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Quantifying Strain Dynamics of CRISPR-Induced Host-Viral Coevolution: Sweeps and Coalitions

The dynamics of hosts and pathogens are driven by ecological interactions and evolutionary events. As the processes of ecology and evolution lead to complex behavior which are difficult to follow experimentally, ecoevolutionary models describing the dynamics of host-pathogen interactions are necessary to determine the essential factors driving growth and diversification of populations. The recent discovery of the CRISPR (Clustered Regularly Interspaced Short Palindromic Repeats) system which acts as an immune defense in over 40% of bacteria and 90% of archaea (hosts) alters how evolution facilitates the interaction of hosts and viruses. The CRISPR immune system uses host-incorporated viral DNA to provide immunity against invading genetic material, such as viruses.

Recently, we introduced a multi-scale model of dynamic coevolution between hosts and viruses in an ecological context that incorporates CRISPR immunity principles [1]. In that work, we analyzed the model to test whether and how CRISPR immunity induces host and viral diversification and maintenance of coexisting strains. We showed that hosts and viruses coevolve to form highly diverse communities through punctuated replacement of extant strains. The populations have very low similarity over long time scales. However over short time scales, we observe evolutionary dynamics consistent with incomplete selective sweeps of novel strains, recurrence of previously rare strains, and sweeps of coalitions of dominant host strains with identical phenotypes but different genotypes.

Here, we analyze our previously developed multi-scale model of coevolution between hosts and viruses involving the CRISPR immune mechanism to explore the molecular drivers of strain dynamics. We show that diversity of strains develops and is maintained within the populations through a combination of overlapping ecological and evolutionary times-scales as well as phenotype similarities resulting from disparate genotypes. Furthermore this observed diversity is not a constant set of co-existing strains but rather involves an ever-changing set of strains. We present metrics to quantitatively distinguish dynamics when one strain (sweep) versus multiple strains (coalition) dominant the population and describe characteristic signatures of each of these population level signatures. The analysis of our model will help understand the implications of signatures found in metagenomic data of microbial communities where CRISPR systems are found.

[1] L. M. Childs, N. L. Held, M. J. Young, R. J. Whitaker and J. S. Weitz, (in press). Multi-scale Model of CRISPR-induced Co-evolutionary Dynamics: Diversification at the Interface of Lamarck and Darwin, *Evolution*.