



## **Metaproteomic analysis reveals microbial metabolic activities in the deep ocean**

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The deep sea is the largest habitat on earth and holds many and varied microbial life forms. However, little is known about their metabolic activities in the deep ocean. Here, we characterized protein profiles of particulate ( $>0.22 \mu\text{m}$ ) and dissolved (between 10 kDa and  $0.22 \mu\text{m}$ ) fractions collected from the deep South China Sea using a shotgun proteomic approach. SAR324, Alteromonadales and SAR11 were the most abundant groups, while Prasinophyte contributed most to eukaryotes and cyanophage to viruses. The dominant heterotrophic activity was evidenced by the abundant transporters (33%). Proteins participating in nitrification, methanogenesis, methyltrophs and  $\text{CO}_2$  fixation were detected. Notably, the predominance of unique cellular proteins in dissolved fraction suggested the presence of membrane structures. Moreover, the detection of translation proteins related to phytoplankton indicated that other process rather than sinking particles might be the downward export of living cells. Our study implied that novel extracellular activities and the interaction of deep water with its overlying water could be crucial to the microbial world of deep sea.