

Bacterial community structure in the Bohai Strait and its response to environmental changes

Xiaoke Hu*, Yibo Wang, Caixia Wang, Bin Wang

Key Laboratory of Coastal Biology and Bioresource Utilization, Yantai Institute of Coastal Zone Research, Chinese Academy of Sciences, Yantai 264003, China
Laboratory for Marine Biology and Biotechnology, Qingdao National Laboratory for Marine Science and Technology, Qingdao 266237, China

Introduction

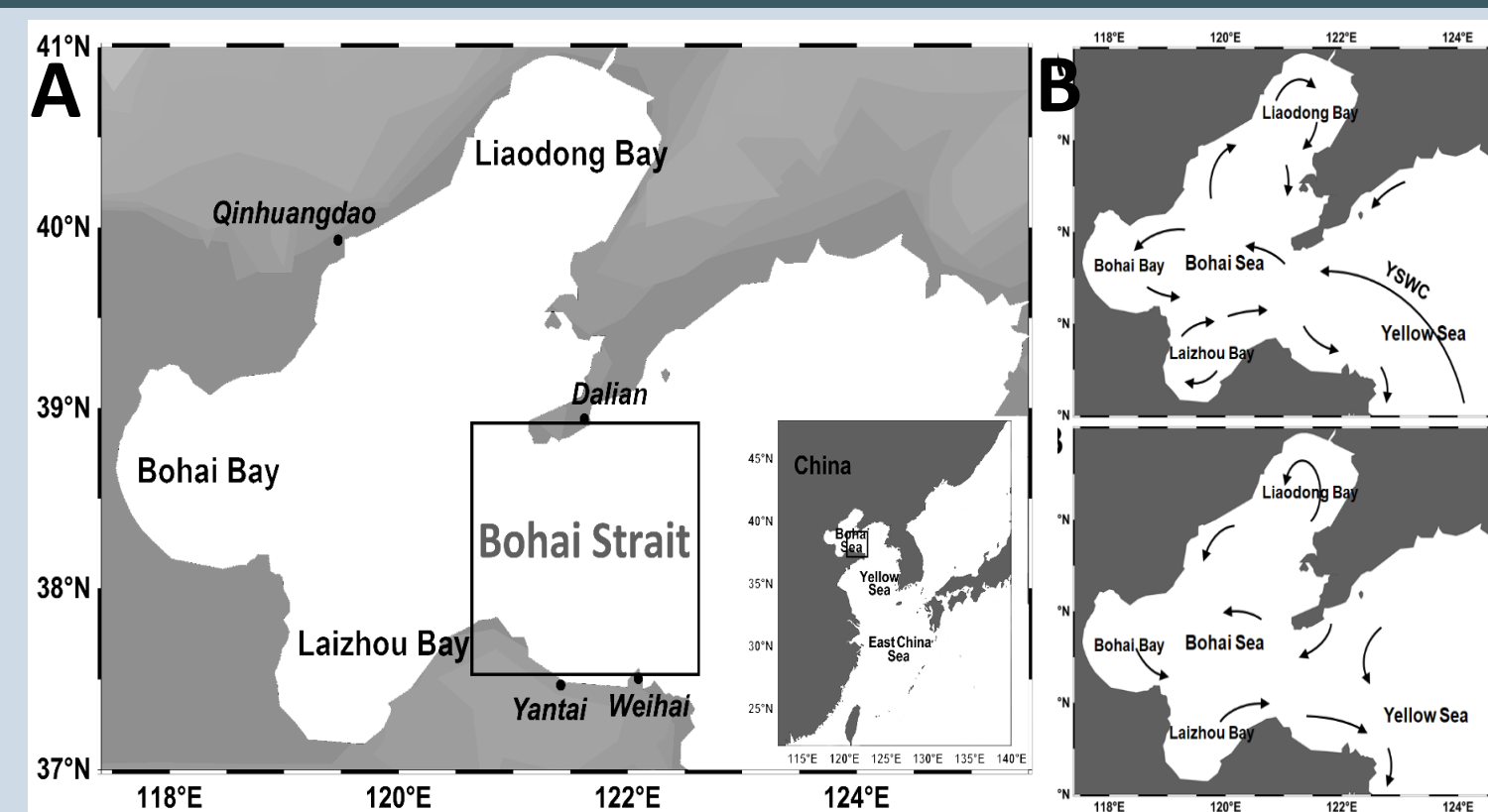


Fig. 1. Location of the Bohai Strait (A) and the features of the currents around the Bohai Strait in winter and summer (B), redrawn from Guan (1994) and Liu (2015).

