

Impact of seasonally recurring hypoxia on biogeochemical sulfur cycles and microbial communities in coastal sediments

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Hypoxia (dissolved $O_2 \leq 2 \text{ mg L}^{-1}$ or $63 \text{ } \mu\text{mol O}_2 \text{ L}^{-1}$) is expanding globally, and drastically affects the ecological and biogeochemical processes. Coastal sediments underlying the hypoxic water column are the dynamic environment where active sulfur cycles in accordance with other elements occur (redox reaction, adsorption/desorption, release/precipitation, etc.). Although it is well known that hypoxia alters ecological and biogeochemical processes in water column, relatively little is known about the impact of hypoxic conditions in the water column on biogeochemical processes and microbial communities in sediments.

We investigated geochemical properties, microbial sulfate reduction rate (SRR), and the benthic bacterial communities at different stages of water-column hypoxia (pre-hypoxia, early-hypoxia, late-hypoxia and post-hypoxia) at Dangdong (DD site) and center of the bay (CB site) in Jinhae Bay, located on the southeast coast of South Korea. During hypoxia, The SRR in surface sediments (0 - 2 cm) in DD (average $682 \text{ nmol cm}^{-3} \text{ d}^{-1}$) and CB sites (average $490 \text{ nmol cm}^{-3} \text{ d}^{-1}$) was 5 and 10 times, respectively, higher than that measured at pre-hypoxia period, which resulted in elevated sulfide accumulation in both sediment sites. Interestingly, sulfide concentrations at DD site remained high (average $323 \text{ } \mu\text{M}$) even under the post-hypoxic (normoxic) condition in water column, whereas the sulfide at CB site substantially decreased (average $9.9 \text{ } \mu\text{M}$), which indicates that there is a time-lag between the water column and sediment due to development of intense hypoxia at DD site.

Molecular microbiological analysis revealed that deltaproteobacterial members (*Desulfobacteraceae* and *Desulfobulbaceae*) were always the key sulfur-reducer in both sites. Meanwhile, shifts in the taxa related to sulfur-oxidizing bacteria (SOB) were observed according to sulfidic conditions. *Thiopfundaceae* (γ -SOB) was abundant in the less sulfidic pre- and early-hypoxia periods. *Sulfurovaceae* (ϵ -SOB) was always abundant in highly sulfidic conditions at both sites. Especially, *Chlorobiaceae* (green sulfur bacteria) predominated in highly sulfidic late- and post-hypoxia periods at DD site. These results suggest that shifts in hypoxic conditions of the water column greatly control sulfur cycles and the composition of diverse SOB in sediments.