Metagenomic insight into methanogenic pathways in seagrass sediments

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Background

Methanogenesis is important to the net carbon burial capacity in seagrass sediments. In marine sediments, where sulfate is abundant, hydrogenotrophic and acetoclastic methanogenesis are usually inhibited because of the competition for hydrogen and acetate with sulfate-reducing bacteria. Thus, methylotrophic methanogenesis is crucially important.

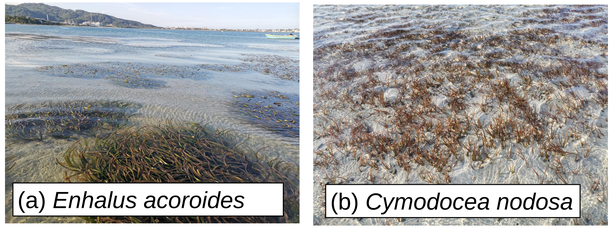

Figure 1. Seagrass meadows of (a) *Enhalus acoroides* and (b) *Cymodocea nodosa* in Li'an Bay, along the east coast of Hainan Island.

Hydrochemistry of the porewater

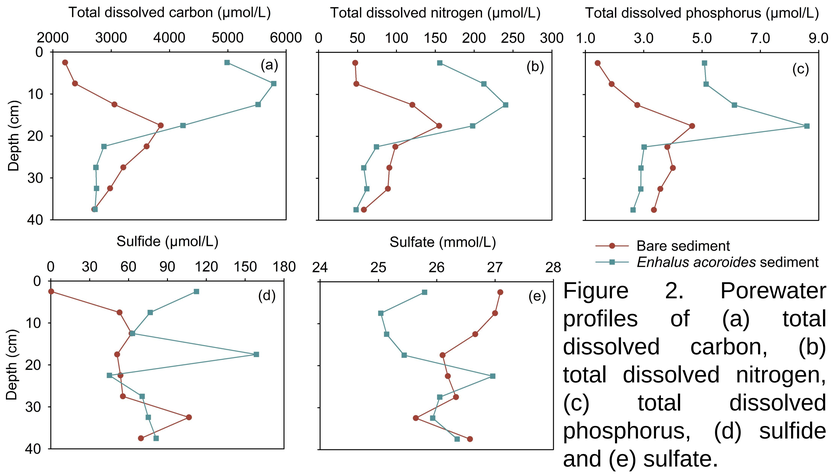

Figure 2. Porewater profiles of (a) total dissolved carbon, (b) total dissolved nitrogen, (c) total dissolved phosphorus, (d) sulfide and (e) sulfate.

From 0 to 20 cm, the total dissolved carbon, nitrogen, phosphorus and sulfide in *Enhalus acoroides* sediment were higher than those in bare sediments. These may be caused by the stronger organic matter degradation in *Enhalus acoroides* sediment.

Methanogenic pathways in seagrass meadows

In bare sediment, *methanococcoides*, which is a strictly anaerobic, methylotrophic marine methanogen, in the bottom was 41% higher than that in the surface because of the lower oxygen in the bottom (Fig. 3). However, it was 43-82% higher in the surface sediment covered by seagrasses due to the higher fresh organic matter contents in the surface, which could provide methylotrophic methanogens with abundant substrates.

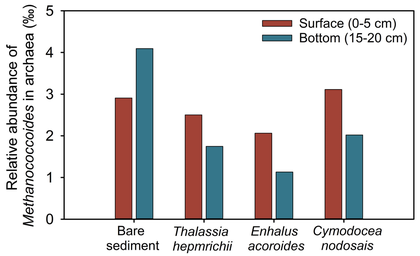

Figure 3. Relative abundance of *methanococcoides* in archaea.

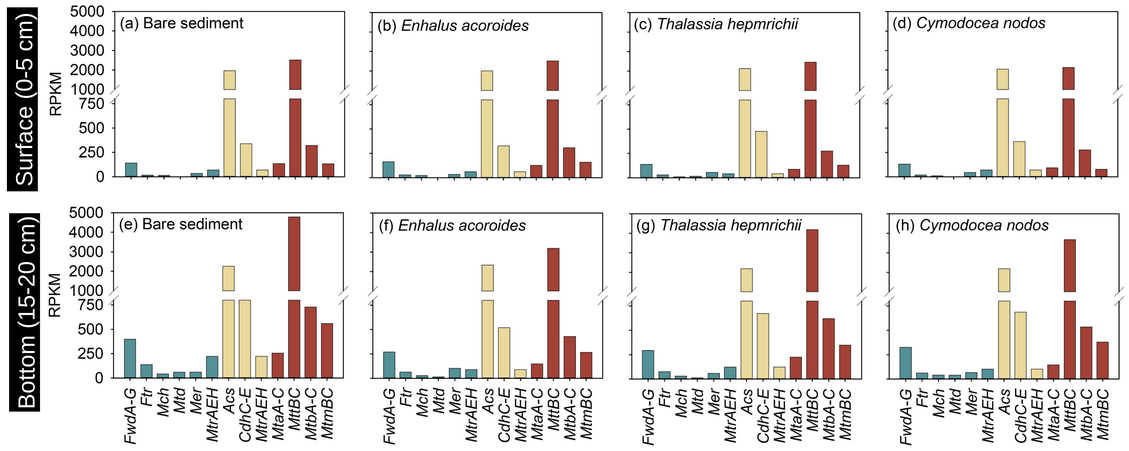

Figure 4. Abundance of genes involved in methanogenic pathways. FRPKM denotes reads per kilobase million. The bule, yellow and red bars denote hydrogenotrophic, acetoclastic and methylotrophic methanogenesis, respectively.

The abundance of genes involved in methylotrophic methanogenesis was greater than that in hydrogenotrophic and acetoclastic methanogenesis (Fig. 4), suggesting that methylotrophic methanogenesis may be dominated in the study area, which validates the results from figure 3 that the *methanococcoides* was the only detected genus. The abundance of genes involved in methanogenesis in the bottom was higher than that in the surface.

Conclusion:

- Our work reveals the importance of methylotrophic methanogenesis in seagrass meadows. The methane production in the sediment of the seagrass meadows was dominated by methylotrophic methanogenesis.
- The distribution of *methanococcoides* was influenced by oxygen contents in bare sediment and the availability of the substrates in the sediment covered by seagrasses.
- We have a better understanding of the methanogenic mechanism and influence factors of methanogenesis in the seagrass meadows. These findings help to estimate the carbon burial capacity of the seagrass meadows accurately in future studies.

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