

Supplementary Data

Manuscript: Plastid genome evolution across the genus *Cuscuta* (Convolvulaceae): two clades within subgenus *Grammica* exhibit extensive gene loss

Authors: Thomas Braukmann, Maria Kuzmina, and Saša Stefanović

Supplementary Table 2 – Oligonucleotides used in this study. Primers were used to amplify hybridization probes for the plastid and mitochondrial genes surveyed.

Gene	Primer name	Primer sequence (5' to 3')
16S rDNA	16S-F2	GACACGGCCCAGACTCCTAC
	16S-R4	ATCCAGCCGCACCTTCCAG
23S rDNA	23S 5F	GGCTTACGGTGGATACCTAG
	23S 4R	TTCAACATCAGTCGGTTCGG
<i>ndhA</i>	<i>ndhA</i> .ex1-F2	GAAGTCTATGGGATCATATG
	<i>ndhA</i> .ex1-R2	GACATAAGAAGTCCAACGGG
	<i>ndhA</i> .ex2-F1	TAAYAGTTYAAGTACAGTTG
	<i>ndhA</i> .ex2-F2	GGTAAAGTCCATCTTGTTCG
<i>ndhB</i> ¹	7F	GGAAGTTTSATTTTCCCAGAATG
	10R	CCTTCGTAGACGTCAGGAGTCCATTG
	12F	CTTTCTGTTACTTCGAAAGTAGC
	14R	GGTATAGTAGATGCTATCACACA
<i>ndhC</i>	<i>ndhC</i> -F1	GTTTCTGCTTTACGAATATG
	<i>ndhC</i> -R1	ATAAGCACGAAAATGAAAGC
<i>ndhD</i>	<i>ndhD</i> .5'-F1b	CTCCTTCTAACGACTTATGC
	<i>ndhD</i> .5'-R2	AATATAGAATGGGCATGAGG
	<i>ndhD</i> .3'-F2	GCAGCTTTAACATCTCTTGG
	<i>ndhD</i> .3'-R1b	ATGAAAGAACGAAATCCGGG
<i>ndhE</i>	<i>ndhE</i> -F1	ATGTACTIONTTTTGAGTGCC
	<i>ndhE</i> -R1tob	TTATTCAACAAATTTGATTG
<i>ndhF</i> ²	536F	TTGTAATAATCGTAGGGGA
	1318R	CGAAACATATAAAATGCRGTTAATCC
<i>ndhG</i>	<i>ndhG</i> -F1	CCAATACATGATTTTCTTTT
	<i>ndhG</i> -R3	CGAGCTACAGCAATTGCACC
<i>ndhH</i>	<i>ndhH</i> .5'-F1	CTCATGATAGTCAATATGGG
	<i>ndhH</i> .5'-R2	TCTGCGACCAATATCCGCC
	<i>ndhH</i> .3'-F3	GAAGGAGATTCATTAGCTCG
	<i>ndhH</i> .3'-R3b	TTGATAAAAACCTGGTGGGCG
<i>ndhI</i>	<i>ndhI</i> -F2	ATGCTCCCTATGATAACTG
	<i>ndhI</i> -R1	TGTGTAATCATCAATTACTG
<i>ndhJ</i>	<i>ndhJ</i> -F1	TCGTTTGTCTGTTTGGCTAG
	<i>ndhJ</i> -R1	CAATGAGCATCTTGTATTTT
<i>ndhK</i>	<i>ndhK</i> -F2b	ACTCTCTAGTTTATGGCCCG

