

Abundance, Dissemination, and Diversity of Escherichia Coli in a Watershed in Northern Michigan

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Contamination of recreational waters with disease-causing microorganisms is a significant, but poorly understood, environmental problem. Effective management of water resources for recreational quality requires improved understanding of the delivery and dissemination of bacteria. An interdisciplinary study, being conducted by a collaboration between the U.S. Geological Survey and Michigan State University, addresses patterns of delivery and dissemination of *Escherichia coli*, a representative enteric bacterium and an indicator of fecal contamination, to surface and ground water in a watershed in northern Michigan. To date, 234 *E. coli* isolates have been collected on three sampling dates (September 1997, May 1998, and October 1998) from 25 surface-water sites within the watershed. Ground water (28 wells) contained no *E. coli*. Isolates have been characterized by DNA fingerprints (rep-PCR profiles), and are being further characterized by patterns of resistance to the antibiotics streptomycin, tetracycline and ampicillin. At each site and date, 15 common water-chemistry parameters (for example, nutrients, major ions, dissolved oxygen) were evaluated. At selected sites and dates, indicator contaminants, such as fecal sterols, caffeine, human drugs, hormones, antibiotics and selected pesticides, have been analyzed. All sites have been mapped and characterized with respect to land-use patterns and other environmental and socioeconomic features using a geographic information system. Preliminary results suggest that on the September and October sampling dates, *E. coli* abundance and rep-PCR patterns were related to the percentage of urban land use at a site as well as to concentrations of chloride, magnesium, and nitrate. These patterns did not occur in May. *E. coli* rep-PCR profiles were very diverse in this watershed, indicating multiple, diffuse sources over short-flow paths and variation in source from day to day. Our results have significant implications for the design of monitoring programs, for modeling of bacterial contamination of recreational waters, and for understanding how to manage watersheds for bacteriological water quality. Models of bacterial contamination of recreational waters that use point sources and in-stream die-off to account for bacterial numbers would not accurately describe our observations. Our data indicate that management of watersheds for bacteriological water quality may require more information than is typically obtained in monitoring programs that simply determine bacterial numbers. Finally, our isolate characterizations provide insight into the genotypic and phenotypic diversity of environmentally-derived *E. coli* and reveal challenges that will be encountered in programs designed to detect specific pathogenic bacteria in recreational waters.

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