

1077-92-241

**Lauren M Childs\*** (lauren.childs@biology.gatech.edu), **Nicole Held**, **Mark J Young**,  
**Rachel J Whitaker** and **Joshua S Weitz**. *Multi-scale Model of CRISPR-induced Coevolutionary  
Dynamics: Diversification at the Interface of Lamarck and Darwin*. Preliminary report.

The CRISPR (Clustered Regularly Interspaced Short Palindromic Repeats) system is a recently discovered immune defense in bacteria and archaea (hosts) that functions via directed incorporation of viral DNA into host genomes. Here, we introduce a multi-scale model of dynamic coevolution between hosts and viruses in an ecological context that incorporates CRISPR immunity principles. We analyze the model to test whether and how CRISPR immunity induces host and viral diversification and maintenance of coexisting strains. We show that hosts and viruses coevolve to form highly diverse communities through punctuated replacement of extant strains. The populations have low similarity over long time scales. However over short time scales, we observe evolutionary dynamics consistent with incomplete selective sweeps, recurrence of previously rare strains, and sweeps of coalitions of dominant host strains with identical phenotypes but different genotypes. Our explicit eco-evolutionary model of CRISPR immunity can help guide efforts to understand the drivers of diversity seen in microbial communities where CRISPR systems are active. Understanding the role of the CRISPR system in bacterial survival has important consequences in environmental cleanup, probiotics, and agriculture management. (Received August 16, 2011)