

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

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Table. S2A. List of repeated sequences in the chloroplast genome of *Colobanthus acicularis*

Repeat length (bp)	Strat site of repeat A	Repeat A location	Repeat A region	Strat site of repeat B	Repeat B location	Repeat B region	Repeat type
30	23989	IGS (<i>psaC-ndhE</i>)	SSC	24014	<i>ndhE</i>	SSC	F
30	52308	<i>ycf2</i>	IR	52350	<i>ycf2</i>	IR	F
30	52310	<i>ycf2</i>	IR	52328	<i>ycf2</i>	IR	F
30	66785	<i>trnS-GCU</i>	LSC	93269	<i>trnS-UGA</i>	LSC	F
30	66785	<i>trnS-GCU</i>	LSC	102808	<i>trnS-GGA</i>	LSC	P
30	87815	IGS (<i>psbM-trnD-GUC</i>)	LSC	89204	IGS (<i>trnE-UUC-trnT-GGU</i>)	LSC	F
30	87816	IGS (<i>psbM-trnD-GUC</i>)	LSC	87819	IGS (<i>psbM-trnD-GUC</i>)	LSC	F
30	87818	IGS (<i>psbM-trnD-GUC</i>)	LSC	87818	IGS (<i>psbM-trnD-GUC</i>)	LSC	R
30	87818	IGS (<i>psbM-trnD-GUC</i>)	LSC	87819	IGS (<i>psbM-trnD-GUC</i>)	LSC	F
30	87818	IGS (<i>psbM-trnD-GUC</i>)	LSC	129669	<i>clpP</i> (intron1)	LSC	R
30	87818	IGS (<i>psbM-trnD-GUC</i>)	LSC	129669	<i>clpP</i> (intron1)	LSC	F
30	87819	IGS (<i>psbM-trnD-GUC</i>)	LSC	87819	IGS (<i>psbM-trnD-GUC</i>)	LSC	R
30	93269	<i>trnS-UGA</i>	LSC	102808	<i>trnS-GGA</i>	LSC	P
30	96444	<i>psaB</i>	LSC	98668	<i>psaA</i>	LSC	F
30	100169	IGS (<i>psaA-ycf3</i>)	LSC	118169	<i>ycf4</i>	LSC	P
30	100309	IGS (<i>psaA-ycf3</i>)	LSC	118030	IGS (<i>psaI-ycf4</i>)	LSC	P
31	52331	<i>ycf2</i>	IR	52355	<i>ycf2</i>	IR	F
31	68397	<i>trnG-UCC</i>	LSC	94203	<i>trnG-GCC</i>	LSC	F
31	87815	IGS (<i>psbM-trnD-GUC</i>)	LSC	129668	<i>clpP</i> (intron1)	LSC	F
31	87816	IGS (<i>psbM-trnD-GUC</i>)	LSC	87818	IGS (<i>psbM-trnD-GUC</i>)	LSC	F
31	87818	IGS (<i>psbM-trnD-GUC</i>)	LSC	87818	IGS (<i>psbM-trnD-GUC</i>)	LSC	R
31	87819	IGS (<i>psbM-trnD-GUC</i>)	LSC	129668	<i>clpP</i> (intron1)	LSC	R
31	87819	IGS (<i>psbM-trnD-GUC</i>)	LSC	129669	<i>clpP</i> (intron1)	LSC	F
31	89203	IGS (<i>trnE-UUC-trnT-GGU</i>)	LSC	129667	<i>clpP</i> (intron1)	LSC	F
38	87187	IGS (<i>petN-psbM</i>)	LSC	87187	IGS (<i>petN-psbM</i>)	LSC	P
40	26624	<i>ndhA</i> (intron)	SSC	45872	IGS (<i>trnV-GAC-rps7</i>)	IR	P
41	33205	<i>ycf1</i>	SSC	33205	<i>ycf1</i>	SSC	R
141	100198	IGS (<i>psaA-ycf3</i>)	LSC	118030	IGS (<i>psaI-ycf4</i>)	LSC	P

IGS (*psaC-ndhE*) means spacer between *psaC* and *ndhE*, P means palindromic match, F means forward (direct) match and R means reverse match

Table S2B. List of repeated sequences in the chloroplast genome of *Colobanthus affinis*

