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Comparative metagenomic analysis of the microbial communities in the surroundings of Iheya north and Iheya ridge hydrothermal fields reveals insights into the survival strategy of microorganisms in deep-sea environments

Hai-liang Wang [a,b,c], Li Sun [a,b,*]

[a] Key Laboratory of Experimental Marine Biology, Institute of Oceanology, Chinese Academy of Sciences, Qingdao, China
[b] Laboratory for Marine Biology and Biotechnology, Qingdao National Laboratory for Marine Science and Technology, Qingdao, China
[c] University of Chinese Academy of Sciences, Beijing, China

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ABSTRACT

In this study, metagenomic analysis was performed to investigate the taxonomic compositions and metabolic profiles of the microbial communities inhabiting the sediments in the surroundings of Iheya North and Iheya Ridge hydrothermal fields. The microbial communities in four different samples were found to be dominated by bacteria and, to a much lesser extent, archaea belonging to the phyla Proteobacteria, Actinobacteria, Planctomycetes, Firmicutes, Deinococcus-Thermus, and Nitrospirae, which play important roles in the cycling of carbon, nitrogen, and sulfur. All four microbial communities (i) contained chemoautotrophs and heterotrophs, the former probably fixed CO_2 via various carbon fixation pathways, and the latter may degrade organic matters using nitrate and sulfate as electron acceptors, (ii) exhibited an abundance of DNA repair genes and bacterial sulfur oxidation mediated by reverse sulfate reduction, and (iii) harbored bacteria and archaea involved in anaerobic methane oxidation via intra-aerobic denitrification and reverse methanogenesis, which were found for the first time in hydrothermal areas. Furthermore, genes involved in DNA repair, reductive acetyl-CoA pathway, and ammonia metabolism were possibly affected by distance to the vent fields. These findings facilitate our understanding of the strategies of the microbial communities to adapt to the environments in deep sea areas associated with hydrothermal vents.

1. Introduction

Deep-sea hydrothermal vents distribute along mid-oceanic ridges, back-arc basins, volcanic arcs, and active seamounts (Tyler et al., 2003). Since the first discovery of hydrothermal vents in 1977 (Corliss et al., 1979), more than 500 vent sites have been found (Zelnio et al., 2011). The vent habitats harbor rich microbial communities, which are fascinating ecosystems on Earth and provide unique models for understanding the living strategies in deep-sea extreme environments (Wang et al., 2009).

Okinawa Trough is a back-arc basin located behind the Ryukyu trench and Ryukyu Islands (Glasby and Notsu, 2003). Many hydrothermal fields have been discovered in Okinawa Trough, including the hydrothermal fields of Iheya North and Iheya Ridge in the mid-Okinawa Trough (Glasby and Notsu, 2003; Tokeshi, 2011). The hydrothermal field of Iheya North discovered in 1995 is located in the western cove of the Central Valley of Iheya North Knoll (27°47′50N, 126°53′80E) (Kawagucci et al., 2011; Momma et al., 1996). Active and dead sulfide-rich chimneys are present in this area (Glasby and Notsu, 2003; Kawagucci et al., 2011). The North Big Chimney (NBC) vent has the highest temperature (over 300 °C) and is situated in the centre of Iheya North Knoll (Glasby and Notsu, 2003). With increasing distance from NBC, the hydrothermal mounds have lower temperatures (Kawagucci et al., 2011). High concentrations of CO_2 at the field of Iheya North are largely derived from the magmatic CO_2 input, while methane is from hydrogenotrophic methanogenesis using CO_2 derived from sedimentary organic carbons (Kawagucci et al., 2011). The hydrothermal field in Iheya Ridge is located about 25 km south of the Iheya North Knoll. At the eastern foot of the Iheya Ridge, it is the CLAM site (27°33′N, 126°58′E) discovered in 1988, which is characterized by a thick blanket of muddy sediments consisting of volcanic sands containing amorphous silica-mangano-calcite and anhydrite-calcite with disseminated minor sulfide (Sakai et al., 1990). Clear hydrothermal fluids with temperatures of 220 °C or less are discharged from the

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* Corresponding author at: Institute of Oceanology, Chinese Academy of Sciences, 7 Nanhai Road, Qingdao 266071, China.
E-mail address: lsun@qdio.ac.cn (L. Sun).

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hydrothermal mounds (Ishibashi et al., 1995). Submarine hydrothermal fluids from the CLAM vent site are characterized by anomalously high alkalinity and ammonia and significantly higher SO_4^{2-} than ambient seawater (Gamo et al., 1991).

Some vent-associated biological communities have been investigated in the hydrothermal fields of Iheya North and Iheya Ridge. The megafaunal species and community structures varied in different vent sites (Ohta and Kim, 2001; Tokeshi, 2011). Microbial compositions have been investigated in the inactive chimney structures, subseafloor muds, and deep-sea sediments from the hydrothermal fields of Iheya North (Suzuki et al., 2004; Yanagawa et al., 2013; Yanagawa et al., 2014; Zhang et al., 2015). These studies showed that the potential microbial community stratification and transition in the subseafloor sediment cores in Iheya North were controlled by fluid flow and geothermal gradient (Yanagawa et al., 2014), and the predominant bacterial population in Iheya North inactive chimney was *Gammaproteobacteria* or Nitrospirae, while the predominant archaeal populations were Crenarchaeota and Euryarchaeota (Suzuki et al., 2004). However, information about the microbial communities inhabiting the sediments in Iheya Ridge hydrothermal field is very scarce (Zhang et al., 2015).

