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Spatial distribution characteristics of bacterial community structure and gene abundance in sediments of the Bohai Sea

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This study investigated differences in the community structure and environmental responses of the bacterial community in sediments of the Bohai Sea. Illumina high-throughput sequencing technology and real-time PCR were used to assay the bacterial 16S rDNA in the surface sediments of 13 sampling stations in the Bohai Sea. The results showed that heavy metal pollution showed regional characteristics, most of the sediments were contaminated by Hg, and the 16S rDNA abundance of bacteria appeared low in the northern regional station. The main phyla of bacteria recorded included Proteobacteria (52.92%), *Bacteroidetes* (11.76%), *Planctomycetes* (7.39%) and Acidobacteria (6.53%). The genus with the highest relative abundance was *Desulfobulbus* (4.99%), which was the dominant genus at most sampling stations. The main factors influencing bacterial community structure were total organic carbon, followed by the depth and total phosphorus. The content of lead, cadmium, chromium, copper, and zinc had a consistent effect on community structure. Arsenic showed a negative correlation with bacterial community structure in most samples, while the more polluted mercury and chromium in sediments had no significant effect on bacterial community structure. The bacterial community in sediment samples from the Bohai Sea was rich in diversity and displayed an increase in diversity from high to low latitudes. The data indicated that the Bohai Sea had abundant microbial resources and was rich in bacteria with the potential to metabolize many types of pollutants.

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