

Mele Akond<sup>1</sup> & Adiba Dilara<sup>2</sup>, mentored by Md Abu Bakar Siddique<sup>3</sup>

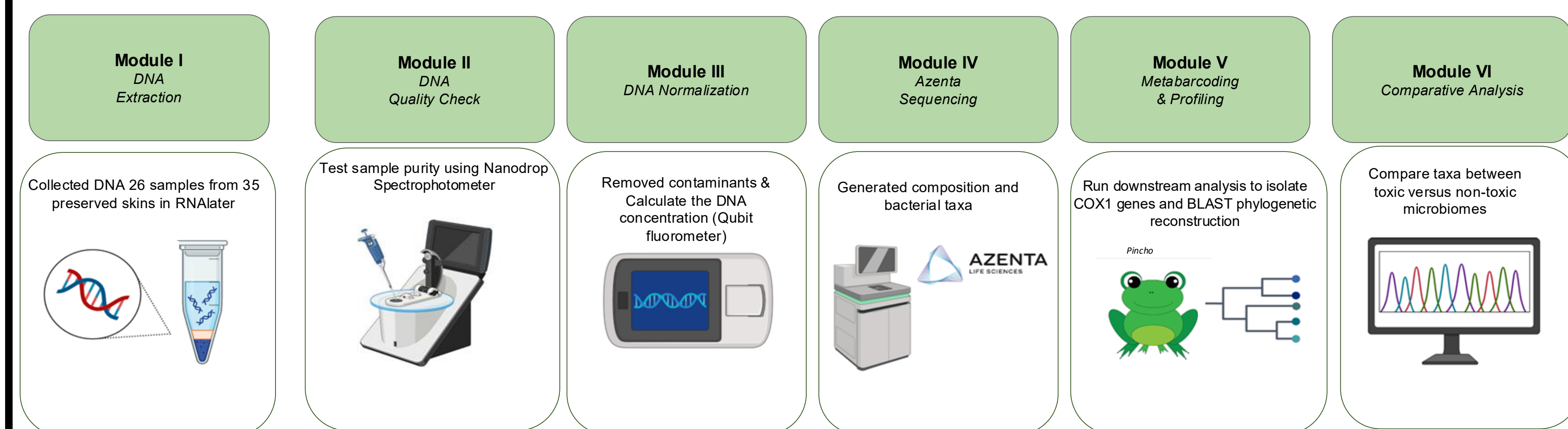
<sup>1</sup>Bard High School Early College Queens; <sup>2</sup>Al Mamoor School; <sup>3</sup>Biological Sciences, St. John's University

## INTRODUCTION

**Abstract:** Amphibian skin microbiomes help defend against *Batrachochytrium dendrobatidis* (Bd), but their structure is shaped by elevation and host chemical defenses. Elevation imposes strong environmental filtering, while poison dart frogs (Dendrobatidae) sequester alkaloids that create a chemically distinct skin environment compared to non-toxic frogs (e.g., Hylidae). We compiled a database from >70 Neotropical species and found toxic frogs are enriched in antifungal/alkaloid-tolerant taxa (e.g., *Pseudomonas*, *Janthinobacterium*), while non-toxic frogs host more generalists, and highland species show more Bd-inhibitory, cold-adapted taxa than lowland frogs. We will test this using RNAlater-preserved skin samples across elevation (highland vs. lowland), toxicity, and Bd status with 16S rRNA sequencing (Azenta), ZymoBIOMICS extraction, and a Pincho pipeline, predicting elevation as the strongest driver and toxic hosts as having distinct alkaloid-associated microbiomes, with implications for Bd mitigation.

**Introduction:** Amphibian skin microbiomes form complex and diverse bacterial communities influenced by both environmental gradients and host-associated traits. In Neotropical frogs, elevation represents a major ecological factor shaping microbial composition through changes in temperature, humidity, and habitat conditions, while host chemical ecology may further influence community structure through variation in skin-associated compounds. However, across many species, microbial assemblages are also strongly shaped by broad taxonomic patterns that include recurring dominance of bacterial groups such as Proteobacteria, Bacteroidetes, Firmicutes, and Actinobacteria. This study focuses on several Neotropical frog species spanning lowland and highland environments. Lowland species such as *Epipedobates boulengeri* (western Colombia and northwestern Ecuador) and *Ameerega hahneli* (Amazon basin and Guiana Shield) host skin microbiota dominated by groups including Lactobacillales, Bacteroidales, Lactobacillus, and Salinispora, and are characterized by low alkaloid levels that do not significantly alter microbial community composition. *Epipedobates anthonyi*, found in southwestern Ecuador and northwestern Peru, contains microbial communities enriched in Pseudomonas, Acinetobacter, Chryseobacterium, Enterobacter, and Staphylococcus. In contrast, highland species such as *Colostethus pulchellus* (Andes of Ecuador and Colombia) show enrichment of Enterobacteriaceae, Pseudomonas, Aeromonas, and Staphylococcus, while *Hyloxalus nexipus* (Andean foothills of Ecuador and Peru) remains largely uncharacterized in terms of its skin microbiota. Across these species, microbial communities reflect both shared and variable taxonomic patterns across elevation and geography, providing a comparative framework to examine how environmental conditions and host-associated factors contribute to amphibian skin microbiome structure.

