

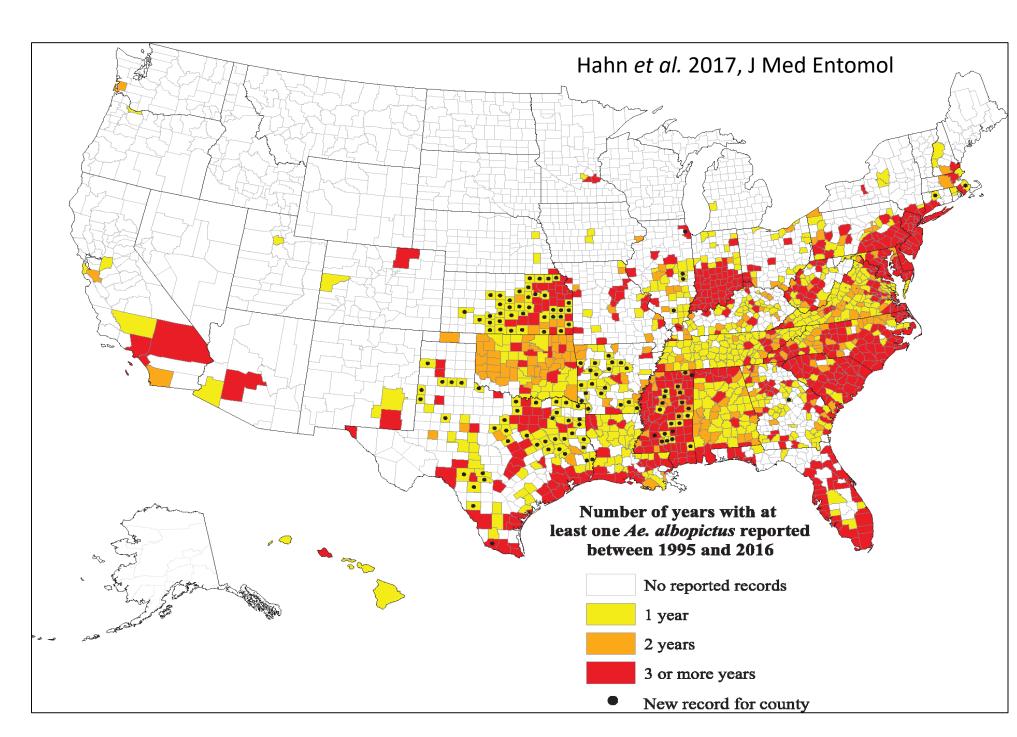
NC STATE UNIVERSITY

Introduction

Urban ecosystems can facilitate all stages of the invasion process. Landscape genetics reveal how anthropogenic features drive dispersal in invasive populations. Here, I explore the impact of urban landscape features on genetic connectivity in the highly invasive Asian tiger mosquito Aedes albopictus.

What landscape features are important for genetic connectivity?





Methods

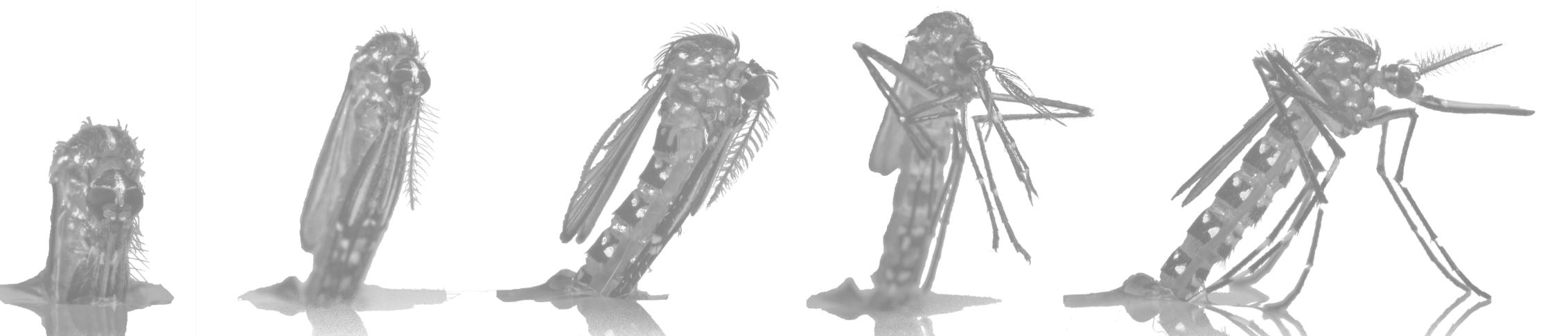
- Location: Wake County, North Carolina (2016)
- Collection: 15 sites using egg traps. Example site (A), egg trap (B) , and egg paper with mosquito eggs (C & D).



Sequencing: 192 individuals using ddRADseq

•Resistance Surfaces: National Land Cover Database classifications, streets, impervious surfaces, and contiguous suburbs

•Analysis: Calculated least cost paths to test whether any of these features explained genetic variation using Mantel tests.



