

Virus-Host Coevolution, Killing the Winner, and the Red Queen

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Extended Abstract

Viruses are the most abundant replicating entities on Earth, with an estimated 10^{30} virus particles in Earth's oceans alone (Suttle, 2005). Viruses play an important role in the marine carbon cycle, by viral mortality effects on the food web and by the 'viral shunt' of material from higher to lower trophic levels (Fuhrman, 1999). Understanding the ecological and evolutionary interactions between viruses and their hosts is thus an important challenge if we are to understand the marine ecosystem and the global carbon cycle. Viruses are obligate parasites that replicate by taking control of infected cells and forcing them to create new virus particles, which are released during cell lysis. Each lysis (cell burst) event may release $\sim 10^1$ - 10^2 new virus particles. Growth rate asymmetries and time-lags during viral infection mean that virus-host population dynamics are hard to model as a standard predator-prey interaction. Furthermore, population-based and analytical approaches to modelling host-virus coevolution are problematic due to massive viral diversity and rapid evolution. Here I describe a novel individual-based simulation model of host-virus coevolution in a spatial aquatic environment. Individual host cells grow at a density-dependent rate up to a parameterised carrying capacity. Virus particles may adsorb to and infect host cells with which they come into contact. After a latent period during which virus particles are replicated inside an infected cell, lysis of the infected cell releases a large number of new virus particles into the environment. This asymmetric and time-lagged interaction results in boom-bust cycles of virus and host abundance, in which uninfected host populations grow until they are infected and destroyed, with associated exponential growth and collapse of viral abundance. To explore virus-host coevolution, the model focuses on the process of adsorption, in which virus tail-fibres bind to nutrient uptake receptors on the cell surface, allowing viral DNA to be injected into the cell. The 'fit' between receptors and tail-fibres is thus an important locus for coevolution. The model represents this interaction in abstract form using evolvable bit-strings that represent nutrient uptake receptor configuration of host cells and tail-fibre orientation of viruses; infection occurs when these bit-strings match. This creates a coevolutionary pursuit in which hosts evolve novel strings to avoid infection, while viruses evolve strings that match their host. The need for host nutrient uptake receptors to fulfil their primary function of nutrient acquisition limits the ability of hosts to evade viral attack and creates an evolutionary trade-off between growth rate maximisation and defence. Results from the model support and quantify a theoretical prediction known as the 'kill-the-winner' hypothesis (Thingstad et al, 1997), in which hosts that become abundant due to uptake efficiency become targets of viral attack. This negative density-dependent selection leads to increased host diversity. The coevolutionary dynamics of the model are characteristic of the well known 'Red Queen' effect (Van Valen, 1973), whereby both viruses and hosts show continual evolutionary adaptation while maintaining broad constancy in relative fitness. Interestingly, the Red Queen effect is most pronounced in abundant host populations, while scarce host populations can achieve progressive fitness increase by improving uptake efficiency until they reach a critical abundance at which viral mortality becomes significant.

References

- Fuhrman, J.A. (1999) Marine viruses and their biogeochemical and ecological effects. *Nature* 399: 541-548.
- Suttle, C.A. (2005) Viruses in the sea. *Nature* 437:356-361.
- Thingstad, T.F. (2000) Elements of a theory for the mechanisms controlling abundance, diversity, and biogeochemical role of lytic bacterial viruses in aquatic systems. *Limnology and Oceanography* 45(6): 1320-1328.
- Van Valen, L. (1973) A new evolutionary law. *Evolutionary Theory* 1: 1—30.