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Chlorobenzene biodegradation under consecutive aerobic-anaerobic conditions

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Abstract:

The biodegradation of monochlorobenzene, the main contaminant in a quaternary aquifer at Bitterfeld, Central Germany, was studied in microcosm experiments employing either original groundwater or defined mineral media together with the indigenous microbial community from the polluted site. The impact of consecutive aerobic–anaerobic–aerobic incubations on monochlorobenzene biodegradation, microbial diversity, and pH development was examined. The related changes in microbial community composition were analyzed by 16S rRNA gene-based single-strand conformation polymorphism (SSCP) fingerprints and sequencing of dominant bands and by quantitative analysis of bacterial respiratory chain quinones as biomarkers. Under aerobic conditions, the indigenous microbial community of the groundwater degraded monochlorobenzene mainly via the modified ortho-pathway. Respiratory chain quinones and SSCP analysis suggested dominance of the genera *Acidovorax* and *Pseudomonas*. A shift to anoxic conditions resulted in monochlorobenzene biotransformation but no dechlorination. The ability to degrade monochlorobenzene aerobically remained preserved throughout a fortnightly anoxic period at sufficiently high buffer capacity. Acidification, caused by monochlorobenzene biodegradation, was alkalinity-controlled. At low initial alkalinity a substantial decrease in pH, monochlorobenzene degradation, and total counts of live cells, accompanied by a change of the microbial community composition, was observed.

Key-words: Chlorobenzene biodegradation, dechlorination, microbial diversity, alkalinity, groundwater aeration, optode principle