**主要从事厚壳贻贝相关功能基因研究，海洋微生物宏基因组及微生物分子生态学方向研究**

*FIELD*

研究方向

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*EXPERIENCE*

工作经历

**2009.09-2013.07 浙江海洋学院 生物技术专业 学士**

**2014.09-2016.06 浙江海洋大学 海洋科学专业 硕士**

**2015.02-2015.07 台湾海洋大学 交流学习**

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教育背景

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何建瑜

**Multiple forces drive the host-associated microbial community in *Mytilus coruscus***

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**Abstract:** Aquatic organisms are the habitat for microbial colonization. Microbes also impact the growth and development of host organisms. However, large knowledge gaps are still missing with regard to the the underlying principles of assembly in host-associated microbes. Here, using 16S rDNA amplicon sequencing and absolute qualification, we investigated the tissue-specific compositional variation of microbiota in *Mytilus coruscus*, and reported the assembly rules of these host-associated microbiota. Results suggested that tissue-related taxa significantly differed from that in seawater with regard to alpha and beta diversity. Estimates of ecological process revealed that these host-associated microbiota are more likely to form through dispersal and homogeneous selection. Host-filtering process was also important in governing the compositional distribution. These results suggest that the multiple forces govern the tissue-associated microbiota in *M. coruscus*. In addition, some functions performed by microbiota, such as C-cycle-related and N-cycle-related, were strengthen in *M. coruscus*. Our findings supported the concept that the mussel-associated micobiota may provide essential functions for host development, physiology, and health. All these observations are attributed to better understand mussel-microbiota holobiont in aquatic system.

**Key words:** Assembly principles; mussel-associated microbes; 16S rRNA gene, Mytilus coruscus