

Taxonomy, phylogeny and biogeography of the monophyletic clade *Anthurium* section *Dactylophyllium*

For many biological groups the Neotropics is the region with the highest diversity. (Myers et al., 2000; Antonelli & Sanmartín, 2011; Antonelli et al., 2018). For example, there are ca. 111.000 species of seed plants, more than Asia and Africa together (Antonelli & Sanmartín, 2011). Besides its taxonomic diversity, the Neotropics holds a great diversity regarding phylogenetic, functional traits and ecosystems. This diversity is believed to be the result of high speciation rates as a consequence of several biological and geological events. Also, it is suggested that dispersion is the main factor influencing the actual geographic distribution of the species.

The family Araceae with 3750 species (Boyce & Croat, 2018), is one of the most diverse groups of angiosperms. Additionally, is common to find Araceae as one of the most abundant families in tropical rainforest below 2000 m of altitude (Leimbeck et al., 2004). Although Araceae is widespread around the world, the Neotropics, with 2200 species is the most diverse region, not only in species number but also regarding morphology and ecological characters (Mayo et al., 1997). Despite its diversity, taxonomic work is still needed, and researchers estimate around of 6400 species (Boyce & Croat, 2018), meaning that 44% of the species are still undescribed. Regarding the evolutionary history of the geographic distribution, there are very few studies at global scales, mainly in the tropics of Asia and America (e.g., Nauheimer et al., 2012a, Zuluaga et al., 2019). It has been hypothesized that species of Araceae have restricted and narrow geographic distributions, with each geographic region having high endemism levels (Croat, 1992; Croat et al., 2010; Nauheimer et al., 2012b; Croat & Hannon, 2015).

Anthurium, with 950 described species, is the richest genus in Araceae, it encompasses 26% of the total species richness of the family, and is one of the 20 richest genera of angiosperms. *Anthurium* is restricted to the Neotropics, ranging from southern Mexico and the Antilles to southern Brazil and northern Argentina and Paraguay (Carlsen & Croat 2013, 2019). Ecologically, *Anthurium* is a very important genus in neotropical forests due to its richness and abundance in the understory and as epiphytes. According to studies focused on the distribution patterns of Araceae, *Anthurium*, largely explains the patterns at the family level (Sierra-Giraldo et al., 2013, Mora et al., 2013). Therefore, because of the wide ecological range and high diversity of *Anthurium*, studying its richness, endemism and biogeography, in a phylogenetic context may contribute to understand general patterns of diversity and endemism in the Neotropics and their underlying causes.

The most recent phylogenetic analysis of *Anthurium* supported its monophyly (Carlsen & Croat 2013). However, the understanding of the infrageneric relationships is still limited, due, firstly, to an incomplete taxon sampling (only 10% of the described species were included in the study), and secondly, to low divergence among the markers used. This being a common problem in the different studies that tried to reconstruct the phylogenetic relationships at the species level within Araceae, it has been suggested that it is necessary to adopt a multigenic approach that includes a large number of DNA regions. Even so, Carlsen and Croat (2013) showed that the infrageneric classification based on morphology did not represent the evolutionary history of the genus. For instance, based on morphology, all the species of *Anthurium* with leaves with three or more free segments were classified

into section *Dactylophyllium*; and those species with leaves composed of five or more segments fused at the base, into section *Schizoplacium* (Croat & Sheffer 1983). According to Carlsen and Croat (2013), these two sections should be grouped into a monophyletic section named *Dactylophyllium* with the exception of three species that are not part of this clade.

Recently, the section *Dactylophyllium* has been re-delimited to include 24 species (Croat & Carlsen 2013), but species boundaries are still confusing, especially because the group was last revised completely in 1978 (Madisson 1978). New species are definitely awaiting description, and species limits need better clarification. *Dactylophyllium* is not that large in terms of number of species, which makes this clade ideal for testing phylogenetic and biogeographical hypotheses. Therefore, in this project a thorough taxonomic revision will be carried out (in collaboration with Dr. Monica Carlsen-Missouri Botanical Garden). Additionally, the few studies that have dealt with the molecular systematics of this genus, have shown the need to expand the number of genes use for phylogenetic reconstructions, using tools such as High-throughput DNA sequencing.

To understand the importance and evolutionary history of *Anthurium* in the neotropical forests a complete geographical and morphological database, combined with a well sampled phylogeny are necessary. One of the goals of this research is to provide a molecular phylogeny of all *Anthurium* section *Dactylophyllium*, using High-throughput DNA sequencing. It will be the first molecular phylogeny of a complete monophyletic clade within *Anthurium* and will serve both to test the phylogenetic relationships within the *Dactylophyllium*, and to study the evolution of characters and geographical distributions of this clade. To achieve this goal, we will use tissue samples gathered from extensive field work the last three years, especially in the the Andes of Colombia. Additionally, we will use DNA tissue obtained from herbarium specimens (CUVC, COL and MO) and living collections (Missouri Botanical Garden). We will extract DNA using the Qiagen DNeasy Minikit and quality will be assessed using a Qubit fluorometer (Life Technologies). Molecular data will be obtained using the probes designed by Carlsen (unpublished data) that include the ones designed by Johnson et al. (2018) for 353 nuclear regions available at myBaits® Expert Panels – Plant Universal – Angiosperms (ArborBiosciences). DNA sequences will be. Sequences will be organized and processed using the software Geneious, phylogenetic reconstructions will be done using the software ASTRAL (Mirarab et al., 2014) and Bucky (Larget et al., 2010) and data will be deposited in repositories like GENBANK.

We have almost complete the taxonomical sampling and the resources requested from this fund will be used to do field work looking for some of the missing species, travel to herbaria in Colombia, and more important to cover the sequencing costs of molecular data. The data obtained with the funds of this grant (together with the morphological and geographical data) is expected to be used to produce two articles, one about taxonomic revision, including new species, and another about historical biogeography and evolution of characters.

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