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First Attempts Using High-Throughput Sequencing in Senecio from the Andes

Authors : L. Salomon, P. Sklenar

Abstract : The Andes hold the highest plant species diversity in the world. How this occurred is one of the most intriguing questions in studies addressing the origin and patterning of plant diversity worldwide. Recently, the explosive adaptive radiations found in high Andean groups have been pointed as triggers to this spectacular diversity. The Andes is the species-richest area for the biggest genus from the Asteraceae family: Senecio. There, the genus presents an incredible diversity of species, striking growth form variation, and large niche span. Even when some studies tried to disentangle the evolutionary story for some Andean species in Senecio, they obtained partially resolved and low supported phylogenies, as expected for recently radiated groups. The high-throughput sequencing (HTS) approaches have proved to be a powerful tool answering phylogenetic questions in those groups whose evolutionary stories are recent and traditional techniques like Sanger sequencing are not informative enough. Although these tools have been used to understand the evolution of an increasing number of Andean groups, nowadays, their scope has not been applied for Senecio. This project aims to contribute to a better knowledge of the mechanisms shaping the hyper diversity of Senecio in the Andean region, using HTS focusing on Senecio ser. Culcitium (Asteraceae), recently recircumscribed. Firstly, reconstructing a highly resolved and supported phylogeny, and after assessing the role of allopatric differentiation, hybridization, and genome duplication in the diversification of the group. Using the Hyb-Seq approach, combining target enrichment using Asteraceae COS loci baits and genome skimming, more than 100 new accessions were generated. HybPhyloMaker and HybPiper pipelines were used for the phylogenetic analyses, and another pipeline in development (Paralogue Wizard) was used to deal with paralogues. RAxML was used to generate gene trees and Astral for species tree reconstruction. Phyparts were used to explore as first step of gene tree discordance along the clades. Fully resolved with moderated supported trees were obtained, showing Senecio ser. Culcitium as monophyletic. Within the group, some species formed well-supported clades with morphologically related species, while some species would not have exclusive ancestry, in concordance with previous studies using amplified fragment length polymorphism (AFLP) showing geographical differentiation. Discordance between gene trees was detected. Paralogues were detected for many loci, indicating possible genome duplications; ploidy level estimation using flow cytometry will be carried out during the next months in order to identify the role of this process in the diversification of the group. Likewise, TreeSetViz package for Mesquite, hierarchical likelihood ratio congruence test using Concaterpillar, and Procrustean Approach to Cophylogeny (PACo), will be used to evaluate the congruence among different inheritance patterns. In order to evaluate the influence of hybridization and Incomplete Lineage Sorting (ILS) in each resultant clade from the phylogeny, Joly et al.'s 2009 method in a coalescent scenario and Paterson’s D-statistic will be performed. Even when the main discordance sources between gene trees were not explored in detail yet, the data show that at least to some degree, processes such as genome duplication, hybridization, and/or ILS could be involved in the evolution of the group.

Keywords : adaptive radiations, Andes, genome duplication, hybridization, Senecio
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