	ndhK-R1tob	TCTCGAGATATTTTCTTACG
<i>psaA</i>	psaA 5'F	TCGAGGAATGGGCCAGAC
	psaA 5'R	GGCCCCTGACCTAGTAAATGG
<i>psaB</i>	psaB angio F1	CATTAMGATTTCCAAGGTTTAGC
	psaB angio R1	ATACTGTGCCCAATCCCG
	psaB angio F3	RGGKCGTGGRCAATAAGG
	psaB angio R3	CCTACMGAAAAGTGRGCTAATCCA
<i>psaC</i>	psaC angio F	TGTGTHCGAGCHTGYCCYACDGAT
	psaC angio R	CCCATRCTKCGRGTGTMTCT
<i>psbA</i>	psbA angio F	TGGGGTCGCTTCTGTAA
	psbA angioR	AGGTCTAGAGGGAAGTTRTGA
<i>psbB</i>	psbB f	AGCGGTTTTTGATCCTTCTG
	psbB r	CTGACGCCGTTGAGTTCAC
<i>psbC</i>	psbC 46F	GGTTYGCTTGGTGGGCGYGGGAATCG
	psbC 49R	GTATTATTGAACCAGACAAAACAACAAGC
<i>psbD</i>	psbD 40F	ATGACTGGTTACGRAGGGACCG
	psbD 45R	CCTCCTCAGGGAATATAAGRTTTTCAT
<i>psbE</i>	psbE angio F	GGAAGCACAGGAGAACG
	psbE angio R	AATBCCTTGTCGGCTCTCT
<i>rbcl</i>	rbcl 3F	GGAGAAAAAGATCAATATATTGC
	rbcl 14R	GGTAAAGAAACCCAATCTTGAG
<i>petA</i>	petA f	CGGACATCCATTTCAAGTGC
	petA 1R	TTGGTCAATTGGACCTTCTC
<i>petB</i>	petB exon 2 F	GAAGAACGTCTCGAGATTCAAGC
	petB exon 2 R	GGCCCAGAAATACCTTGTTTACG
<i>petD</i>	petD exon 2 F	GGAGAGCCCCGCATGG
	petD 3' exon R	GTAATGTTGCACCAATGCCC
<i>atpA</i>	atpA angio F1	ATCCGTGAACGTATTGARCA
	atpA angio R1	CCAKYTYTCTGAATAGCTT
<i>atpB</i>	atpB H ³	TGTCCTGAAGTTCTTTGTAACGTTG
	atpB P ³	CCCCTTGATAATTTAGGTCC
<i>atpF</i>	atpF angio F	GTTTHYTTGGGYCACTG
	atpF angio R	RCTAKAGCTCCTYGTAAHGCTT
<i>atpH</i>	atpH angio F	ATGAATCCAYTGRTTKCTGC
	atpH angio R	GCTACRACCARRCCRTAAA
<i>atpI</i>	atpI angio F	TCCARRTYCATGSCCARG
	atpI angio R	ACAGGTATAGGAACYACYRARGGTAC
<i>rpoA</i>	rpoA F1	SAGTGGAAARTGTGKGAATCA
	rpoA R3	TCYTBVSTSTTABTCAAAAGKTCC
<i>rpoB</i>	rpoB F2	TAGTYCTATYATCAGCTATGGG
	rpoB R4	TCCAAYCCMGTCCAACAATGC
<i>rpoC1</i>	rpoC1 F2	GATACACTTCTTGATAATGG

<i>rpoC2</i>	rpoC1 3`R5 rpoC2 F3 rpoC2 R5	GACCAACAGTGGTTCGAATG CATTAAGAACTTTTCATACYGG ATCCGYTGGACATAGATCCA
<i>rps2</i>	rps2 1 rps2 3c	GCGAATACTAATTTGTTAAG GGAACATAAATTTGGAAGAG
<i>rps4</i>	rps4 angio F	GCTTTACCNGGACTAACTA
	rps4 angio R	CTATCTATKATTTGATTDACTAATCC
<i>rps7</i>	rps7 angio F	GAAACAAATCCACTATCYGTTTTAC
	rps7 angio R	GCAAAAAGCTCTATTTGCCCTCT
<i>rps16</i>	rps16 3`F1b rps16 3`R1b	GAGCCGTCTATCGAATCG TTAGGATTGATTAGGACG
<i>rpl2¹</i>	20F 25R	AAAGGTCGTAATGCCAGAGGAGGAAT TTCCAAGYGCAGGATAACCCCA
<i>rpl14</i>	rpl14 angio F	GGGCTCGAGAATTGATGTG
	rpl14 angio R	CCTCRGGAGCTARKGAACTAT
<i>rpl20</i>	rpl20 angio F	CGGAGRCGTMGAACAAAAAT
	rpl20 angio R	TTGTGCAAGTATTTTACGRTTAAGAAG
<i>rpl23</i>	rpl23 angio F	GGATGGAATCAAATATGCAG
	rpl23 angio R	YTMTAAGAGGTGGAATAGAATAACC
<i>rpl32</i>	rpl32 F rpl32 R	GGCAGTTCCAAAAAACG ACTTATTTATTTTGTGGCGTA
<i>accD</i>	accD 5`F1 accD 5`R3 cus F cus R	GGGGGCAAGAAAACCTATG CAAATGATATCCACATTGTTTAC CRTTAGGGATAKSAMCGGAG AAGYACSGGGTTCGGTAA
<i>ccsA</i>	ccsA ang F ccsA ang R	GGATTATTARTTACTCGTTGG TCCAAGTAATAAAWGCCCAAG
<i>cemA</i>	cemA ang F cemA ang R	GGRTTACTAATTGGTGAATAC TTGAATGATAAATCACTACAAG
<i>clpP</i>	clpP intr1/2F clpP 2Rb	CCTAATCAACCGACTTTATC AGCGTGAGGGAATGCTAGAC
<i>matK</i>	trnK 685F matK 1932R matK MonoEx 4F matK MonoEx R3	GTATCGCACTATGTATCATTTGA CAGAACGGATTACTAATGGG ATCTCAGAATTTACGATCAATTC CCCAAGCTTTGTAAAAAAGCGCG
<i>ycf1 5`</i>	ycf1 5` F1 ycf1 5` R2	AAATTCGGTCGTTGTGGTCGGAC AAGATATTCKTTSTTTTCCATCA
<i>ycf2 3`</i>	ycf2 ang 3`F ycf2 ang 3`R	TTGTAGCACTTACCAATGAGG TCATTTTATCCGGGAAAAGCC
<i>paf2 (ycf4)</i>	ycf4 angio F	GGCGATCAGAACATATATGG

