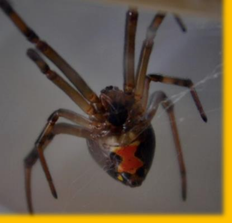

DNA methylation in Black Widow Spiders: The Epigenome of An Urban Pest

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Introduction

- Urbanization alters community structure and challenges organisms to respond to new conditions [1].
- DNA methylation alters genetic codes, which plays a role in stress response, development, and adaptation [2].
- DNA methylation patterns may explain why some species tolerate urban disturbance [3].
- Western Black Widow spiders (*Latrodectus hesperus*) are a pest species of medical importance often forming dense urban infestations [4].
- **We hypothesize urbanization triggers DNA methylation variation ("epimutations"). We predict spiders collected from urban habitats will display heightened methylation.**

Methods

- N=3 adult female spiders were collected from both urban and desert populations.
- These 6 spiders were weighed (mg) in the field and immediately frozen at –80 °C.
- Oxford Nanopore long-read sequencing will quantify genome-wide methylation patterns from the cephalothorax.

Preliminary Results

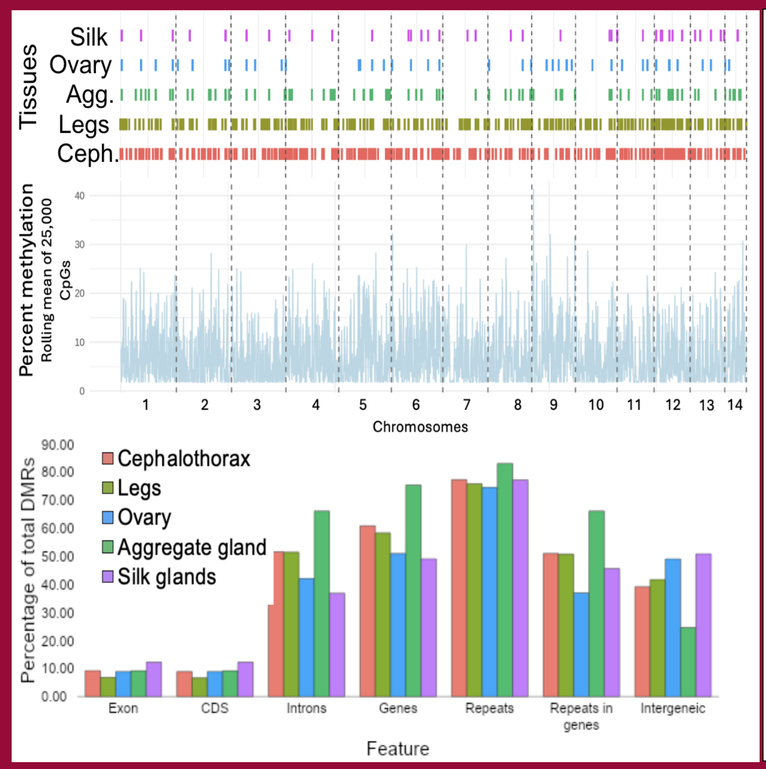

Figure 1. Whole genome methylation and tissue-specific DMR. Overall, methylation is low (3-7%). There is differential methylation regions (DMR) across tissue types. The differentially methylated regions disproportionately occur in repetitive regions of the genome and introns compared to coding regions of the genome.

Future Directions

- Ultimately, we will sample at least 10 spiders from each habitat, representing at least 3 different collection sites within each habitat.
- We will compare methylation across development and sexes.
- We will manipulate urban heat island stress in the lab to explore if that specific urban stressor heightens methylation.

Literature Cited

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