



Microbiome of Spider Abdomens

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Abstract

Microbial communities within three separate species of arachnids were closely examined. It was expected that arachnids of the same species would possess many of the same microbiota and could then be grouped together when data is displayed. Samples were collected, identified, and DNA was isolated. Microbial communities were determined using 16s rDNA. It was found that species 1 and 3 had some of the same distinct bacteria not found within species 2. Species 1 and 3 were collected from the same location, suggesting that location may play a bigger factor than initially considered when it comes to microbial makeup of arachnids.



Introduction

- Research of insect diversity based on microbiota present is a topic of increasing interest as the roles of microbiota are crucial to the development and livelihood of many organisms. The roles of microbiota include regulation of metabolic pathway, protection from parasites and pathogens, modulation of immune responses, communication, and more (Engel et. al, 2013).
- One study recorded the bacterial diversity within eight different species of spiders. It was reported that similarities between bacterial communities were far more common in spiders of the same species than those not of the same species. Endosymbionts and other bacteria were detected. This study was the first like it to be done on multiple species of arachnids (Zhang et. al, 2018).
- Since the insect microbiome is less diverse than the mammalian microbiome, insect microbial species are more easily identifiable. Also, since insect microbiome analysis is much more feasible than mammalian microbiome analysis, results gathered can be used as the basis for various hypotheses which concern mammals as well (Douglas, 2012).

Research Aim: *Uncover the correlation between species of spiders and the types of microbiota present within their abdominal regions.*

