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Co-transmission and the evolution of virulence

Host are often co-infected by several genotypes of the same pathogen species or even by different species and this is known to affect virulence evolution. However, epidemiological models typically assume that only one of the co-infecting strains can be transmitted at the same time. Here, we study the effect of co-transmission on virulence evolution in a case where parasites compete for host resources. For co-infections by two strains of the same species, we find that increased co-transmission selects for less virulent strains. For co-infection caused by different pathogen species, the evolutionary outcome depends on the respective virulence of the two pathogen species. These results are discussed in the light of kin selection theory. This study has several implications for predicting virulence evolution, one of which is that considering the prevalence of co-infections is not sufficient to predict the optimal level of virulence.

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Investigation of the genetic diversity of cyprinid herpesvirus-3 in enzootic areas

Cyprinid herpesvirus-3 (CyHV-3) is responsible for high mortalities in aquaculture of both common carp (*Cyprinus carpio carpio*) and koi carp (*C. carpio koi*) worldwide. CyHV-3 has emerged and spread on all continents in less than 15 years due to fish trade of latently infected koi carps. In spite of an important international effort for data acquisition on this new viral threat, little is known about the diversity and the origin of CyHV-3.

Comparison of the complete genome sequences of three CyHV-3 isolates revealed the presence of numerous short tandem repeats. Eight of them were tested for investigating the genetic diversity of CyHV-3 isolates. They proved efficient and allowed to classify genotypes within 2 main lineages. Subsequently, a wide molecular survey has been recently undertaken in West Java (Indonesia). Results will be presented, and epidemiological features of outbreaks induced by this deadly virus will be discussed in light of these findings.

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A new genus-level geminivirus lineage isolated from the South African fynbos

A new genus-level geminivirus lineage isolated from the South African fynbos. The state of the art on the diversity of plant viruses mainly concerns those causing symptoms affecting plants of economic interest. However, wild plants have the potential to be reservoirs of viral biodiversity which contribute to the emergence of virus without necessarily showing symptoms. We have carried out over the past 10-months a preliminary study aiming at assessing the diversity of circular ssDNA viruses present at the interface between crops and wild plants in the South African fynbos. We have discovered a new geminivirus, which infects a wild spurge (*Euphorbia caput-medusae*). This virus is highly divergent from the current known members of the family Geminiviridae and is likely to represent a new previously unknown genus of this agriculturally highly relevant family of viruses. This virus, which is not obviously a recombinant of viruses in the known geminivirus genera, has features most similar to viruses in the genus Mastrevirus but it also has unique features among geminiviruses.

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Selection on virulence in emergent epidemics

Our ability to control emerging pathogens requires an understanding of the interaction between epidemiology and pathogen evolution. Theory suggests that epidemic spread feeds back on pathogen evolution, but empirical evidence is scarce. Here we demonstrate that selection on virulence can actually be reversed between emergence and progression of an epidemic. We compete the temperate bacteriophage lambda and its virulent mutant λ bdacI857 throughout a developing epidemic in a chemostat setup. Whereas the virulent λ bdacI857 is strongly favored at epidemic emergence, it loses competition as the epidemic progresses to high prevalence. This reversion of selection on virulence can be explained by a non-equilibrium model using the tools of evolutionary epidemiology. We show that evolutionary epidemiology can predict selection on virulence in our experiments without separation of epidemic and evolutionary time scale and provides, for the first time, a dynamic measure of selection on virulence in emerging infectious diseases.

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