The Bohai Strait is the only pathway connecting the Bohai Sea and the Yellow Sea in China. The seasonal pattern of the hydrodynamics in the Bohai Strait is striking, especially between summer and winter (Chen 2009, Bi et al. 2011). In winter, the Yellow Sea Warm Current (YSWC) enters the northern Bohai Strait, while the Bohai Sea Coastal Water (BSCW) occupies the southern Bohai Strait (Hainbucher et al. 2004, Chen 2009). In contrast, the hydrodynamics in summer is relatively weak, and the differences in temperature and salinity between the northern and southern strait become less evident. This area is also experiencing heavy anthropogenic impacts. There are a number of important ports and agricultural areas centered around the cities of Dalian, Yantai and Weihai, on both sides of the Bohai Strait. Previous studies in the Bohai Strait have largely focused on the physical processes (Cheng et al. 2004, Li et al. 2015, Bi et al. 2011, Guo et al. 2016), whereas little is known about the biotic communities and their response to environmental changes (Wang et al. 2016). Bacteria can respond rapidly to physicochemical gradients and environmental changes, resulting in specific spatial and temporal patterns (Lindh et al., 2015; Bunse and Pinhassi, 2017). The microbial communities in the Bohai Strait are supposed to show a variation pattern in response to these environmental forces as a result of both hydrodynamic and anthropogenic impacts.

In this study, we investigated the bacterial communities in the seawater and sediments of the Bohai Strait using 16S rRNA amplicon sequencing and flow cytometry. The aim of this study was to illuminate how the bacterial assemblages respond to complex environmental changes.



Dr Xiaoke Hu

Phone: +86-535-2109127
E-mail: xkhu@yic.ac.cn

Results & Discussion

Part 1 Distribution of bacterial communities in the surface water of the Bohai Strait and its environmental associations

