

Microarray-Based Method for Representative, Sensitive and Quantitative Detection and Analysis of Microbial Genomes in Microbial Communities

Disclosure Number

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Technology Summary

The subject invention disclosed herein is a method for monitoring microbial community activities in natural environments. The method of the subject invention utilizes a rolling-circle amplification (RCA)-assisted microarray-based hybridization method for representative, sensitive and quantitative detection of microbial genomes in a microbial community. In the present invention, a microbial community is defined as any assemblage of more than two microbial species or strains. The method of the subject invention is rapid and can simultaneously generate information on many of the microbial members of a microbial community. A unique feature of the subject invention is that whole microbial community DNAs are randomly amplified by DNA polymerases and then detected by microarray hybridization. This avoids the problem that individual gene-based PCR amplification methods are incompatible with the high throughput genome-wide microarray hybridization methods. The method of the subject invention uses a modified buffer for significantly improved detection sensitivity and representation. Results obtained have shown that the whole microbial community is amplified representatively and quantitatively within a wide range of DNA template concentrations. Applications of the method of the subject invention to groundwater samples contaminated with uranium and other metals indicate that this technology is very powerful for analyzing and monitoring the structure and composition of microbial communities. A key advantage of this method is that it permits the analysis of the structure and composition of microbial communities whose members would not be detected by using conventional microarray-based technology. The RCA-assisted microarray-based hybridization method of the subject invention is important for addressing questions concerning microbial communities associated with human health, plant, animal health, forestry, oceanography, fisheries, ecology, biodiversity discovery and management (e.g., pharmaceutical discovery), bioprocessing of industrial products, waste-water treatment, water and food safety and bioremediation of metal and radioactive contaminants, because microbial communities play important roles in each of these areas.

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