

Evolutionary dynamics of the chloroplast genome sequences of six *Colobanthus* species

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Table S6. RNA editing sites predicted in the CP genomes of eight *Colobanthus* species using the PREP program.

Gene	Nucleotide position	Amino acid position	Codon change	Amino acid change	Score
<i>accD</i>	74	25	ACG => ATG	T => M	1.00
	229	77	CCT => TCT	P => S	1.00
<i>atpA</i>	914	305	TCA => TTA	S => L	1.00
	1270	424	CCC => TCC	P => S	1.00
<i>atpB</i>	419	140	ACA => ATA	T => I	0.86
<i>atpF</i>	–	–	–	–	–
<i>atpI</i>	–	–	–	–	–
<i>ccsA</i>	–	–	–	–	–
<i>clpP</i>	559	187	CAT => TAT	H => Y	1.00
<i>matK</i>	637	213	CAT => TAT	H => Y	1.00
<i>ndhA</i>	566	189	TCA => TTA	S => L	1.00
	1073	358	TCC => TTC	S => F	1.00
<i>ndhB</i>	149	50	TCA => TTA	S => L	1.00
	467 ^s	156 ^s	CCA => CTA	P => L	1.00
	542	181	ACG => ATG	T => M	1.00
	586	196	CAT => TAT	H => Y	1.00
	611	204	TCA => TTA	S => L	0.80
	737	246	CCA => CTA	P => L	1.00
	746	249	TCT => TTT	S => F	1.00
	830	277	TCA => TTA	S => L	1.00
	836	279	TCA => TTA	S => L	1.00
	1481	494	CCA => CTA	P => L	1.00
<i>ndhD</i>	29	10	ACG => ATG	T => M	1.00
	53	18	ACA => ATA	T => I	1.00
	94	32	CTT => TTT	L => F	1.00
	410	137	TCA => TTA	S => L	1.00
	637	213	CCG => TCG	P => S	1.00
	1325	442	TCA => TTA	S => L	0.80
	1337	446	TCA => TTA	S => L	0.80
	1366	456	CTT => TTT	L => F	0.80
	1424	475	ACT => ATT	T => I	1.00
	1487	496	GCT => GTT	A => V	0.80
<i>ndhF</i>	290	97	TCA => TTA	S => L	1.00
	586	196	CTT => TTT	L => F	0.80
	1769 ^ε	590 ^ε	CCT => CTT	P => L	0.80
<i>ndhG</i>	166	56	CAT => TAT	H => Y	0.80

	250	84	CCA => TCA	P => S	1.00
	314	105	ACA => ATA	T => I	0.80
<i>petB</i>	418	140	CGG => TGG	R => W	1.00
<i>petD</i>	–	–	–	–	–
<i>petG</i>	–	–	–	–	–
<i>petL</i>	–	–	–	–	–
<i>psaB</i>	–	–	–	–	–
<i>psaI</i>	28	10	CTT => TTT	L => F	0.86
<i>psbB</i>	–	–	–	–	–
<i>psbE</i>	–	–	–	–	–
<i>psbF</i>	–	–	–	–	–
<i>psbL</i>	17	6	ACG => ATG	T => M	1.00
<i>rpl2</i>	–	–	–	–	–
<i>rpl20</i>	–	–	–	–	–
<i>rpoA</i>	–	–	–	–	–
<i>rpoB</i>	169	57	CAT => TAT	H => Y	1.00
	473	158	TCA => TTA	S => L	0.86
	551	184	TCA => TTA	S => L	1.00
	566	189	TCG => TTG	S => L	1.00
	2033/2036*	678/679*	GCA => GTA	A => V	1.00
	2177/2180*	726/727*	GCG => GTG	A => V	1.00
<i>rpoC1</i>	41	14	TCA => TTA	S => L	1.00
<i>rpoC2</i>	1493	498	ACG => ATG	T => M	0.86
	2278	760	CGG => TGG	R => W	1.00
<i>rps14</i>	80	27	TCA => TTA	S => L	1.00
<i>rps16</i>	–	–	–	–	–
<i>rps2</i>	248	83	TCA => TTA	S => L	1.00
<i>rps8</i>	–	–	–	–	–
<i>ycf3</i>	–	–	–	–	–

[§] - RNA editing site not observed for *C. lycopodioides*;

[‡] - RNA editing site not observed for *C. acicularis*;

*- RNA editing sites with shifted position revealed for *C. quitensis*