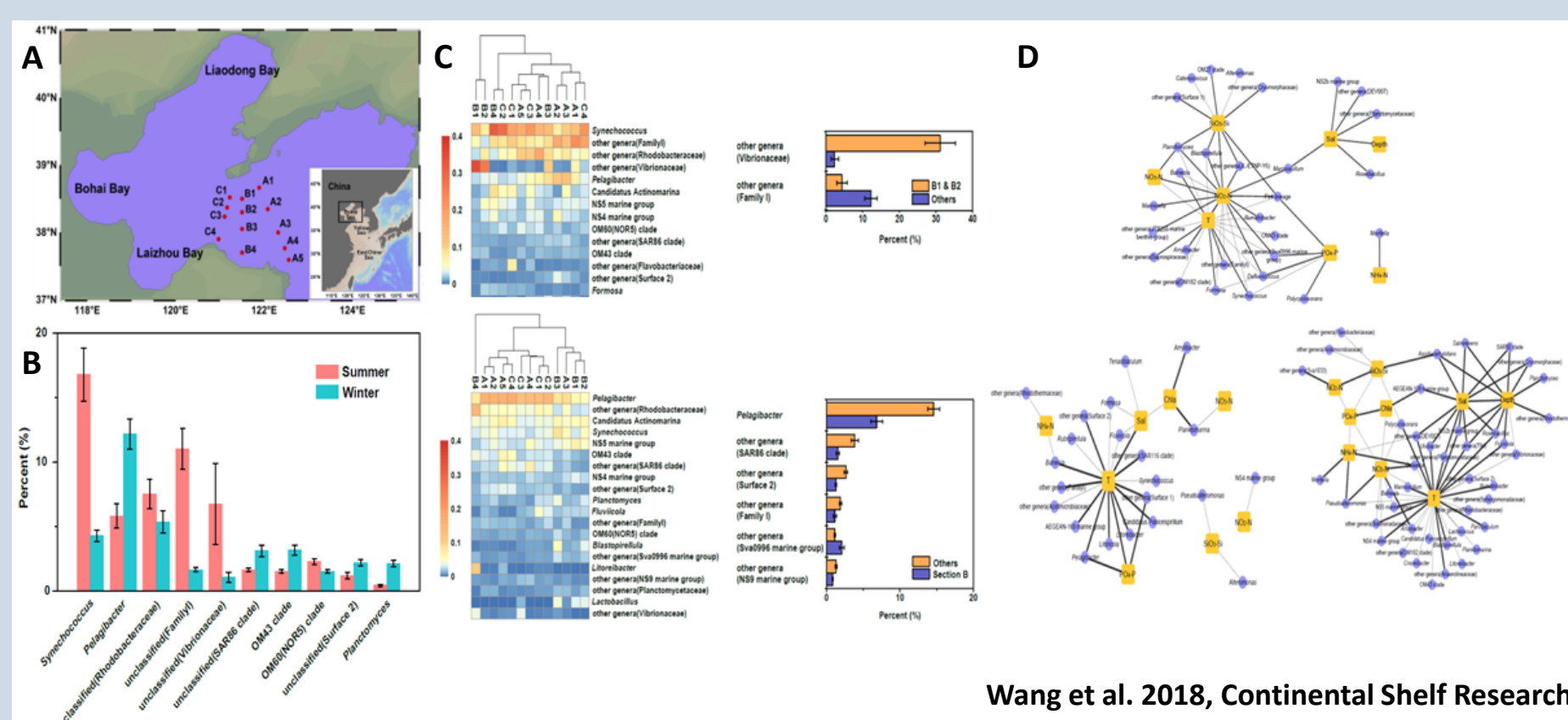


Fig. 2 Location of sampling sites (A), genera with significant variations between seasons (B), genera with significant variations between different areas (C), network between the most common genera and environmental factors (D).

The bacterial community in the surface water of the Bohai Strait exhibited a robust seasonal and spatial pattern. In response to environmental changes between seasons, especially the dramatic changes of temperature and nutrient ($\text{NO}_2\text{-N}$ and $\text{PO}_4\text{-P}$) level, *Synechococcus* and unclassified genera in Family I predominated in summer while some oligotrophic taxa (e.g., *Pelagibacter*, OM43 clade) are more abundant in winter. However, the spatial heterogeneity of the bacterial communities can be attributed to factors other than the measured environmental parameters. Some taxa (e.g., *Vibrionaceae*, Sva0996 marine group, SAR11) exhibited spatial heterogeneity or patchiness most likely related to the patchiness of organic matter (OM) derived from algae or aquaculture organisms, while other taxa, e.g. OM43 clade, showed a correlation with currents. Also, the spread range of currents might have influenced the size of patchiness to a certain degree. In conclusion, our results suggested that OM niche partitioning among bacterial communities was crucial to the community structure in the Bohai Strait. The relationship between bacterial communities and different sources of OM substrates, such as algae-derived OM, animal-derived OM, and external organic pollutants, etc., should be further explored. Our results support the hypothesis that local factors have a greater impact on bacterial community structure than dispersal purely due to hydrodynamics.

Part 2 Distribution of bacterial communities in the surface sediment of the Bohai Strait and its environmental associations

In the summer of 2014, six stations across the strait were selected to explore the taxonomic composition of microbial communities and their ecological associations in the surface sediments. The four most abundant classes were Gammaproteobacteria, Deltaproteobacteria, Bacilli and Flavobacteriia. The shifts in the relative abundance of predominant microbes under different environmental conditions can reflect the adaptations of microbial communities to habitat filtering. Temperature, total carbon, depth, nitrate, fishery breeding and cold water masses influenced the microbial communities, as suggested by representational difference and composition analyses. Network analysis of microbial associations revealed that the key families included Flavobacteriaceae, Pirellulaceae and Piscirickettsiaceae. The three key families have high phylogenetic diversity and wide distributions. The high phylogenetic diversity may imply high overlap of the ecological functions within the community. If some microbes in the three families that have certain ecological functions were removed, other microbes could perform similar functions accordingly. Our findings suggest that the families with high phylogenetic diversity are key populations in the microbial association network that ensure the stability of microbial ecosystem. Our study contributes to a better understanding of microbial ecology in complex hydrological environments.