Aedes albopictus is important to the SE United States, as this is the region of initial introduction in the 1980s and the source of subsequent spread north- and westward

Landscape genetic tools can be used to identify habitat corridors and understand how invasive species are affected by land use

Emily MX Reed & Martha Burford Reiskind Department of Biological Sciences, North Carolina State University

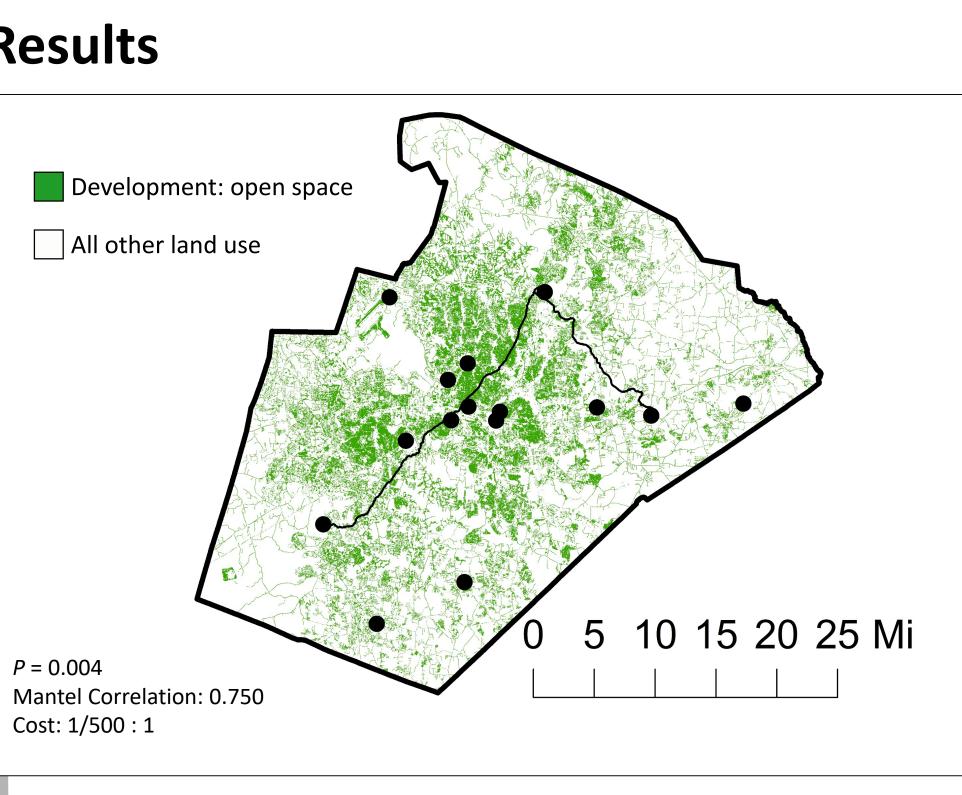
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SECASC Science Priorities

1: Exposure. My research demonstrates how genetics can be used as a method to *identify habitat corridors*, especially in highly fragmented and urban environments. **2: Impacts.** One of the opportunities of Science Priority 2 is to understand how invasive species are affected by land use, which closely aligns to my project goals.

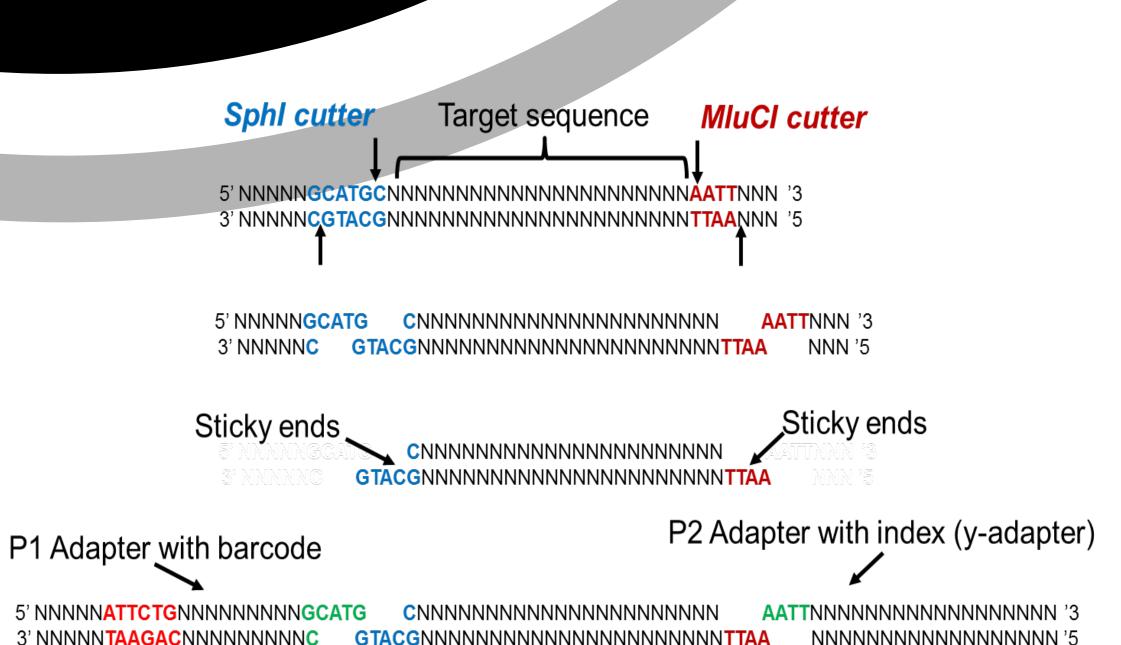
3: Adaptation. One of the greatest advantages of landscape genetics is that it is *multi-scalable*. These techniques can be applied to different scales depending on the needs of the stakeholder and the ecology of the species.

Results



P = 0.028Cost: 100 : 1

I identified 1067 unique SNPs used in subsequent analyses. Using Nei'sD, I identified developed open spaces (mostly vegetated lawns, parks, & golf courses) facilitated gene flow (top), while impervious surfaces acted barriers to gene flow (bottom).



Double digest RAD sequencing method. Genetic and genomic techniques allow us to investigate dispersal in hard or hard-to-track organisms.

