

Genetic Diversity and Spatial Genetic Structure of *Guzmania monostachia* (Bromeliaceae) in Florida

Introduction

Bromeliaceae are a neotropical plant family consisting of around 3140 species in eight traditional subfamilies [1]. The origin of Bromeliaceae is estimated to have occurred roughly 100 Ma in the Guyana Shield [2]. *Guzmania* is traditionally placed in the largest subfamily of Bromeliaceae, Tillandsioideae, which also includes *Tillandsia*, *Vriesea*, *Catopsis*, and *Glomeropitcairnia* [3]. The subject of my research, *Guzmania monostachia* (L.) Rusby ex Mez has the widest distribution range of any *Guzmania*, spanning the Andes, Central America, the Caribbean, and South Florida [2]. Many bromeliads in Florida were already threatened prior to the 1990s due to habitat loss and overharvesting by humans. However, in 1989, an invasive bromeliad-eating weevil, *Metamasius callizona* Chevrolat (Coleoptera: Curculionidae), was introduced into Florida from Mexico, further endangering these species. In all, twelve of Florida's native bromeliad species are being destroyed by *M. callizona*, including *G. monostachia*, whose soft leaves make it particularly vulnerable [4]. Research is desperately needed to assess the full impact of *M. callizona* on *G. monostachia* populations in Florida, as well as to identify sources of population-level diversity that may be important for future pest-mitigation and targeted conservation efforts.

Objectives

My dissertation research combines field botany, phylogenomics, genomics, and population genomics to understand the evolutionary origins of Florida *Guzmania* and their genetic diversity. As part of my proposed project, my goals are to:

- 1) Reconstruct the evolutionary history of Tillandsioideae using phylogenomic approaches, with special emphasis on Florida lineages
- 2) Assemble a high-quality reference genome for *G. monostachia*
- 3) Use population genomic approaches to quantify the genetic diversity and spatial genetic structure of Florida populations of *G. monostachia*.

Specifically, I hypothesize the following:

- 1) There will be little to no gene flow among the fragmented Florida populations of *G. monostachia* due to their autogamous nature and short seed dispersal distances
- 2) Different populations will harbor unique genetic characteristics due to possible long-term isolation
- 3) The genetics of the Florida populations of *G. monostachia* will differ significantly from those observed elsewhere in the Neotropics.

Materials and Methods

As part of *Goal 1*, I will employ high-throughput sample processing, targeted sequence capture (Hyb-seq [5]), and second-generation sequencing techniques to generate a large-scale sequence dataset and a robust phylogenomic framework for Tillandsioideae, identifying the closest relatives of Florida *Guzmania*. Towards this goal, I will use the reference genome for *G. monostachia* generated under *Goal 2* to design a probe set targeting phylogenetically informative

sites. Tissue samples for DNA extraction, sample prep, and Illumina sequencing will come from both herbarium specimens as well as from living accessions collected across Florida; notably, the latter efforts will generate many new voucher specimens for accession into the University of Florida Herbarium (FLAS) and other herbaria. Lastly, as part of *Goal 3*, I will employ low-coverage whole-genome sequencing techniques to collect genome-scale data from *G. monostachia* accessions representing populations across Florida. Single nucleotide polymorphisms (SNPs) identified from reads mapped to the *G. monostachia* reference genome (*Goal 2*) will be used to quantify the genetic diversity within and among populations. These SNPs will also be used to estimate the pairwise kinship coefficient which will then be regressed on the logarithm of the spatial distance between individuals to analyze spatial genetic structure.

Significance

The collection resources, phylogenomic and genomic data, and results from my project will serve as a resource for ongoing bromeliad research and, most importantly, inform *G. monostachia* conservation efforts in Florida. Conservation of native bromeliads is critical as a result of the important roles they play in their ecosystems. Water collected in their leaf bases, known as a “phytotelmata”, not only sustains life for a variety of aquatic organisms (including some invertebrates that exist solely on bromeliads) and represent a unique ecosystem in its own right, it also serves as an important source of hydration for animals during the dry winter season [6]. As for *G. monostachia*, it is characterized by selfing and, consequently, low genetic variation. These characteristics make it more susceptible to disease, pests, and parasites. Genetic variation can also have implications for the possibility of evolved resistance to herbivory [7]. Therefore, it is very important to quantify its population-level genetic diversity that can inform effective conservation strategies for Florida populations. The Belizean form of *Tillandsia utriculata* L., another bromeliad native to Florida, exhibits resistance to *M. callizona*, which suggests that resistance has evolved in closely related bromeliad species [8]. In addition to its importance for conservation, my project will also help resolve complex phylogenetic relationships in Tillandsioideae. Only a small sample of *Guzmania* has been used in phylogenetic analyses to date, and my data will improve our evolutionary knowledge of this poorly known taxon. Additionally, a phylogenomic approach has never been employed in Tillandsioideae and my research will significantly help resolving relationships within this charismatic clade.

Budget Justification

I am applying for funds to support each phase of my research. I am focusing my fieldwork activities in Florida with the goal of increasing our knowledge of the morphology and genetic diversity of this species. Additionally, the cost of my phylogenomic and genomic analyses is not insignificant. Therefore, the requested funds would help cover the cost of field supplies, herbarium material, and travel (see itemized budget), in addition to molecular analyses. I expect to spend considerable time traveling throughout South Florida in search of *G. monostachia* due to the sparse amount of locality data available for this species. I am very familiar with Florida ecosystems and have targeted several localities deemed ideal putative habitats to explore. Finally, I want to stress that we currently have only 17 specimens of *Guzmania monostachia* from Florida available for study. The majority of these specimens are maintained in Florida in the collections at Fairchild Tropical Gardens (9 specimens), University of South Florida (4 specimens), and University of Florida (2 specimens), so the requested funds will also help cover the travel to and from these herbaria to collect tissue samples for my genetic work. My fieldwork will generate critically needed material to update our knowledge of the distribution and diversity of this taxon.

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