

TABLA S1. Lista de números de Genbank para las especies de *Dysopsis* y los grupos externos. / Genbank numbers for *Dysopsis* species and outgroups.

Taxon	Numero de Genbank			
	<i>pbsa-trnH</i>	<i>rpl16</i>	<i>YCF1</i>	ITS
<i>Colliguaja integerrima</i>	-	JN249420	-	-
<i>Chrozophora</i> sp.	-	-	-	KSUFS341
<i>Conceveiba martiana</i> Baill.	-	-	-	DQ006004
<i>Conceveiba maynasensis</i> Secco	-	-	-	DQ006005
<i>Dysopsis glechomoides</i> 710	OQ689403	OQ789550	OQ833191	OQ679945
<i>Dysopsis glechomoides</i> 720	OQ689405	OQ789551	OQ833190	OQ679947
<i>Dysopsis glechomoides</i> 730	OQ689404	OQ789552	OQ833189	OQ679946
<i>Dysopsis glechomoides</i> 740	OQ689402	OQ789553	OQ833188	OQ679948
<i>Dysopsis paucidentata</i> 1000	OQ689408	OQ789555	OQ833183	OQ679950
<i>Dysopsis paucidentata</i> 2000	OQ689407	OQ789556	OQ833182	OQ679951
<i>Dysopsis paucidentata</i> 3000	OQ689406	OQ789557	OQ833181	OQ679952
<i>Dysopsis paucidentata</i> 4000	OQ689409	OQ789554	OQ833180	OQ679949
<i>Dysopsis chilensis</i> p181	OQ689401	OQ789536	OQ833187	OQ679984
<i>Dysopsis chilensis</i> p182	OQ689398	OQ789539	OQ833186	-
<i>Dysopsis chilensis</i> p183	OQ689399	OQ789538	OQ833185	OQ679985
<i>Dysopsis chilensis</i> p184	OQ689400	OQ789537	OQ833184	OQ679983
<i>Dysopsis hirsuta</i> CR10	OQ689417	OQ789540	OQ833195	OQ675570
<i>Dysopsis hirsuta</i> CR20	OQ689413	OQ789544	OQ833194	OQ675568
<i>Dysopsis hirsuta</i> CR30	OQ689411	OQ789541	OQ833193	OQ675576
<i>Dysopsis hirsuta</i> CR40	OQ689410	OQ789546	OQ833192	OQ675574
<i>Dysopsis hirsuta</i> MS10	OQ689418	OQ789543	OQ833199	OQ675571
<i>Dysopsis hirsuta</i> MS20	OQ689412	OQ789547	OQ833198	OQ675579
<i>Dysopsis hirsuta</i> MS30	OQ689420	-	OQ833197	OQ675575
<i>Dysopsis hirsuta</i> MS40	OQ689421	-	OQ833196	OQ675577
<i>Dysopsis hirsuta</i> PY20	OQ689419	OQ789545	OQ833201	OQ675573
<i>Dysopsis hirsuta</i> PY30	OQ689416	OQ789542	OQ833200	OQ675578
<i>Dysopsis hirsuta</i> PY40	OQ689414	OQ789549	-	OQ675569
<i>Dysopsis hirsuta</i> PY10	OQ689415	OQ789548	OQ833202	OQ675572
<i>Macaranga subdentata</i> Benth	-	-	-	DQ866583
<i>Macaranga henryi</i> (Pax & K. Hoffm.) Rehder	KR533531	-	-	-
<i>Ricinus communis</i> L.	MT555101	MT555101	MT555101	MN880886

TABLA S2. Lista de partidores. / Primers list.

Marcador	Nombre del primer	Primer	Referencia*
ITS	ITSA	GGAAGGAGAAGTCGTAACAAGG	Blattner 1999
	ITS4	TCCTCCGCTTATTGATATGC	White <i>et al.</i> 1990
Espaciador intergénico <i>psba-trnH</i>	psbAF	GTTATGCATGAACGTAATGCTC	Sang <i>et al.</i> 1997
	trnHR	CGCGCATGGTGGATTCACAATC	Sang <i>et al.</i> 1997
Intron <i>rpl16</i>	rpl16-F71	GCTATGCTTAGTGTGTGACTCGTT	Jordan <i>et al.</i> 1996
	rpl16-R1516	CCCTTCATTCTTCTCTATGTTG	Jordan <i>et al.</i> 1996
YCF1	ycf1-4182F	AAATAYRRATAGAAAATATTTKGATT	Franck <i>et al.</i> 2012
	ycf1-5248R	GAATTCTYAATTCTCTACGACG	Franck <i>et al.</i> 2012

