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Effects of Elevated CO₂ on Microbial Community in a Salt Marsh

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Salt marshes are one of the most productive ecosystems and their ecological importance has been widely acknowledged. Recently, it has been proposed that coastal marshes will be affected in various ways by increases in atmospheric CO₂ concentration. For example, elevated CO₂ accounts for greater exudates of labile C from plant roots compared to ambient air. Such changes in below-ground C quantity and quality may influence the composition and abundance of microbial community, which is likely to alter ecosystem level functions such as decomposition of soil organic matter and nutrient cycling in salt marshes. This study aims to determine effects of elevated CO₂ on microbial community structure and abundance in a salt marsh employing molecular biological techniques.

Wetland soil cores were collected from a salt marsh in North Wales, UK. The area is dominated by *Spartina alterniflora* and *Distichlis spicata*, and salinity varies between 20 to 30 ppt. Eight cores were exposed to two levels of atmospheric CO₂ of ambient air or elevated CO₂ (+ 300 ppm CO₂) using FACE (Free Carbon Dioxide Enrichment) facility for 7 months during a growing season. DNA was extracted from soils, followed by PCR amplification of fragments of eubacterial 16S rRNA, *nirS* and *dsr* genes using FAM-labeled primer pairs. PCR products were digested with *HhaI* and T-RFLP patterns were determined. The abundance of microbial community was determined by real-time PCR using an I-Cycler™.

Elevated CO₂ significantly increased the abundance of SRB by 40%, ($p < 0.01$) (Table 1). Elevated CO₂ appears to stimulate microbial growth and activity via greater exudates of labile C from plant roots. In particular, SRB have been known as main populations involving in organic matter decomposition in saline environments. For example, SRB are capable of degradation up to 94% of organic matters in marine sediments and 67~80% in salt marshes. We speculate that SRB acquired benefits more competitively due to organic matter supplies as root exudates under elevated CO₂. However, eubacteria and denitrifiers did not show any significant changes in the abundance due to elevated CO₂. In contrast, elevated CO₂ led to no significant influences on the diversity of all microbial communities examined, as assessed by

Shannon's index (Table 1). Overall results of this study indicate that elevated CO₂ would increase the abundance of sulfate reducers in a salt marsh, but influences on community structure would be minimal. Further study should focus on interactions between elevated CO₂ and salinity which is another environmental factor expected to vary under future climate changes.

Table 1. Effects of elevated CO₂ on abundance and diversity of Eubacteria, denitrifiers and sulfate reducers in a salt marsh. Values labelled with different letters are significantly different between CO₂ treatments.

| Measurements | Functional Groups | Ambient CO ₂ | Elevated CO ₂ |
|------------------|-------------------|--|--|
| Gene copy number | 16S rDNA | $4.1 \times 10^8 \pm 1.6 \times 10^8$ | $7.6 \times 10^8 \pm 2.9 \times 10^8$ |
| | nirS | $8.6 \times 10^6 \pm 8.3 \times 10^5$ | $9.6 \times 10^6 \pm 1.2 \times 10^6$ |
| | dsr | $1.0 \times 10^6 \pm 8.4 \times 10^4$ ^a | $1.4 \times 10^6 \pm 1.1 \times 10^5$ ^b |
| Shannon's index | 16S rDNA | 2.43 ± 0.73 | 2.27 ± 1.14 |
| | nirS | 1.52 ± 0.41 | 1.56 ± 0.40 |
| | dsr | 2.45 ± 0.68 | 2.42 ± 0.70 |