ABSTRACT

Gut microbiota research in marine invertebrates is an emerging field driven by the interest to understand the microbial association and their impact on animal health. Many microbes in the gut of aquatic animals are either sourced from the environment or food intake. Therefore, some gut microbes remain stable over time, but others are transient and established in the host gut. The bacteria community is mainly species-specific, but members in the gut of marine invertebrates are similar to those of teleost and mammals. Habitat differences, dietary intervention, host age, physiological conditions and environmental disturbances can modulate bacterial community and biomass. Gut microbiota plays a crucial role in food transformation into nutrients and energy and in disease resistance. Potential pathogenic bacteria and resident bacteria may be present in a healthy animal, but the opportunistic pathogens may outcompete endosymbionts during extreme environmental, seasonal and physiological stress to cause epidemic diseases. Furthermore, low food availability can alter intestinal homeostasis leading to a shift of the bacterial species composition. Therefore, sustainable bivalve aquaculture requires a better understanding of gut bacteria. The dynamics of gut bacterial composition due to host phylogeny, seasonal, environmental, and dietary variations is of particular interest to better understand bacterial symbiosis and health management in oysters and mussels. Yet, despite the commercial importance of these bivalves and susceptibility to diseases, little is known regarding the host and environmental pressures that drive gut microbiota composition between inter-genic populations. The research aims to understand bacterial community composition and assess if the gut microbial change is related to species, habitat, season, or feed composition. To achieve these goals, I carried out four experiments with four specific objectives: (1) to compare gut bacteria between oysters and mussels, (2) to compare gut bacterial community in oysters between two different habitats, (3) to investigate the seasonal pattern of gut bacterial community composition in oysters, and (4) to identify the impact of feed composition on gut bacteria in oysters and mussels.

Experiment 1 demonstrates both inter-generic and intra-specific host specificity in colonising bacterial composition in the gut of oysters and mussels from same sampling site. The seasonal change of gut bacteria in oysters differed from mussels. Experiment 2 defines the colonization of host-specific bacteria in oyster gut. The bacterial abundance and diversity were both season and habitat dependent. The gut bacteria of oysters in the oceanic nutrient based Coffin Bay had higher diversity than those in local nutrient-based habitat Franklin Harbor. This trend was more obvious in winter than in summer. Experiment 3 shows a significant effect of seasonal temperature on the oyster gut microbial community and its ambient environment whole year-round. Experiment 4 shows that diet type strongly affected the gut microbial composition in oysters and mussels in a laboratory condition, and the response of bacteria to diet change varied with feed composition and bivalve species.

In summary, Tenericutes was the most prevalent bacterial class in oyster guts. The low microbial diversity, especially in summer, provides evidence to partially explain the vulnerability of oysters to bacterial infection and mass mortality in summer. The high bacterial diversity of oysters in winter and oceanic nutrient based Coffin Bay indicates the resistance of oysters to environmental stress. In contrast, the low bacterial diversity of oysters in local nutrient-based Franklin Harbor may be less resilient to environmental stress, triggering oyster disease or mass mortality in summer. Modulation of gut microbes could be used to predict the growth of beneficial bacteria in marine bivalves in aquaculture.