

Complete chloroplast genomes of *Cerastium alpinum*, *C. arcticum* and *C. nigrescens*: genome structures, comparative and phylogenetic analysis

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Table S3A. Distribution of SSR in the *Cerastium alpinum* cp genome.

Type	Repeat unit	Length (bp)	Start	End	Location
Mononucleotide	A	12	11,878	11,889	<i>ycf1</i>
		13	28,119	28,131	<i>ycf1</i>
		12	58,788	58,799	<i>matK</i>
		12	73,365	73,376	<i>rpoC2</i>
		13	83,607	83,619	IGS (<i>psbM-psbD</i>)
		12	85,146	85,157	IGS (<i>psbM-psbD</i>)
		12	95,444	95,455	IGS (<i>psaA-ycf3</i>)
		12	99,608	99,619	IGS (<i>trnT-UGU-trnL-UAA</i>)
		13	133,151	133,163	IGS (<i>rpl14-rpl16</i>)
Trinucleotide	AAT	13	14,074	14,086	<i>ndhF</i>
		12	63,563	63,574	IGS (<i>trnS-GCU-trnG-UCC</i>)
		14	63,906	63,919	IGS (<i>trnS-GCU-trnG-UCC</i>)
		14	97,915	97,928	IGS (<i>ycf3-trnS-GGA</i>)
		17	99,389	99,405	IGS (<i>trnT-UGU-trnL-UAA</i>)
		12	118,910	118,921	IGS (<i>trnP-UGG-psaI</i>)
		12	120,081	120,092	IGS (<i>rpl33-rps18</i>)
Tetranucleotide	ACCT	14	8,761	8,774	<i>rrn23</i>
	AAAT	12	18,720	18,731	<i>ndhD</i>
	AATT	12	63,461	63,472	IGS (<i>trnS-GCU-trnG-UCC</i>)
	AATT	12	100,217	100,228	<i>trnL-UAA</i> (intron)
Pentanucleotide	AATAT	16	99,417	99,432	IGS (<i>trnT-UGU-trnL-UAA</i>)

IGS (*psbM-psbD*) means spacer between *psbM* and *psbD*

Table S3B. Distribution of SSR in the *Cerastium arcticum* cp genome.

Type	Repeat unit	Length (bp)	Start	End	Location
Mononucleotide	A	12	11,877	11,888	<i>ycf1</i>
		13	28,131	28,143	<i>ycf1</i>
		12	58,803	58,814	<i>matK</i>
		12	73,460	73,471	<i>rpoC2</i>
		18	84,321	84,338	IGS (<i>psbM-psbD</i>)
		12	98,695	98,706	IGS (<i>ycf3-trnS-GGA</i>)
		14	98,799	98,812	IGS (<i>ycf3-trnS-GGA</i>)
		13	100,388	100,400	IGS (<i>trnT-UGU-trnL-UAA</i>)
		12	119,927	119,938	IGS (<i>trnP-UGG-psaI</i>)
		14	133,918	133,931	IGS (<i>rpl14-rpl16</i>)
Trinucleotide	AAT	13	14,073	14,085	<i>ndhF</i>
		12	63,567	63,578	IGS (<i>trnS-GCU-trnG-UCC</i>)
		16	71,387	71,402	IGS (<i>rps2-rpoC2</i>)
		14	98,826	98,839	IGS (<i>ycf3-trnS-GGA</i>)
		17	100,304	100,320	IGS (<i>trnT-UGU-trnL-UAA</i>)
		12	119,684	119,695	IGS (<i>trnP-UGG-psaI</i>)
		12	120,864	120,875	IGS (<i>rpl33-rps18</i>)
Tetranucleotide	ACCT	14	8,756	8,769	<i>rrn23</i>
	AAAT	12	18,728	18,739	<i>ndhD</i>
	AATT	12	63,487	63,498	IGS (<i>trnS-GCU-trnG-UCC</i>)
	AGAT	12	101,035	101,046	<i>trnL-UAA</i> (intron)
	AATT	12	134,509	134,520	<i>rpl16</i> (intron)
Hexanucleotide	AAATCC	19	29,127	29,145	<i>ycf1</i>

IGS (*psbM-psbD*) means spacer between *psbM* and *psbD*

Table S3C. Distribution of SSR in the *Cerastium nigrescens* cp genome.

