



Paepalanthus subg. *Platycaulon* Mart. ex Körn. (Eriocaulaceae): Taxonomy, Phylogeny and Biogeography

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Introduction

Paepalanthus subg. *Platycaulon* Mart. ex Körn. can be distinguished from its allies by the presence of fused scapes (Giulietti & al 2012) with many sessile or free capitula at apex (Giulietti & Hensold 1990). The group currently comprises 49 species with disjunct distribution between Brazil and Andean Region. Brazil comprises the greatest diversity of the subgenus, with 33 species distributed in the *Campo Rupestre*, *Altitude Grassland* and *Campos Gerais* (Sauthier 2019). The remnant species occur in the Andean Regions of Venezuela, Colombia, Ecuador, Peru, Costa Rica and Panama (Tissot-Squalli 1997).

The Altitude Grassland and Andean Region are related due to their remarkable floristic similarity (Safford 2007) and by the disjunct geographic distribution of the taxa they harbour (Fiaschi & Pirani 2009). There are many cases of few restrict species to subtropical or tropical high-altitude areas of southern

Brazil and belongs to genera best represented in the Andes (see Fiaschi & Pirani 2009). On the other hand, richness and distribution of *P. subg. Platycaulon* suggests the opposite scenario, which is corroborated by *Agarista* D.Don ex G.Don (Judd 1984), *Bromelioideae* Burnett (Givnish 2011), *Gaylussacia* Kunth (Romão 2011), and *Leandra* Raddi s.str. (Reginato & Michelangeli 2019). The cause of these disjunct patterns and asymmetric diversity has been poorly investigated. In the case of *Leandra* s.str., range expansions during Pleistocene colder periods followed by local extinctions during interglacial periods associated with short-dispersion by stepping-stone were possibly related with the shaping of its currently distribution (Reginato & Michelangeli 2019).

Recent phylogenetic reconstructions using an incomplete sampling of *Paepalanthus* subg. *Platycaulon* recovered different evolutionary scenarios (Peña 2016, Andrino 2018). Whereas the available phylogenetic inferences had not included all *Paepalanthus* subg. *Platycaulon* species, the evidence for its evolutionary and biogeographical history is still limited. Therefore, the aims of the present study are to perform a phylogenetic analysis including a wider taxon sampling of this subgenus, estimating the date of divergence among the species and the ancestral range of distribution. In this thesis, we will use *P. subg. Platycaulon* as model to test species hypotheses about the origin and maintenance of biodiversity in the Andes and Brazilian *Campo Rupestre*, *Altitude Grassland* and *Campos Gerais*. In order to establish a more comprehensive picture on the evolution of the Neotropical biota, the results derived from this study will be analyzed in the light of existing phylogenetic data for other groups of plants and animals.

Objectives

The aims of the present study are (1) to test the monophyly of *P. subg. Platycaulon* based on a molecular phylogeny; (2) to estimate divergence times and reconstruct the ancestral areas of *P. subg. Platycaulon*; (3) to monograph the Andean species, updating data of geographic distribution, morphological variation and conservation status.

Material and Methods

At the moment, I already sampled 12 Brazilian species. The other 21 will be obtained by field expeditions in sites according to the data from reference collections of Eriocaulaceae in SPF, R and BHCB Herbaria. The Andean species will be sampled in 2021 according to the data available in GBIF database (<https://www.gbif.org/>).

Vegetal tissue for molecular analyses will be dried in silica gel (Chase & Hills 1991) and extracted by CTAB (Doyle & Doyle 1987). Sequences of the 49 species will be obtained by *Next Generation Sequencing* (NGS). Target genes will be selected using the Probe kit myBaits Angiosperms 353 v1 48 rxns (Johnson & al 2018) and sequenced on the platform MiSeq (Illumina). The obtained sequences will be edited by Trimmomatic (Bolger & al 2014) and analysed with the pipeline HybPiper (Johnson & al 2016) using reference for the 353 genes (<http://github.com/mossmatters/Angiosperms353>). The inference will be performed by Parsimony (TNT 1.5); Maximum Likelihood (RAxML 8.9.2); and Bayesian (MrBayes 3.2). The calibration will use data of Poales and *P. subg. Xeractis*, the sister group of *P. subg. Platycaulon*.