***REFERENCIAS**

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- Franck, A., Cochrane, B., Garey, J. 2012. Low-copy nuclear primers and YCF1 primers in Cactaceae. American Journal of Botany: e405-e407. <https://doi.org/10.3732/ajb.1200128>
- Jordan, W.C., Courtney, M.W., Neigel, J.E. 1996. Low levels of intraspecific genetic variation at a rapidly evolving chloroplast DNA locus in North American duckweeds (Lemnaceae). American Journal of Botany 83: 430-439.
- Sang, T., Crawford, D., Stuessy, T. 1997. Chloroplast DNA phylogeny, reticulate evolution, and biogeography of Paeonia (Paeoniaceae). American Journal of Botany 84: 1120-1136.
- White, T., Bruns, T., Lee, S., Taylor J. 1990. Amplification and direct sequencing of fungal ribosomal DNA genes for phylogenetics. En: Innis, M., Gelfand, D., Snrnsky, J., White, T. (Eds.) PCR Protocols: a guide to methods and amplifications, pp. 315-322. Academic Press, New York.

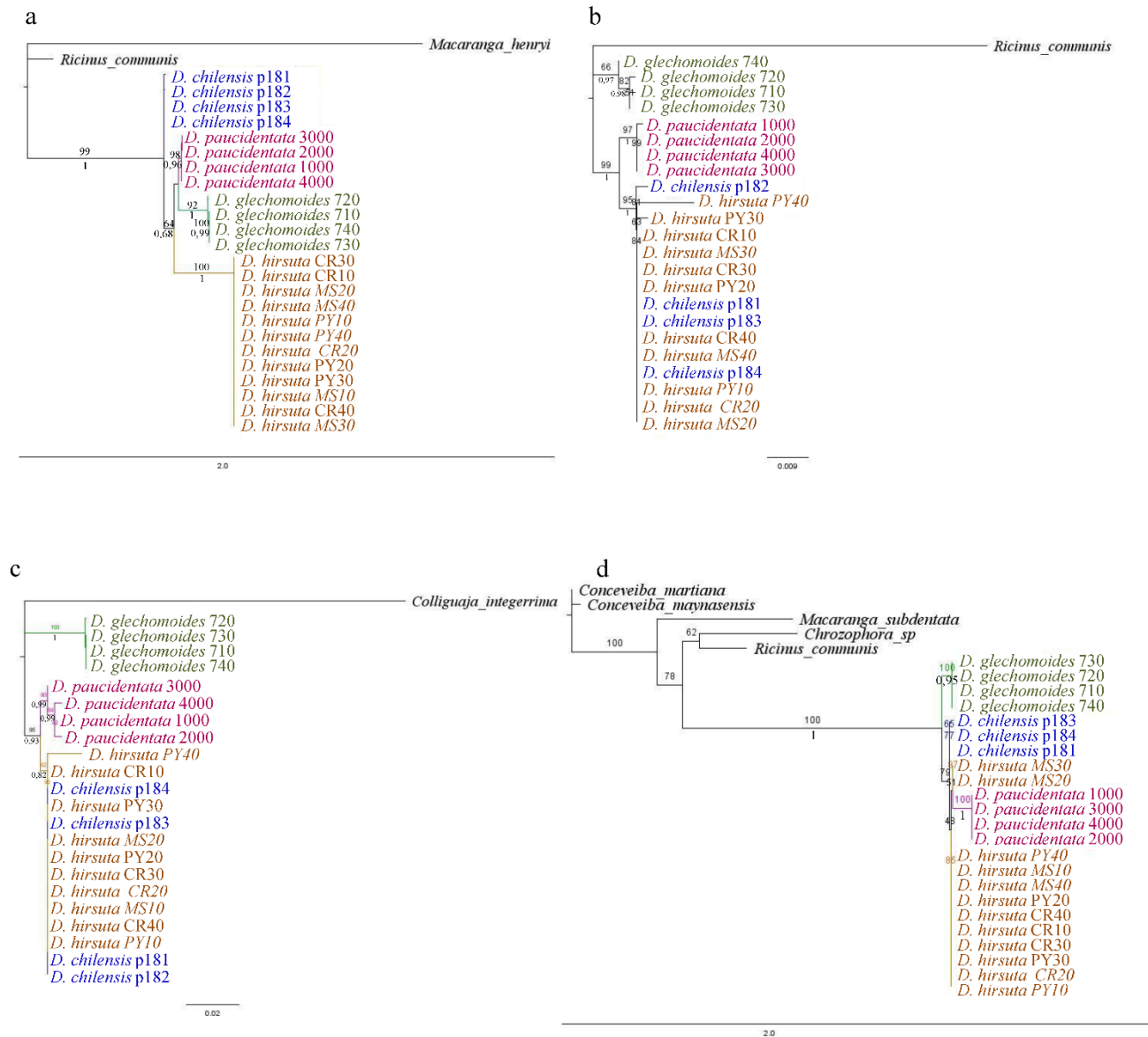


