

Spatial and Seasonal Trends for Microbial Community Structure and Biomass across a Pollutant Gradient in the Western Basin of Lake Erie

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Abstract

The relationship between sedimentary microorganisms and lipophilic pollutants is complex in that many pollutants can serve as a resource at moderate concentrations but are toxic at higher concentrations. The western basin of Lake Erie has a natural pollutant gradient due to sedimentation patterns from the Detroit and Maumee Rivers with polychlorinated biphenyl (PCB) and polycyclic aromatic hydrocarbon (PAH) concentrations increasing northward toward Canada. Three stations were established along the gradient to elucidate the response of microbial communities to changing pollutant concentrations: low (PCB 36.83 ± 14.56 ng gdw⁻¹, PAH 1.14 ± 0.39 µg gdw⁻¹), intermediate (PCB 63.96 ± 4.06 ng gdw⁻¹, PAH 1.62 ± 0.16 µg gdw⁻¹) and high (PCB 135.23 ± 59.52 ng gdw⁻¹, PAH 3.25 ± 0.60 µg gdw⁻¹). Sediment samples were collected in May, July and September by SCUBA-assisted divers. Sediment samples collected in September were taken from within and between *Dreissenid* mussel beds (zebra and quagga mussels) to compare differences in microbial biomass and community structure as well as pollutant concentration. Sediment samples were extracted for microbial lipids, PCBs and PAHs using the modified, Bligh and Dyer lipid extraction. Microbial community structure was analyzed using phospholipid fatty acid analysis and pollutants by mass spectroscopy. Microbial biomass showed a trend of greater biomass at the low pollutant concentration station compared to the high pollution concentration station in May and July, with low and high pollutant stations having comparable microbial biomass in September. Microbial biomass was significantly higher between mussel beds compared to within beds at the low and high pollutant stations with no detectable difference at the intermediate pollutant station. Microbial community structure, analyzed using principal component analysis, showed a seasonal pattern with changes in dominance between phototrophic microeukaryotes and heterotrophic prokaryotes dependent on sampling date and independent of pollutant concentration. Stations showed significant differences in sediment surface areas; these changes did not correlate with microbial biomass, community structure or pollutant concentration. Once seasonal variation in community structure was removed, changes in microbial community structure correlated with pollutant concentration. Two marker fatty acids (i17:0 and a17:0; associated with gram-positive and anaerobic gram-negative bacteria) were enriched with increasing PCB and PAH concentration. These findings indicate that

bacterial communities in Lake Erie sediments respond to pollutants and the presence of mussels within the sediments. This research is dependent upon SCUBA-based sediment collection techniques which facilitate the analysis of spatial affects on microbial communities in Lake Erie sediments.