<i>ycf15</i>	ycf4 angio R	ATACTTCAATTGGTACACGC
	solanac F	ATGTTACTGCTGAAACACGG
	solanac R	CGCCTGTTGGCATTCCAGCC
<i>atp1</i>	5	GAGCTGCGGAACTMACVAVTC
	4	CATTGATCACAGAAKCCRTT

¹Primer names and sequences after Graham and Olmstead (2000).

²Primer names and sequences after Olmstead and Sweere (1994).

³Primer names and sequences after Hoot et al. 1995.

Supplemental Table 3 – List of probes used in the hybridizations. The length (bp), GC content, and the structural location within the plastome of *Nicotiana tabacum* (tobacco) are provided for each probe. The typical plastome of a green plant is divided into three partitions; the inverted repeat (IR), small single copy region (SSC), and large single copy region (LSC)

Gene	length	GC	Location	Gene	length	GC	Location
<i>16S</i>	1185	0.567	IR	<i>atpA</i>	1459	0.411	LSC
<i>23S</i>	747	0.534	IR	<i>atpB</i>	862	0.425	LSC
<i>ndhA ex1</i>	380	0.379	SSC	<i>atpF</i>	1132	0.348	LSC
<i>ndhA ex2</i>	429	0.347	SSC	<i>atpH</i>	212	0.495	LSC
<i>ndhB ex1</i>	692	0.379	IR	<i>atpI</i>	550	0.369	LSC
<i>ndhB ex2</i>	680	0.366	IR	<i>rpoA</i>	872	0.35	LSC
<i>ndhC</i>	306	0.359	LSC	<i>rpoB</i>	1162	0.387	LSC
<i>ndhD 5'</i>	698	0.355	SSC	<i>rpoC1</i>	979	0.392	LSC
<i>ndhD 3'</i>	583	0.365	SSC	<i>rpoC2</i>	1292	0.386	LSC
<i>ndhE</i>	289	0.322	SSC	<i>rps2</i>	655	0.395	LSC
<i>ndhF</i>	808	0.361	SSC	<i>rps4</i>	494	0.379	LSC
<i>ndhG</i>	509	0.334	SSC	<i>rps7</i>	293	0.44	IR
<i>ndhH 5'</i>	358	0.411	SSC	<i>rps16</i>	218	0.376	LSC
<i>ndhH 3'</i>	323	0.375	SSC	<i>rpl2</i>	1315	0.423	IR
<i>ndhI</i>	462	0.368	SSC	<i>rpl14</i>	318	0.406	LSC
<i>ndhJ</i>	467	0.411	LSC	<i>rpl20</i>	267	0.401	LSC
<i>ndhK</i>	390	0.415	LSC	<i>rpl23</i>	266	0.38	IR
<i>psaA</i>	936	0.439	LSC	<i>rpl32</i>	164	0.335	SSC
<i>psaB 5'</i>	898	0.431	LSC	<i>accD</i>	785	0.341	LSC
<i>psaB 3'</i>	898	0.431	LSC	<i>ccsA</i>	613	0.336	SSC
<i>psaC</i>	185	0.465	SSC	<i>cemA</i>	579	0.33	LSC
<i>psbA</i>	969	0.425	LSC	<i>clpP</i>	298	0.416	LSC
<i>psbB</i>	1104	0.444	LSC	<i>matK</i>	1256	0.326	LSC
<i>psbC</i>	791	0.43	LSC	<i>ycf1 5'</i>	1229	0.36	IR
<i>psbD</i>	978	0.438	LSC	<i>ycf2 3'</i>	1284	0.411	IR
<i>psbE</i>	183	0.437	LSC	<i>paf2</i>	543	0.39	LSC
<i>rbcL</i>	842	0.416	LSC	<i>ycf15</i>	187	0.417	IR
<i>petA</i>	866	0.426	LSC				
<i>petB</i>	617	0.42	LSC				
<i>petD</i>	367	0.401	LSC				