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Differences of microbial diversities in sediments depending on the hydrothermal areas
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Key Word: microbial diversity, hydrothermal area, 16S rRNA gene, clone library

Little are known about microbial diversity in sub-surface sediment in hydrothermal area, although the microbial diversities in hydrothermal vent fluid and/or chimney used as sample have been reported. In this study, several submarine sediments, which were obtained from hydrothermal area around Japan, were used for investigations and comparisons of microbial diversities. Submarine sediments were obtained from Myojin knoll, Genroku seamount and Bayonnaise knoll in Izu-Bonin back-arc, and Izena caldron in Okinawa trough. Some parts of cores below about 2 m from submarine surface were used for the analyses of the microbial diversities using clone library analysis with 16S rRNA gene. Almost clones were related to Proteobacteria, particularly g-Proteobacteria clone were abundant in Myojin knoll, Genroku seamount and Izena caldron. This group includes many marine bacteria. The clones related to e-Proteobacteria were not detected, sulfur-metabolizing bacteria seem to be minority in these sediments. In Myojin knoll sediment, other phylogenetic group such as Bacteroides, Chloroflexi, Firmicutes and other accounts for about 20% in clone library. On the other hand, the diversity in Bayonnaise knoll was richer than other areas. No e-Proteobacteria clone was detected from all hydrothermal areas. This fact suggested that some microbes related sulfur metabolism were minority in these sediments. Clone libraries of archaea obtained from these sediments had much less diverse than eubacteria. Especially, in Bayonnaise knoll sediment, 90% of archean clones belonged to Thaumarchaeota.

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Application of ribosomal intergenic spacer analysis (RISA) for monitoring bacterial population responsible for the rapid tissue necrosis (RTN) of stony coral
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Key Word: RISA, RTN, Story Coral, Bacterial monitoring

Microbial infection has been recognized as one of the local threats to coral reefs. Bacteria so far identified as causative for infectious coral diseases include Vibrio, Serratia and some cyanobacteria, most of which are common members of bacterial population in coastal environments. It is therefore important to monitor bacterial population in the coral reef environments in order to help protect corals from the infectious diseases. In the present study, we applied RISA to monitor bacterial population responsible for RTN of a stony coral, Acropora microphthalmia that have been maintained in Okinawa Churaumi Aquarium, Okinawa, Japan. We isolated bacterial colonies from coral branch with or without epidermal lesion and from seawater near the coral. A total of 13 bacterial isolates obtained from the tissue specimens were all affiliated with the family Vibrionaceae, two of which were closely related to coral-pathogenic Vibrios (V. shiloi and V. harveyii). Internal transcribed spacer (ITS) regions that were amplified from the isolates as well as those from the coral specimens and seawater were electrophoresed with a capillary sequencer (ABI 3130x). The ITS fragments used for the analysis ranged from 100 to 850 bp in size. One of the distinctive fragments (770-775 bp) was found across the ITS profiles from half of the bacterial isolates, a heavily-necrotized coral branch and seawater near the coral branch. These results demonstrated that RISA is a suitable method of choice for monitoring dynamics of bacterial population including causative pathogens for RTN in coral reef environments.

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