

## PHYLOGEOGRAPHY OF THE ARGENTINE MISTLETOE, *LIGARIA CUNEIFOLIA* (LORANTHACEAE)

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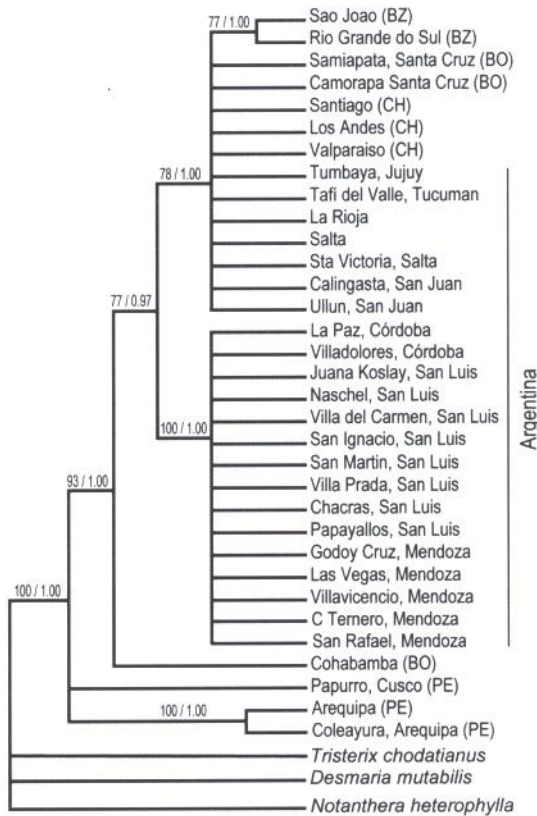
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South America harbors several mistletoes considered relictual in Loranthaceae (Barlow, 1983), including the genus *Ligaria* which has two endemic stem-parasitic species in South America (Kuijt, 1990). The most widely distributed is *Ligaria cuneifolia* (R. et P.) Tiegh. which is found from Peru to Central Argentina and is also present in Bolivia, central Chile, Uruguay and southern Brazil. In Argentina, it has a disjunct distribution between three regions: the Andes from Jujuy-Salta to Mendoza (its primary range), the central part of the country (Sierra of San Luis and Córdoba) and in the Mesopotamia region (Corrientes and Entre Ríos) (Abbiatti, 1946). The primary hosts for *L. cuneifolia* are members of Fabaceae such as *Prosopis*. Hummingbirds pollinate the flowers of *L. cuneifolia*, attracted to its large, tubular, bright red flowers with bright yellow filaments, anthers and style. Fruits are black at maturity and are dispersed by birds. The objective of the present study is to reconstruct the phylogeography of *L. cuneifolia* using molecular markers. Two DNA chloroplast regions (*trnL-F* and *atpB-rbcL*) were amplified from

33 samples collected from various localities (Fig. 1). Three other South American loranth species were also sampled and used as outgroups. DNA extraction, amplification and sequencing protocols followed Amico et al. (2007). Individual sequences were aligned manually using BioEdit. Both chloroplast regions had indels that were manually coded as present or absent. Gaps were considered homologous only when they shared identical boundaries and length. Nine indels were coded for the *atpB-rbcL* and seven for the *trnL-F* partitions. Maximum parsimony (MP) analyses with the branch-and-bound search option were implemented in PAUP\*. Nodal support was assessed using the nonparametric bootstrap (BS) with 100 pseudoreplicates. Bayesian inference (BI) was also performed using MrBayes where the model of sequence evolution was determined using MrModeltest.

Including the outgroup, the aligned positions, variable sites, and parsimony informative sites for the two partitions were as follows: *atpB-rbcL* (897, 151, 45) and *trnL-F* (660, 116, 56). MP and BI of both chloroplast regions resulted in trees



**Fig. 1.** Cladogram obtained from the combined chloroplast regions for each individual representing the different localities. Numbers above lines are bootstrap values for maximum parsimony and posterior probabilities from Bayesian inference analyses, respectively. Abbreviations: **BO**, Bolivia, **BZ**, Brazil, **CH**, Chile; **PE**, Peru.

with congruent topologies, thus they were concatenated into one chloroplast partition. Analysis of this partition yielded seven equally parsimonious trees ( $L = 307$ ). All analyses provided strong support for a monophyletic ingroup (*Ligaria*). The three localities from Peru were resolved as sister to the remaining ones (Fig. 1). One sample

(Cohabamba) from Bolivia is sister to a clade composed of the remaining localities. The latter comprises two clades, one of localities from the central portion (the Central clade) and another of localities mainly from the north of its distribution (the Northern clade). The localities from this last clade form a polytomy involving individuals from Bolivia, Chile, northwest Argentina (from Salta to San Juan), and a clade of the two localities from Brazil. Unfortunately this study did not include samples from the Mesopotamia region of Argentina, but presumably they would resolve as sister to the Brazilian samples. The Central clade includes all the localities from Mendoza, San Luis and Córdoba (central part of Argentina). Interestingly, although separated by 200 km, the Mendoza localities are genetically more similar to those from central Argentina than to the geographically closer localities from San Juan and Chile.

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