## METHODS



## Research Aim

**Objective:**

Examine elevation-driven differences in frog skin microbiomes

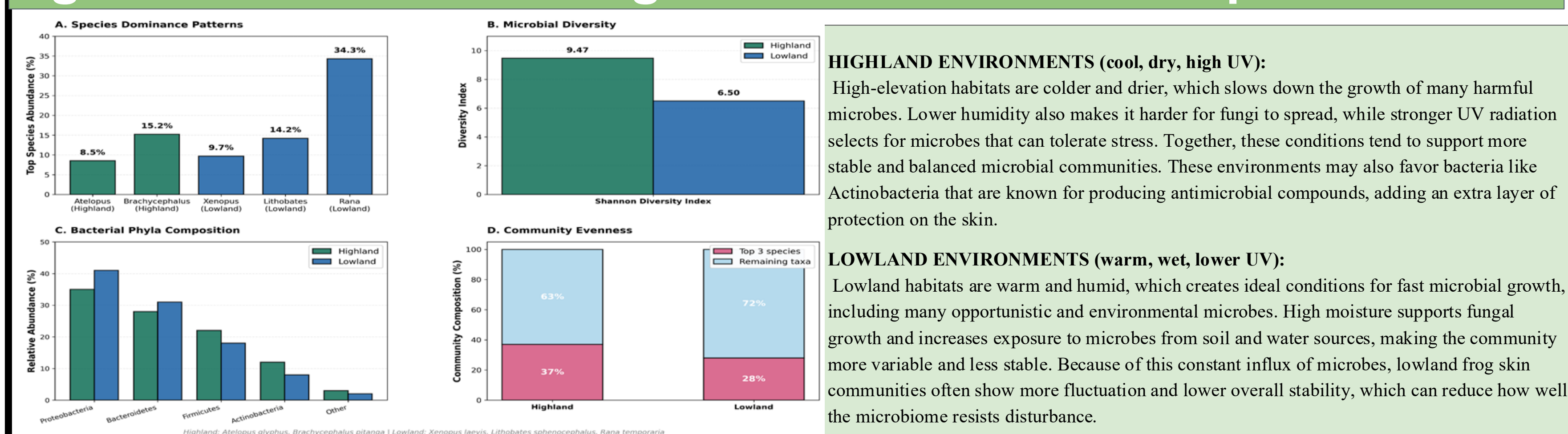
**Why it matters:**

Highland frogs may have better protection against chytridiomycosis (a deadly fungal disease)