Repeat length (bp)	Strat site of repeat A	Repeat A location	Repeat A region	Strat site of repeat B	Repeat B location	Repeat B region	Repeat type
30	26881	<i>ndhA</i> (intron)	SSC	26892	<i>ndhA</i> (intron)	SSC	R
30	52356	<i>ycf2</i>	IR	52374	<i>ycf2</i>	IR	F
30	52354	<i>ycf2</i>	IR	52396	<i>ycf2</i>	IR	F
30	63572	IGS (<i>trnK-UUU-rps16</i>)	LSC	63576	IGS (<i>trnK-UUU-rps16</i>)	LSC	F
30	89089	IGS (<i>trnE-UUC-trnT-GGU</i>)	LSC	89121	IGS (<i>trnE-UUC-trnT-GGU</i>)	LSC	F
30	66850	<i>trnS-GCU</i>	LSC	93527	<i>trnS-UGA</i>	LSC	F
30	96696	<i>psaB</i>	LSC	98920	<i>psaA</i>	LSC	F
30	66850	<i>trnS-GCU</i>	LSC	103088	<i>trnS-GGA</i>	LSC	P
30	93527	<i>trnS-UGA</i>	LSC	103088	<i>trnS-GGA</i>	LSC	P
31	52377	<i>ycf2</i>	IR	52401	<i>ycf2</i>	IR	F
31	63572	IGS (<i>trnK-UUU-rps16</i>)	LSC	66696	IGS (<i>psbI-trnS-GCU</i>)	LSC	P
31	68460	<i>trnG-UCC</i>	LSC	94460	<i>trnG-GCC</i>	LSC	F
32	63572	IGS (<i>trnK-UUU-rps16</i>)	LSC	63574	IGS (<i>trnK-UUU-rps16</i>)	LSC	F
34	89077	IGS (<i>trnE-UUC-trnT-GGU</i>)	LSC	89109	IGS (<i>trnE-UUC-trnT-GGU</i>)	LSC	F
38	87263	IGS (<i>petN-psbM</i>)	LSC	87263	IGS (<i>petN-psbM</i>)	LSC	P
40	26641	<i>ndhA</i> (intron)	SSC	45918	IGS (<i>trnV-GAC-rps7</i>)	IR	P
41	19979	IGS (<i>rpl32-trnL-UAG</i>)	SSC	20034	IGS (<i>rpl32-trnL-UAG</i>)	SSC	F
41	33244	<i>ycf1</i>	SSC	33244	<i>ycf1</i>	SSC	R
61	19959	IGS (<i>rpl32-trnL-UAG</i>)	SSC	20014	IGS (<i>rpl32-trnL-UAG</i>)	SSC	F
103	100519	IGS (<i>psaA-ycf3</i>)	LSC	118296	IGS (<i>psaI-ycf4</i>)	LSC	P
134	100488	IGS (<i>psaA-ycf3</i>)	LSC	118296	IGS (<i>psaI-ycf4</i>)	LSC	P
169	100453	IGS (<i>psaA-ycf3</i>)	LSC	118296	IGS (<i>psaI-ycf4</i>)	LSC	P

IGS (*trnK-UUU-rps16*) means spacer between *trnK-UUU* and *rps16*, P means palindromic match, F means forward (direct) match and R means reverse match

Table S2C. List of repeated sequences in the chloroplast genome of *Colobanthus lycopodioides*

Repeat length (bp)	Strat site of repeat A	Repeat A location	Repeat A region	Strat site of repeat B	Repeat B location	Repeat B region	Repeat type
30	52273	<i>ycf2</i>	IR	52315	<i>ycf2</i>	IR	F
30	52275	<i>ycf2</i>	IR	52293	<i>ycf2</i>	IR	F
30	63516	IGS (<i>trnK-UUU-rps16</i>)	LSC	63518	IGS (<i>trnK-UUU-rps16</i>)	LSC	F
30	63516	IGS (<i>trnK-UUU-rps16</i>)	LSC	63520	IGS (<i>trnK-UUU-rps16</i>)	LSC	F
30	63615	IGS (<i>trnK-UUU-rps16</i>)	LSC	110958	IGS (<i>trnM-CAU-atpE</i>)	LSC	P
30	63615	IGS (<i>trnK-UUU-rps16</i>)	LSC	130085	<i>clpP</i> (intron1)	LSC	F
30	66856	<i>trnS-GCU</i>	LSC	93695	<i>trnS-UGA</i>	LSC	F
30	66856	<i>trnS-GCU</i>	LSC	103222	<i>trnS-GGA</i>	LSC	P
30	93695	<i>trnS-UGA</i>	LSC	103222	<i>trnS-GGA</i>	LSC	P
30	96869	<i>psaB</i>	LSC	99093	<i>psaA</i>	LSC	F
30	100720	IGS (<i>psaA-ycf3</i>)	LSC	118440	IGS (<i>psaI-ycf4</i>)	LSC	P
30	122218	IGS (<i>petA-psbJ</i>)	LSC	122219	IGS (<i>petA-psbJ</i>)	LSC	F
31	52296	<i>ycf2</i>	IR	52320	<i>ycf2</i>	IR	F
31	68472	<i>trnG-UCC</i>	LSC	94640	<i>trnG-GCC</i>	LSC	F
31	71794	IGS (<i>atpF-atpH</i>)	LSC	71834	IGS (<i>atpF-atpH</i>)	LSC	P
38	87379	IGS (<i>petN-psbM</i>)	LSC	87379	IGS (<i>petN-psbM</i>)	LSC	P
40	26595	<i>ndhA</i> (intron)	SSC	45837	IGS (<i>trnV-GAC-rps7</i>)	IR	P
41	33164	<i>ycf1</i>	SSC	33164	<i>ycf1</i>	SSC	R
42	63403	IGS (<i>trnK-UUU-rps16</i>)	LSC	63443	IGS (<i>trnK-UUU-rps16</i>)	LSC	F
134	100616	IGS (<i>psaA-ycf3</i>)	LSC	118440	IGS (<i>psaI-ycf4</i>)	LSC	P
169	100581	IGS (<i>psaA-ycf3</i>)	LSC	118440	IGS (<i>psaI-ycf4</i>)	LSC	P

