# Characterization of Squamate Microbiomes



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# Background

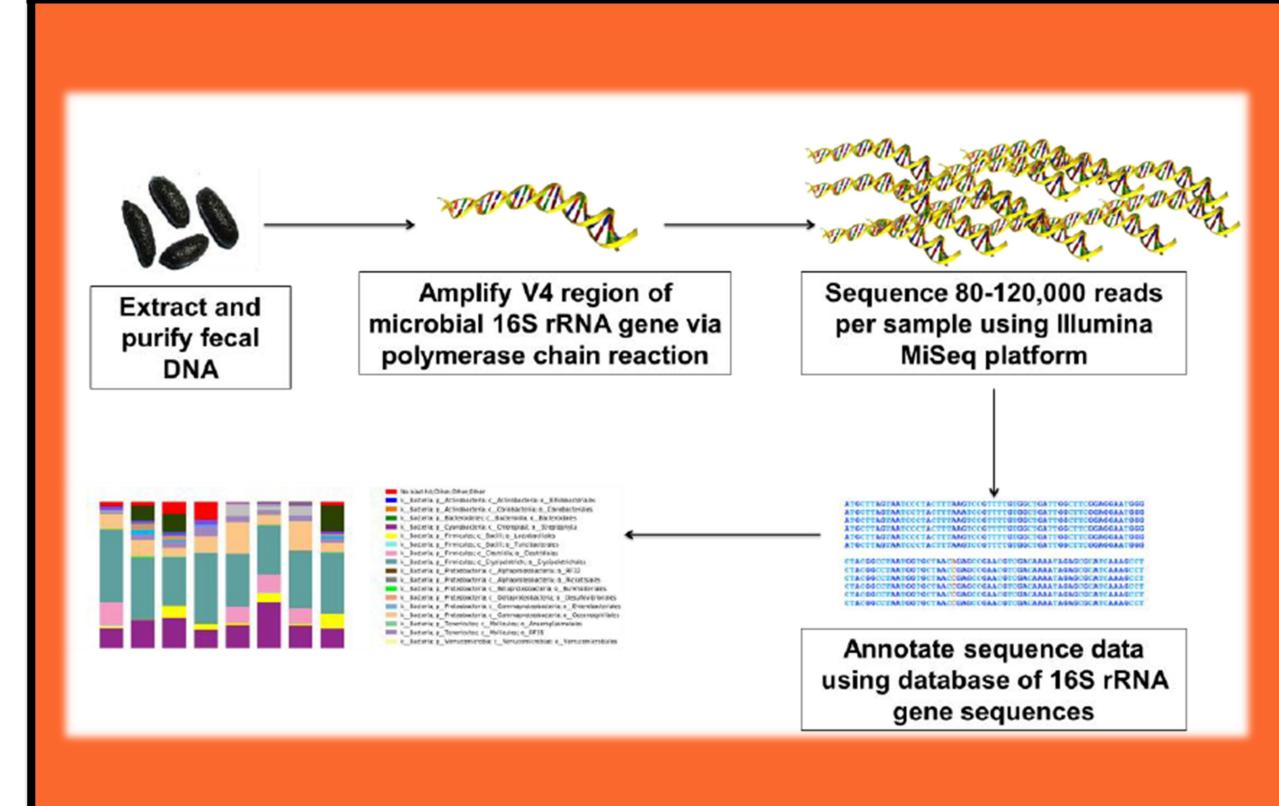
- Microbiome research has expanded the role of microbes in health and disease beyond classical roles of aiding in digestion, immune system development & pathogen defense.
- Only 2 papers have investigated the intestinal microbiome on snakes (McLaughlin et. Al 2015, Qin et. Al, 2019).
- All medicines used for snakes are off label.
- Snake's feces is representative of their health status.







### Microbiome Analysis Pipeline



### Informatics and Statistics

- DNA sequences assembled with FLASH software
- Principal coordinate analyses and alpha-diversity determined with PAST software
- Differences assessed with ANOVA and PERMANOVA



# **PERMANOVA** Permutation N: 9999 Total sum of squares: Within-group sum of squares: 16.32 ariation Snake Horse $\triangle$ PCo1 11.67% Variation

Figure 1: PCoA of 6 snakes, 4 rats, and 44 horses showing a significant difference between species