Type	Repeat unit	Length (bp)	Start	End	Location
Mononucleotide	A	12	11,878	11,889	<i>ycf1</i>
		13	28,118	28,130	<i>ycf1</i>
		12	58,787	58,798	<i>matK</i>
		12	73,368	73,379	<i>rpoC2</i>
		13	83,610	83,622	IGS (<i>psbM-psbD</i>)
		12	85,149	85,160	IGS (<i>psbM-psbD</i>)
		12	99,615	99,626	IGS (<i>trnT-UGU-trnL-UAA</i>)
		13	133,146	133,158	IGS (<i>rpl14-rpl16</i>)
Trinucleotide	AAT	13	14,074	14,086	<i>ndhF</i>
		12	63,566	63,577	IGS (<i>trnS-GCU-trnG-UCC</i>)
		15	64,281	64,295	<i>trnG-UCC</i> (intron)
		14	97,927	97,940	IGS (<i>ycf3-trnS-GGA</i>)
		17	99,401	99,417	IGS (<i>trnT-UGU-trnL-UAA</i>)
		12	118,915	118,926	IGS (<i>trnP-UGG-psaI</i>)
		12	120,090	120,101	IGS (<i>rpl33-rps18</i>)
Tetranucleotide	ACCT	14	8,761	8,774	<i>rrn23</i>
	AAAT	12	18,720	18,731	<i>ndhD</i>
	AATT	12	63,464	63,475	IGS (<i>trnS-GCU-trnG-UCC</i>)
	AATT	12	100,224	100,235	<i>trnL-UAA</i> (intron)
	AAAT	13	119,006	119,018	IGS (<i>trnP-UGG-psaI</i>)

IGS (*psbM-psbD*) means spacer between *psbM* and *psbD*

Table S3D. Distribution of SSR in the *Cerastium glomeratum* cp genome.

Type	Repeat unit	Length (bp)	Start	End	Location
Mononucleotide	A	12	11,891	11,902	<i>ycf1</i>
		13	15,556	15,568	<i>ycf1</i>
		12	21,753	21,764	IGS (<i>ndhI-ndhG</i>)
		12	58,751	58,762	<i>matK</i>
		12	62,984	62,995	IGS (<i>psbK-psbI</i>)
		12	73,367	73,378	<i>rpoC2</i>
		13	98,611	98,623	IGS (<i>ycf3-trnS-GGA</i>)
		12	104,764	104,775	IGS (<i>ndhC-trnV-UAC</i>)
Dinucleotide	AT	13	89,161	89,173	IGS (<i>psbC-trnS-UGA</i>)
Trinucleotide	AAT	13	29,502	29,514	<i>ndhF</i>
		12	63,517	63,528	IGS (<i>trnS-GCU-trnG-UCC</i>)
		13	63,653	63,665	IGS (<i>trnS-GCU-trnG-UCC</i>)
		14	98,738	98,751	IGS (<i>ycf3-trnS-GGA</i>)
		12	120,777	120,788	IGS (<i>rpl33-rps18</i>)
		13	145,896	145,908	IGS (<i>trnL-CAA-ndhB</i>)
Tetranucleotide	ACCT	14	8,775	8,788	<i>rrn23</i>
	AAAT	12	24,995	25,006	<i>ndhD</i>
	AATT	12	98,268	98,279	<i>ycf3</i> (intron 1)
	AATT	13	99,791	99,803	IGS (<i>rps4-trnT-UGU</i>)
	AAAT	12	110,398	110,409	IGS (<i>rbcl-accD</i>)
	AAAG	12	118,080	118,091	IGS (<i>psbE-petL</i>)
	AAAT	12	124,724	124,735	<i>clpP</i> (intron 1)

IGS (*ndhI-ndhG*) means spacer between *ndhI* and *ndhG*