FIGURA S1. Árboles de genes de *Dysopsis* obtenidos por Máxima Verosimilitud. a. Espaciador intergénico *psba-trnH*, b. *ycf1*, c. intron *rpl16*, d. ITS. Cada una de las especies es está representada por cuatro accesiones, excepto *D. hirsuta* que tiene 10 a 12. Los números encima de las ramas son valores de ultrafast bootstrap y los números debajo de las ramas son probabilidad posterior. / *Dysopsis* genes trees obtained by Maximum likelihood. a. intergenic spacer *psba-trnH*, b. *ycf1*, c. intron *rpl16*, d. ITS. Each of the species is represented by four accessions, except *D. hirsuta* which has between 10 to 12. The numbers above the branches are ultrafast bootstrap values and the numbers below the branches are posterior probability.

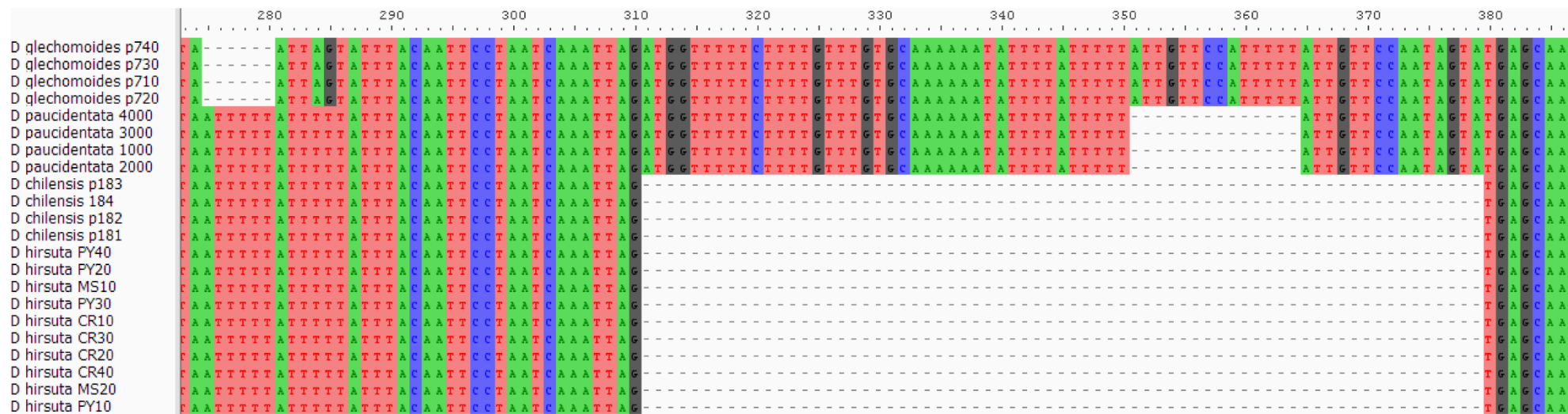


FIGURA S2. Región del *rpl16* para mostrar los indels presentes en las especies de *Dysopsis*. / *rpl16* region showing the indels in *Dysopsis* species

