Wild Sea Lion Gut Microbe and Parasite Communities: A One-Health Tool for Host and Ocean Monitoring

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Marine animals such as pinnipeds offer a unique perspective into wildlife and ocean function in an era of intensifying anthropogenic stressors and environmental change. Pinnipeds are recognized as sentinel species because they have long lifespans, feed at high trophic levels and accumulate toxicants, and share many of the same environmental pressures as humans. Changes in pinniped health, therefore, indicate changes in ecosystem structure, disease transmission, and climate change, and elucidate risks to other organisms that would otherwise be difficult to observe. However, pinniped health monitoring poses challenges, and marine disease dynamics are complex.

To better understand pinniped health, an investigation led by the Carlson College of Veterinary Medicine at Oregon State University (OSU CCVM), in collaboration with the Oregon and Washington Departments of Fish and Wildlife, is using bioinformatics tools to explore associations between California and Steller sea lion gut microbial and parasite communities and host health. The development of high-throughput sequencing has become essential to our understanding of the composition and interactions of genetic material within living organisms. In wildlife studies, for example, high-throughput sequencing is used to study biodiversity, infectious disease, and importantly, to characterize the dynamic consortia of bacteria, viruses, phages, and archaea (i.e. the microbiome) and protozoa, helminths, and fungi (i.e. the eukaryome) present within a space, host, or ecosystem. The microbiome and eukaryome have the potential to serve as non-invasive indicators of wild sea lion health, and, by extension, may also provide insights into ecosystem health.

Extensive evidence supports the intricate association between the gut microbiome and host physiology, fitness, and ecology, and it is becoming increasingly clear the gut eukaryome has similar impacts on health. Gut communities in symbiosis contribute to homeostasis and important biochemical functions, whereas severe community imbalance, known as dysbiosis, may lead to dysregulation and disease. In addition, host and environmental conditions, like diet, behavior, geography, pollution, and disease, can alter the composition and function of gut communities. For example, once beneficial microbes may become harmful (and vice versa) or certain groups of microbes may link to disease indicators or various environmental conditions. Both the microbiome and eukaryome modulate host responses through a spectrum of symbiotic and dysbiotic interactions, but these interactions are largely unexplored in wild sea lion populations.

Anthropogenic stressors in the marine ecosystem may contribute to the inability to maintain commensal gut communities, promoting dysbiotic states in sea lions (e.g. low diversity, substitution of normal gut flora, abundance of pathogenicity). Sea lion gut dysbiosis may then compromise immune function and increase susceptibility to pathogen burden *(*e.g. pathogenic *Leptospira* spp.*, Toxoplasma gondii,* Otarine herpesvirus-1*),* contaminant accumulation (e.g mercury, PBDEs), and severe pathophysiological consequences (e.g. high creatinine levels and kidney dysfunction), potentially threatening pinniped behavior, health, and survival as well as ecosystem dynamics.

OSU CCVM's work aims to characterize the gut microbiome and eukaryome present within California and Steller sea lions and explore variation across host health, immune function, and disease. These associations can be leveraged to provide meaningful early indicators of anthropogenic impacts, strengthen One Health monitoring efforts, and inform management interventions in the future. Ultimately, this project paves the way for long-term studies to evaluate variations in health patterns associated with environmental changes in the marine ecosystem.