

Genetic variation in pathogen populations

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Abstract

We study the patterns of molecular variation in populations with a complex demographic history, such as those of microbes that can cause human diseases. This is an important subject in evolutionary biology, interdisciplinary physics and biomedical sciences. The standard neutral model of M. Kimura, that has provided us with a null model against which we can test interesting alternative hypothesis to understand molecular evolution and variation, is far too simple for understanding pathogen genetic diversity. With this motivation we have studied a non standard neutral model that aims at being simple enough, but not too simple, so as to account for demographic processes that will occur in natural pathogen populations. Our work is the border between population genetics and epidemiology and constitutes an effort towards integrating results from these areas and providing new results towards the ultimate aim of identifying pathogen genes that are evolving under selection and thus have immunological and medical importance. Towards that aim, we cannot forget that the underlying population structure that will govern patterns of pathogen variation is that imposed by the contact structure of their hosts. We have therefore explored different models that have been taken as a standard in network epidemiology. Our results show that levels of genetic variation are maximal for intermediate values of the pathogen basic reproductive number and that the patterns of that variation are in general similar to those expected in the simple standard neutral model. However in a complex host