

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

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Table S3A. Distribution of SSR in the *Colobanthus acicularis* cp genome.

Type	Repeat unit	Length (bp)	Start	End	Location
Mononucleotide	A	12	31 124	31 135	<i>ycf1</i>
		14	32 047	32 060	<i>ycf1</i>
		12	60 849	60 860	<i>trnK-UUU</i>
		17	63 539	63 555	IGS (<i>trnK-UUU-rps16</i>)
		12	65 850	65 861	IGS (<i>trnQ-UUG-psbK</i>)
		15	65 896	65 910	IGS (<i>trnQ-UUG-psbK</i>)
		13	66 485	66 497	IGS (<i>psbK-psbI</i>)
		14	71 130	71 143	<i>atpF</i> (intron)
		18	74 579	74 596	IGS (<i>rps2-rpoC2</i>)
		15	74 712	74 726	IGS (<i>rps2-rpoC2</i>)
		12	76 784	76 795	<i>rpoC2</i>
		23	87 819	87 841	IGS (<i>psbM-trnD-GUC</i>)
		17	89 208	89 224	IGS (<i>trnE-UUC-trnT-GGU</i>)
		13	90 483	90 495	IGS (<i>trnT-GGU-psbD</i>)
		16	93 106	93 121	IGS (<i>psbC-trnS-UGA</i>)
		13	106 246	106 258	IGS (<i>trnF-GAA-ndhJ</i>)
		14	114 876	114 889	IGS (<i>rbcL-accD</i>)
		13	123 654	123 666	IGS (<i>psbE-petL</i>)
		15	123 857	123 871	IGS (<i>psbE-petL</i>)
		12	127 886	127 897	IGS (<i>rpl20-rps12</i>)
24	129 670	129 693	<i>clpP</i> (intron1)		
12	133 706	133 717	<i>petB</i> (intron)		
Dinucleotide	AT	13	63 527	63 539	IGS (<i>trnK-UUU-rps16</i>)
		12	117 293	117 304	IGS (<i>accD-psaI</i>)
Trinucleotide	AAT	12	20 533	20 544	IGS (<i>trnL-UAG-ccsA</i>)
		13	103 784	103 796	IGS (<i>rps4-trnT-UGU</i>)
		12	137 244	137 255	IGS (<i>rpoA-rps11</i>)
Tetranucleotide	AAAT	12	18 715	18 726	IGS (<i>ndhF-rpl32</i>)
	AATT	12	27 329	27 340	<i>ndhA</i> (intron)
	ACCT	14	38 520	38 533	<i>rrn23</i>
	AATT	12	63 758	63 769	IGS (<i>trnK-UUU-rps16</i>)
	AATG	13	68 446	68 458	IGS (<i>trnG-UCC-trnR-UCU</i>)
	AAAC	12	68 883	68 894	<i>atpA</i>
	AAGG	13	71 794	71 806	IGS (<i>atpF-atpH</i>)
	AAAT	16	87 164	87 179	IGS (<i>petN-psbM</i>)
	AAAC	13	93 968	93 980	IGS (<i>psbZ-trnG-GCC</i>)
	AACT	13	100 123	100 135	IGS (<i>psaA-ycf3</i>)
	AATT	12	117 617	117 628	IGS (<i>accD-psaI</i>)
	AAAG	12	128 669	128 680	<i>clpP</i> (intron2)
AAAT	12	135 112	135 123	<i>petD</i> (intron)	
Pentanucleotide	AAATT	18	19 803	19 820	IGS (<i>rpl32-trnL-UAG</i>)
	AAATC	16	24 409	24 424	IGS (<i>ndhE-ndhG</i>)
	AATCT	15	123 764	123 778	IGS (<i>psbE-petL</i>)
Hexanucleotide	AATACT	25	94 365	94 389	IGS (<i>trnG-GCC-trnfM-CAU</i>)

IGS (*trnK-UUU-rps16*) means spacer between *trnK-UUU* and *rps16*

Table S3B. Distribution of SSR in the *Colobanthus affinis* cp genome.