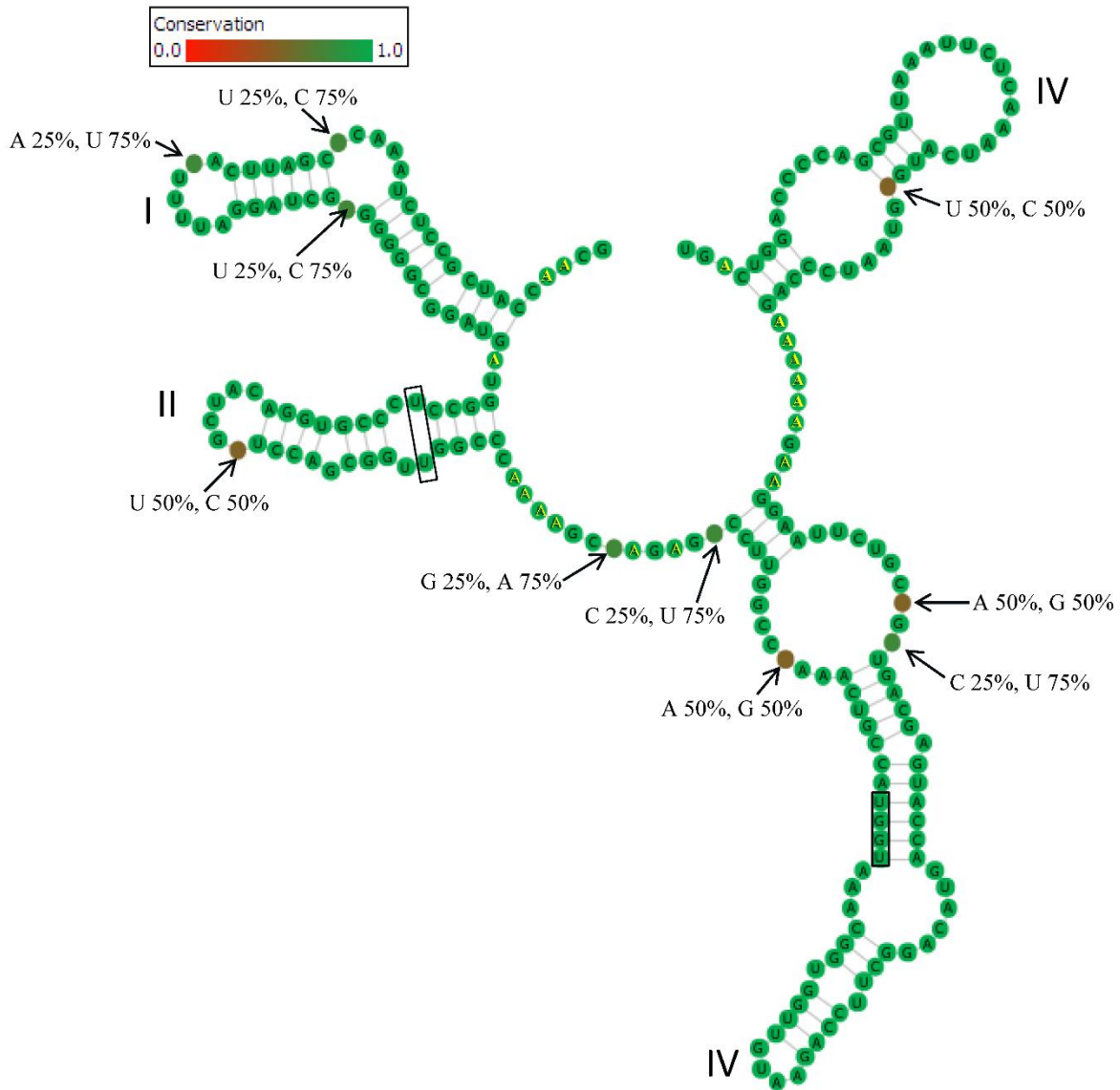


FIGURA S3. Estructura secundaria de consenso del ITS2 obtenida de una accesión de cada especie de *Dysopsis*. Las regiones conservadas en angiospermas se reconocen en la estructura secundaria de *Dysopsis* (Los stem se numeran de I a IV), y están marcadas en cuadros (hélice II: mismatch U U, hélice III UGGU) y como letras amarillas (alto contenido de A) entre los stem. El grado de conservación de la estructura secundaria va de pardo (altamente variable) a verde (conservado). Se incluye la frecuencia de las bases en los sitios variables. / Consensus secondary structure of ITS2 obtained from one accession of each *Dysopsis* species. Regions conserved in angiosperms are recognized in *Dysopsis* secondary structure (stems are numbered I to IV), and are marked in boxes (helix II: mismatch U U, helix III UGGU) and as yellow letters (high A content) among the stems. The degree of preservation of secondary structure ranges from brown (highly variable) to green (conserved). The frequency of the bases at the variable sites is showed.