

2018 Research Week Proposal

Title: A Stream Continuum Analysis of Bacteria Community Assembly in Association with Crayfish and their Symbionts

Program of Study: Biomedical Sciences

Presentation Type: PowerPoint

Mentor Name and Email: Kyle Harris, M.S. (kjharris@liberty.edu)

Student Contributors and Emails:

Kaleb Bohrnstedt (kmbornstedt@liberty.edu)

Matthew Cooke (mmcooke@liberty.edu)

Luke Fischer (lfischer1@liberty.edu)

Thomas Kepler (takepler@liberty.edu)

Category: Applied

Abstract:

Microbial community assemblages have long been understood as key components within freshwater ecosystems (e.g. nutrient cycling). However, patterns of microbial presence and persistence along stream continuums, in relation to specific host organisms, have been understudied. The identification of such patterns may provide additional insight into the dynamics of microbial framework, consequently shaping other community assemblages. One such pattern was observed in a recent lab-based experiment that involved crayfish with and without branchiobdellidan ectosymbionts (Cooke et al., 2017). Microbial 16S genes were isolated and sequenced, revealing that bacterial taxa present on specimens with symbionts were unique from those without symbionts. This current study builds on the previous lab-based experiment by collecting crayfish microbial samples from a local stream. The microbial community assembly on crayfish with and without ectosymbionts was examined to see if similar assembly patterns exist within a physical stream continuum. Ten crayfish and six environmental microbial samples were

obtained from five different collection sites along the length of the Opossum Creek Tributary, using aseptic technique. The bacterial swabs were taken to the lab, and microbial DNA was extracted using a Qiagen Blood and Tissue Kit. Subsequently, qPCR was performed for quantitative analysis of microbial composition and abundance. In the future, PCR will be used for 16s gene amplification. Illumina sequencing will be employed, and the resulting data will be sorted and analyzed using the bioinformatics software QIIME. It is hypothesized that shifts in microbial makeup and community assembly will be observed along the continuum length, not only in the environment (water and substrate), but also on the crayfish. In addition, the community assembly of bacteria is predicted to differ significantly for specimens with ectosymbionts compared to those without.

References:

Cooke, M., Fischer, L., Griffin, T., & Jeffers, S. (2017). Identification of microbiota associated with the ectosymbiotic community structure of the Appalachian Brook Crayfish (*Cambarus bartonii*). DOI: 10.13140/RG.2.2.34798.10563