

Introduction

Araliaceae is a diverse plant family (c. 46 genera and 1500 species) distributed mainly in tropical and subtropical regions (Wen et al. 2001). Despite the importance of this family due to the ornamental (e.g. *Hedera*, *Schefflera*), medicinal (e.g. *Panax*, *Eleutherococcus*), and nutritional (e.g. *Aralia*, *Metapanax*) use of some of its members (Li et al., 2013), and how extensively it has been studied from an evolutionary perspective, its evolutionary history has still not been unravelled.

The “Asian Palmate Group” (AsPG) includes more than 50% of generic and species diversity of the family (21-23 genera and c. 850 species, Valcárcel & Wen, 2019; Lowry et al. 2019) and is distributed across four continents, with the highest diversity occurring in Asia (18 genera, c. 400 spp.) and Neotropical America (4 genera, c. 300 spp.). Although the most highly diversified genera of the AsPG exhibit tropical affinity, most of the poorly diversified ones have temperate climate preferences and appear scattered across the group phylogeny (Valcárcel et al. 2014).

Despite the fact that attempts to elucidate the evolutionary history of the AsPG have been made for a long time now (see below), evolutionary relationships of the group remain unclear. First reconstructions, using Sanger techniques, lacked enough resolution (e.g. Wen et al., 2001; Plunkett et al., 2004; Li & Wen, 2016). Valcárcel et al. (2014) found basal incongruences between phylogenies constructed with nuclear and plastid genes, interpreted as hybridization between genera. Subsequent research employing complete plastomes obtained through next generation sequencing (NGS) techniques has provided more resolved phylogenies, yet not totally resolved deep in the AsPG tree (e.g. Li et al., 2013; Valcárcel & Wen, 2019). Altogether these results point to an ancient radiation with inter-genera hybridization occurred at the origin of the AsPG (Valcárcel & Wen, 2019). However, increasing taxonomic sampling and providing with a nuclear NGS phylogeny is necessary to properly evaluate (1) the hybridization-radiation hypothesis and (2) the role of niche differentiation as a determinant factor to understand current biogeographic and diversity patterns in the AsPG.

Objectives

The main objective of the project is to study the evolutionary history of the Asian Palmate Group. We hypothesize that the spatial evolutionary patterns of the group are more conditioned by phylogenetic and ecologic constraints than by dispersal limitations. The first objective will be obtaining both nuclear and plastid NGS phylogenies representing the AsPG species diversity. The second objective will be the ecomorphological characterization of each genus as part of the study of niche differentiation.

Material and Methods

The project, that constitutes part of my PhD project, will be developed at the National Museum of Natural Sciences of the Smithsonian Institution from July 2020 to September 2020. Work will be divided into two working packages: 1) phylogenomic reconstruction of AsPG at Dr. Jun Wen’s lab, and 2) ecomorphological characterization of AsPG genera at the US National Herbarium.

Phylogenetic reconstruction. The next-generation sequencing (NGS) technique HybSeq will be used to provide extensive data of nuclear and chloroplast genes for 102 species of the AsPG group, improving the sampling of the most recent research using plastomes (Valcárcel et al., 2019; 29 species). The first library for this objective has already been obtained in the analytical biology laboratories of the National Museum of Natural

Sciences by Dr. Wen. My work will focus on the obtention of a second library. Plastid genomes will be assembled and analyzed together with the Araliaceae plastomes already available on GenBank (currently c. 25 species). A large dataset of nuclear loci will be obtained from the HybSeq library. This will be the first study to apply NGS techniques for nuclear phylogenetic reconstruction in the Araliaceae family and will allow testing the hypotheses of radiation and hybridization in the AsPG origin.

The laboratory work of this objective will be performed at the analytical biology laboratories of the National Museum of Natural Sciences, as well as the training process for data parsing and assembling techniques. Afterwards, genome assembly and phylogenetic analyses will be performed at the Universidad Autónoma de Madrid. Dr. Jun Wen is one of world experts on Araliaceae, and the HybSeq technique has already been optimized for Araliaceae on her lab. Therefore, her help and this visit are essential for the correct development of my PhD project.

Ecomorphological characterization of the AsPG genera. Herbarium specimens of the AsPG clade collected after 1950, in good conservation status, and belonging to known species will be selected. Among these specimens, functional traits will be measured for those with sufficient plant material and representative of the morphological variation and distribution of the genus, trying to sample the maximum number of specimens as possible. We will try to include a minimum of 20% of species diversity of each lineage and to represent each lineage distribution as accurately as possible with the available material. A preliminary search has indicated that the US National Herbarium has useful material for all of the studied lineages, therefore providing a unique opportunity to study AsPG functional diversity.

Traits will be measured in all the plant structures present in herbarium sheets: leaves (area, dry mass, specific leaf area, serrated margin (y/n), lobulation (y/n), lobe number, leaflet number, division pattern, nerve pattern, symmetry, trichome presence (y/n) and density, stomatal density and morphology), fruits (number, type, length, width), inflorescence (number of flowers, type of inflorescence), branches (spine presence (y/n), spicule presence (y/n)). We also count with the support and knowledge of Dr. Jun Wen, who is a US Herbarium curator, for this part of the project.

The data obtained in this visit will be complemented by additional ecomorphological data obtained from the Royal Botanic Garden of Madrid (Spain), although the representation of the AsPG genera is much lower in this institution. This makes my visit to the US herbarium crucial to obtain enough data. This information will be analyzed with genomic data from the previous objective, as well as distribution and climate data that have already been obtained by our research group. Integrative analysis will be performed at the Universidad Autónoma de Madrid.

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