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Microbial community shift under exposure of dredged sediments from a tropical eutrophic bay

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Microbial communities occur in almost every habitat. To evaluate the homeostasis disruption of in situ microbiomes, dredged sediments from Guanabara Bay-Brazil (GB) were mixed with sediments outside the bay (D) in three different proportions (25%, 50% and 75%) which we called GBD25, GBD50 and GBD75. Grain size, TOC and metals -as indicators of complex contamination;- dehydrogenase (DHA) and esterases enzymes (EST) – as indicators of microbial community availability, were determined. Microbial community composition was addressed by amplifying the 16S rRNA gene for DGGE analysis and sequencing using MiSeq platform (Illumina). We applied the Quality Ratio index (QR) to the GB, D and every GBD mixture to integrate geochemical parameters with our microbiome data. QR indicated high environmental risk for GB and every GBD mixture; and low risk for D. The community shifted from aerobic to anaerobic profile, consistent with the characteristics of GB. Sample D was dominated by JTB255 marine benthic group, related to low impacted areas. Milano-WF1B-44 was the most representative of GB, often found in anaerobic and sulfur enriched environments. In GBD, the denitrifying sulfur-oxidizing bacteria, *Sulfurovum*, was the most representative, typically found in suboxic or anoxic niches. The canonical correspondence analysis was able to explain 60% of the community composition variation and exhibit the decrease of environmental quality as the contamination increases. Physiological and taxonomic shifts of the microbial assemblage in sediments was inferred by QR, which was suitable to determinate sediment risk. The study produced sufficient information to improve dredging plan and management.