Characterization of the Internal Microbiome of a Lab-Reared Urban Arthropod Pest, the Western Black Widow Spider

Hasti Asrari[1], Juan Maldonado Ortiz[2], Keaton Coker[1], Todd Sandrin[1], and J. Chadwick Johnson[1]
[1]School of Mathematical and Natural Sciences, Arizona State University, Glendale, AZ 85304
[2]Genomics Core, Biodesign Institute, Arizona State University, Tempe, AZ 85281

INTRODUCTION

- What mechanisms make organisms thrive in cities?
- Black widow spiders are a medically-important pest of the Western U.S. where they form urban infestations.
- The microbiome of this spider species has been relatively unstudied.
- We predict that lab-reared widows will have highly similar microbiome compositions across the sample batch due to controlled rearing conditions.

METHODOLOGY

- We selected 4 F2 lineage sub-adult spiders, lab-reared for preliminary analysis.
  - Whole spiders were stored at -80℃, preserved in SSC buffer prior to microbiome sample prep.
- Whole lab-reared spiders were surfaced washed with SSC buffer and homogenized with sterile motorized pestles.
- DNA was extracted using Qiagen's PowerSoil Pro Kit and PCR amplified with bacterial V4 region primers.
- 16s rRNA gene sequencing was performed using an Illumina MiSeq instrument and the data was processed with the QIIME2 bioinformatics tool for microbial community analyses.

REFERENCES

[1] Trubl, Patricia and J. C. Johnson. *Journal of Arid Environments* 163 (2019): 18-25
[2] Sugden, S., Sanderson, D., Ford, K. et al. *Sci Rep* 10, 22207 (2020).
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Figure 1. Unfiltered bar plot of the relative frequencies of specific bacterial taxa in 4 lab-reared black widow spiders.

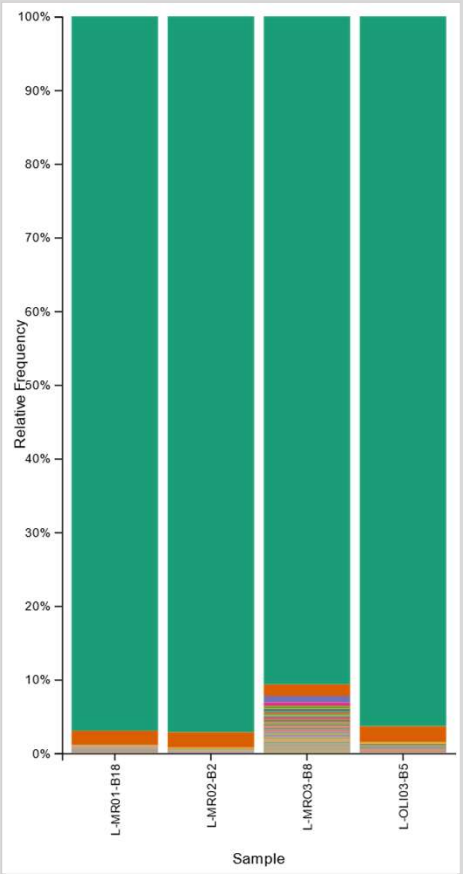
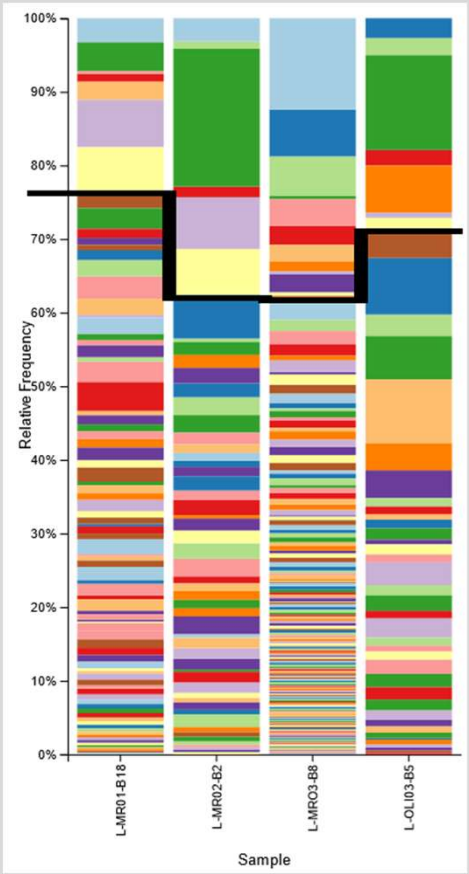


Figure 2. Bar plot of the relative frequencies of bacterial taxa in 4 lab-reared black widow spiders, filtered for those minimally identified at the genus level.



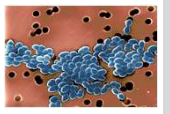
		Taxonomy: Lowest Known Rank	Approx. Frequency (%)	Functional Characteristics
Figure 1.		k_Bacteria; ?	96%	~~~
		k_Bacteria; p_Firmicutes; ?	2%	~~~
Figure 2.		*Blautia*	0.88%	Liu et. al. (2021): Probiotic properties
		Bacteriodes	0.45%	Significant gut anaerobic pathogen
		Faecalibacterium prausnitzii	0.38%	Promotes good gut health; biomarker
		Enterococcus	0.16%	Normally gut commensal; linked to infections
		Prevotella copri	0.26%	Enriched in those with Rheumatoid Arthritis
		Coprococcus	0.18%	Butyrate-producing bacterium in feces
		Clostridium clostridioforme	0.16%	~~~
		f_Lachnospiraceae; *g_ ; s_*	0.10%	~~~
		o_Bacteroidales; f_ *; g_ ; s_*	0.07%	~~~
		Bifidobacterium adolescentis	0.18%	Linked to gut-brain axis interactions
		Pseudomonas stutzeri	0.06%	Found in many different environments

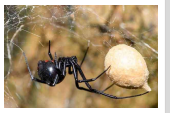
RESULTS

- A high frequency of bacterial taxa are of unknown origin, identified as k__Bacteria.
  - Greengenes 99% OTUs (V4 region bound by the 515F/806R primer pair) classifier.
  - NCBI BLAST: Uncultured Prokaryotic Clone (83.54% Identity) Mycoplasma sp. (81.48% Identity)
- There is high individual variation between all four lab-reared spiders, some microbes more abundant than others but similarly present amongst all samples.
- Microbiome *diversity* differs between the F2 generation widows genetically originated from two separate sites.
- Microbial taxa identified as beneficial gut bacteria in humans are also present in widows.

FUTURE DIRECTIONS

- We expect differences between urban, desert, and controlled lab habitats to produce microbiome differences in the next dataset.
  - Goal: Identify the mechanisms that shape traits favoring urban winners.
  - Looking at urban spiders may reinforce the view that cities are complex, spatially dynamic ecosystems, especially as urban widows have extensive nutrient variation [1].
- Internal microbiome comparison attempts to identify the role diet and environment play, like previous studies with coyotes [2].
- Future studies will ask how spider behavior (e.g. cannibalism) shapes the microbiome, which may then shape future behavior.
- More generally, we hope to disentangle the functional importance of microbes in living organisms (e.g., metabolizing vitamins essential for reproductive success [3]).





ACKNOWLEDGEMENTS

This work is supported by the National Science Foundation under Grant No. DEB-1832016, Central Arizona-Phoenix Long-Term Ecological Research Program (CAP-LTER). Additional funding for this project was provided by Barrett, The Honors College and the NCUIRE program at Arizona State University. I am honored to acknowledge Ryan Clark for assisting in desert widow collection and the members of the Johnson lab for their support and input throughout this work.