

# Niche partitioning of key bacterial and archaeal groups along the Changjiang River Estuary to the East China Sea

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## Introduction

The Changjiang River estuary and its adjacent area show unique phenomena such as dilute water diversion, anoxic, frontal migration, and maximum turbidity zone, which directly or indirectly affect the physical and chemical factors such as temperature, salinity, suspended particulate matter and nutrients, represent a unique ecosystem (Zhang et al. 2007, ). In this study, During the R/V “Zheyuke#2” cruises (July, 1st, 2017 – July, 8th, 2017), niche partitioning of the key bacterial and archaeal groups from two size fractions (0.2–3 μm and >3 μm) was investigated in three regions including estuary area, maximum turbidity zone, and sea area along the Changjiang estuary to the East China Sea. To explore the relationship between the specific microbial taxa and environmental conditions, advanced the understanding of preferences of specific bacterial and archaeal taxa for distinct niches within the estuarine environment.

## Sampling

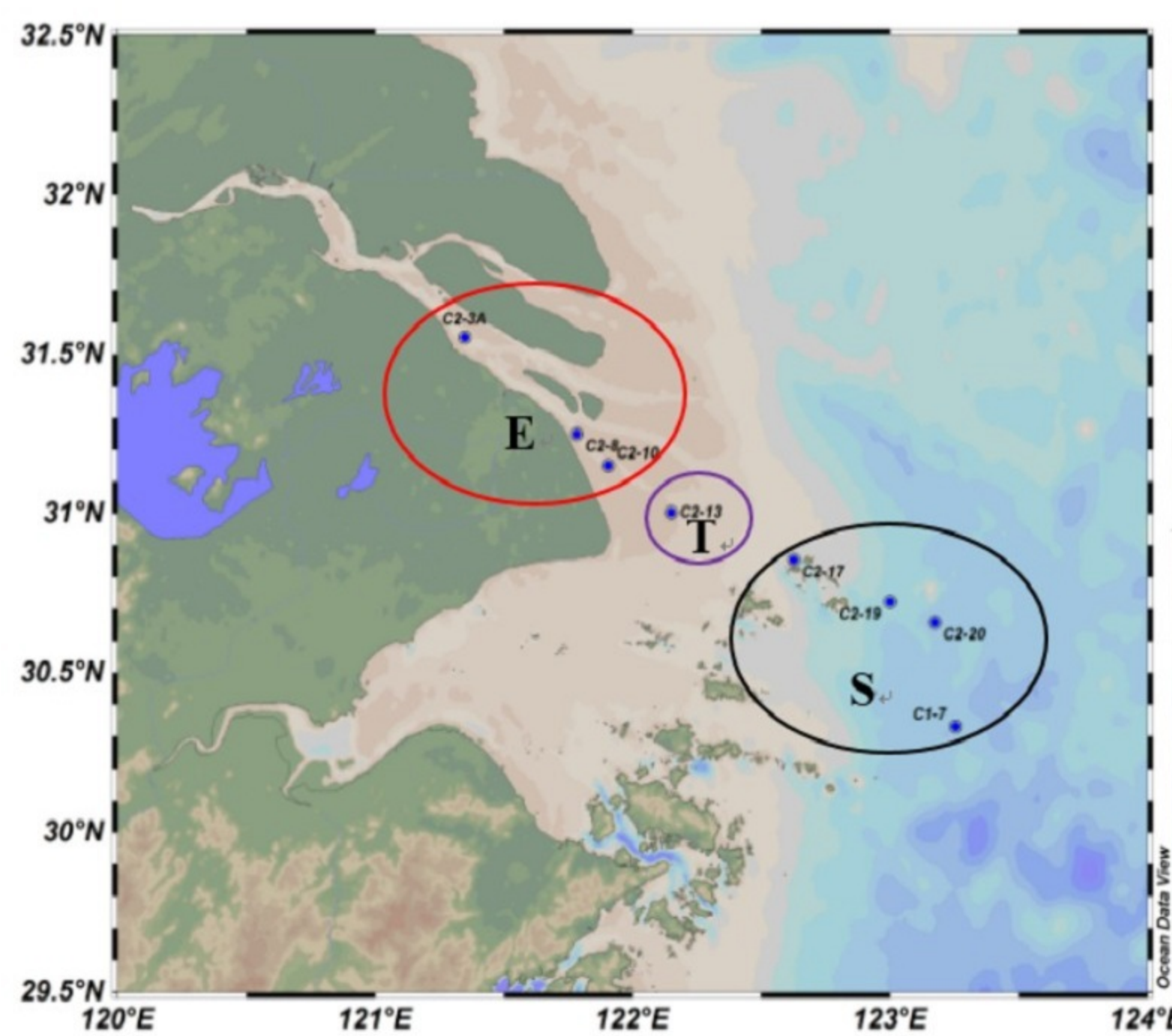


Fig. 1 Map showing the sampling stations, based on the sampling locations and physicochemical parameters, eight stations were separated into three groups: Group E included three stations collected from low salinity zones (C2-3A, C2-8 and C2-10), where near to estuary area. Group T included stations C2-13, which in the TMZ. Group S included four stations south near to the East China Sea (C2-17, C2-19, C2-20 and C1-7) with high salinity.

## Results and discussion

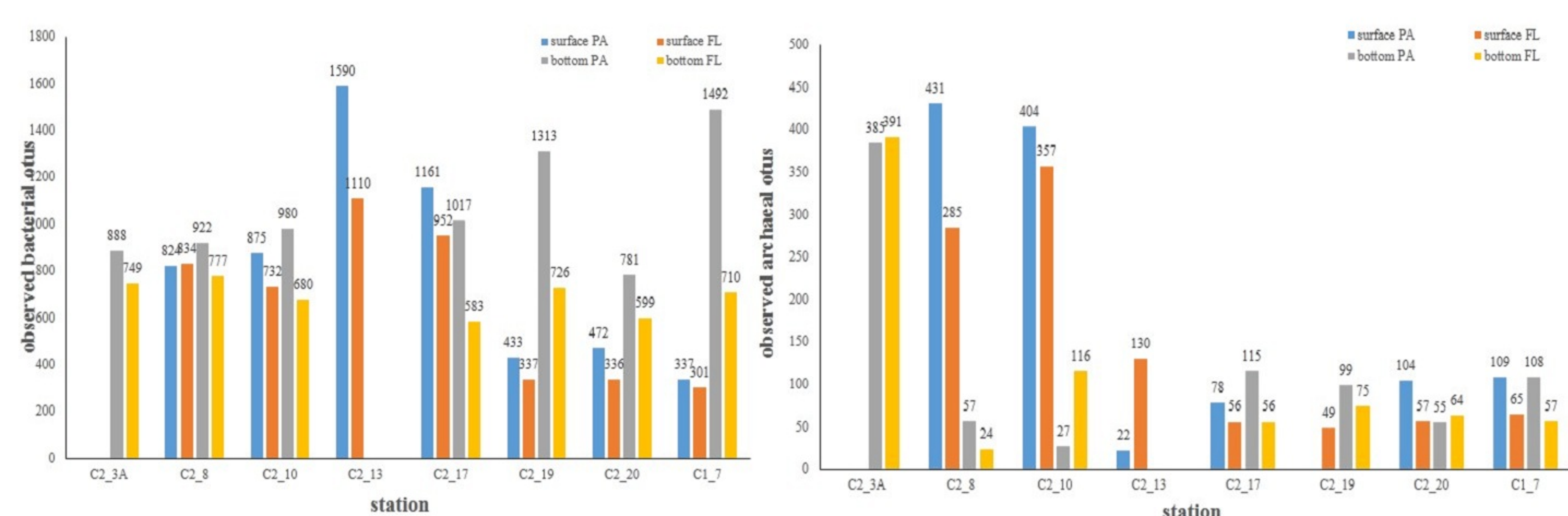


Fig. 2a Actual measured number of bacterial OTUs.

