Dynamics at the host-microbe interface

Recent advancements in sequencing technology drive a new and astounding appreciation for diverse, microbial worlds in biotic and abiotic environments. Many animal-associated communities often establish intimate and sometimes dependent relationships with each other but can also gain diverse functions that can be harmful for their host. Two routes for understanding these complex relationships are to (i) study organisms in pure culture or (ii) in defined model systems. For example, in the human oral microbiome, culture-independent studies have linked the previously uncultured Desulfobulbus genus and TM7 phylum with periodontal disease. Isolation and characterization of these novel species has uncovered how such microorganisms have coevolved with human hosts and to the emergence of pathogenic traits. Specifically, horizontal gene acquisitions, such as toxins including leukotoxin and hemolysins, permit D. oralis to trigger a proinflammatory response in oral epithelial cells. Likewise, within the TM7 phylum, comparative genomics with free-living relatives has identified traits important for human host association, such as protein families of known virulence factors and novel viral defense mechanisms. Furthermore, we can utilize a simple animal model, such as the Nasonia parasitoid wasp model system, to investigate adaptions of the host to its microbes. The vertically transmitted bacterium, Wolbachia, inhabits the reproductive organs of these wasps and provides an opportunity to disentangle complex host-microbe interactions through the lens of a single host-microbe association. Utilizing these two approaches, we can begin to understand the complex dynamics that establish stable relationship between hosts and their microbiome.