

**Ethan Berg, Sean Stettner: Cell Biology & Neuroscience, Bioengineering**  
**Mentor: Steve Hamner -- Microbiology**  
***Microbial Source Tracking of Escherichia coli in the Little Big Horn River, Montana***

The method of microbial source tracking was used to determine the source of the gram-negative bacterium *Escherichia coli*. When *E. coli* is isolated from a water source, it indicates a possible public health risk due to fecal contamination of the water. Knowing the source of the *E. coli* can aid in elimination of the contamination. This project was a continuation of an ongoing project that examined *E. coli* isolates from various cattle ranches at various points along the Little Big Horn River and its tributaries in southeast Montana. This experiment used polymerase chain reaction (PCR) coupled with gel electrophoresis to create a database of DNA fingerprints. Multiple primers were to be used originally, however the BOXA1R and (GTG)5 primers displayed far too complex fingerprints for accurate analysis, therefore the ERIC primer set was used as a basis for creating the fingerprint database. That database was created using the GelCompar II software by Applied Maths. Using this software, all fingerprints were compared using a similarity matrix to create a list of possible matches of *E. coli* obtained from the various ranches, the river, and its tributaries. Preliminary results suggest possible matches between some of the manure lots on the largest ranch and various drainage sites into the river. Current work is being done using the BOXA1R and (GTG)5 primers to confirm validity of the matches found by the ERIC primer set.