Fig. 2b Actual measured number of archaeal OTUs.

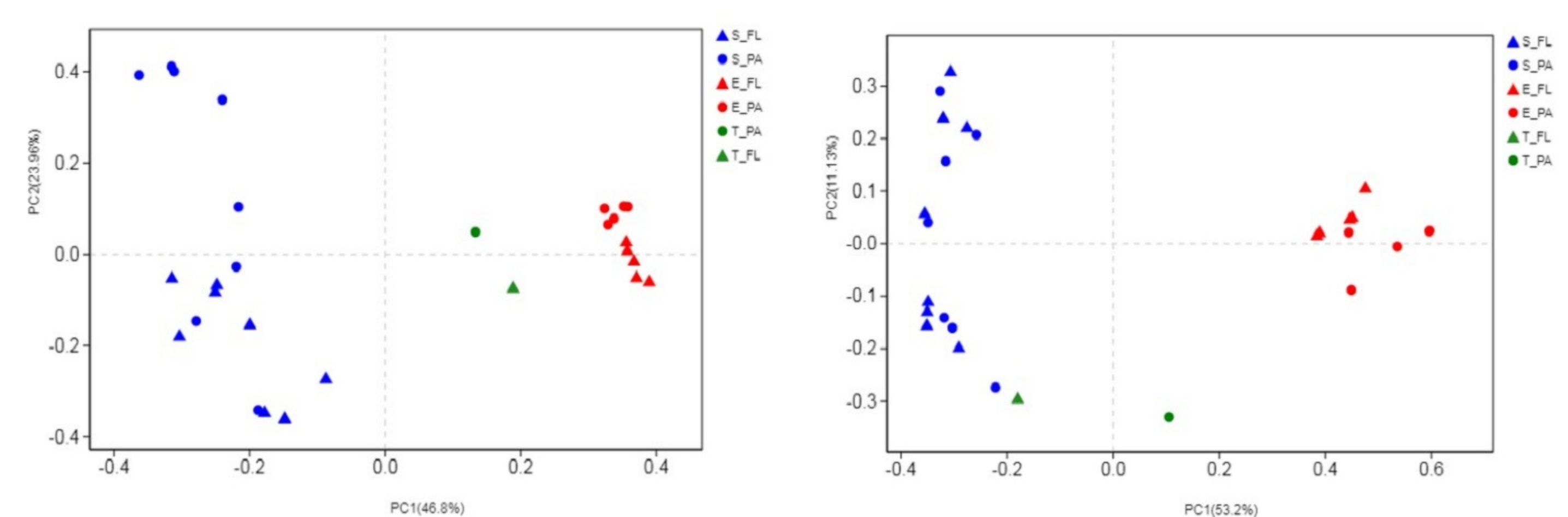


Fig. 3a PCoA analysis of bacteria.

Fig. 3b PCoA analysis of archaea.

Overall, the abundance of PA bacteria and archaea is greater than FL one. The maximum abundance of bacteria occurs in the TMZ(C2-13), and there are relatively high abundances of archaea at several stations near the estuary. The PCoA figure shows significant differences in the distribution of bacteria and archaea in three regions, Verified the rationality of our partition.

