Coinfections and evolutionary emergence of novel infectious diseases

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Infection of humans with nonhuman pathogens (zoonoses) is common, but sustained transmission of zoonotic pathogens in human populations is rare. Since most nonhuman pathogens have $R_0 < 1$ in humans, sustained transmission cannot occur unless the pathogen evolves $R_0 > 1$, a process known as evolutionary emergence. Since mutations occur in the course of replication within a host, there is a high probability that genotypes with different R_0 values will end up occupying the same host. We use a multi-type branching process model to show that the probability of evolutionary emergence is strongly dependent on the R_0 of coinfections. We then use a within-host model to show how the phenotypes of coinfecting strains shape the overall R_0 of a coinfection and identify types of mutations that are more or less favorable for emergence. Finally, we demonstrate that the effects of other factors known to influence emergence - such as mutation rates and transmission bottlenecks - differ quantitatively and even qualitatively depending on the phenotypes of the coinfecting strains.

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[*]Mini-Symposium: Immuno-epidemiological models