

Table Appendix 3: Table with target-specific primer pair sequences and citations for each gene region (and segments).

Gene Region	Ex-pected Length (bp)	Primer Pair Name	5' Primer	5' Sequence	5' Reference	3' Primer	3' Sequence	3' Reference
ITS	650	ITS	ITS-5	ggAAggAgAAgTCgTAACAAgg	White <i>et al.</i> (1990); Baldwin (1992)	ITS-4	TCCTCCgCTTATTgATATgC	White <i>et al.</i> (1990); Baldwin (1992)
atpB	1497	atpB1	S1494R	TCAgTACACAAAgATTTAAggTCAT	Hoot <i>et al.</i> (1995)	S611	AACgTACTCgTgAAggAAATgATCT	Hoot <i>et al.</i> (1995)
		atpB2	S766R	TAAcATCTCggAAATATTCcGCAT	Hoot <i>et al.</i> (1995)	S2	TATgAgAAATCAATCCTACTACTTCT	Hoot <i>et al.</i> (1995)
ndhF	2086	ndhF1	ndhF 5'-PCR	ATggAACAgACATATCAATATgSgTgg	Olmstead and Sweere (1994)	ndhF 803R	gAAAAATTCCCgCCgCTACCATAg	Olmstead and Sweere (1994)
		ndhF2	ndhF 803	CTATggTAgCggCgggAATTTTTC	Olmstead and Sweere (1994)	ndhF 1318R	CgAAACATATAAAATgCRgTTAATCC	Olmstead and Sweere (1994)
		ndhF3	ndhF 1318	ggATTAACYgCATTTTATATgTTTCg	Olmstead and Sweere (1994)	ndhF 3'-PCR	CCCYASATATTTgATACCTTCKCC	Olmstead and Sweere (1994)
matK	1491	matK1	matK1F	ACTgTATCgCACTATgTATCA	Sang <i>et al.</i> (1997)	matK4R	gCATCTTTTACCCARTAgCgAAg	Bremer <i>et al.</i> (2002)
		matK2	matK3F	AAgATgCCTCTTCTTTGCAT	Sang <i>et al.</i> (1997)	matK3R	gATCCgCTgTgATAATgAgA	Sang <i>et al.</i> (1997)
rbcL	1408	rbcL	rbcL 5'-PCR	ggCCgTCgACATgTCACCACAAACAgARACTAAAgC	Olmstead and Palmer (1994)	rbcL Z674R	gATTTCgCCTgTTTCggCTTgTgCTTTATAAA	Olmstead and Palmer (1994)
trnTLF	1500	trn.ab	^a (B48557)	CATTACAAATgCgATgCTCT	Taberlet <i>et al.</i> (1991)	^b (A49291)	TCTACCgATTTCgCCATATC	Taberlet <i>et al.</i> (1991)
		trn.cf	^c (B49317)	CgAAATCggTAgACgCTACg	Taberlet <i>et al.</i> (1991)	^f (A50272)	ATTgAACTggTgACACgAg	Taberlet <i>et al.</i> (1991)

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References

Baldwin B.G. 1992. Phylogenetic utility of the internal transcribed spacers of nuclear ribosomal DNA in plants: an example from the compositae. *Molecular Phylogenetics and Evolution* 1:3–16.

Bremer B., Bremer K.A., Heidari N., and Erixon P. 2002. Phylogenetics of asterids based on 3 coding and 3 non-coding chloroplast DNA markers and the utility of non-coding DNA at higher taxonomic levels. *Molecular Phylogenetics and Evolution* 24:274–301.

8 Hoot S.B., Culham A., and Crane P.R. 1995. The Utility of *atpB* Gene Sequences in Resolving Phylogenetic Relationships: Comparison with *rbcL* and 18S Ribosomal DNA Sequences in the Lardizabalaceae. *Annals of the Missouri Botanical Garden* 82:194–207.

Olmstead R.G. and Palmer J.D. 1994. Chloroplast DNA Systematics: A Review of Methods and Data Analysis. *American Journal of Botany* 81:1205–1224.

Olmstead R.G. and Sweere J.A. 1994. Combining Data in Phylogenetic Systematics: An Empirical Approach Using Three Molecular Data Sets in the Solanaceae. *Systematic Biology* 43:467–481.

Sang T., Crawford D., and Stuessy T. 1997. Chloroplast DNA phylogeny, reticulate evolution, and biogeography of *Paeonia* (Paeoniaceae). *American Journal of Botany* 84:1120–1136.

Taberlet P., Gielly L., Pautou G., and Bouvet J. 1991. Universal primers for amplification of three non-coding regions of chloroplast DNA. *Plant Molecular Biology* 17:1105–1109.

White T., Bruns T., Lee S., and Taylor J. 1990. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. *In* *PCR Protocols: A Guide to Methods and Applications* (M. Innis, D. Gelfand, J. Shinsky, and T. White, eds.), pages 315–322, Academic Press.