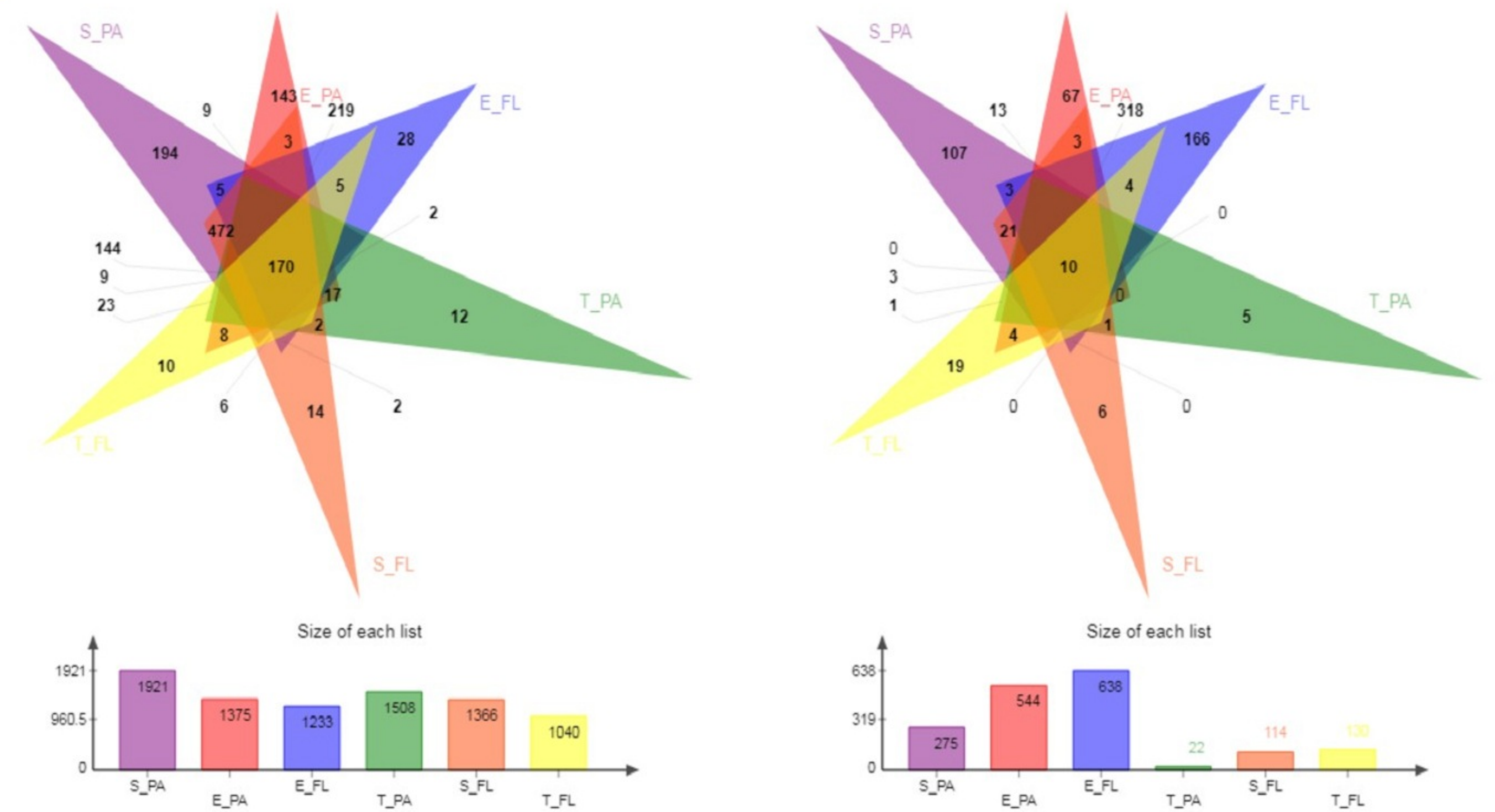


Fig. 3a Venn diagram of bacterial species at OTU level.

Fig. 3b Venn diagram of archaeal species at OTU level.

Different colors represent different groups, overlapping parts represent OTUs shared by multiple groups, and no overlapping parts represent OTUs unique to the groups, numbers in the chart represent the corresponding number of OTUs.

Within the bacterial domain, we found the niche specificity of SAR11 in the various regions. Phylogenetic analysis showed that *hgI* clade was dominant in the estuary area and *flavobacterial* groups were abundant in the sea area. In addition, we found that certain *Cyanobacteria* are abundant in the collection of bacteria above 3μm, which closely related to an obtained clone from *Karenia brevis* bloom water on the west Florida shelf (Jones et al. 2010) suggesting a connection with blooms. Notably, the co-occurrence of sequences belonging to different groups of *SAR11*, *hgI* clade and *flavobacterial* class in the maximum turbidity zone, indicating there are complicated metabolic pathways in this area.

