CONTROL ID: 1817701

TITLE: Elucidating Microbial Adaptation Dynamics via Autonomous Exposure and Sampling

AUTHORS (FIRST NAME, LAST NAME): Joseph M Grace1, 4, Cyprien Verseux4, Diana Gentry2, 4, Amy Moffet1, Ramanen Thayabaran3, Nathan Wong3, Lynn Rothschild4

INSTITUTIONS (ALL): 1. University of California, Santa Cruz, Santa Cruz, CA, United States.
2. Stanford University, Stanford, CA, United States.
3. San Jose State University, San Jose, CA, United States.
4. NASA Ames Research Center, Moffett Field, CA, United States.

ABSTRACT BODY: The adaptation of micro-organisms to their environments is a complex process of interaction between the pressures of the environment and competition. Reducing this multifactorial process to environmental exposure in the laboratory is a common tool for elucidating individual mechanisms of evolution, such as mutation rates [Wielgoss et al., 2013]. Although such studies inform fundamental questions about the way adaptation and even speciation occur, they are often limited by labor-intensive manual techniques [Wassmann et al., 2010].

Current methods for controlled study of microbial adaptation limit the length of time, the depth of collected data, and the breadth of applied environmental conditions. Small idiosyncrasies in manual techniques can have large effects on outcomes; for example, there are significant variations in induced radiation resistances following similar repeated exposure protocols [Alcántara-Díaz et al., 2004; Goldman and Travisano, 2011].

We describe here a project under development to allow rapid cycling of multiple types of microbial environmental exposure. The system allows continuous autonomous monitoring and data collection of both single species and sampled communities, independently and concurrently providing multiple types of controlled environmental pressure (temperature, radiation, chemical presence or absence, and so on) to a microbial community in dynamic response to the ecosystem’s current status. When combined with DNA sequencing and extraction, such a controlled environment can cast light on microbial functional development, population dynamics, inter- and intra-species competition, and microbe-environment interaction.

The project’s goal is to allow rapid, repeatable iteration of studies of both natural and artificial microbial adaptation. As an example, the same system can be used both to increase the pH of a wet soil aliquot over time while periodically sampling it for genetic activity analysis, or to repeatedly expose a culture of bacteria to the presence of a toxic metal, automatically adjusting the level of toxicity based on the number or growth rate of surviving cells.

We are on our second prototype iteration, with demonstrated functions of microbial growth monitoring and dynamic exposure to UV-C radiation and temperature. We plan to add functionality for general chemical presence or absence by Nov. 2013. By making the project low-cost and open-source, we hope to encourage others to use it as a basis for future development of a common microbial environmental adaptation testbed.

References:

INDEX TERMS: 0465 BIOGEO SCIENCES Microbiology: ecology, physiology and genomics, 0456 BIOGEO SCIENCES Life in extreme environments.
(No Image Selected)
(No Table Selected)

Additional Details
Previously Presented Material:

Contact Details
CONTACT (NAME ONLY): Joseph Grace
CONTACT (E-MAIL ONLY): josephmgrace@gmail.com
TITLE OF TEAM: