

## Spatial-temporal distribution and environmental effects of Anammox bacteria in typical estuary ecosystem

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### Abstract

Anaerobic ammonium oxidation (anammox) as an important process of nitrogen cycle has been studied in the Pearl River Estuary (PRE) in last several years. However, knowledge about the effects of salinity on the diversity and activity of anammox bacteria remains scarce in this environment. Here we employed both the quantitative PCR and high throughput sequencing to document the spatiotemporal distribution of anammox bacteria in sediments samples of the PRE, which have a strong gradient of salinity range from 0.3 ‰~31‰. The quantitative PCR results showed that the *hzsB* gene of anammox bacteria gradually decreases from  $1.06 \times 10^4$  to  $1.85 \times 10^2$  copies per gram of wet weight along with the increasing of salinity. Moreover, the *hzsB* high throughput sequencing results showed that, the anammox bacteria '*Ca. Scalindua*', '*Ca. Brocadia*', '*Ca. Jettenia*' and '*Ca. Kuenenia*' were detected in PRE sediments. Meanwhile, the genera of '*Ca. Brocadia*' dominated at samples with low salinity concentration (0.3 ‰), but their relative abundance sharply decreased along with the increasing of salinity. In contrast, the relative abundance of '*Ca. Scalindua*' increased from 0.5 to 31‰ along with the salinity increasing. Surprisingly, the '*Ca. Kuenenia*' was detected as the dominant anammox genera at the samples with salinity range from 10‰ ~ 31‰. Combining the physicochemical characteristics of the PRE sediment samples and their correlations with anammox bacteria community structure, our results indicated that the salinity was a key environmental factor defining the geographical distribution and diversity of the anammox bacterial community in the PRE ecosystem.