Reconstructing evolutionary relationships in the genus *Packera* (Asteraceae: Senecioneae)

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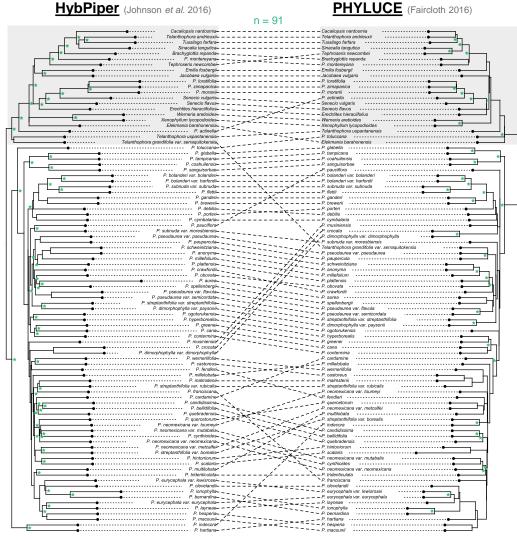
INTRODUCTION

Packera is a genus that contains about 88 species and varieties that are endemic to North America. It was previously included in the genus *Senecio* as the informal group known as "aureoid senecios" but was eventually determined to be a separate genus in 1981 based on chromosome numbers (x=22,23), various morphological differences, and molecular phylogeny data. Ecologically, *Packera* is adapted to a variety of habitats, with some species being abundant and widely distributed, while others are narrow endemics, restricted to specialized or isolated habitats. Taxonomy within *Packera* remains complex due to the species' ability to easily hybridize and polyploidy being common throughout the genus with roughly 40% of taxa being polyploids.

The goal of this study is to better understand the evolutionary history and species relationships within this complicated genus. To do this, I am testing various bioinformatic and tree inference methods to determine which workflow works best with my data to then generate the best fitting tree once sampling is complete. Preliminary trees are shown containing ~85% of *Packera* taxa.

> *Packera* is a good model system to address questions relating to polyploidy, hybridization, and introgression in complex genera.

METHODS

75 *Packera* and 16 outgroup taxa have been sequenced using Hyb-Seq methods that target 1061 COS loci (Mandel *et al.* 2014). PHYLUCE (Faircloth 2016) and HybPiper (Johnson *et al.* 2016) were used for ortholog detection since both methods treat paralogous sequences differently, potentially leading to conflicting results. Initial nuclear phylogenies follow pseudocoalescent (ASTRAL-III) methods (Zhang *et al.* 2018) and were generated using RAxML (Stamatakis 2014). The resulting trees were visualized using the package *phytools* (Revell 2012) in R.

HybPiper (Johnson *et al.* 2016)   **PHYLUCE** (Faircloth 2016)

n = 91

0.05
*Scale bar shows the mean number of nucleotide substitutions per site

Transformed tree with all LPP values can be found here:

LPP values over 0.85 starred (★) at node
Outgroup taxa are shaded

RESULTS & DISCUSSION

The ASTRAL-RAxML trees generated using HybPiper and PHYLUCE are incongruent and appear paraphyletic. Fortunately, most of the *Packera* taxa in the outgroups are believed to be misidentified as *Packera* when they should remain as *Senecio* or reclassified into other genera, so that was to be expected. Unfortunately, some *Packera* varieties are not grouping with their autonyms within both trees (e.g., *P. subnuda* var. *subnuda* and *P. subnuda* var. *moresbiensis*), showing that there is potentially introgression or hybridization between taxa.

Overall, HybPiper is considered a better fit to the data. The HybPiper tree retained more loci than PHYLUCE and appears to have better support; however, there are many paralog warnings using HybPiper which raises concern (Table 1). Paralogs were expected since polyploidy typically leads to more paralogous sequences (Zhang *et al.* 2019). Given this, I am investigating the paralogs within HybPiper and exploring approaches to prune the loci that have extensive paralog warnings. In addition, I am currently investigating further into the PHYLUCE and HybPiper data. An interesting discovery made so far is that the underlying PHYLUCE alignment has many '?'s (~84% of alignment), potentially biasing the results. Further investigations are required.

Table 1. Summary statistics of HybPiper and PHYLUCE phylogenies

ASTRAL - RAxML	HybPiper	PHYLUCE
Sequence length (bp)	543,269	439,880
# loci retained (out of 1,061)	1,027	863
# loci w/ paralog warnings	848	N/A
Pairwise % identity	58.6%	87.8%
Parsimony informative sites (PIS; bp)	107,259	48,929

CITATIONS Faircloth (2016). *Bioinformatics*, 32(5), 786–788.; Johnson *et al.* (2016). *Appl Pl Sci*, 4(7), 1600016.; Mandel *et al.* (2014). *Appl Pl Sci*, 2(2), 1300085.; Revell (2012). *Methods Ecol Evol*, 3(2), 217–223.; Stamatakis (2014). *Bioinformatics*. 30(9), 1312-1313.; Zhang *et al.* (2018) *BMC Bioinformatics*, 19(Suppl 6), 15-30.; Zhang *et al.* (2019). *Horticultural Plant Journal*, 5(6), 231-239.

Top images (left to right): *Packera werneriifolia*, *P. glabella*, & *P. greenei*