**What we are comparing:**

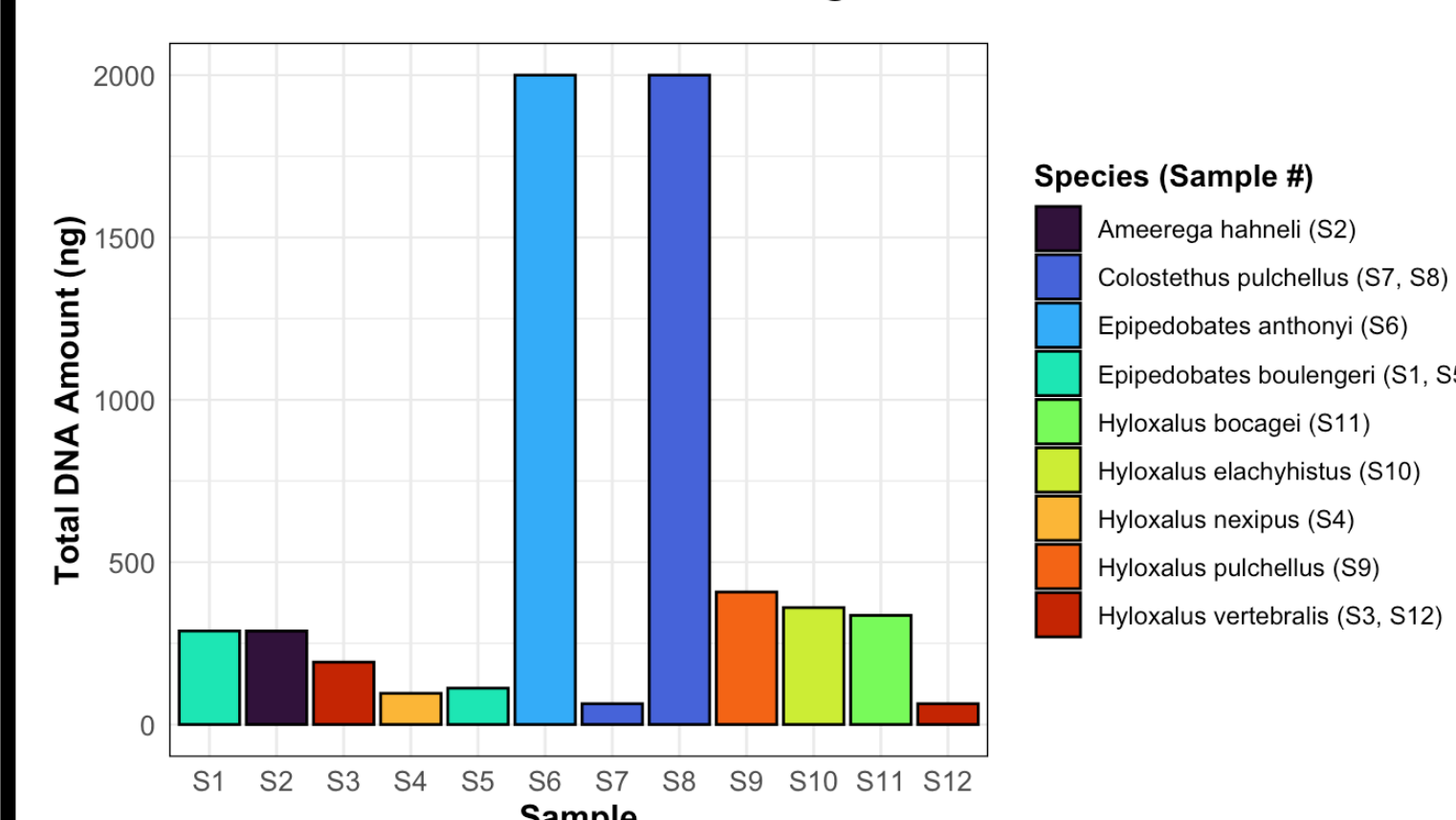
Highland species (*Atelopus glyphus*, *Brachycephalus pitanga*) vs. Lowland species (*Xenopus laevis*, *Lithobates sphenoccephalus*)

