

基于高通量测序分析的大鹏澳海域沉积物古菌群落结构初步研究

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Preliminary study on archaeal community in the sediment of Dapeng Cove using high-throughput sequencing

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摘要

于2014年夏季(8月)利用柱状采泥器采集了大亚湾大鹏澳海域养殖区、对照区5 cm层和30 cm层沉积物样品,并通过高通量测序方法对沉积物样品古细菌生物群落结构进行了分析。结果显示,大鹏澳沉积物深层样品中古菌占原核生物的比例高于表层。5 cm层和30 cm层沉积物古菌群落优势种存在明显差异,分别为广古菌门(Euryarchaeota)的热原体纲(Thermoplasmata)和泉古菌门(Crenarchaeota)的MCG纲(Miscellaneous Crenarchaeotic Group)。总体上,泉古菌门相对丰度高于广古菌门。养殖区古菌优势种的数量显著高于非养殖区。养殖区表层和深层沉积物之间古菌群落物种组成和数量的差异明显大于非养殖区。古菌群落的空间差异一定程度上反映了大鹏澳沉积物古菌群落受到了养殖活动的影响,但影响的机制还需要深入研究。

关键词: 沉积物, 古菌群落, 16S rRNA, 高通量测序, 近海养殖

Abstract :

We analyzed the archaeal community in tropical aquaculture farm sediments in Dapeng Cove, located in the southwest of Daya Bay, southern China. Sediment cores samples (5 cm and 30 cm in depth) were collected by a core-sampler in summer (August, 2014). Results show that the abundance of archaea in deep layers was higher than that in surface layer. The dominant species in surface and deep layers were Class Thermoplasma, Phylum Euryarchaeota, and Class MCG (Miscellaneous Crenarchaeotic Group), Phylum Crenarchaeota. In general, the abundance of Crenarchaeota was higher than that of Euryarchaeota. The abundance of predominant species was higher in aquaculture farms than in non-aquaculture area. The difference in archaeal community structure between surface and deep layers was more significant in aquaculture farms than that in non-aquaculture area. Results indicate that the archaeal community structure might be affected by intensive aquaculture activities, whose underlying mechanism needs further study.

Key words: sediment archaeal community 16S rRNA high-throughput sequencing nearshore aquaculture

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