Ancestral range reconstruction will be made with the package BioGeoBears (Matzke 2015), based at the tree obtained in BEAST. The Brazilian geographic unities will be based in Sauthier (2019) and Colli-Silva & al (2019) and the Andean ones will be in accordance with the distributional data obtained. A dispersion matrix will be incorporate to account the distance changes between the regions along the time: 44.9-30 Ma; 30–10 Ma; e 10 Ma-21 ka. The layer 44.9 Ma correspond to the origin of Eriocaulaceae (Bouchenak-Khelladi & al 2014); 30 Ma, to the origin of *Paepalanthus* (Peña 2016); 10 Ma, to the closure of the Isthmus of Panama in the Middle Miocene (Montes & al 2012) and 21 Ka, to the Last Glacial Maximum (Reginato & Michelangeli 2019).

The taxonomic review will include the Andean species, and will be incorporated into the review carried out for the Brazilian species (Sauthier 2019). This review will be based in analysis of herbarium material, field expeditions and bibliography (Körnicke 1863; Ruhland 1903; Tissot-Squalli 1997).

Justification

The different understandings about *Paepalanthus* along its taxonomic history and biogeography constitute a considerable point for this research. Martius (1835) recognised four subgenera in *Paepalanthus*, while Körnicke (1863) recognised 14 and Ruhland (1903) recognised six subgenera, seven sections, six subsections and five series, distinguished by the organization of the capitula and scape, ramification patterns and flower structure (Giulietti & Hensold 1990).

Nowadays, many of the names allocated in those categories were synonymized or had their taxonomic status modified. *Paepalanthus* subg. *Platycaulon* remains in the infrageneric level, besides the morphology of its inflorescence be exclusive. Based on morphological evidences Giulietti & al (1998) suggested that *P. subg. Platycaulon* could be splitted from *Paepalanthus*. However, the most recent phylogenies could not rescue this scenario. Peña (2016) found *P. subg. Platycaulon* as paraphyletic using species of Brazil and Andean Paramos, while Andrino (2018) found it as monophyletic, based only Brazilian species and a new molecular marker, the nuclear region ETS.

Geographic studies in the context Brazil-Andes are scarce (Sánchez-Baracaldo 2004; Givnish 2011; Peña 2016; Reginato & Michelangeli 2019), and the disjunct distribution in *P. subg. Platycaulon* remains unclear. Dispersal events from Brazilian *Campo Rupestre* and Altitude Grassland to Andean Paramos likely explain the currently *P. subg. Platycaulon* distribution pattern (Peña 2016). However, the *Campos Gerais* in South of Brazil, an important area of *P. subg. Platycaulon* occurrence area was not considered in this analysis.

Previous phylogenies of *Paepalanthus* applying Sanger methods resulted in conflicting topologies. Therefore, NGS sequencing will be a better tool to investigate these relationships, once the volume of obtained data is larger than Sanger (Mamanova & al 2010). Finally, to clarify if *P. subg. Platycaulon* can be segregated from *Paepalanthus* and to understand its geographical distribution, a representative sampling of the species is necessary.

This proposal seeks for US\$2000 to cover the costs of fieldwork in Brazil. For the fieldwork in Andes region, I count to Brazilian public foundation Coordination for the

Improvement of Higher Education Personnel (CAPES). Partnerships with researchers in COL, QCA and USM Herbaria was already established as well.

As outputs of this project, I intend to publish at least three papers: (1) the list of Andeans species and their distribution and conservation in the *Kew Bulletin* or *PhytoKeys*; (2) the phylogeny of *P. subg. Platycaulon* in the *Botanical Journal of the Linnean Society*; (3) the biogeographic history of the group in the *Journal of Biogeography*.

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