ABIGAIL O'CONNOR and JAMES WOOD, Dept of Biological Sciences, West Liberty University, West Liberty, WV 26074. Investigation of environmental and land use influence on watershed bacterial contamination using *E. coli* quantification and 16s identification.

Wheeling Creek in the Northern Panhandle of West Virginia was monitored for fecal indicator bacterium *Escherichia coli* (*E. coli*). Since Wheeling Creek is used recreationally, elevated fecal coliform levels pose potential human health risks including gastrointestinal or respiratory illness.

The current study included 12 sites spanning 18 stream km. For each site, weekly or bi-weekly bacteria samples were collected from the water column and water chemistry parameters were recorded. Seasonal trends in bacterial contamination and correlations with site parameters including rainfall, water chemistry, and land use were recorded.

Additionally, monthly water samples from each site were enriched for coliform bacteria, amplified using 16s rRNA primers, and sequenced using Oxford Nanopore's Flongle technology. Metagenomic analysis was used to determine patterns in the microbial community and note correlations between indicator bacteria and pathogens.

Concentration of *E. coli* regularly exceeded the USEPA recommendation of 235 CFU/100 mL at many sites. Two sites averaged over 3,000 CFU/100 mL, while five sites averaged less than 126 CFU/100 mL. Development in the watershed correlated with *E. coli* concentration. Within the water chemistry parameters measured, turbidity, rainfall, pH, and temperature were the best predictors of site-level *E. coli* concentration, while pH, temperature, and percent developed land use were the best predictors of watershed *E. coli* levels. Collectively, these data can elucidate human health risk and inform remediation efforts in the Wheeling Creek watershed.