



Microbial community structure associated with submarine groundwater discharge in northern Java (Indonesia)

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Fresh submarine groundwater discharge (FSGD) is an important pathway for nutrients and other forms of pollutants from land to the ocean. Microbial communities in SGD may have an effect on sediments and coastal waters. In this study, we examined microbial community composition along the hydrological continuum of a SGD site in an urban tropical area in Indonesia.

Microbial communities in coastal water were clustered according to salinity. The bacterial taxa *Novosphingobium*, *Flavobacterium* and *Burkholderiaceae* were predominantly found in low salinity samples, including those from terrestrial groundwater and brackish SGD, while cyanobacteria of the genus *Synechococcus* CC9902 were indicative of saline SGD and seawater samples. The microbial community composition of each sample pointed towards a mixture of shallow and deep groundwater contribution into the SGD sites, as well as a high influence of seawater recirculation. Ammonia oxidation and denitrification likely were the dominant biochemical processes occurring along the SGD pathway based on the taxonomic composition of the microbial community. The identification of fecal and potentially pathogenic bacteria along the land-ocean interface also suggested biological contamination from anthropogenic activities.

Results from this study suggest that groundwater and coastal pore water were related based on their microbial community composition and it supports previous findings regarding the occurrence of fresh SGD in the area. Furthermore, microbial analyses in SGD studies can determine the quality of SGD; thus, it could be a useful tool for environmental policy makers in formulating water management strategies in coastal areas.