Hayes, M., R. I. Eytan and M. E. Hellberg. 2010. High amino acid diversity and positive selection at a putative coral immunity gene (*tachylectin-2*). BMC Evolutionary Biology, in press.

Genes involved in immune functions, including pathogen recognition and the activation of innate defense pathways, are among the most genetically variable known, and the proteins that they encode are often characterized by high rates of amino acid substitutions, a hallmark of positive selection. The high levels of variation characteristic of immunity genes make them useful tools for conservation genetics. To date, highly variable immunity genes have yet to be found in corals, keystone organisms of the world's most diverse marine ecosystem, the coral reef. Here, we examine variation in and selection on a putative innate immunity gene from *Oculina*, a coral genus previously used as a model for studies of coral disease and bleaching. In a survey of 244 Oculina alleles, we find high nonsynonymous variation and a signature of positive selection, consistent with a putative role in immunity. Using computational protein structure prediction, we generate a structural model of the Oculina protein that closely matches the known structure of tachylectin-2 from the Japanese horseshoe crab (Tachypleus tridentatus), a protein with demonstrated function in microbial recognition and agglutination. We also demonstrate that at least three other genera of anthozoan cnidarians (Acropora, Montastrea and Nematostella) possess proteins structurally similar to tachylectin-2. Taken together, the evidence of high amino acid diversity, positive selection and structural correspondence to the horseshoe crab tachylectin-2 suggests that this protein is 1) part of Oculina's innate immunity repertoire, and 2) evolving adaptively, possibly under selective pressure from coral-associated microorganisms. Tachylectin-2 may serve as a candidate locus to screen coral populations for their capacity to respond adaptively to future environmental change.