

LARGE-SCALE EVOLUTIONARY SIMULATIONS OF COMPLEX MICROBIAL BEHAVIORS IN DYNAMIC ENVIRONMENTS

V. Mozhayskiy and I. Tagkopoulos*

Department of computer science and Genome Center

University of California Davis

451 Health Sciences Dr.

Davis, CA 95620

**Email: itagkopoulos@ucdavis.edu*

Recent phylogenetic studies show that Horizontal Gene Transfer (HGT) events are ubiquitous in the Tree of Life, however our knowledge of its role in evolution is limited. Incorporation of foreign DNA may confer advantageous traits to host organisms, which in turn results in increased fitness, as in the case of antibiotic resistance. Similarly, at a social context HGT may induce cooperative or defective behavior, changing the population dynamics in competitive environments. We investigate to what extent HGT facilitates phenotypic changes by building a model of microbial evolution. Towards this goal, we built a parallelized simulation framework (EVE: Evolution in Variable Environments) which enables large scale simulations of microbial ecologies in fluctuating environments and is scheduled to run in NCSA's Blue Waters Petascale Supercomputer in summer 2011. We will present preliminary data and parameter sweeps on environmental parameters such as mutation rates, uptake probabilities and fluctuating signals show that HGT significantly accelerates the emergence of complex traits and contributes to the population resiliency to environmental perturbations.

* Corresponding author.