Type	Repeat unit	Length (bp)	Start	End	Location
Mononucleotide	A	13	16 448	16 460	<i>ndhF</i>
		12	31 163	31 174	<i>ycf1</i>
		13	60 894	60 906	<i>trnK-UUU</i> (intron)
		16	63 591	63 606	IGS (<i>trnK-UUU-rps16</i>)
		20	65 946	65 965	IGS (<i>trnQ-UUG-psbK</i>)
		13	66 540	66 552	IGS (<i>psbK-psbI</i>)
		18	74 630	74 647	IGS (<i>rps2-rpoC2</i>)
		15	74 763	74 777	IGS (<i>rps2-rpoC2</i>)
		12	76 835	76 846	<i>rpoC2</i>
		18	89 308	89 325	IGS (<i>trnE-UUC-trnT-GGU</i>)
		12	90 745	90 756	IGS (<i>trnT-GGU-psbD</i>)
		13	93 367	93 379	IGS (<i>psbC-trnS-UGA</i>)
		14	106 515	106 528	IGS (<i>trnF-GAA-ndhJ</i>)
		14	115 142	115 155	IGS (<i>rbcL-accD</i>)
		14	124 100	124 113	IGS (<i>psbE-petL</i>)
		12	125 281	125 292	IGS (<i>trnP-UGG-psaJ</i>)
		12	128 147	128 158	IGS (<i>rpl20-clpP</i>)
		21	129 933	129 953	<i>clpP</i> (intron1)
13	133 963	133 975	<i>petB</i> (intron)		
Dinucleotide	AT	19	63 573	63 591	IGS (<i>trnK-UUU-rps16</i>)
		21	66 709	66 729	IGS (<i>psbI-trnS-GCU</i>)
		12	117 559	117 57	IGS (<i>accD-psaI</i>)
Trinucleotide	AAT	12	20 579	20 590	IGS (<i>trnL-UAG-ccsA</i>)
		13	104 064	104 076	IGS (<i>rps4-trnT-UGU</i>)
		12	137 508	137 519	IGS (<i>rpoA-rps11</i>)
Tetranucleotide	AAAT	12	18 722	18 733	IGS (<i>ndhF-rpl32</i>)
	AATT	12	27 367	27 378	<i>ndhA</i> (intron)
	ACCT	14	38 560	38 573	<i>rrn23</i>
	AATT	12	63 811	63 822	IGS (<i>trnK-UUU-rps16</i>)
	AAAC	12	68 942	68 953	<i>atpA</i>
	AAGG	13	71 854	71 866	IGS (<i>atpF-atpH</i>)
	AAAT	12	87 240	87 251	IGS (<i>petN-psbM</i>)
	AAAC	13	94 225	94 237	IGS (<i>psbZ-trnG-GCC</i>)
	AACT	13	100 407	100 419	IGS (<i>psaA-ycf3</i>)
	AATT	12	117 883	117 894	IGS (<i>accD-psaI</i>)
	AAAG	12	128 930	128 941	<i>clpP</i> (intron2)
AAAT	12	135 376	135 387	<i>petD</i> (intron)	
Pentanucleotide	AAATC	16	24 429	24 444	IGS (<i>ndhE-ndhG</i>)
	AATCT	15	124 007	124 021	IGS (<i>psbE-petL</i>)

IGS (*trnK-UUU-rps16*) means spacer between *trnK-UUU* and *rps16*

Table S3C. Distribution of SSR in the *Colobanthus lycopodioides* cp genome.

