

Microbial Source Tracking (MST)

MST is the attempt to match a microbe (e.g. bacterium) from a polluted site (e.g. water body) and a known source to suggest the origin of fecal pollution. This can be achieved using a variety of target organisms in either library-dependent or library-independent approaches. The Rose WQEMM laboratory has established protocols for MST projects using bacterial targets such as the evaluation of the putatively human-specific *esp* surface protein marker for *Enterococcus faecium*, and human and bovine markers for *Bacteroides*. The polymerase chain reaction-based MST methods can be extended to other target organisms by adapting the assays as necessary. In turn these protocols can be adapted based on the characteristics of the geographical location of interest e.g. areas dominated by specific breeds of livestock or wildlife. The evolving field of MST requires that the laboratory is able to evaluate and apply new source tracking protocols as they become available, and improve our expertise in the application of new methods.

MST Approaches used by the Rose WQEMM Laboratory

Bacterial

- Putatively human-specific *Enterococcus faecium* surface protein (*esp*) gene
- *alpha mannanase* gene targeted in *Bacteroides thetaiotaomicron*
- 16S rRNA in *Bacteroides* in humans
- *E. coli* (*uid* gene)
- Enterococci (23S rRNA)

Viral

- Human Adenoviruses (F40 and F41)
- Human Enteroviruses
- Norovirus Genotype I and II
- Bovine Enteroviruses (1,2 and 4-8)
- Hepatitis A virus