IGS (*trnK-UUU-rps16*) means spacer between *trnK-UUU* and *rps16*, P means palindromic match, F means forward (direct) match and R means reverse match

Table S2D. List of repeated sequences in the chloroplast genome of *Colobanthus nivicola*

Repeat length (bp)	Strat site of repeat A	Repeat A location	Repeat A region	Strat site of repeat B	Repeat B location	Repeat B region	Repeat type
30	19876	IGS (<i>rpl32-trnL-UAG</i>)	SSC	19897	IGS (<i>rpl32-trnL-UAG</i>)	SSC	F
30	52316	<i>ycf2</i>	IR	52334	<i>ycf2</i>	IR	F
30	52314	<i>ycf2</i>	IR	52356	<i>ycf2</i>	IR	F
30	89058	IGS (<i>trnE-UUC-trnT-GGU</i>)	LSC	89090	IGS (<i>trnE-UUC-trnT-GGU</i>)	LSC	F
30	66802	<i>trnS-GCU</i>	LSC	93487	<i>trnS-UGA</i>	LSC	F
30	96649	<i>psaB</i>	LSC	98873	<i>psaA</i>	LSC	F
30	66802	<i>trnS-GCU</i>	LSC	103043	<i>trnS-GGA</i>	LSC	P
30	93487	<i>trnS-UGA</i>	LSC	103043	<i>trnS-GGA</i>	LSC	P
30	110793	IGS (<i>trnM-CAU-atpE</i>)	LSC	110793	IGS (<i>trnM-CAU-atpE</i>)	LSC	R
30	74728	IGS (<i>rps2-rpoC2</i>)	LSC	110794	IGS (<i>trnM-CAU-atpE</i>)	LSC	F
31	52337	<i>ycf2</i>	IR	52361	<i>ycf2</i>	IR	F
31	63536	IGS (<i>trnK-UUU-ndhA</i>)	LSC	63540	IGS (<i>trnK-UUU-ndhA</i>)	LSC	F
31	87862	IGS (<i>psbB-trnD-GUC</i>)	LSC	87862	IGS (<i>psbB-trnD-GUC</i>)	LSC	R
31	68413	<i>trnG-UCC</i>	LSC	94420	<i>trnG-GCC</i>	LSC	F
33	63536	IGS (<i>trnK-UUU-ndhA</i>)	LSC	63538	IGS (<i>trnK-UUU-ndhA</i>)	LSC	F
34	89046	IGS (<i>trnE-UUC-trnT-GGU</i>)	LSC	89078	IGS (<i>trnE-UUC-trnT-GGU</i>)	LSC	F
38	87230	IGS (<i>petN-psbM</i>)	LSC	87230	IGS (<i>petN-psbM</i>)	LSC	P
40	26617	<i>ndhA</i> (intron)	SSC	45878	IGS (<i>trnV-GAC-rps7</i>)	IR	P
41	33199	<i>ycf1</i>	SSC	33199	<i>ycf1</i>	SSC	R
97	100478	IGS (<i>psaA-ycf3</i>)	LSC	118250	IGS (<i>psaI-ycf4</i>)	LSC	P
134	100441	IGS (<i>psaA-ycf3</i>)	LSC	118250	IGS (<i>psaI-ycf4</i>)	LSC	P
169	100406	IGS (<i>psaA-ycf3</i>)	LSC	118250	IGS (<i>psaI-ycf4</i>)	LSC	P