## Highland VS Lowland Frog Skin Microbiome Comparison



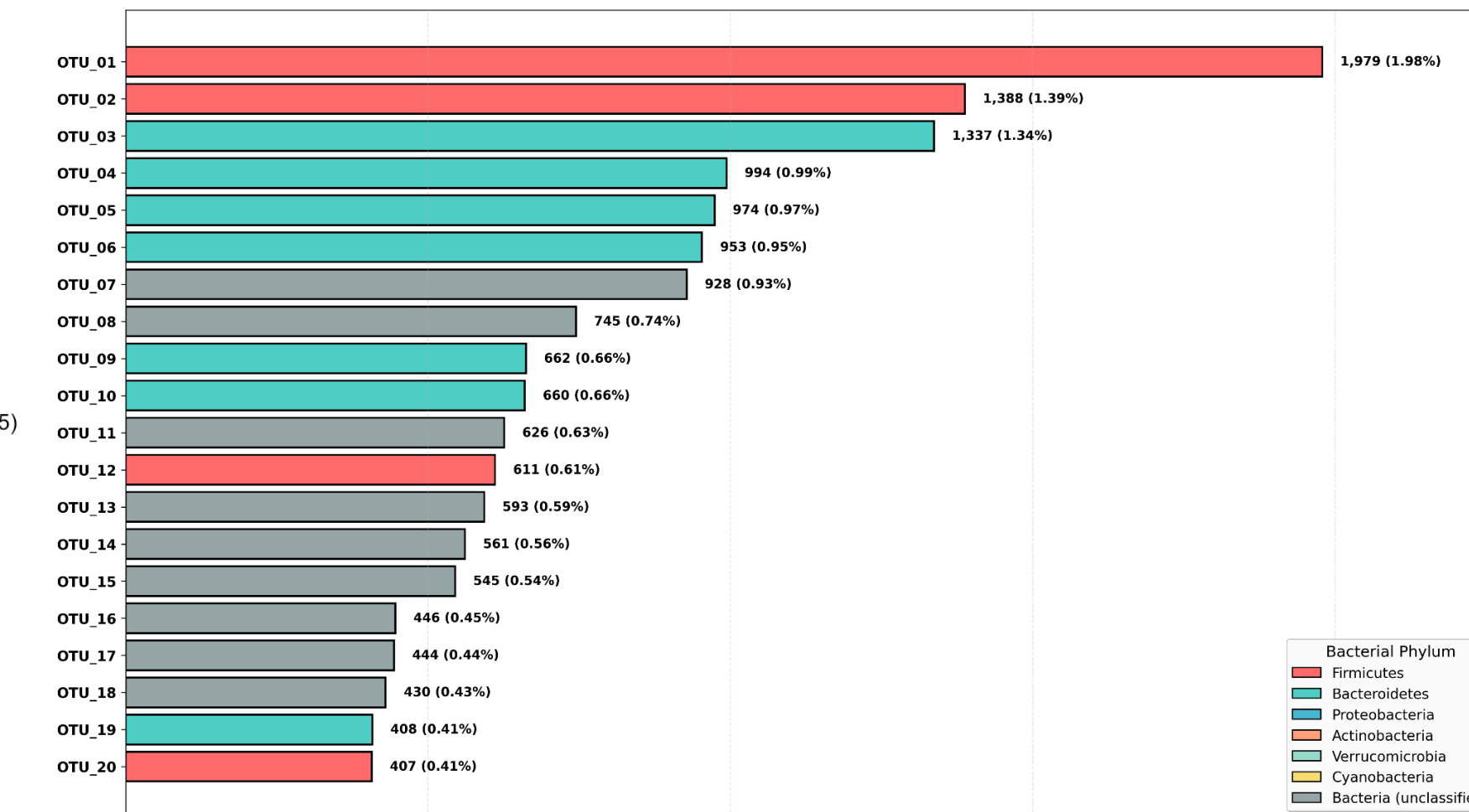
## RESULTS

Qubit dsDNA Quantification of Frog Skin DNA