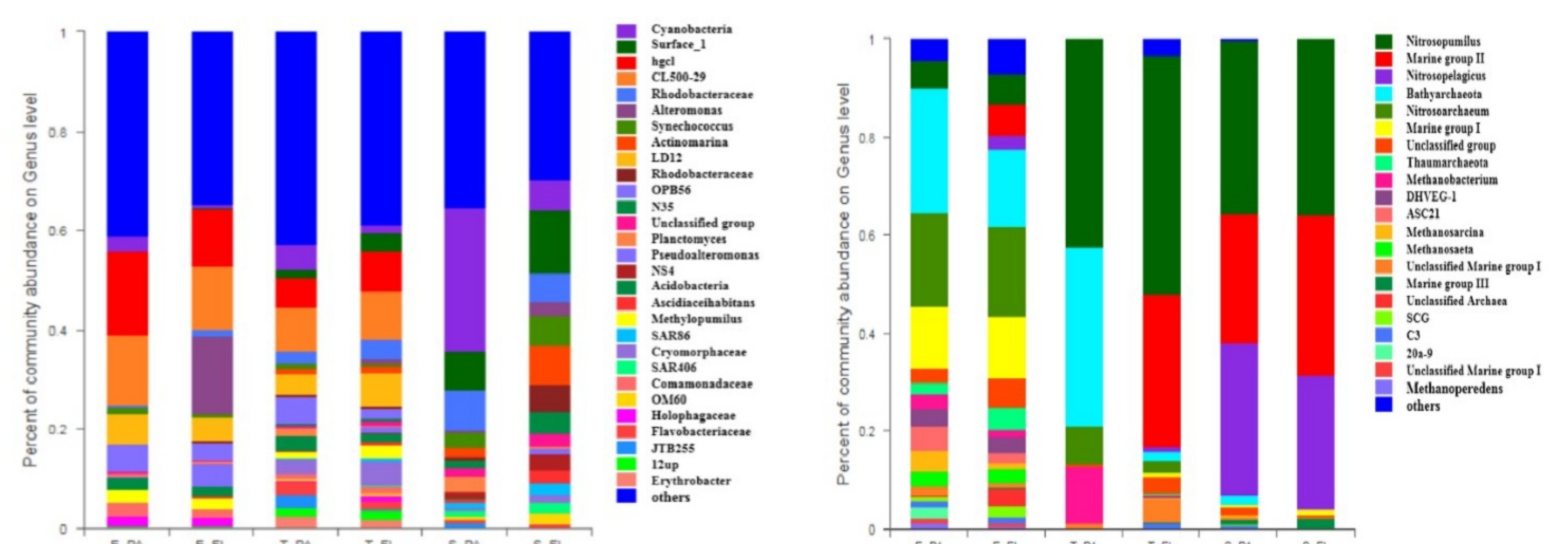


Fig. 4a Relative abundance of bacterial sequences classified at the genus level of the Yangtze River Estuary and its adjacent area.

Fig. 4b Relative abundance of archaeal sequences classified at the genus level of the Yangtze River Estuary and its adjacent area.

Within the archaeal domain, the *Nitrosoarchaeum* group and several novel groups belonging to *marine group I* were frequently detected in the estuary area, showing these potential ammonia-oxidizing archaea may be more adaptable in low salinity condition. Sequences affiliated with heterotrophic *Maine Group II* were predominant in the sea area, indicating they may prefer utilize marine organic matters. Also, a distinct distribution of *bacthyarchaeal* groups was observed in both size fractions in the bottom water, suggesting the metabolic specialists exist in our studied sites.

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## References

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- [2]. Jones K L, Mikulski C M, Barnhorst A, et al.FEMS microbiology ecology, 2010.