

Vertical Profiles of Microbial Communities along a Salinity Gradient in a Coastal Aquifer Subject to Seawater Intrusion

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In aquifers subject to saline water intrusion, the mixing zone between freshwater and saltwater shows distinct physico-chemical characteristics. Although the microbial components of these specific environments has been largely disregarded, the contribution of microorganisms to biogeochemical reactions impacting water geochemistry has previously been considered. Here we characterize and compare bacteria community diversity and composition along a vertical saline gradient in a coastal aquifer using high-throughput sequencing of 16S rRNA genes. At different depths of the mixing zone, unique geochemical and hydrological conditions were associated with indigenous bacterial communities harboring clearly distinct structures. While *Proteobacteria* was highly identified in freshwater samples, a greater portion of the phylum *Firmicutes* was predominantly observed in high saltwater samples. The mixing zone shows complexed bacterial composition compare with freshwater and saltwater. Interestingly, above region of mixing zone observed similar bacterial compositions with saltwater than freshwater. In addition, we identified 920 shared operational taxonomic units (OTUs) with mixing zone, among which the freshwater sample shared greater number of bacterial species with mixing zone (90.8%). In contrast, saltwater sample only shared 11.3% of OTUs with mixing zone. This work presents characterization of bacterial community composition and diversity along a freshwater-saltwater mixing zone in a coastal aquifer. Our results may provide insights in understanding geochemical-hydrological dynamics at coastal areas.

Keywords: microbial diversity, seawater intrusion, coastal aquifer