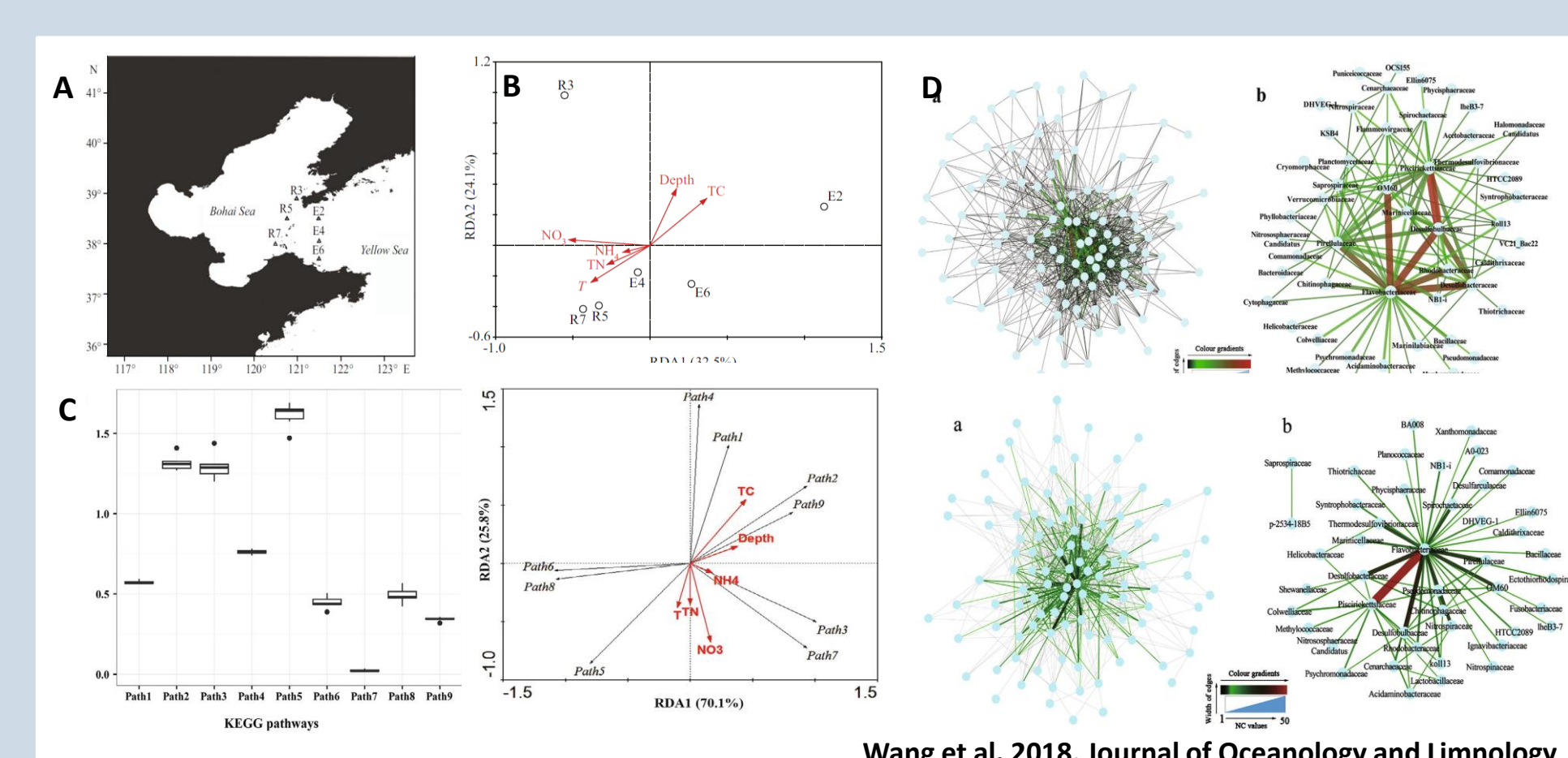


Fig. 3 Location of the nine survey stations (A), relationship between bacterial communities and environmental factors (B), summary of the predicted KEGG pathways of energy metabolism (C), network showing the positive and negative associations at the family level (D).

Part 3 Distribution of heterotrophic bacterial abundance in the Bohai Strait and its environmental associations

