Seasonal and spatial variations in microbial activity at various phylogenetic resolutions at a groundwater – surface water interface

We investigated the seasonal and spatial variation in activity and density of the metabolically active in situ microbial community (AIMC) at a landfill leachate-impacted groundwater – surface water interface (GSI). A series of AIMC traps were designed and implemented for AIMC sampling and microbial activity and density examinations. Measurements were made not only at the level of bacterial domain but also at the levels of alphaproteobacterial Rhizobiales order and gammaproteobacterial Pseudomonas genus, both of which included a large number of iron-oxidizing bacteria as revealed from previous analysis. Consistently higher microbial activities with less variation in depth were measured in the AIMC traps than in the ambient sediments. Flood disturbance appeared to control AIMC activity distributions at the gradually elevated GSI. The highest AIMC activities were generally obtained from locations closest to the free surface water boundary except during the dry season when microbial activities were similar across the entire GSI. A clone library of AIMC 16S rRNA genes was constructed, and it confirmed the predominant role of the targeted alphaproteobacterial group in AIMC activity and composition. This taxon constituted 2%–14% of all bacteria with similar activity distribution profiles. The Pseudomonas group occupied only 0.1‰–0.5‰ of the total bacterial density, but its activity was 27 times higher than the bacterial average. Of the 16S rRNA sequences in the AIMC clone library, 7.5% were phylogenetically related to putative IOB, supporting the occurrence and persistence of active microbial iron oxidation across the studied iron-rich GSI ecosystem.