Type	Repeat unit	Length (bp)	Start	End	Location
Mononucleotide	A	15	18 781	18 795	IGS (<i>ndhF-rpl32</i>)
		12	31 083	31 094	<i>ycf1</i>
		13	60 790	60 802	<i>trnK-UUU</i> (intron)
		14	63 535	63 548	IGS (<i>trnK-UUU-rps16</i>)
		14	63 627	63 640	IGS (<i>trnK-UUU-rps16</i>)
		14	65 932	65 945	IGS (<i>trnQ-UUG-psbK</i>)
		14	65 980	65 993	IGS (<i>trnQ-UUG-psbK</i>)
		12	66 570	66 581	IGS (<i>psbK-psbI</i>)
		13	68 787	68 799	IGS (<i>trnR-UCU-atpA</i>)
		16	71 214	71 229	<i>atpF</i> (intron)
		12	71 284	71 295	<i>atpF</i> (intron)
		14	74 747	74 760	IGS (<i>rps2-rpoC2</i>)
		17	74 879	74 895	IGS (<i>rps2-rpoC2</i>)
		12	76 944	76 955	<i>rpoC2</i>
		13	89 485	89 497	IGS (<i>trnE-UUC-trnT-GGU</i>)
		12	90 912	90 923	IGS (<i>trnT-GGU-psbD</i>)
		14	93 534	93 547	IGS (<i>psbC-trnS-UGA</i>)
		12	93 985	93 996	IGS (<i>trnS-UGA-psbZ</i>)
		12	102 560	102 571	IGS (<i>ycf3-trnS-GGA</i>)
		12	109 212	109 223	IGS (<i>ndhC-trnV-UAC</i>)
		18	122 231	122 248	IGS (<i>petA-psbJ</i>)
		16	124 283	124 298	IGS (<i>psbE-petL</i>)
		12	128 306	128 317	IGS (<i>rpl20-clpP</i>)
14	129 942	129 955	<i>clpP</i> (intron1)		
22	130 097	130 118	<i>clpP</i> (intron1)		
12	134 121	134 132	<i>petB</i> (intron)		
Dinucleotide	AT	19	63 517	63 535	IGS (<i>trnK-UUU-rps16</i>)
		12	117 703	117 714	IGS (<i>accD-psaI</i>)
Trinucleotide	AAT	12	20 526	20 537	IGS (<i>trnL-UAG-ccsA</i>)
		13	104 198	104 210	IGS (<i>rps4-trnT-UGU</i>)
		12	137 659	137 670	IGS (<i>rpoA-rps11</i>)
Tetranucleotide	AAAT	12	18 721	18 732	IGS (<i>ndhF-rpl32</i>)
	AATT	12	27 287	27 298	<i>ndhA</i> (intron)
	ACCT	14	38 479	38 492	<i>rrn23</i>
	AATT	12	63 849	63 860	<i>rps16</i>
	AATG	13	68 521	68 533	IGS (<i>trnG-UCC-trnR-UCU</i>)
	AAAC	12	68 960	68 971	<i>atpA</i>
	AAGG	13	71 949	71 961	IGS (<i>atpF-atpH</i>)
	AAAT	12	87 356	87 367	IGS (<i>petN-psbM</i>)
	AAAC	13	94 404	94 416	IGS (<i>psbZ-trnG-GCC</i>)
	AACT	13	100 535	100 547	IGS (<i>psaA-ycf3</i>)
	AAAT	15	111 001	111 015	IGS (<i>trnM-CAU-atpE</i>)
	AATT	12	118 027	118 038	IGS (<i>accD-psaI</i>)
	AAAG	12	129 089	129 100	<i>clpP</i> (intron2)
AAAT	12	135 527	135 538	<i>petD</i> (intron)	
Pentanucleotide	AATTC	15	24 370	24 384	IGS (<i>ndhE-ndhG</i>)

	AATCT	15	124 190	124 204	IGS (<i>psbE-petL</i>)
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IGS (*tmK-UUU-rps16*) means spacer between *tmK-UUU* and *rps16*

Table S3D. Distribution of SSR in the *Colobanthus nivicola* cp genome.

Type	Repeat unit	Length (bp)	Start	End	Location
Mononucleotide	A	13	16 453	16 465	<i>ndhF</i>
		12	18 787	18 798	IGS (<i>ndhF-rpl32</i>)
		12	31 118	31 129	<i>ycf1</i>
		12	32 338	32 349	<i>ycf1</i>
		15	60 855	60 869	<i>trnK-UUU</i>
		19	63 553	63 571	IGS (<i>trnK-UUU-rps16</i>)
		15	63 639	63 653	IGS (<i>trnK-UUU-rps16</i>)
		16	65 913	65 928	IGS (<i>trnQ-UUG-psbK</i>)
		12	66 503	66 514	IGS (<i>psbK-psbI</i>)
		12	67 187	67 198	IGS (<i>trnS-GCU-trnG-UCC</i>)
		21	74 593	74 613	IGS (<i>rps2-rpoC2</i>)
		17	74 729	74 745	IGS (<i>rps2-rpoC2</i>)
		12	76 803	76 814	<i>rpoC2</i>
		15	87 871	87 885	IGS (<i>psbM-trnD-GUC</i>)
		13	89 277	89 289	IGS (<i>trnE-UUC-trnT-GGU</i>)
		13	90 703	90 715	IGS (<i>trnT-GGU-psbD</i>)
		14	93 326	93 339	IGS (<i>psbC-trnS-UGA</i>)
		14	106 471	106 484	IGS (<i>trnF-GAA-ndhJ</i>)
		15	110 797	110 811	IGS (<i>trnM-CAU-atpE</i>)
		Dinucleotide	AT	17	63 537
12	117 513			117 524	IGS (<i>accD-psaI</i>)
Trinucleotide	AAT	12	20 555	20 566	IGS (<i>trnL-UAG-ccsA</i>)
		13	104 019	104 031	IGS (<i>rps4-trnT-UGU</i>)
		12	137 403	137 414	IGS (<i>rpoA-rps11</i>)
Tetranucleotide	AAAT	12	18 727	18 738	IGS (<i>ndhF-rpl32</i>)
	AATT	12	27 322	27 333	<i>ndhA</i>
	ACCT	14	38 514	38 527	<i>rrn23</i>
	AATT	12	63 855	63 866	IGS (<i>trnK-UUU-rps16</i>)
	AAAC	12	68 895	68 906	<i>atpA</i>
	AAGG	13	71 808	71 820	IGS (<i>atpF-atpH</i>)
	AAAT	12	87 207	87 218	IGS (<i>petN-psbM</i>)
	AAAC	13	94 185	94 197	IGS (<i>psbZ-trnG-GCC</i>)
	AACT	13	100 360	100 372	IGS (<i>psaA-ycf3</i>)
	AATT	12	117 837	117 848	IGS (<i>accD-psaI</i>)
	AAAG	12	128 880	128 891	<i>clpP</i> (intron2)
Pentanucleotide	AAATT	18	19 816	19 833	IGS (<i>rpl32-trnL-UAG</i>)
	AAATC	16	24 405	24 420	IGS (<i>ndhE-ndhG</i>)
	AATCT	15	123 965	123 979	IGS (<i>psbE-petL</i>)
Hexanucleotide	AAGAAT	19	41 278	41 296	IGS (<i>trnA-UGC-trnI-GAU</i>)