IGS (*rpl32-trnL-UAG*) means spacer between *rpl32* and *trnL-UAG*, P means palindromic match, F means forward (direct) match and R means reverse match

Table S2E. List of repeated sequences in the chloroplast genome of *Colobanthus pulvinatus*

Repeat length (bp)	Strat site of repeat A	Repeat A location	Repeat A region	Strat site of repeat B	Repeat B location	Repeat B region	Repeat type
30	52284	<i>ycf2</i>	IR	52326	<i>ycf2</i>	IR	F
30	52286	<i>ycf2</i>	IR	52304	<i>ycf2</i>	IR	F
30	66692	<i>trnS-GCU</i>	LSC	93377	<i>trnS-UGA</i>	LSC	F
30	66692	<i>trnS-GCU</i>	LSC	102933	<i>trnS-GGA</i>	LSC	P
30	74474	IGS (<i>rps2-rpoC2</i>)	LSC	129737	<i>clpP</i> (intron1)	LSC	C
30	74605	IGS (<i>rps2-rpoC2</i>)	LSC	129736	<i>clpP</i> (intron1)	LSC	C
30	74618	IGS (<i>rps2-rpoC2</i>)	LSC	110690	IGS (<i>trnM-CAU-atpE</i>)	LSC	F
30	87750	IGS (<i>psbM-trnD-GUC</i>)	LSC	129743	<i>clpP</i> (intron1)	LSC	F
30	96539	<i>psaB</i>	LSC	98763	<i>psaA</i>	LSC	F
30	110686	IGS (<i>trnM-CAU-atpE</i>)	LSC	129736	<i>clpP</i> (intron1)	LSC	P
31	52307	<i>ycf2</i>	IR	52331	<i>ycf2</i>	IR	F
31	63506	IGS (<i>trnK-UUU-rps16</i>)	LSC	63512	IGS (<i>trnK-UUU-rps16</i>)	LSC	F
31	68303	<i>trnG-UCC</i>	LSC	94310	<i>trnG-GCC</i>	LSC	F
31	74611	IGS (<i>rps2-rpoC2</i>)	LSC	110683	IGS (<i>trnM-CAU-atpE</i>)	LSC	R
31	87752	IGS (<i>psbM-trnD-GUC</i>)	LSC	87752	IGS (<i>psbM-trnD-GUC</i>)	LSC	R
31	87752	IGS (<i>psbM-trnD-GUC</i>)	LSC	110684	IGS (<i>trnM-CAU-atpE</i>)	LSC	C
31	87752	IGS (<i>psbM-trnD-GUC</i>)	LSC	110684	IGS (<i>trnM-CAU-atpE</i>)	LSC	P
31	87752	IGS (<i>psbM-trnD-GUC</i>)	LSC	129737	<i>clpP</i> (intron1)	LSC	R
31	87752	IGS (<i>psbM-trnD-GUC</i>)	LSC	129737	<i>clpP</i> (intron1)	LSC	F
31	87753	IGS (<i>psbM-trnD-GUC</i>)	LSC	110685	IGS (<i>trnM-CAU-atpE</i>)	LSC	P
31	87753	IGS (<i>psbM-trnD-GUC</i>)	LSC	110686	IGS (<i>trnM-CAU-atpE</i>)	LSC	C
31	110675	IGS (<i>trnM-CAU-atpE</i>)	LSC	129737	<i>clpP</i> (intron1)	LSC	C
31	110683	IGS (<i>trnM-CAU-atpE</i>)	LSC	129735	<i>clpP</i> (intron1)	LSC	P
31	110686	IGS (<i>trnM-CAU-atpE</i>)	LSC	110689	IGS (<i>trnM-CAU-atpE</i>)	LSC	F
31	110688	IGS (<i>trnM-CAU-atpE</i>)	LSC	129739	<i>clpP</i> (intron1)	LSC	P
31	110691	IGS (<i>trnM-CAU-atpE</i>)	LSC	129745	<i>clpP</i> (intron1)	LSC	C
32	74615	IGS (<i>rps2-rpoC2</i>)	LSC	110683	IGS (<i>trnM-CAU-atpE</i>)	LSC	F

