



UNDERGRADUATE RESEARCH SUMMER INSTITUTE

Characterization of the Skin Microbiome in Wood Frog (*Rana sylvatica*) Tadpoles



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INTRODUCTION

Very few studies have investigated the formation of microbiome of tadpoles, and yet the microbiome likely provides essential functions for these organisms, including aiding digestion and pathogen defense. Our research sought to provide one of the first characterizations of the composition and diversity of the skin bacterial communities on tadpoles of wood frogs. In addition, we determined if the skin microbiome differed across the bodies of individual tadpoles using skin tissue samples from two different locations: the tail and the ventral surface. This research will inform best sampling techniques for assessing skin microbial diversity in future studies aimed at understanding the effects of environmental stressors on the formation of the microbiome.

Hypothesis: The ventral surface will have a more diverse bacterial community than the tail, because the ventral surface comes into contact with the diverse microbial communities of the pond bottom, and because tail tissue degenerates and is resorbed during metamorphosis.



Woodfrog tadpoles at Gosner Stage 39-40



Collecting tadpoles for DNA sequencing

METHODS

- We collected tadpoles (Gosner stage 39-40) from a single pond thirteen days apart (N=8 per time point) and extracted tissue samples from the tail and the ventral surface
- We amplified the 16s rRNA gene to characterize bacterial diversity and relative abundance
- We compared diversity across time and body region



RESULTS

Our results supported our hypothesis. The ventral surface was more diverse and had greater species richness (ANOVA: Bodyregion: $F_{1,14} = 9.3$, $P = 0.009$) than the tail for both time points (ANOVA: Bodyregion * Time: $F_{1,14} = 0.2$, $P = 0.66$).

