

Modifications to bacterial biological communities relevant with grown shellfish

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ABSTRACT

In China's very profitable marine aquaculture business, crustaceans (*Crassostrea gigas*) are grown on a vast scale. However, there have been numerous mass fatalities of farmed oysters in recent years owing to disease and environmental factors (such as high temperatures). We employed high-throughput sequencing to evaluate the dynamics of bacterial and protist communities in oysters at different growth stages to investigate potential links between microorganisms and oyster farming mortality.

As a result, the microbial communities of farmed oysters evolved dramatically and differed significantly from those of natural oysters and ambient bacteria. As the oysters grew larger, the number of biomarker taxa between them and their surroundings dropped. The number of ecologically useful genes in the microbial community changed during the mass extinction of cultivated oysters, and inter-microbial connections vanished. These findings add to our understanding of the microbial community dynamics of cultured oysters at various growth stages and characterise microorganism interactions during mass mortality in cultured oysters. Our research contributes to the promotion of healthy oyster farming.

Keywords: Pacific oyster; Bacteria; Protists; Mass death

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INTRODUCTION

Oysters (Phylum *Mollusca*, *Ostreidae* family) are sessile benthic metazoans found worldwide in intertidal zones. Oysters are filter-feeding bivalves that provide crucial ecological roles such as water filtration and habitat restoration, particularly on coastal oyster reefs. Oysters are one of the most frequently farmed crustaceans in the world, and they are a vital economic and protein source for humans [1-3]. Because of their flexibility, great fertility, rapid growth and abundant nutrition, crustaceans are the world's most productive and economical oysters and China is the world's top producer.

Given the importance of oysters, various research have been conducted to investigate the effects of environmental conditions on oyster genetics, reproduction, aquaculture and disease. Microbial communities are directly tied to oyster farming and have a significant role in the formation and development of macroorganisms. Bacterial communities linked with various oyster tissues have previously been examined, mostly in stomach and overall microbiota research. Several research have been conducted to explore various stages of oyster growth. Microorganisms are required for oyster growth and health at various phases of development and knowing the shifting patterns of microbial communities is critical for oyster farming.

Many researches have been conducted on the dynamics of bacterial communities in oyster farming situations. Several studies have studied the bacterial populations of oysters and their surrounding ecosystems. Previous research has revealed that the oyster microbiome and its environment (seawater and sediments) are inextricably linked, with major interactions between these biotopes [4-6]. In contrast, sediment suspension and subsidence in marine aquaculture sites had a significant impact on oyster microbial communities. The richness and organisation of bacterial communities in final sediments, on the other hand, tended to alter dramatically with increased aquaculture activity. Several studies have also found that sediment suspension is a crucial interaction process between water and sediment for microbial populations. However, research that profile bacterial and protist communities associated with cultivated oysters and their environment at the same time are scarce.

DESCRIPTION

Pacific oyster (*Crassostrea gigas*) is one of the most important aquaculture species in China and oyster raft farming using mussel shells as an artificial substrate is widely used by fishermen. Shell

biofilms are essential for *C. gigas* attachment and growth and several infectious diseases originate from here [7-9]. In this study, high-throughput sequencing was used to compare biofilm bacterial and protist communities at different developmental stages and environments in farmed, diseased and wild oysters.

C. larva after 15 days of culture. *Gigas* attached to its shell. After 48 days, *C. gigas* had significantly increased in size. Growth stages (15 and 48 days) were inconsistent. The Shannon index and Chao-1 index observed after 15 days were significantly lower than those observed after 48 days. After using the raft culture, *C. gigas* began to attach to the shell and altered the microbial diversity of the shell biofilm. As *C. gigas* grew, the diversity of the microbial community changed, increased and eventually stabilized. Bacterial strains Firmicutes and Actinobacteriota became more frequent after 15 days and Bacteroidota and Cyanobacteria strains were more enriched after 48 days. Based on the evidence, we concluded that bacterial community function was more concentrated at the attachment stage (day 15) and then changed gradually during growth (day 48) [10-12]. Phyla Firmicutes and Actinobacteriota were consistently detected in sediments, suggesting that early stages of oyster attachment may be highly correlated with sediment microbes.

CONCLUSION

We evaluated the bacterial and protist community compositions

of oysters at various growth stages, habitats, healthy and diseased oysters and their environs in this study. The diversity of the oyster microbial community closely paralleled that of the surrounding saltwater as the oysters developed. However, the microbial community's makeup can be split into three types. As a result, we discovered that bacterial and protist communities in oysters exhibit various community dynamics mechanisms at different times. The microbial community of infected oysters differs significantly from that of healthy oysters, according to an analysis of microbial biomarker taxa and possible community roles. Furthermore, the co-occurrence network considerably reduced interactions between diseased oyster microbial communities, demonstrating that the correlation between protist populations and disease was stronger in oysters than in bacterial communities. Changes in microbial interactions, particularly those connected with protists, may be linked to oyster mortality. To reduce disease-related losses in oyster farming, regular monitoring of microbial populations and the installation of early warning methods are proposed. Our research presents a preliminary examination of the dynamics of the oyster microbial community and its environment, and additional research is suggested to allow for a more systematic comparative investigation of different tissues in the oyster. Furthermore, sophisticated molecular biological techniques to improve our ability to recognise protists are promoted.

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