Title: Immunogenetic diversity and transcriptomic response to disease in Hawaiian green sea turtles

Authors: Jamie Adkins[1], Katherine R. Martin[2], Jennifer M. Lynch[3,6], Shreya Banerjee[1,4], Camryn D. Allen[5], Anna E. Savage[2], Vipheaviny Chea[1], Marc Rice[7], T. Todd Jones[8], George Balazs[9], Lisa M. Komoroske[1]

1 Department of Environmental Conservation, University of Massachusetts, Amherst, MA, USA

2 Department of Biology, University of Central Florida, Orlando, FL, USA

3 Chemical Sciences Division, National Institute of Standards and Technology, Hawai'i Pacific University, Waimanalo, HI, USA

4 Department of Biological Sciences, Stanford University, Stanford, CA, USA

5 Marine Turtle Biology and Assessment Program, Protected Species Division, Pacific Islands Fisheries Science Center, National Marine Fisheries Service, National Oceanic and Atmospheric Administration, Honolulu, HI, USA

6 Center for Marine Debris Research, Hawai'i Pacific University, Waimanalo, HI, USA

7 Sea Turtle Research Program, Hawaii Preparatory Academy, Kamuela, HI, USA

8 Fisheries Research and Monitoring Division, Pacific Islands Fisheries Science Center, National Marine Fisheries Service, National Oceanic and Atmospheric Administration, Honolulu, HI, USA

9 Golden Honu Services of Oceania, Honolulu, HI, USA

Abstract:

Wildlife diseases threaten population sustainability, particularly in conjunction with other anthropogenic threats. In wild populations, the role of host genetics is understudied yet crucial to understanding patterns of disease prevalence. Sea turtles face several known diseases in conjunction with other human threats to population viability, yet we know little about the capacity of these organisms to respond to disease from an immunogenetic perspective. Using Hawaiian green sea turtles (honu), a closed population where

fibropapillomatosis (FP) has been documented for decades, we (1) quantify genes responsive to FP affliction and associated biological processes in blood, and (2) characterize diversity of major histocompatibility complex class I (MHCI) immune loci. We find 116 differentially expressed genes between clinically healthy and FP-afflicted honu. These genes were associated with enrichment for immune response, regulation of cell adhesion, interferon-gamma production, and detection of biotic stimulus. Patterns of expression of these enriched genes share commonalities with human responses to cancers and suggest a basis for how FP neoplasms evade the host immune system. We also identify 17 unique nucleotide sequence variants in the MHCI region that fall into three distinct functional supertypes, a subset of which are also represented in FP-associated differentially expressed genes. We find evidence of up to three MHCI gene copies per individual, with most individuals possessing a heterogeneous mixture of functional supertypes. We also compare the Hawai‘i MHCI sequence variants to those in Florida green, Florida loggerhead, and Cape Verde loggerhead sea turtle populations. We find evidence of trans-species polymorphism as well as shared polymorphisms between green turtle populations. One of the shared sequence variants between green turtle populations in Florida and Hawai‘i was previously associated with tumor regression. Overall, we see levels of MHCI diversity in the closed honu population are greater than have been reported for some endangered species but are less than previous findings in loggerhead sea turtles, the mixed-stock Florida green turtle population, and many avian species. We next plan to sequence the MHCI region of additional individuals with known FP status to associate sequence variants with this disease. Collectively, these findings are an important step in understanding sea turtle immunogenetics and can inform future studies investigating disease susceptibility, adaptation, and potentially the development of diagnostic disease biomarkers.