

From genomics to epidemiology of influenza

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The seasonal influenza A virus undergoes rapid evolution to escape human immune response. In this talk, I discuss a fitness model for this process, which links the genome evolution of influenza A (H3N2) with its epidemiological characteristics. The model explains the observed pattern of recurrent selective sweeps. It shows that mode and speed of influenza evolution are governed not only by positive selection within, but also by background selection outside antigenic epitopes: immune adaptation and conservation of other viral functions interfere with each other. We discuss the consequences for predicting the evolution of influenza A.