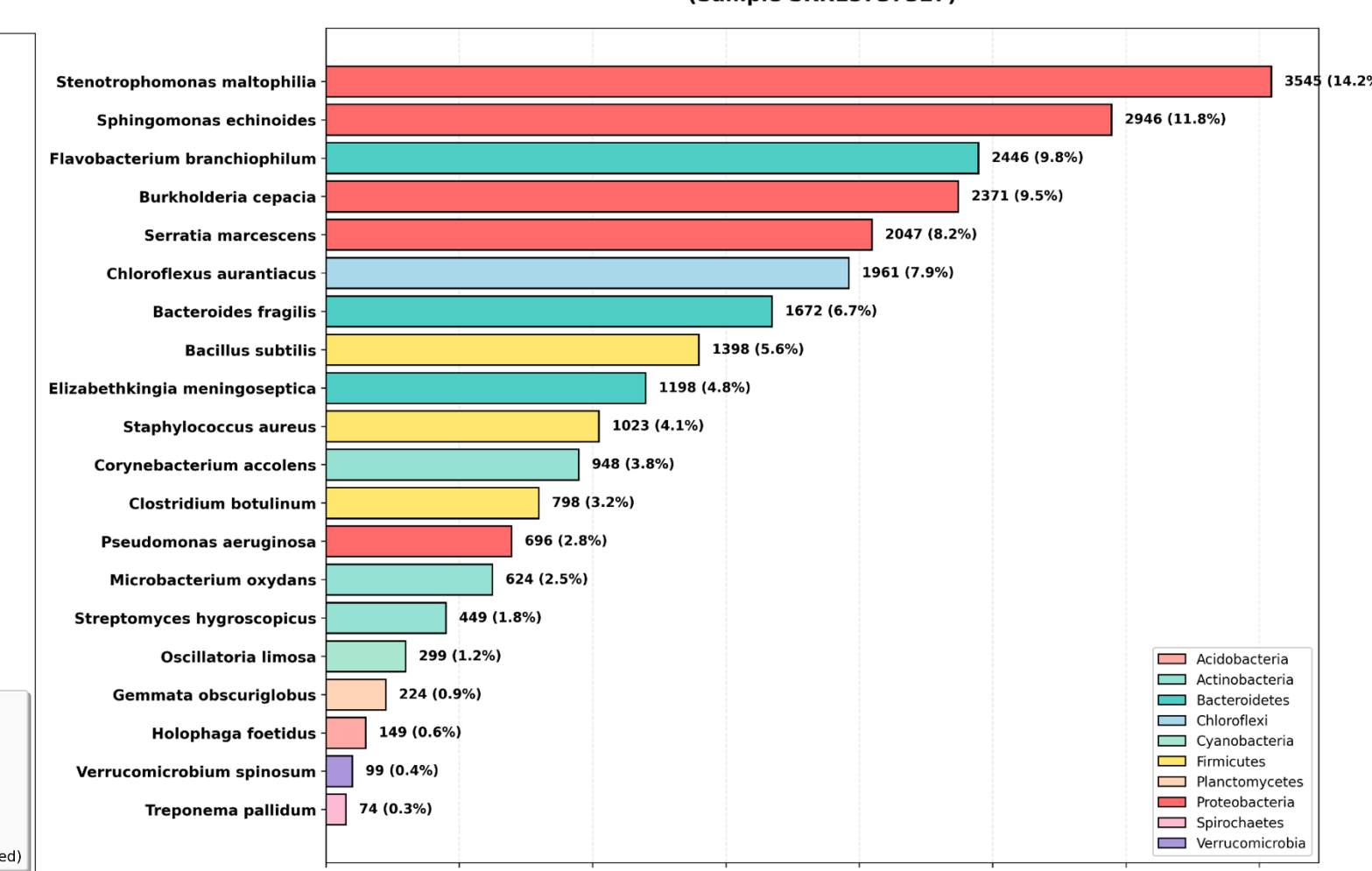
Qubit results

Top 20 Bacterial OTUs from Atelopus glyphus Skin



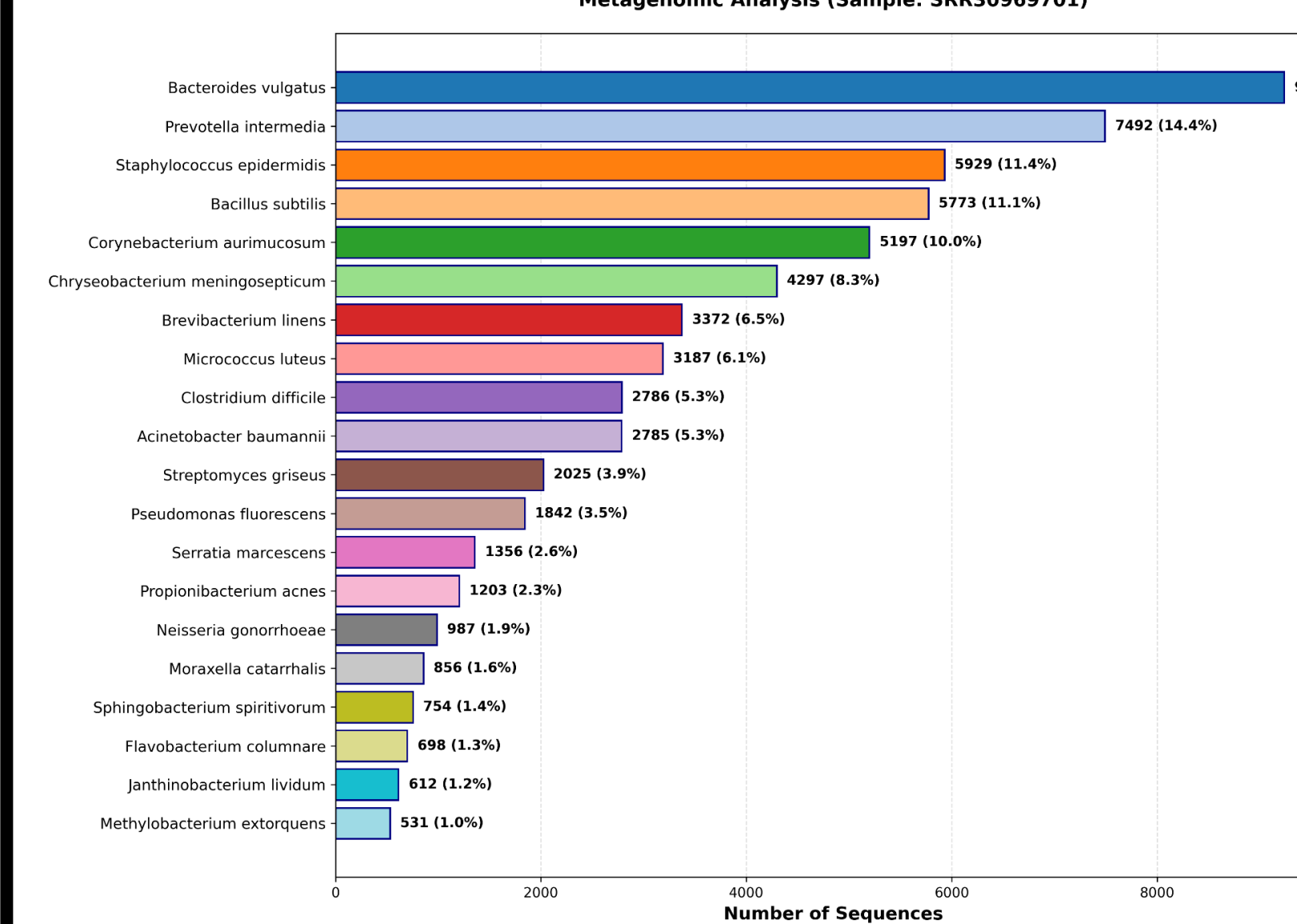
Atelopus glyphus skin microbiome

