Evaluation of sulfate reducing bacteria community composition in a surface sediment of seasonally hypoxic enclosed bay by using *dsr*A and 16S rRNA genes

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Abstract

As decline in dissolved oxygen (DO) concentration of bottom water exerts fundamental impacts on biogeochemical processes that are driven by diverse bacterial populations in aquatic environments, knowledge on the dynamics of bacterial community composition (BCC) in the sediment-water interface is indispensable for the sustainable management and utilization of the ecosystem services. Recently, bacterial community composition (BCC) in surface sediment has been shown to be more responsive to bottom DO conditions than previously thought (Mori et al. 2018, *FEMS Microbiol Ecol*). A combination of 16SrRNA gene sequencing and finger-printing of the ribosomal intergenic transcribed spacer (ITS) regions revealed that relative proportion of gamma-proteobacteria population in the surface sediment tended to increase during oxic conditions, while sulfate reducing delta-proteobacteria (sulfate reducing bacteria; SRB) became predominant during hypoxia in an enclosed bay (Omura Bay). Predominance of SRB under hypoxic condition was well reflected in the buildup of sediment sulfide. We further demonstrated that BCC of the uppermost layers of sediment within 1cm depth (0–5 and 5–10 mm depth) became similar to one another under lower DO condition. In contrast, SRB community structure assessed by using another finger printing method (i.e., T-RFLP) of the dissimilatory sulfite reductase (dsrA) gene, significantly differed between the two sediment layers regardless of the DO levels (Mori et al. 2018, *Microbes Environ*). The result, however, could be substantially skewed due to a lack of consistent resolution across the finger printing methods. The two contrasting results prompted us to further perform amplicon sequencing of the bacterial 16Sr RNA gene for the surface sediment layers for two consecutive years (2012–2013). Amplicon sequence variants (ASVs) generated from the sequence results were assigned to known families of SRB. Relative abundance of ASVs from Sva0081_sediment_group (Desulfobacteraceae) contributed most to the total ASVs in the sediment layers across the sampling months. No significant shift in the SRB community was observed between normoxic and hypoxic periods, while it was significantly different between two layers. On the other hand, the relative abundance of ASVs from *Desulfobacter* drastically increased under anoxic condition. These results demonstrated that (1) the predominant SRB in the surface sediment of Omura Bay were made up of a group of bacteria ubiquitous in marine sediment and (2) were shaped in depth-related manner.