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Wide scale mapping of the Southern Ocean Microbial Diversity

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Key carbon and nutrient cycling processes within the Southern Ocean (SO) are microbially driven and ecologically regulated as a balance between surface photosynthetic carbon dioxide fixation and remineralisation by heterotrophic bacteria/archaea within the twilight and dark ocean. Despite their pivotal role, most of the SO microbial community structure, particularly within the pelagic dark oceans, remains unexplored. This study aims to map the SO microbes and explore the potential roles of ocean circulation and hydrologically distinct water masses in structuring the SO microbial community. From several multi-latitudinal transects spanning the Indian, Australian and Pacific sectors (71°E – 170°W) of the SO, we sampled seawater at multiple points transversing the water column from surface to abyssal depths, and examined bacterial, archaeal and eukaryotic community compositions through high resolution 16S and 18S rRNA tag sequencing. Surface samples across all transects were dominated by the Pelagibacteraceae (SAR11) family with shifts in different Pelagibacteraceae oligotypes observed from low to high latitude samples. Longitudinal distance was not observed to drive community differences between samples at similar latitudes or surface water zones, and we found temperature to be a major driving force for surface community selection. The biogeographical distribution of microbes were explained in part by distinct hydrographies of the water masses, but bacteria and archaea from deeper (Antarctic bottom-lower circumpolar) water masses, which spread across a wide range of latitudes, displayed niche communities with varying abundances of specific phylotypes that were not explained by hydrography or geographical distance. Together, these results provide a baseline for evaluation of future changes towards an improved trend assessment of the principle SO nutrient cycle drivers.