Abstract for a Poster Presentation given at the 2010 annual meeting of the Association of Southeastern Biologists, UNC-Ashville, NC.

E.R. Tripp, J.Q. Lyerly, M.-K. Liao, and G.P. Lewis. 2010. The impact of urbanization on bacterial community compositions in watersheds of Upstate South Carolina.

Background. Streams draining urban areas have increased nutrients and pollutants and lower macroinvertebrate and fish diversity. However, little is known about the impact of urbanization on bacterial community composition. In this study, we investigated the community compositions of antibioticresistant (ABR) bacteria in Brushy Creek (BC), a stream draining a commercial watershed, South Pacolet River (SPR), a stream draining a residential watershed, and Middle Saluda River (MSR), a stream draining a forested watershed. Additional commercial, residential, and forested samples from watersheds throughout upstate South Carolina were also analyzed. The fecal indicator bacteria concentrations in all samples were determined. Methods. Water samples were filtered through 0.45µm membranes. The diversity of 431 bacterial isolates from different sampling sites was analyzed by the restriction pattern (ImageJ) or the sequences of 16S rRNA genes (BLAST). Fecal indicator bacteria were quantified using IDEXX's Colilert and Enterolert kits. Results. Our data showed that the concentrations of fecal indicator bacteria were greatest in BC, followed by SPR and MSR. Additionally, samples from residential areas throughout upstate South Carolina had greater concentrations of fecal indicator bacteria than those found in samples from commercial areas. There was a greater abundance of ABR bacteria in BC, followed by SPR and MSR. However, there was greater diversity in ABR bacteria in MSR than either BC or SPR. Similar ABR bacterial profiles were seen in commercial, residential, and forested samples throughout the upstate. Conclusion. Our research suggested that urbanization produces increased abundance and decreased diversity in antibiotic-resistant bacterial community.