
Temporal Variability of *E. coli* Genetic Fingerprints and Microbial Source Tracking

Why Does it matter?

Microbial source tracking (MST) pertains to methods of identifying sources of fecal contamination impacting surface waters. Once a fecal source is identified measures can be taken to correct the problem. This is important in light of the total maximum daily load or TMDL regulations. Libraries of genetic finger prints of *E. coli* from cattle, swine, poultry, and humans have been proposed as a MST tool, but for this tool to be effective the collection of genetic fingerprints must show stability or little change over time.

What was done?



More than 450 *E. coli* were isolated from feces of 6 steers per sampling time at four sampling times over a grazing season. DNA was isolated and genetic fingerprints were developed for each *E.coli* isolate. Genetic fingerprints were analyzed to determine the number of identical fingerprints.

What was found?

Of 451 genetic fingerprints 240 were identified as being distinct. Only 20 of the 240 genetic fingerprints were shared between isolates, and only two of the 20 fingerprints were observed at three of the four sampling times while the remaining 18 shared fingerprints were observed at two sampling times. The implication of this is that a library containing over 1000 distinct fingerprints would be necessary for the library to be effective at identifying environmental *E. coli* isolates. In addition the library would require continuous updating.

What is the impact?

Since the economics of establishing and maintaining a host origin library of *E. coli* fingerprints for one animal source is formidable, our results suggest that this method of microbial source tracking may not be feasible and other methods need to be explored.

Research Team and Contact information

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