

Molecular Level Interactions between Organisms and Environment

Mark V. Brown

*Institute for Astronomy
University of Hawaii, Manoa
Physical Sciences Building Room 213
2565 McCarthy Mall
University of Hawaii, Manoa
Honolulu, HI 96822
USA*
mbrown@ifa.hawaii.edu

Andrew K. Boal

*Institute for Astronomy
University of Hawaii, Manoa
USA*

Brian T. Glazer

*Institute for Astronomy
University of Hawaii, Manoa
USA*

Kim Binsted

*Information and Computer Sciences Department
University of Hawaii, Manoa
USA*

Eric Gaidos

*Department of Geology & Geophysics
University of Hawaii, Manoa
USA*

Microbial survival in extreme environments requires specific adaptation at the molecular level, selected to maintain functionally stable protein structures under potentially denaturing conditions. Such adaptations are known to include alterations in peptide residue frequencies and preferential utilization of specific protein motifs (patterns of amino acid sequences within a protein structure). Our work aims to couple environmental conditions with specific molecular adaptations to investigate whether a physico-chemical determinant for structural motifs can be established. As well as utilizing available structural and sequence databases, novel molecular data will be obtained from environments considered to be analogous to potential ecosystems on Mars and Europa (subseafloor material, sub-glacial lake water, tephra and sediment).

Local adaptation may require a trade off between the ability to survive in an extreme environment and an organism's ability to successfully disperse across environments to which it is not adapted, potentially leading to populations evolving in isolation. Examination of analogous but geographically or physiochemically isolated populations will provide us with further insights into the mechanisms by which environmental

conditions shape molecular structures (e.g. co-evolution, endemism .) and determine the potential to predict which structures are stable in an environment of a given set of physical parameters. In parallel to this study, we will computationally derive sets of peptides predicted to be the “most stable” in a given environment and confirm predictions through systematic laboratory studies of synthetic peptides.