SCCWRP #0728

Community analysis-based methods

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ABSTRACT

Microbial communities are each a composite of populations whose presence and relative abundance in water or other environmental samples are a direct manifestation of environmental conditions, including the introduction of microbe-rich fecal material and factors promoting persistence of the microbes therein. As shown by culture-independent methods, different animal-host fecal microbial communities are distinctive, suggesting that their community profiles can be used to differentiate fecal samples and to potentially reveal the presence of host fecal material in environmental waters. Cross-comparisons of microbial communities from different hosts also reveal relative abundances of genetic groups that can be used to distinguish sources. In increasing order of their information richness, several community analysis methods hold promise for MST applications: phospholipid fatty acid (PLFA) analysis, denaturing gradient gel electrophoresis (DGGE), terminal restriction fragment length polymorphism (TRFLP), cloning/sequencing, and PhyloChip. Specific case studies involving TRFLP and PhyloChip approaches demonstrate the ability of community-based analyses of contaminated waters to confirm a diagnosis of water quality based on host-specific marker(s). The success of community-based MST for comprehensively confirming fecal sources relies extensively upon using appropriate multivariate statistical approaches. While community-based MST is still under evaluation and development as a primary diagnostic tool, results presented herein demonstrate its promise. Coupled with its inherently comprehensive ability to capture an unprecedented amount of microbiological data that is relevant to water quality, the tools for microbial community analysis are increasingly accessible, and community-based approaches have unparalleled potential for translation into rapid, perhaps real-time, monitoring platforms.