Ocean acidification and the Southern Ocean

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Ocean acidification, the decrease in seawater pH, negatively impacts several marine organisms such as molluscs, fish, and corals by affecting their physiology and function. Microbial communities (bacteria, archaea, and fungi) form the basis of ocean ecosystems by cycling key nutrients throughout the entire trophic structure, especially within iron-limited regions such as the Southern Ocean. It is hypothesised that microbial communities may be resistant to external perturbations such as decreasing pH, although the direct effects of these changes on community structure, interactions and functionality remains largely under investigated. In this study, we performed a mesocosm experiment on Southern Ocean seawater, where bacterioplankton communities were subjected to future predicted pH decreases (0.4 and 0.8 units). Amplicon sequencing of the 16S rRNA gene and ITS 1 region was used to determine the effect of ocean acidification on microbial community structure and interactions. Furthermore, we assessed community functionality through extracellular enzyme activities. Results show that acidification causes significant increases in the diversity of bacterioplankton communities, while in contrast has no effect on fungal communities. Network analyses reveal the loss of putative keystone taxa and a decrease in community interactions as a response to lower pH levels. Bacterioplankton shift from generalist to specialist community members, suggesting a specialised stress response to unfavourable conditions. N-Acetyl-β-D-Glucosamine and leucine aminopeptidase activities (proxies for nitrogen acquisition) are lower at reduced pH levels, whereas the activities of enzymes involved in carbon acquisition were not significantly different across treatments. Taken together, our findings suggest that bacterioplankton communities may not be as resistant to climate perturbations as previously proposed.