In recent years, metagenomic analysis has become a routine approach to simultaneously explore taxonomic diversity and biological function of microbial communities in shallow-sea and deep-sea environments (Cao et al., 2014; Tang et al., 2013; Xie et al., 2011). However, this technique has not been applied to systematic study of microbial populations in the sediments of different hydrothermal fields in Okinawa Trough. In this study, we aimed to utilize metagenomics to investigate the compositions and metabolic profiles of the microbial communities in the sediments of the hydrothermal fields of Iheya North and Iheya Ridge.

2. Materials and methods

2.1. Sampling sites and sample collection

The four samples used in this study were collected in April 2014 during the cruise conducted by the scientific research vessel KEXUE in Iheya North and Iheya Ridge fields, Okinawa Trough. Information of the sampling sites and the samples are shown in Fig. 1 and Table 1. Of the four samples, INT4 and INT6 were from the areas surrounding the vent field in Iheya North, while IRS6 and IRT2 were from the areas surrounding the vent field in Iheya Ridge. Samples INT4, INT6, and IRT2 were collected using electro hydraulic grab with underwater television camera, and IRS6 was collected using a gravity corer. The samples were stored at −80 °C immediately and kept on dry ice during transportation.

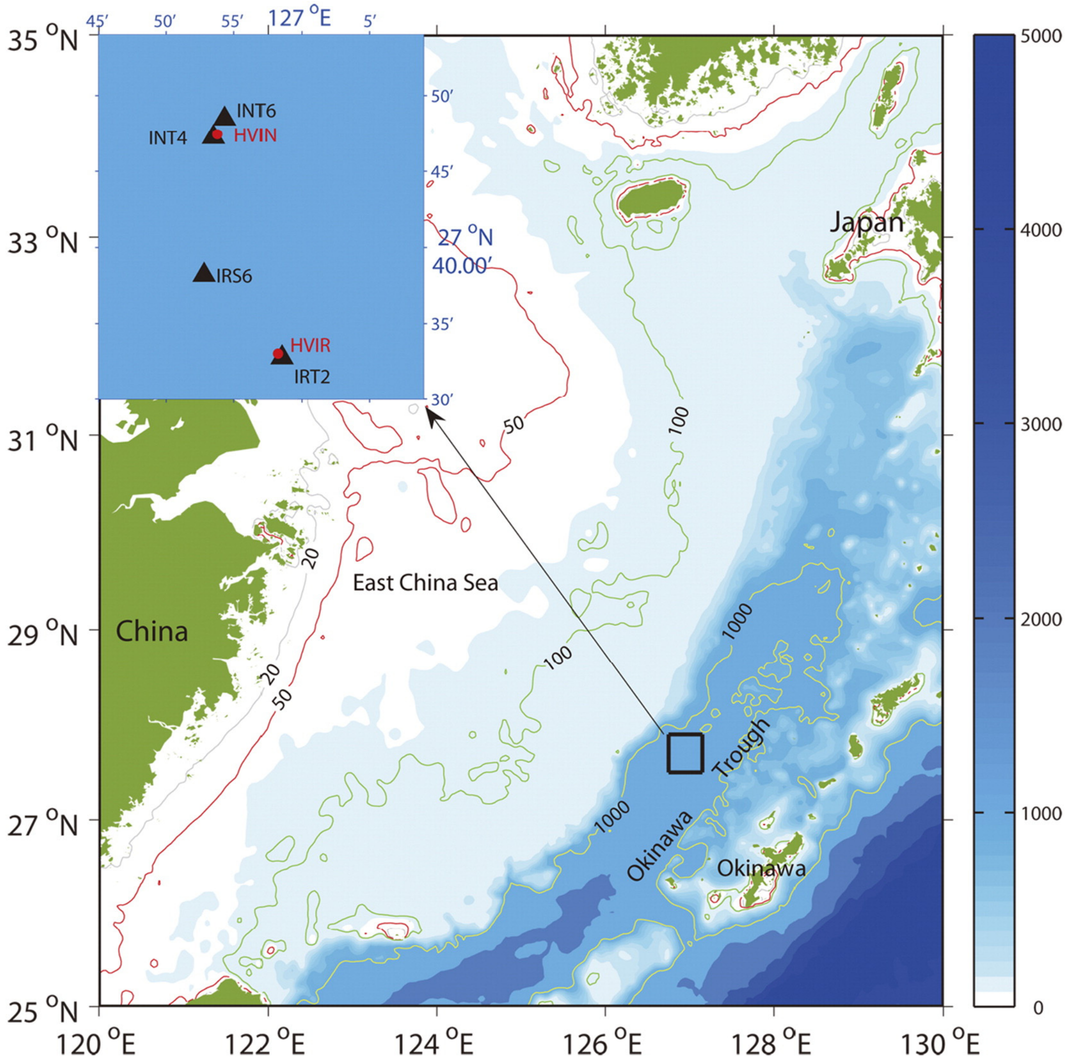

Fig. 1. Location of sampling sites and active vents in Okinawa Trough. The black triangles represent four sampling sites, and the two red circles represent vents HVIN and HVIR in Iheya North and Iheya Ridge, respectively. Map was generated using Matlab R2014a. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

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