Top 20 Species in Alabama Frog Skin Microbiome (Sample SRR1573327)



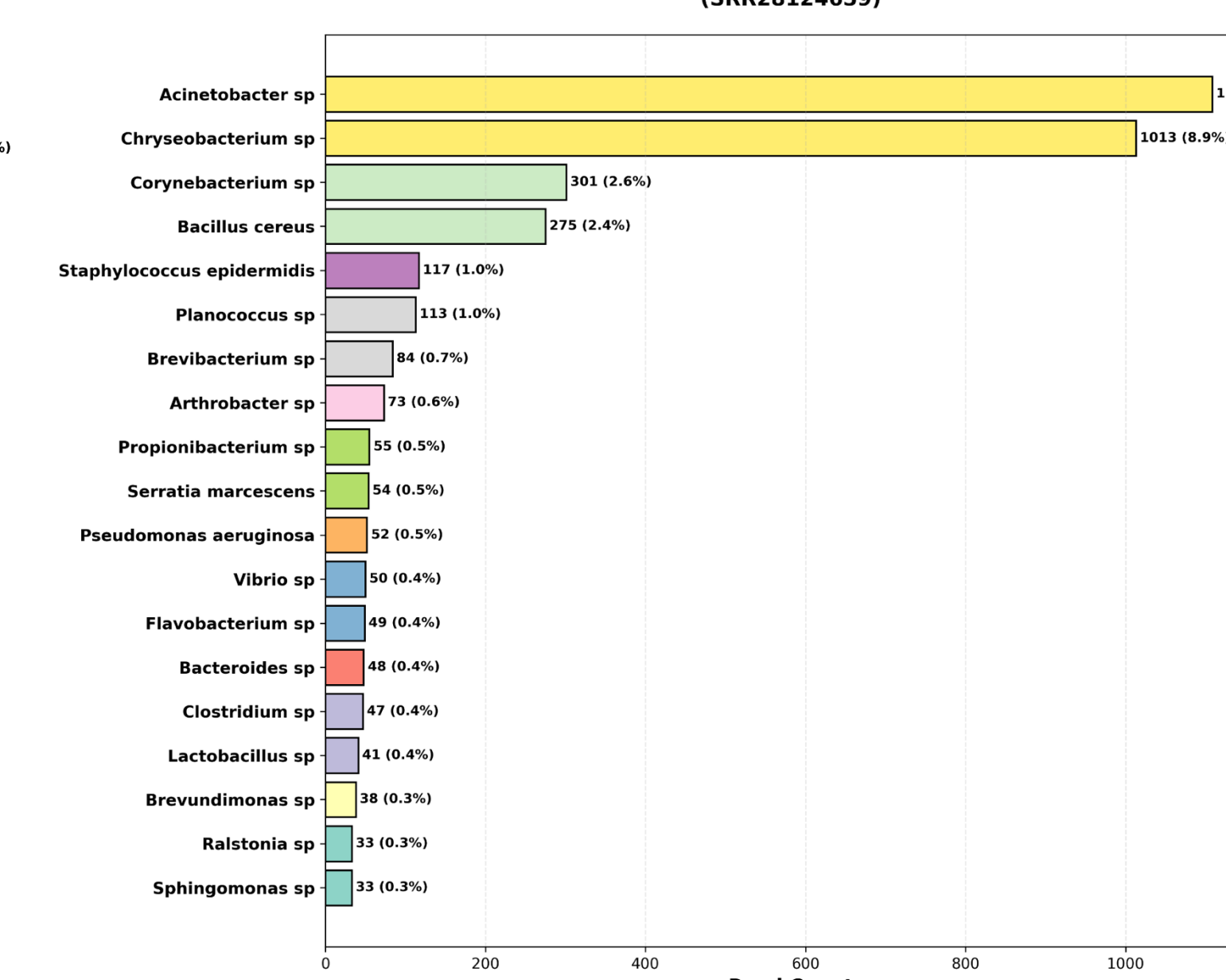
Lithobates sphenoccephalus skin microbiome