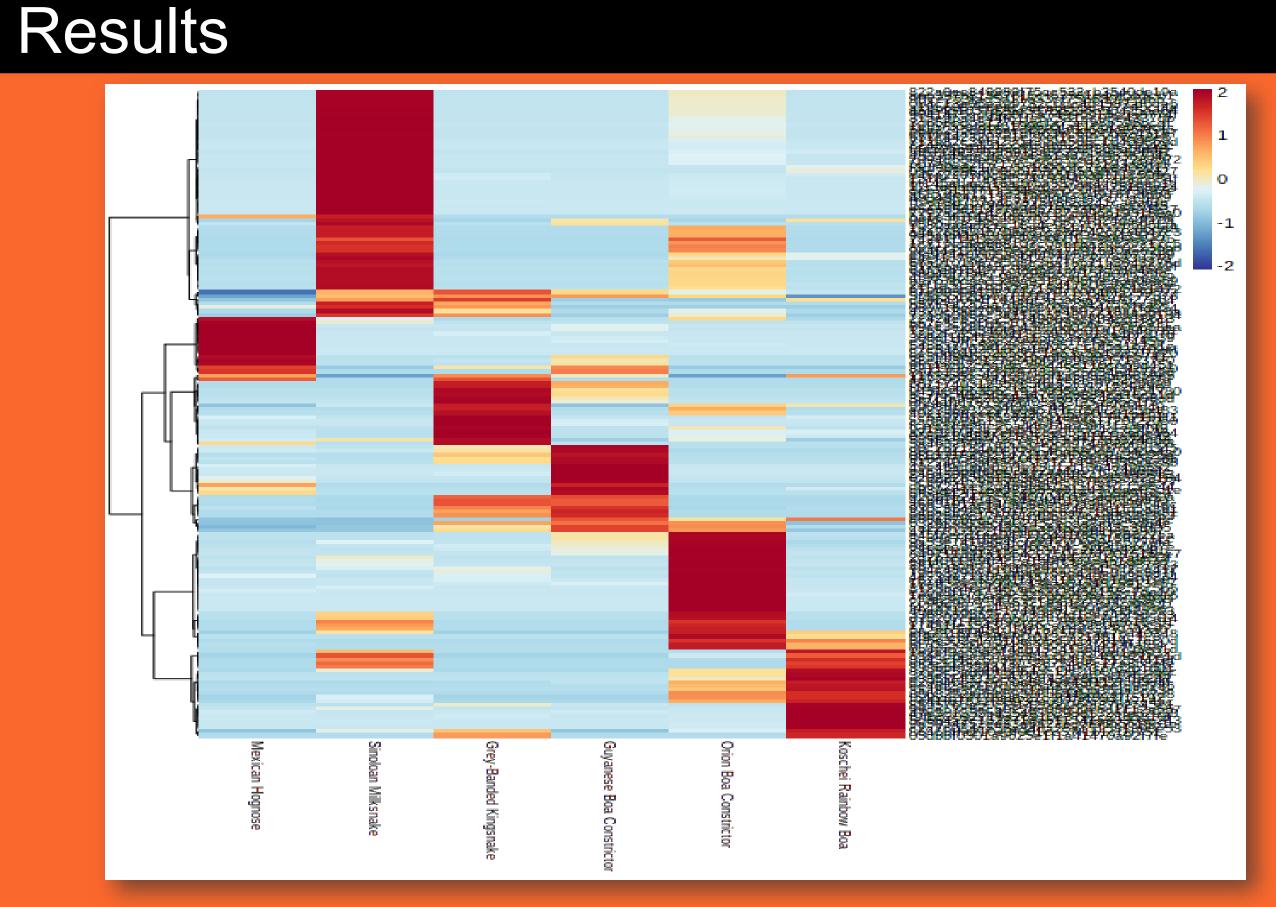


Figure 2: Heatmap of the 6 snake samples collected showing marked variation in amplicon sequence variants (ASVs) of snake fecal samples



Metadata Example

#### Conclusions

- Significant differences in microbiome composition were found when comparing snake samples to two other species.
- As expected, snake samples showed marked variation in microbiome composition.
- Six institutions have agreed to participate in this project, and we are in discussion with another 35 institutions.

# **Future Directions**

- Additional sample analysis will allow for comparisons of different independent variables including species, environment and disease states.
- This information will serve as a baseline of snake fecal microbiome data that can be used for future development of therapeutic and preventative medicines.

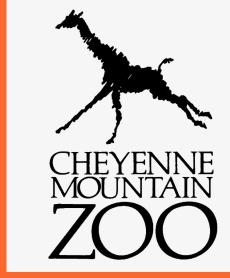
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