Lyme disease is rapidly expanding and is of a great public health concern in the United States. The emergence of Lyme disease is the consequence of a confluence of the causative agent, *Borrelia burgdorferi*, *Ixodes* tick vectors, hosts, and the ecological and climatic conditions supporting tick and host populations. The complexity of Lyme disease transmission impedes our ability to predict its migration patterns and areas of high risk. This study was conducted at the index sites where established populations of blacklegged ticks (*Ixodes scapularis*) were first identified in Ohio to investigate the current infection prevalence of *B. burgdorferi* sensu lato, *B. burgdorferi* sensu stricto, and *B. mayonii* in questing blacklegged ticks and small mammals. Multi-locus sequence typing (MLST) analysis was performed to find the diversity of Ohio *B. burgdorferi* sensu stricto strains related to the reported strains in other regions in the public databases for molecular typing and microbial genome diversity (PubMLST.org). Pathogen-tick-host relationships of the Ohio small mammal community were also studied by trapping a variety of host species during peak tick activity and assessing tick burden. My research indicates the current infection prevalence, strain diversity, and small mammal host ecology of *Borrelia* in Ohio.

Advisor: Dr. Risa Pesapane

**TUESDAY, APRIL 12, 2022**
**10:00 A.M. - 12:30 P.M.**

**Join the seminar via Zoom:**
https://osu.zoom.us/j/92891649580?pwd=MlITRmdSR2xneXpnNW0rWHFSbTBMZz09
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