Results

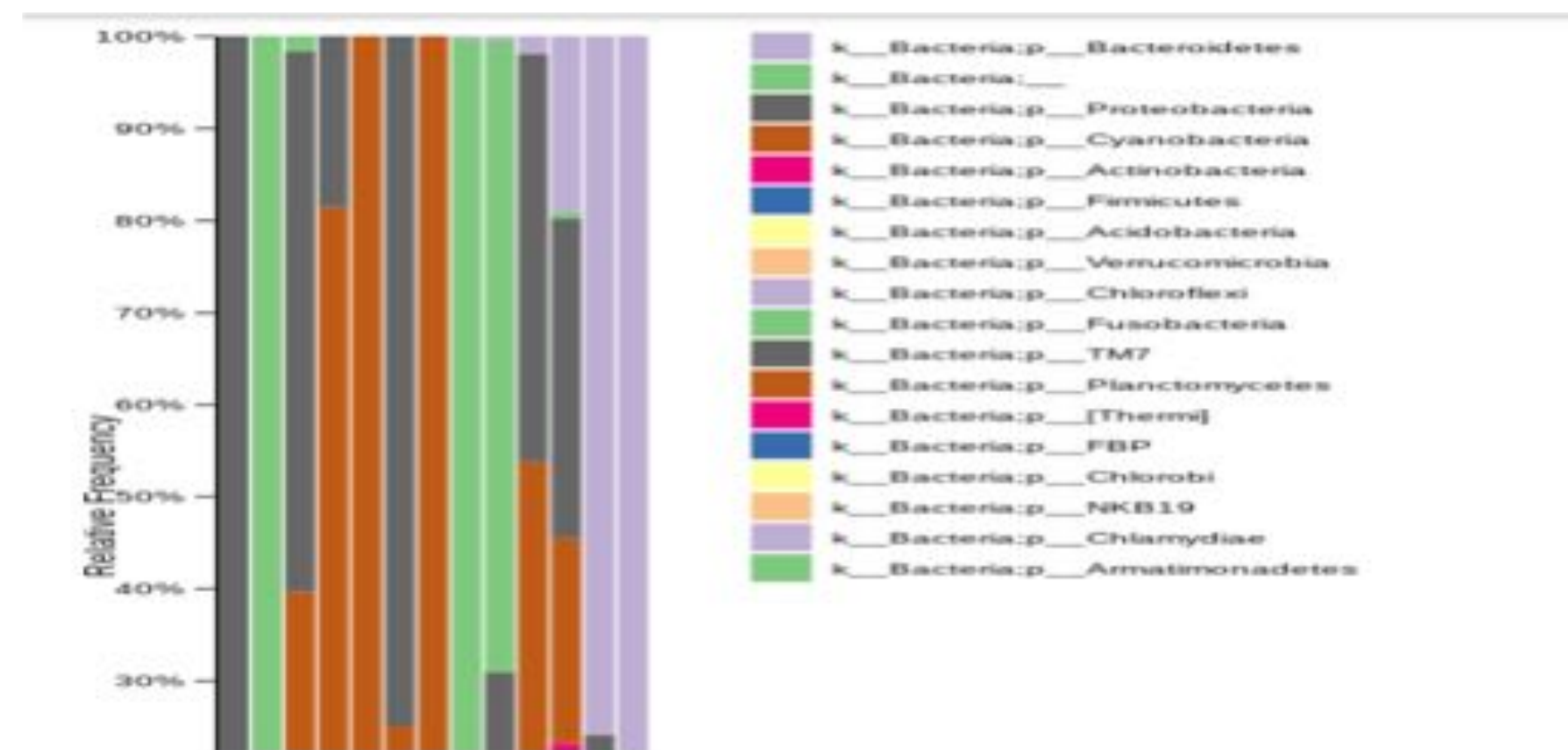


Figure 1 displays level 2 taxonomic level.

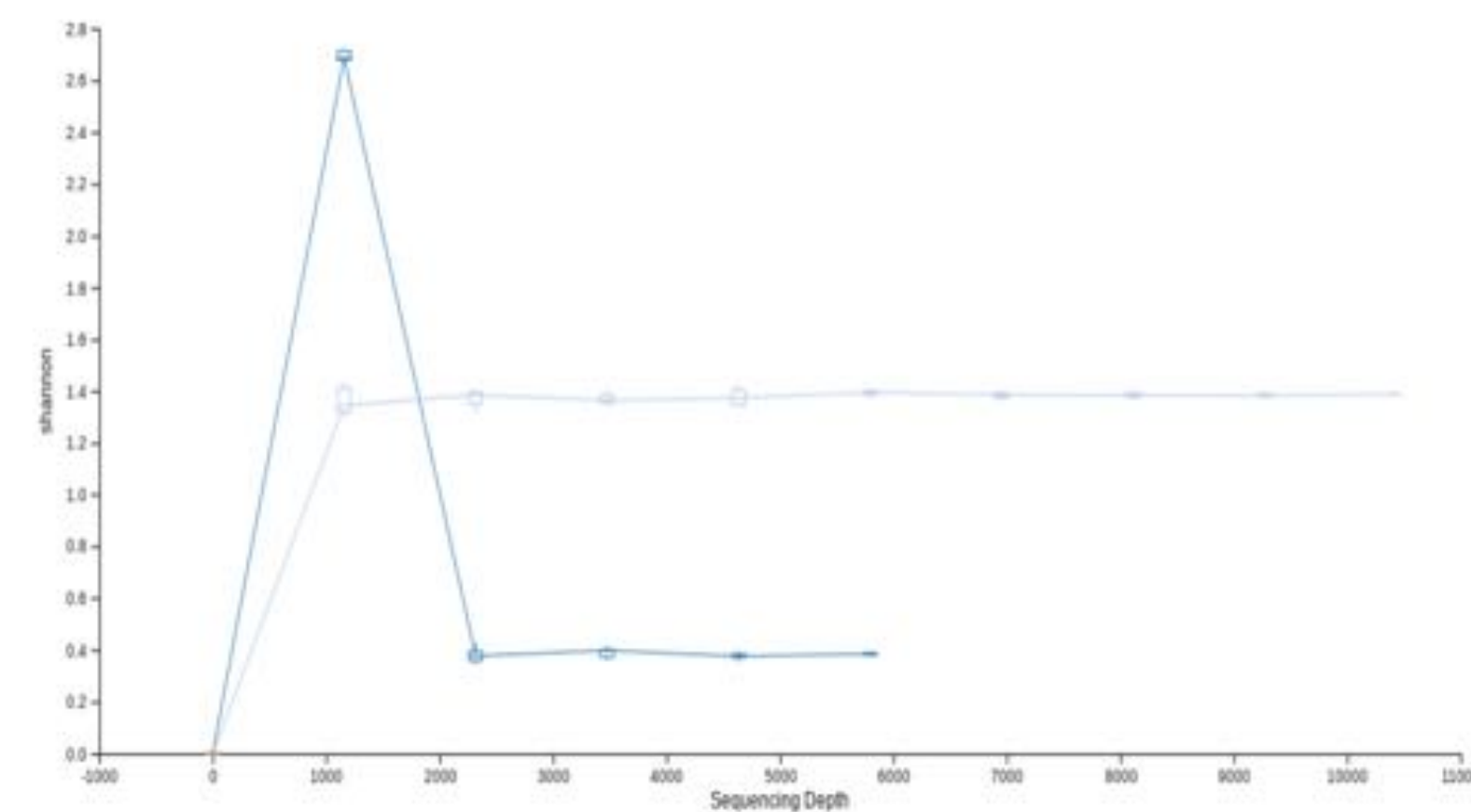
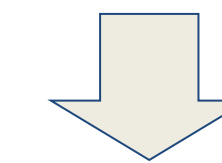