Figure 1: Diversity of bacteria across time and body region

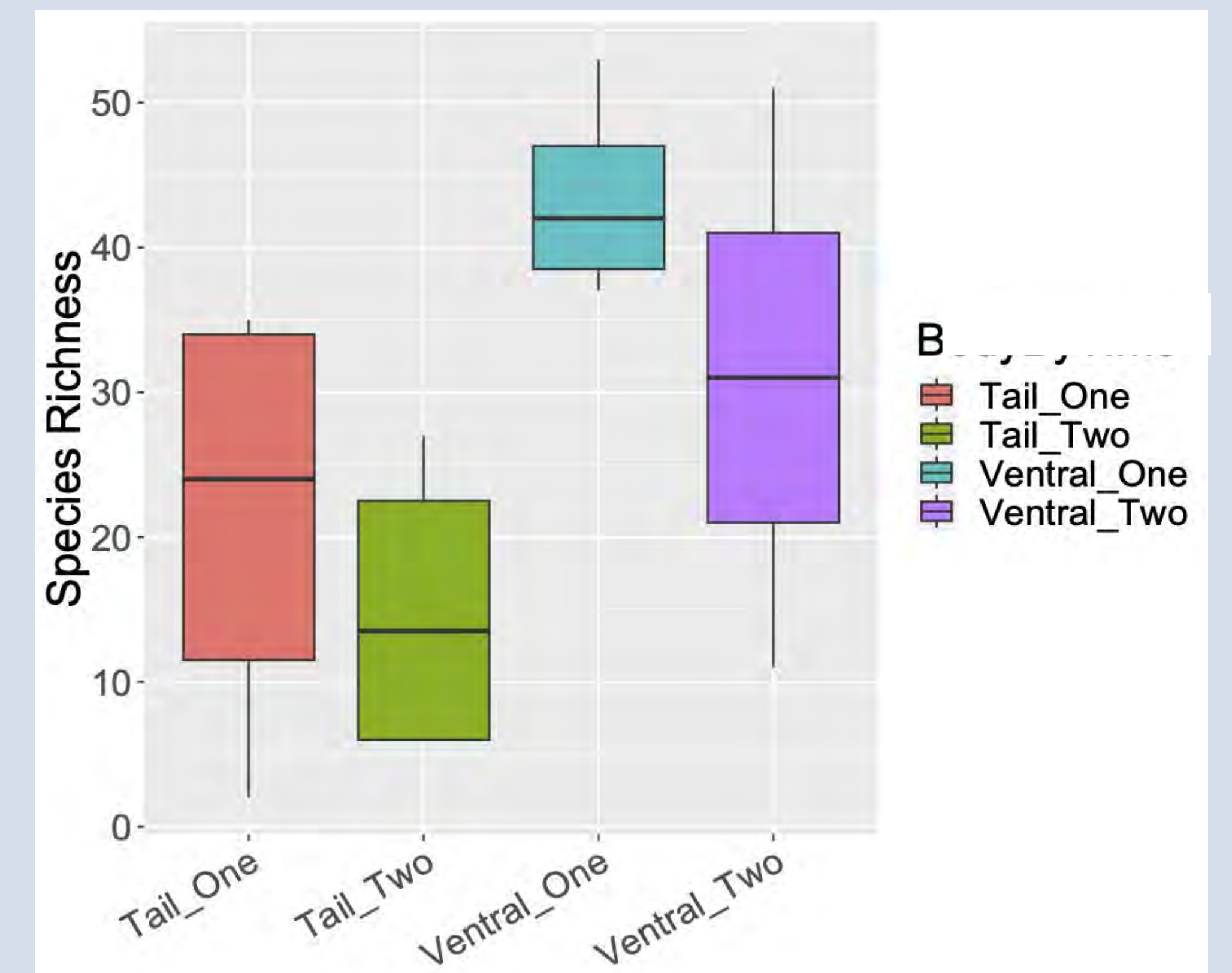
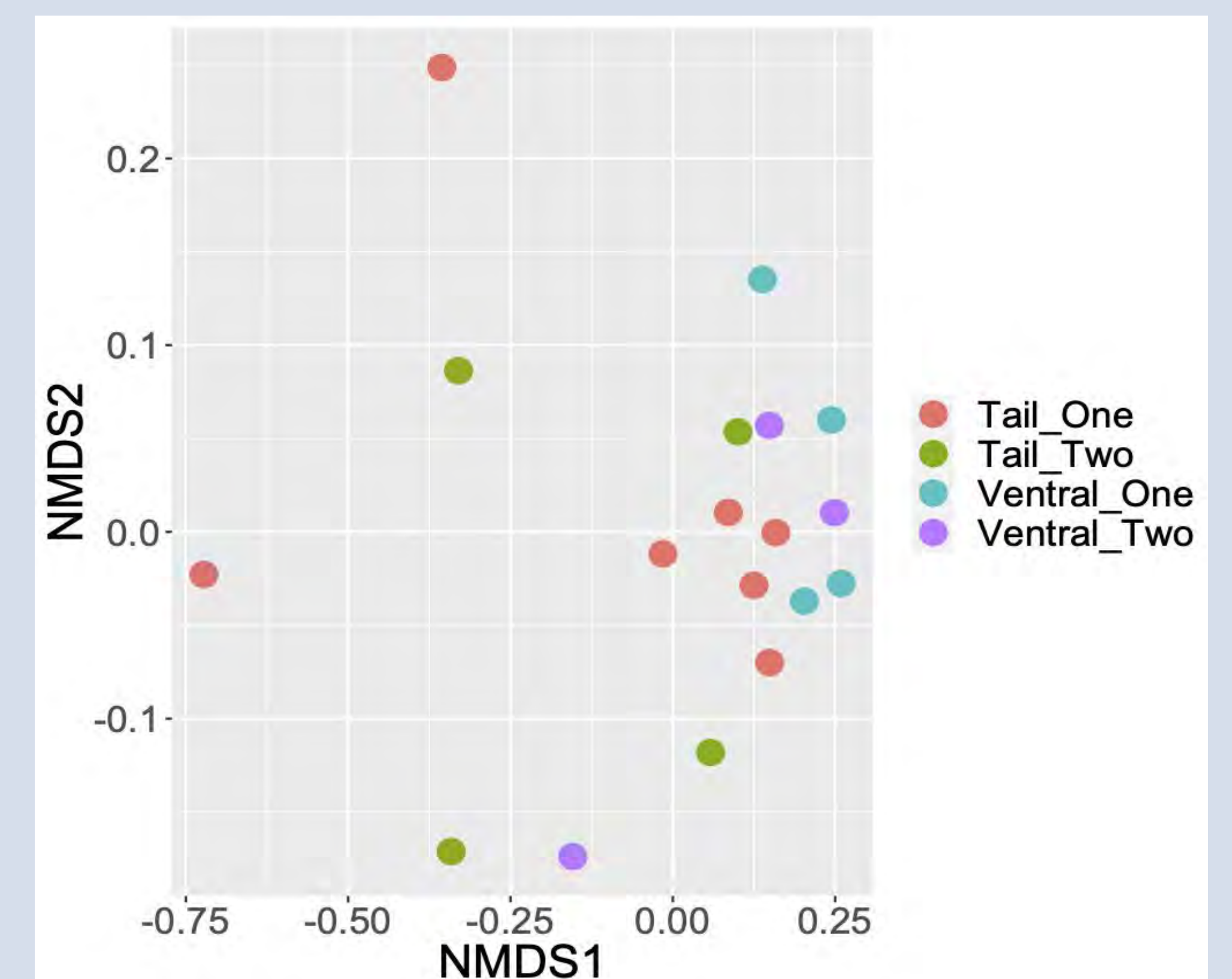


Figure 2: Community composition across time and body region



Species composition also differed between the tail and the ventral surface, a pattern that was consistent across the two time points (PERMANOVA: Bodyregion: $PseudoF_{1,17} = 1.7$, $P = 0.03$; Time: $PseudoF_{1,17} = 1.4$, $P = 0.07$).

CONCLUSIONS

- The tail and the ventral surface harbored different communities of skin bacteria in terms of both the number and kinds of species present.
- However, tadpoles maintained the same skin bacterial communities across the two time points despite the pond environment changing dramatically.
- These findings are important to consider when determining methods to assess the skin microbiome.

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