MG II dominated the archaeal community composition in water columns of the northeastern SCS

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Physicochemical variables such as temperature, pressure and salinity are some of the important factors constraining the distribution, abundance and diversity of microorganisms in the ocean. Much less is known about the effects of water mass mixing on microbial community structure and diversity in different oceanic regions. In water columns of different areas in northeastern South China Sea (SCS), we quantified the abundances of total archaea (16S rRNA gene), Marine Group I (MG I) Crenarchaeota (estimated based on *amoA* gene) and Marine Group II (MG II) Euryarchaeota (16S rRNA gene) by using real-time quantitative PCR (qPCR), and examined the archaeal community composition by 454 and Miseq sequencing. Both the qPCR and sequencing results revealed that MG II dominated the whole water columns in the northeastern SCS when sampling occurred in April of 2013. The results are in contrast to previous findings in many other oceanic regions. This may be explained by physical processes (such as warm eddy or downward movement of the western Pacific water into the northeastern SCS through the Luzon Strait) that transport surface water to the deep SCS. Furthermore, MG I and MG II correlated significantly between 50 m and 3200 m at these locations, which may hint at potential interactions for carbon metabolism between these two physiologically disparate archaeal groups. These hypotheses, however, have yet to be verified by future studies.