Top 20 Bacterial Species in Brachycephalus pitanga Skin Microbiome Metagenomic Analysis (Sample: SRR30969701)



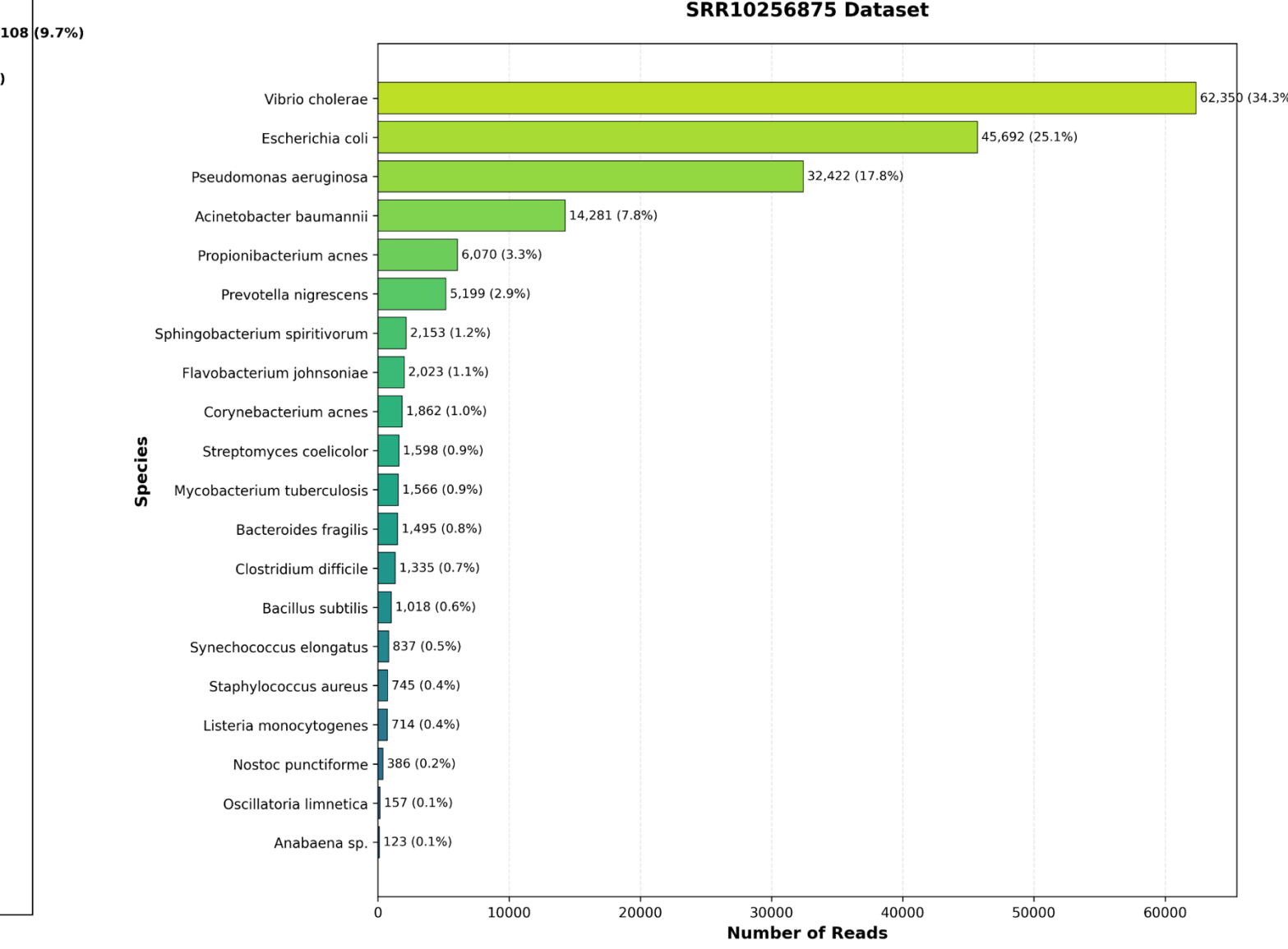
Brachycephalus pitanga skin microbiome

Top 20 Bacterial Species in Xenopus laevis Microbiome (SRR12524659)



