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A DGGE-Based E. coli Community Profiling Method for Bacterial Source Tracking

Current bacterial source tracking methods are limited in their ability to match polluted sinks with potential sources. Our overall aim is to develop an *E. coli* community fingerprinting method that can differentiate and match among such sources and sinks. Therefore, this study aimed to (i) assess the environmental distribution of genes that detect *E. coli*, (ii) test the sensitivity of these genes, (iii) identify the gene that provided the best fingerprint-based differentiation of *E. coli* communities, and (iv) test the method on a lake with a defined source of bacterial pollution.

The distribution of 13 gene fragments (23S rRNA, *gadAB*, *lacZ*, *lamB*, *uidR*, *mdh, phoE*, 2 fragments of 16S rRNA and 4 of *uidA*) was assessed by PCR on 176 environmental *E. coli* isolates. The sensitivity of these fragments was determined by PCR following serial dilution of *E. coli* cultures. Each gene fragment was screened with DGGE for its ability to differentiate (i) artificial *E. coli* assemblages (generated by combining DNA from eight *E. coli* isolates determined to be different by BOX-PCR), and (ii) total *E. coli* communities grown from animal fecal material.

PCR detection of the 13 gene fragments showed that all fragments were 100% distributed among the *E. coli* isolates except for one of the *uidA*- (97.1%) and *16S* fragments (95.4%). Three fragments of *uidA* and the *16S* rRNA gene provided the lowest detection limit (10^2 *E. coli* cells) in pure cultures. Cluster analysis of DGGE fingerprints showed that *lacZ, phoE* and one *uidA* gene fragment most effectively differentiated mixed *E. coli* communities and indicated the ability of these three gene fragments to match pollution sinks to potential sources.

In conclusion, when distribution, sensitivity and differentiation were collectively considered a fragment of the *uidA* gene was the most appropriate target for *E. coli* community characterization.

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