IGS (*trnK-UUU-rps16*) means spacer between *trnK-UUU* and *rps16*

Table S3E. Distribution of SSR in the *Colobanthus pulvinatus* cp genome.

Type	Repeat unit	Length (bp)	Start	End	Location
Mononucleotide	A	13	16 444	16 456	<i>ndhF</i>
		12	18 778	18 789	IGS (<i>ndhF-rpl32</i>)
		12	31 088	31 099	<i>ycf1</i>
		12	32 308	32 319	<i>ycf1</i>
		15	60 825	60 839	<i>trnK-UUU</i> (intron)
		15	63 529	63 543	IGS (<i>trnK-UUU-rps16</i>)
		16	65 803	65 818	IGS (<i>trnQ-UUG-psbK</i>)
		12	66 393	66 404	IGS (<i>psbK-psbI</i>)
		12	67 077	67 088	IGS (<i>trnS-GCU-trnG-UCC</i>)
		21	74 483	74 503	IGS (<i>rps2-rpoC2</i>)
		17	74 619	74 635	IGS (<i>rps2-rpoC2</i>)
		12	76 693	76 704	<i>rpoC2</i>
		15	87 761	87 775	IGS (<i>psbM-trnD-GUC</i>)
		13	89 167	89 179	IGS (<i>trnE-UUC-trnT-GGU</i>)
		13	90 593	90 605	IGS (<i>trnT-GGU-psbD</i>)
		14	93 216	93 229	IGS (<i>psbC-trnS-UGA</i>)
		14	106 361	106 374	IGS (<i>trnF-GAA-ndhJ</i>)
		21	110 687	110 707	IGS (<i>trnM-CAU-atpE</i>)
		13	114 993	115 005	IGS (<i>rbcL-accD</i>)
		14	123 954	123 967	IGS (<i>psbE-petL</i>)
13	127 963	127 975	IGS (<i>rpl20-clpP</i>)		
23	129 746	129 768	<i>clpP</i> (intron1)		
14	133 780	133 793	<i>petB</i> (intron)		
Dinucleotide	AT	23	63 507	63 529	IGS (<i>trnK-UUU-rps16</i>)
		12	117 409	117 420	IGS (<i>accD-psaI</i>)
Trinucleotide	AAT	12	20 525	20 536	IGS (<i>trnL-UAG-ccsA</i>)
		13	103 909	103 921	IGS (<i>rps4-trnT-UGU</i>)
		12	137 326	137 337	<i>rpoA</i>
Tetranucleotide	AAAT	12	18 718	18 729	IGS (<i>ndhF-rpl32</i>)
	AATT	12	27 292	27 303	<i>ndhA</i> (intron)
	ACCT	14	38 484	38 497	<i>rrn23</i>
	AATT	12	63 745	63 756	IGS (<i>trnK-UUU-rps16</i>)
	AAAC	12	68 785	68 796	<i>atpA</i>
	AAGG	13	71 698	71 710	IGS (<i>atpF-atpH</i>)
	AAAT	12	87 097	87 108	IGS (<i>petN-psbM</i>)
	AAAC	13	94 075	94 087	IGS (<i>psbZ-trnG-GCC</i>)
	AACT	13	100 250	100 262	IGS (<i>psaA-ycf3</i>)
	AATT	12	117 733	117 744	IGS (<i>accD-psaI</i>)
	AAAG	12	128 747	128 758	<i>clpP</i> (intron2)
AAAT	12	135 194	135 205	<i>petD</i> (intron)	
Pentanucleotide	AAATT	18	19 807	19 824	IGS (<i>rpl32-trnL-UAG</i>)
	AAATC	16	24 375	24 390	IGS (<i>ndhE-ndhG</i>)
	AATCT	15	123 861	123 875	IGS (<i>psbE-petL</i>)
Hexanucleotide	AAGAAT	19	41 248	41 266	IGS (<i>trnA-UGC-trnI-GAU</i>)

