

EPI-Net Perspective

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Tracking Microbial Pathogens

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What is Microbial Source Tracking (MST)?

Microbial source tracking (MST) is the use of a suite of methods and experimental protocols to match microorganism in a set of samples to their possible origin. In general, MST is used to help identify sources of fecal contamination in water and sediments, although the approach can be applied to food and other materials that come in contact with microorganisms. MST is useful in helping decision makers to understand contamination dynamics and can be used as part of a “source investigation study”.

Sources of fecal contamination

Fecal contamination in surface waters can be caused by introduction of fecal material from:

- Improperly managed animal production facilities
- Runoff from animal manures applied to land
- Runoff from wastewater treatment land application programs
- Poorly functioning septic tanks
- Wastewater/Combined Sewer Overflow discharging to surface water
- Domestic animals
- Wildlife

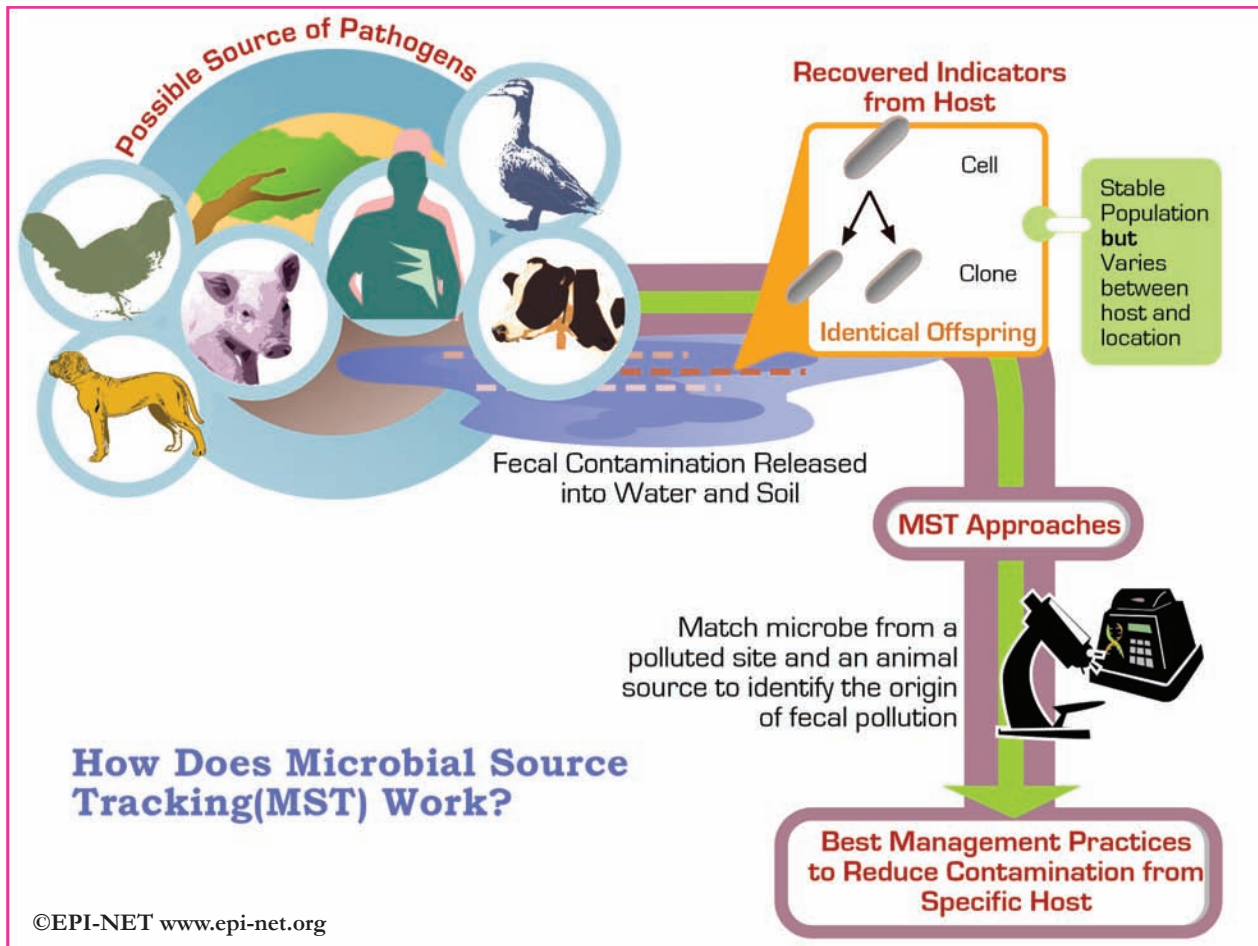
The Microbial Source Tracking Premise

MST is based on the premise that target (contaminant) microorganism found at some

location can be related (using genetic markers) to a specific host found only at one source location. MST utilizes differences in the genotypic and phenotypic patterns between the resident microorganisms (normal flora) and the introduced microorganisms (contaminant) to describe the relationship. Examples of contaminant microorganisms are: *E. coli*, *Enterococcus*, *Bacterioides*, *Bifidobacterium*, protozoa, and viruses.

Assumptions inherent with MST are:

- For a given bacterial species (i.e., *E. coli*), some members have adapted to the specific environmental condition within a host making them “different” and being different they become traceable.
- Fecal bacteria are genetically adapted to their host environment (animal or human track), also making them different from environmental systems or samples.
- Adaptations in the host allows for the development of a traceable population composed of unique groups of clones (organism with the exact genetic information of its antecessor or mother cell), intestinal microbes of animal groups are expected to be different
- Clonal composition of the population remains stable
- Community composition is controlled locally so it represents the location (either the host or the in the environment.) and new members can be identified.



Microbial Source Tracking Methodology

Through the year's scientist have worked on developing methods for MST. These methods are divided in four categories; microbiological methods, phenotypic methods, genotypic methods and chemical methods.

Microbiological Methods

- Fecal coliform/*streptococcus* ratio (FC/FS)
- *Bifidobacterium* spp.
- Human enteric viruses
- Bacteriophage (a virus that attacks bacteria)
 - *Bacteroides fragilis* bacteriophage
 - F+ coliphage

Phenotypic Methods

- Multiple Antibiotic Resistance (MAR)
- Antibiotic Resistance Analysis (ARA)
- Carbon Utilization Pattern (CUP)

Genotypic Methods

- Amplified Fragment length Polymorphism (AFLP)
- Ribotyping
- Pulse Field Gel Electrophoresis (PFGE)
- Repetitive Extragenic Palindromic Element-PCR (rep-PCR)
- Restriction fragment Length Polymorph (RFLP)
- Random Amplified Polymorphic DNA (RAPD)
- Host specific PCR

Chemical Methods

- Caffeine
- Fecal sterols



A document with descriptions of each method will follow.