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APPLICATION OF HIGH-DENSITY OLIGONUCLEOTIDE MICROARRAYS TO THE STUDY OF *CRENARCHAEOTA* COMMUNITY STRUCTURE AND DYNAMICS IN AN AERATED ACTIVATED SLUDGE WASTEWATER TREATMENT PLANT

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Despite the fact that biological wastewater treatment is practiced widely to remove organics, nutrients, toxics, and pathogens from polluted water, little is known about the ecology of microbial communities in bioreactors. In particular, the prevalence, diversity, functional importance, and population dynamics of nonthermophilic *Crenarchaeota* in aerated activated sludge wastewater treatment systems remain virtually unknown. The aim of this study was to elucidate the diversity and dynamics of nonthermophilic *Crenarchaeota* in aerated activated sludge systems and to link these dynamics to operational or environmental parameters. To this end, we used high-density 16S rDNA phylogenetic microarrays containing 500,000 probes to monitor bacterial and archaeal population dynamics in monthly samples from the aeration basin of a local municipal activated sludge wastewater treatment plant (WWTP) for a period of one year. Operational data were collected concurrently. Our results revealed a highly diverse prokaryotic community in the WWTP, with an average of 1606 bacterial and archaeal phylotypes detected at each sampling point. Eleven distinct and highly dynamic nonthermophilic *Crenarchaeota* phylotypes from groups 1.1a and 1.1b were detected in 11 of the 12 months examined. Within each *Crenarchaeal* phylotype, 16S rRNA gene copy number varied by nearly an order of magnitude during the study period. Seven main covarying archaeal response groups in this time period were identified based on hierarchical clustering. The majority of the identified nonthermophilic *Crenarchaeota* phylotypes fell within the same response group, indicating significant covariation in population size among these phylotypes during the year of sampling. Our results suggest that nonthermophilic *Crenarchaeota* may play a previously unrecognized role in aerated activated sludge bioreactors. To our knowledge, this is the first application of high-density phylogenetic DNA microarray methods to the analysis of microbial community structure in activated sludge bioreactors.

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