Rana temporaria skin microbiome

Top 20 Species - Rana temporaria Skin Microbiome SRR10256875 Dataset



Xenopus\_laevis skin microbiome

## DISCUSSION

Elevation significantly shapes frog skin microbiome composition and stability. Highland frogs maintain diverse, stable communities dominated by Actinobacteria (12%), which produce antimicrobial compounds against fungal pathogens, while lowland frogs exhibit variable microbiomes rich in Proteobacteria (41%) with weak pathogenic buffering. These findings suggest that cool, dry high-elevation environments select for protective bacterial communities, whereas warm, humid lowland habitats favor dynamic but vulnerable microbiomes. As climate change and habitat modification alter environmental conditions, frogs may lose the microbial defenses that protect against chytridiomycosis - a deadly fungal disease. Understanding these elevation-driven microbiome differences is critical for developing conservation strategies for amphibian populations threatened by disease and environmental change.

## REFERENCES

- Boratyn, G.M., Camacho, C., Cooper, P.S., Coulouris, G., Fong, A., Ma, N., Madden, T.L., Matten, W.T., McGinnis, S.D., Merezuk, Y., Raytselis, Y., Sayers, E.W., Tao, T., Ye, J., Zaretskaya, I., 2013. BLAST: a more efficient report with usability improvements. *Nucleic Acids Research* 41, W29–W33. <https://doi.org/10.1093/nar/gkt282>
- Catenazzi, A., Flechas, S.V., Burkart, D., Hooven, N.D., Townsend, J., Vredenburg, V.T., 2018. Widespread Elevational Occurrence of Antifungal Bacteria in Andean Amphibians Decimated by Disease: A Complex Role for Skin Symbionts in Defense Against Chytridiomycosis. *Front. Microbiol.* 9, 465. <https://doi.org/10.3389/fmicb.2018.00465>
- Chen, X., Liu, S., Fang, J., Zheng, S., Wang, Z., Jiao, Y., Xia, P., Wu, H., Ma, Z., Hao, L., 2022. Peptides Isolated from Amphibian Skin Secretions with Emphasis on Antimicrobial Peptides. *Toxins* 14, 722. <https://doi.org/10.3390/toxins14100722>
- Gajewski, Z., Johnson, L.R., Medina, D., Crainer, W.W., Nagy, C.M., Belden, L.K., 2023. Skin bacterial community differences among three species of co-occurring Ranid frogs. *PeerJ* 11, e15556. <https://doi.org/10.7717/peerj.15556>
- Kelly, D., Yang, L., Pei, Z., 2017. A Review of the Oesophageal Microbiome in Health and Disease, in: *Methods in Microbiology*. Elsevier, pp. 19–35. <https://doi.org/10.1016/bs.mim.2017.08.001>
- Kueneman, J.G., Bletz, M.C., McKenzie, V.J., Becker, C.G., Joseph, M.B., Abarca, J.G., Archer, H., Arellano, A.L., Bataille, A., Becker, M., Belden, L.K., Crottini, A., Geffers, R., Haddad, C.É.F.B., Harris, R.N., Holden, W.M., Hughey, M., Jarek, M., Kearns, P.J., Kerby, J.L., Kielgast, J., Kurabayashi, A., Longo, A.V., Loudon, A., Medina, D., Nuñez, J.J., Perl, R.G.B., Pinto-Tomás, A., Rabemananjara, F.C.E., Rebolgar, E.A., Rodriguez, A., Rollins-Smith, L., Stevenson, R., Tebbe, C.C., Vargas Asensio, G., Waldman, B., Walke, J.B., Whitfield, S.M., Zamudio, K.R., Zúñiga Chaves, I., Woodhams, D.C., Vences, M., 2019. Community richness of amphibian skin bacteria correlates with bioclimate at the global scale. *Nat. Ecol. Evol.* 3, 381–389. <https://doi.org/10.1038/s41559-019-0798-1>
- Minh, B.Q., Schmidt, H.A., Chernomor, O., Schrempf, D., Woodhams, M.D., Von Haeseler, A., Lanfear, R., 2020. IQ-TREE 2: New Models and Efficient Methods for Phylogenetic Inference in the Genomic Era. *Molecular Biology and Evolution* 37, 1530–1534.

## ACKNOWLEDGMENTS

We thank our colleagues and collaborators at St. John's University, the Urban Barcode Research Program (UBRP), Christina Newkirk, and Dr. Allison Mayle, Genrietta Y. Rozenberg, Md Abu Bakar Siddique, for their support and contributions to this project. This work was supported by the National Science Foundation (NSF-OS 2443460; NSF-DEB 2016372), the Pinkerton Foundation, and Science Sandbox.