IGS (*trnK-UUU-rps16*) means spacer between *trnK-UUU* and *rps16*

Table S3F. Distribution of SSR in the *Colobanthus subulatus* cp genome.

Type	Repeat unit	Length (bp)	Start	End	Location
Mononucleotide	A	13	16 449	16 461	<i>ndhF</i>
		12	31 091	31 102	<i>ycf1</i>
		12	63 503	63 514	IGS (<i>trnK-UUU-rps16</i>)
		12	63 582	63 593	IGS (<i>trnK-UUU-rps16</i>)
		15	66 030	66 044	IGS (<i>trnQ-UUG-psbK</i>)
		14	66 620	66 633	IGS (<i>psbK-psbI</i>)
		15	74 836	74 850	IGS (<i>atpI-rps2</i>)
		12	76 908	76 919	<i>rpoC2</i>
		14	87 983	87 996	IGS (<i>psbM-trnD-GUC</i>)
		16	88 162	88 177	IGS (<i>psbM-trnD-GUC</i>)
		16	89 360	89 375	IGS (<i>trnE-UUC-trnT-GGU</i>)
		12	104 721	104 732	IGS (<i>trnT-UGU-trnL-UAA</i>)
		15	106 496	106 510	IGS (<i>trnF-GAA-ndhJ</i>)
		18	110 858	110 875	IGS (<i>trnM-CAU-atpE</i>)
		13	115 156	115 168	IGS (<i>rbcL-accD</i>)
		20	124 134	124 153	IGS (<i>psbE-petL</i>)
		17	124 542	124 558	IGS (<i>petL-petG</i>)
15	129 919	129 933	<i>clpP</i> (intron1)		
13	133 944	133 956	<i>petB</i> (intron)		
Dinucleotide	AT	13	63 491	63 503	IGS (<i>trnK-UUU-rps16</i>)
	AT	15	66 790	66 804	IGS (<i>psbI-trnS-GCU</i>)
	AT	12	117 582	117 593	IGS (<i>accD-psaI</i>)
Trinucleotide	AAT	12	20 530	20 541	IGS (<i>trnL-UAG-ccsA</i>)
	AAT	13	104 096	104 108	IGS (<i>rps4-trnT-UGU</i>)
	AAT	12	137 483	137 494	IGS (<i>rpoA-rps11</i>)
Tetranucleotide	AAAT	12	18 723	18 734	IGS (<i>ndhF-rpl32</i>)
	AATT	12	27 295	27 306	<i>ndhA</i> (intron)
	ACCT	14	38 488	38 501	<i>rrn23</i>
	AATT	12	63 801	63 812	<i>rps16</i>
	AATG	13	68 577	68 589	IGS (<i>trnG-UCC-trnR-UCU</i>)
	AAAC	12	69 012	69 023	<i>atpA</i>
	AAGG	13	71 925	71 937	IGS (<i>atpF-atpH</i>)
	AAAC	13	94 269	94 281	IGS (<i>psbZ-trnG-GCC</i>)
	AACT	13	100 444	100 456	IGS (<i>psaA-ycf3</i>)
	AATT	12	117 906	117 917	IGS (<i>accD-psaI</i>)
	AAAG	12	128 917	128 928	<i>clpP</i> (intron2)
AAAT	12	135 351	135 362	<i>petD</i> (intron)	
Pentanucleotide	AATCC	18	23 776	23 793	IGS (<i>psaC-ndhE</i>)
	AAATT	17	19 810	19 826	IGS (<i>rpl32-trnL-UAG</i>)
	AAATC	16	24 385	24 400	IGS (<i>ndhE-ndhG</i>)
	AATCT	15	124 041	124 055	IGS (<i>psbE-petL</i>)

IGS (*trnK-UUU-rps16*) means spacer between *trnK-UUU* and *rps16*