

**Development of Functional Gene Arrays
for Analysis of Microbial Communities in Natural Environments**

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While microarrays are proven tools for whole-genome expression analysis, the technology has not been systematically tested for microbial community studies using diverse environmental samples. To assess the potential of array-based methods for monitoring bacterial populations, DNA microarrays were constructed using selected genes involved in nitrogen cycling: heme- and copper-containing nitrite reductase genes (*nirS* and *nirK*, respectively) and ammonia monooxygenase (*amoA*)-like genes from pure cultures and those cloned from marine sediments. Microarray fabrication and hybridization were optimized in terms of fluorescence intensity by evaluating different glass slides, DNA deposition buffers, rehydration and denaturation times, and probe concentrations. Specific hybridizations were obtained for the different target genes at high stringency (65°C). The limit of detection was approximately 1 ng with pure genomic DNA and 25 ng with soil community DNA. A strong linear quantitative relationship was observed between signal intensity and target DNA concentration within a range of 1 to 100 ng. However, sequence divergence and probe size had significant effects on hybridization intensity. The applicability of functional gene arrays for microbial community analysis was demonstrated by specifically measuring the distribution of *nir* and *amoA* genes present in marine sediment and surface soil environments. Our results show that microarrays can be used as specific, sensitive, quantitative, and parallel tools for characterizing microbial community composition and structure in natural environments.

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