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Undergraduate Research in Biology I: Understanding Pathogens and their Vectors

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9:00-10:00 AM (ROOM 1310) Undergraduate Research in Biology I Understanding Pathogens and their Vectors Chair: Dr. Dayle Daines, Department of Biological Sciences

Habitat preferences of Ixodes scapularis at Hoffler Creek Wildlife Preserve, Portsmouth, Virginia By Leo Notto (Mentor: Dr. Holly Gaff)

Within Virginia, the main vector of *Borrelia burgdorferi*, causative agent of Lyme disease, is the tick species *Ixodes scapularis*. In order to provide better recommendations to wildlife managers and outdoor enthusiast on how to avoid contact with this tick species we need to understand its habitat preferences. To study the habitat of *I. scapularis* we documented variations in plant communities, and distributions of the tick species along two 200-meter transects, on a biweekly basis, at Hoffler Creek Wildlife Preserve in Portsmouth, VA, between October and November. The goal of our study is to reduce human exposure to *I. scapularis*.

Microclimate Variation in Southeastern Virginia

By Tyler Chavers (Mentor: Dr. Holly Gaff)

Ticks are one of many vectors that transmit diseases worldwide. Unlike other vectors, they have the ability to live for long durations both on and off a host. Their extended lifespan allows tick-borne diseases to persist year after year. These vectors reside in ground vegetation and leaf litter when searching for hosts. A fundamental understanding of these microhabitats can improve our approaches to tick surveillance. A pilot study was performed in the summer of 2014 to survey known tick environments in the southeastern Virginia region. These transects were observed for microclimate conditions, including temperature, relative humidity, and soil pH. This survey allowed us to compare each transect for variation, which may correspond to differing vector levels among sites. The results indicated a slight variation of temperature, a significant variation of relative humidity, and overall slightly acidic soil conditions.

A new in cis complementation system for nontypeable Haemophilus influenzae (NTHi)

By Amarilis Dyer (Mentor: Dr. Dayle Daines)

The use of a plasmid to complement a genetic deletion results in multiple copies of the gene *in trans*. The biological relevance of this practice is questionable. The objective of this project was to design and construct a targeted system for chromosomal *in cis*-complementation of NTHi deletion strains. To accomplish this, we used a gene encoding green fluorescent protein, *gfpmut2*, as the reporter for successful insertion into the NTHi genome. Our results indicate that this system will facilitate *in cis* complementation of genetic mutants in a number of clinical isolates.