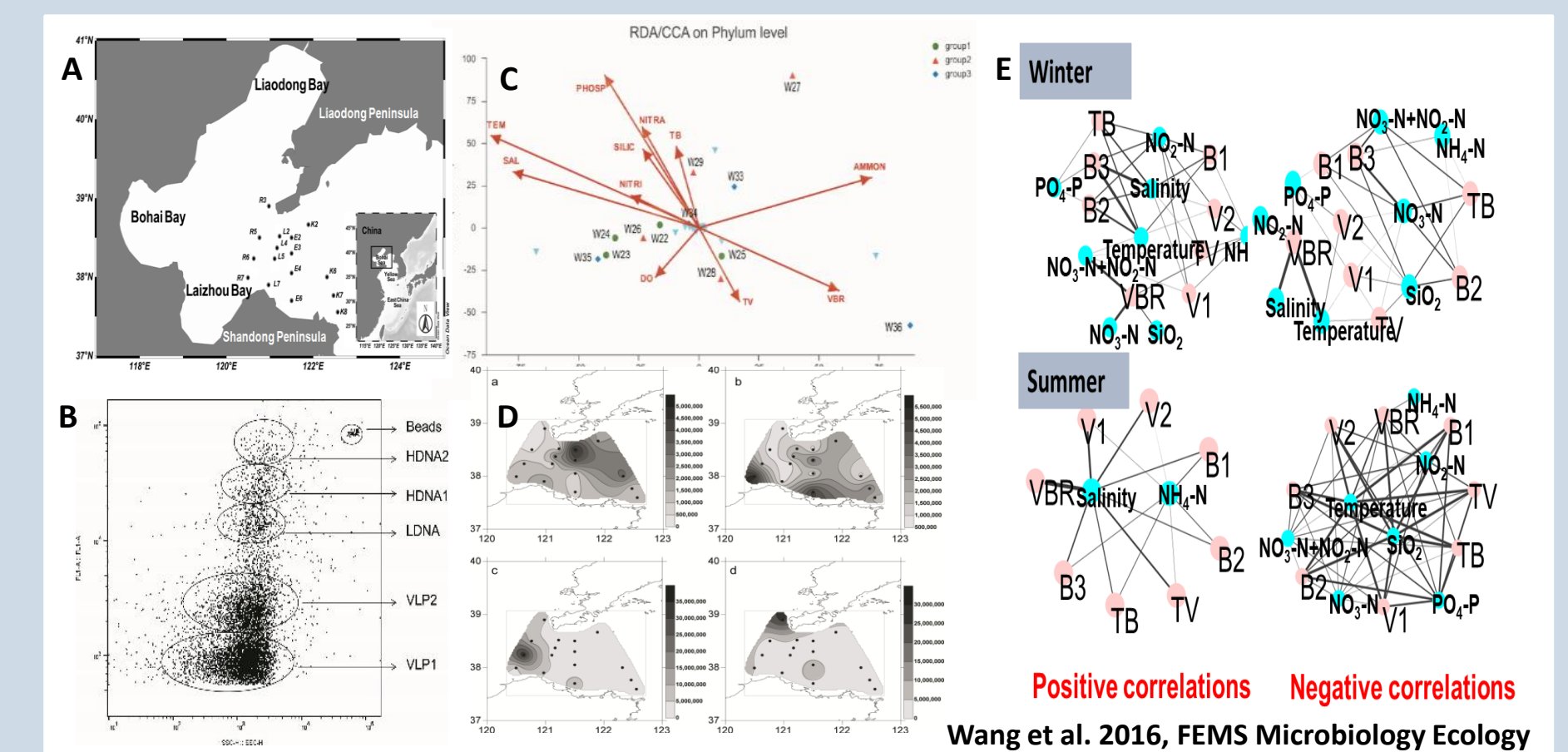


Fig. 4 Location of survey stations (A), representative scatter diagram used for determination of bacterial abundance (B), relationship between environmental factors and heterotrophic bacterial community (C), horizontal distribution of heterotrophic bacterial abundance in the Bohai Strait in winter and summer (D).

The average heterotrophic bacterial abundance was lower in winter (1.84×10^6 cells/mL) than in summer (5.05×10^6 cells/mL). In the horizontal distribution, bacterial abundance was obviously higher near-shore than offshore. In the vertical distribution, the variation of bacterial abundance did not show a clear relationship with depth. Spearman correlation analysis showed that heterotrophic bacterial abundance was correlated with the concentration of $\text{PO}_4\text{-P}$ in winter (positive) and $\text{NO}_3\text{-N}$ in summer (negative). Additionally, heterotrophic bacterial abundance showed a negative correlation with salinity. The water temperature and salinity in the northeast of the Bohai Strait was much higher than in the southwest due to the impact of the YSWC, and the abundance of heterotrophic bacteria showed a similar trend. The negative correlation between bacterial abundance and $\text{NO}_3\text{-N}$ concentration may be caused by the indirect relationship between heterotrophic bacteria and phytoplankton and the resulting antagonistic effects. Together, the above results signified that both salinity and nutrients are critical factors controlling microbial growth in the waters of the Bohai Strait, and the role of the Yellow Sea Warm Current is particularly evident.

Conclusion

Local factors control the bacterial communities in the Bohai Strait. The heterotrophic bacterial abundance in the seawater of the Bohai Strait is significantly correlated to nutrient level, which is closely related to the seasonal presence of the YSWC. While the bacterial community composition in the seawater and sediments in the Bohai Strait implies the significant influence of local agriculture on bacterial communities. Our study contributes to a better understanding of microbial ecology in complex hydrological environments and supports that the taxa with high phylogenetic diversity are crucial in the microbial association network that ensures the stability of microbial ecosystem.

Acknowledgments

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