

## **Comparative Analysis of Microbial Community Structure and Function of Two Deep-Sea Brine Pools from the Red Sea**

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In the middle rift of the Red Sea, two neighboring deep-sea brine pools - the Atlantis II Deep and Discovery Deep, which are characterized by high salinity, high temperature, and high metal contents, have been extensively studied for their geochemical and geological characteristics. Over the past 50 years, the seawater temperature of the Atlantis II Deep has raised from 56 to 68°C, whereas that of the Discovery Deep has maintained relatively stable at about 44 °C. We hypothesized that such a drastic temperature change in the Atlantis II Deep shall have driven the microbial community there through substantial adaptive changes; subsequently, there shall be substantial differences in microbial community structure and function between the Atlantis II Deep the Discovery Deep. In this study, we have analyzed community diversity and functional genes of both bacteria and archaea in the brine pool waters, the overlying deep-sea water, and the brine-seawater interfaces, using most advanced sequencing platform. As expected, the bacteria and archaea communities were significantly different in terms of species diversity, metagenomic reads, functional gene groups. Specifically, in the Discovery Deep, the highest microbial abundance was found in the brine-seawater interface, probably due to a complex mixing environment therein, whereas the upper convective layer of the Atlantis II Deep harbored more microbes than in its interface. Overall, we identified 19 phyla and a high proportion of unclassified groups in both brine pools. The Discovery Deep was dominated by halophilic methanogens, while in contrast, the Atlantis II Deep harbored thermo-tolerant, metal-resistant bacteria that can degrade aromatic compounds and mediate metal precipitation. The presence of aromatic compounds in the Atlantis II Deep was further confirmed by chemical analysis and supported by significantly enriched aromatic degradation pathways in the metagenome of this Deep. These aromatic compounds were believed to be hydrothermally produced under the high temperature. In the Discovery Deep, the most abundant genes from the microbes were related to sugar metabolism pathways and DNA synthesis and repair, suggesting different strategies of utilization of carbon and energy sources between the two brine pools. A substantial divergence in functional profiles of the two pools was further highlighted by different abundances of genes involved in ion transport, signal conduction, and transcription. In summary,

the chemical and ecological differences between these two neighboring brine pools have strongly shaped their microbial communities and led to different functions and evolutionary scenarios. Altogether, the two brine pools are unique ecosystems warrant further exploration.

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