32	110680	IGS (<i>trnM-CAU-atpE</i>)	LSC	129736	<i>clpP</i> (intron1)	LSC	C
33	63506	IGS (<i>trnK-UUU-rps16</i>)	LSC	63510	IGS (<i>trnK-UUU-rps16</i>)	LSC	F
33	129741	<i>clpP</i> (intron1)	LSC	129741	<i>clpP</i> (intron1)	LSC	R
34	88936	IGS (<i>trnE-UCC-trnT-GGU</i>)	LSC	88968	IGS (<i>trnE-UCC-trnT-GGU</i>)	LSC	F
35	63506	IGS (<i>trnK-UUU-rps16</i>)	LSC	63508	IGS (<i>trnK-UUU-rps16</i>)	LSC	F
36	110683	IGS (<i>trnM-CAU-atpE</i>)	LSC	110683	IGS (<i>trnM-CAU-atpE</i>)	LSC	R
38	87120	IGS (<i>petN-psbM</i>)	LSC	87120	IGS (<i>petN-psbM</i>)	LSC	P
40	26587	<i>ndhA</i> (intron)	SSC	45848	IGS (<i>trnV-GAC-rps7</i>)	IR	P
41	33169	<i>ycf1</i>	SSC	33169	<i>ycf1</i>	SSC	R
97	100368	IGS (<i>psaA-ycf3</i>)	LSC	118146	IGS (<i>psaI-ycf4</i>)	LSC	P
134	100331	IGS (<i>psaA-ycf3</i>)	LSC	118146	IGS (<i>psaI-ycf4</i>)	LSC	P
169	100296	IGS (<i>psaA-ycf3</i>)	LSC	118146	IGS (<i>psaI-ycf4</i>)	LSC	P

IGS (*psbM-trnD-GUC*) means spacer between *psbM* and *trnD-GUC*, P means palindromic match, F means forward (direct) match, R means reverse match and C complementary match

Table S2F. List of repeated sequences in the chloroplast genome of *Colobanthus subulatus*

Repeat length (bp)	Strat site of repeat A	Repeat A location	Repeat A region	Strat site of repeat B	Repeat B location	Repeat B region	Repeat type
30	52284	<i>ycf2</i>	IR	52302	<i>ycf2</i>	IR	F
30	52282	<i>ycf2</i>	IR	52324	<i>ycf2</i>	IR	F
30	59167	IGS (<i>trnH-GUG-psbA</i>)	LSC	59199	IGS (<i>trnH-GUG-psbA</i>)	LSC	P
30	66912	<i>trnS-GCU</i>	LSC	93571	<i>trnS-UGA</i>	LSC	F
30	96733	<i>psaB</i>	LSC	98957	<i>psaA</i>	LSC	F
30	66912	<i>trnS-GCU</i>	LSC	103120	<i>trnS-GGA</i>	LSC	P
30	93571	<i>trnS-UGA</i>	LSC	103120	<i>trnS-GGA</i>	LSC	P
30	110857	IGS (<i>trnM-CAU-atpE</i>)	LSC	110858	IGS (<i>trnM-CAU-atpE</i>)	LSC	F
30	100630	IGS (<i>psaA-ycf3</i>)	LSC	118319	IGS (<i>psaI-ycf4</i>)	LSC	P
31	52305	<i>ycf2</i>	IR	52329	<i>ycf2</i>	IR	F
31	64323	<i>rps16</i> (intron)	LSC	64415	<i>rps16</i> (intron)	LSC	F
31	68528	<i>trnG-UCC</i>	LSC	94504	<i>trnG-GCC</i>	LSC	F
38	87341	IGS (<i>petN-psbM</i>)	LSC	87341	IGS (<i>petN-psbM</i>)	LSC	P
40	26604	<i>ndhA</i> (intron)	SSC	45846	IGS (<i>trnV-GAC-rps7</i>)	IR	P
41	33172	<i>ycf1</i>	SSC	33172	<i>ycf1</i>	SSC	R
42	108814	IGS (<i>ndhC-trnV-UAC</i>)	LSC	108856	IGS (<i>ndhC-trnV-UAC</i>)	LSC	F
47	64326	<i>rps16</i> (intron)	LSC	64395	<i>rps16</i> (intron)	LSC	F
70	64326	<i>rps16</i> (intron)	LSC	64372	<i>rps16</i> (intron)	LSC	F
93	64326	<i>rps16</i> (intron)	LSC	64349	<i>rps16</i> (intron)	LSC	F
134	100526	IGS (<i>psaA-ycf3</i>)	LSC	118319	IGS (<i>psaI-ycf4</i>)	LSC	P
169	100491	IGS (<i>psaA-ycf3</i>)	LSC	118319	IGS (<i>psaI-ycf4</i>)	LSC	P

IGS (*trnH-GUG-psbA*) means spacer between *trnH-GUG* and *psbA*, P means palindromic match, F means forward (direct) match and R means reverse match