



Response of an arctic ammonia oxidising community to increased pCO₂

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Ocean acidification has been shown to influence sediment/water nutrient fluxes, possibly by impacting on the microbial process of nitrification, the conversion of ammonia to nitrite and nitrate by both bacteria and archaea and anammox, the anaerobic conversion of nitrite and ammonium to dinitrogen gas by bacteria. To directly investigate the effect of increased pCO₂ on these processes, DNA and RNA was extracted from surface sediment during the EPOCA Svalbard benthic mesocosm and the abundance of bacterial (AOB) and archaeal (AOA) ammonia oxidising (amoA) gene and transcript copies quantified using qPCR and RT-qPCR. While there was an equal abundance of both AOB and AOA gene copies, substantially fewer bacteria were actively expressing amoA within the surface sediments: less than 3% of AOB present within the sediment were active, compared to approximately 30% of AOA. Lowering the pH by 0.4 units (to pH 7.7) reduced sediment AOB transcriptional activity by 40% and this was accompanied by a shift in diversity as the population tried to adapt to the changing pCO₂ concentration. However, this decrease in AOB activity was masked by the dominance of AOA activity within the sediment. While there was no change to the diversity of the AOA community, reducing the pH by 0.9 units (to pH 7.2), doubled both AOA gene and transcript copies. PCR primers targeting anammox-specific 16S rRNA PCR indicated this activity also doubled at pH 7.2. This suggests that ammonia oxidising bacteria and archaea have different pH optima, and that the response of sediments to increased pCO₂ may depend on the ratios of microbes present. At this point in time, the majority of sediments are thought to be dominated by archaeal ammonia oxidisers. If this is the case, pH would need to drop by 0.9 units (beyond current projections) before a response is evident, and this could be an increase, not decrease in nitrification.