Figure 2 displays an alpha rarefaction plot using the Shannon metric

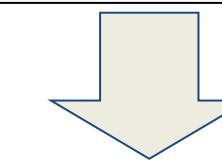
- Species 2 showed high amounts of cyanobacteria (displayed by the rust colored bars) and bacteroidetes (displayed by the lilac colored bars) in taxonomic level 2.
- Also in taxonomic level 2, proteobacteria (displayed by the black colored bars) were common in species 1 and 3.
- The darker blue line shown in figure 2 is representative of species 1 while the lighter blue line is representative of species 2. Species 1 has a much higher initial Shannon index but as sequencing depth increases, the Shannon index of species 1 falls below the Shannon index of species 2. Note that species 3 cannot be seen on the graph for unknown reasons.

Materials and Methods

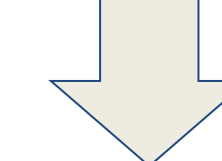
Collect arachnid samples with the use of transects and quadrats, freeze until DNA extraction



Verify the presence of true triplicates using standard DNA barcoding of the COI gene



Determine bacterial composition of arachnid abdomens through the use of PCR amplification of 16S ribosomal DNA, use gel electrophoresis to ensure successful isolation of genes



Use DNA Subway Purple Line to analyze data

Discussion

- As stated in the results section, species 2 showed high amounts of cyanobacteria and bacteroidetes in taxonomic level 2. Cyanobacteria are a type of photosynthetic bacteria. Bacteroidetes are rod-shaped bacteria which are commonly found in soil, sediments, sea water, and in the guts and on the skin of animals.

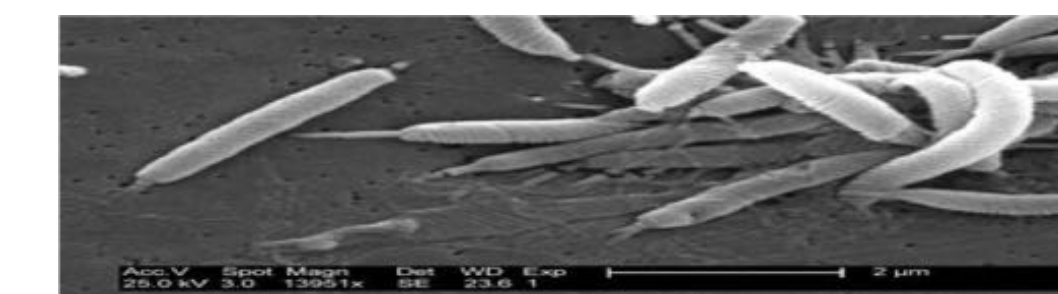


cyanobacteria
("What Are Cyanobacteria?", 2019)



bacteroidetes
("The Bacteria In Your Gut May Reveal Your True Age", 2019)

- Additionally, in taxonomic level 2, proteobacteria were common in species 1 and 3. Proteobacteria are gram negative bacteria and many common human pathogens are found within this phylum.



proteobacteria
("Epsilon Proteobacteria", 2020)

- Species 1 and 3 had some distinct commonly shared bacteria which may suggest that location plays a stronger role in determination of microbiota present since species 1 and 3 were collected from the same location while species 2 was collected from a separate location
- The higher Shannon index of species 1 indicates less diversity among the samples collected from that species than from the samples collected from species 2. This suggests there may be a factor present in the location that species 1 came from that influences the microbiota of spiders from that region heavily, making them have more similar microbiomes than spiders collected from the location that species 2 was taken from. Further research should be conducted.

Acknowledgments

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References

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