

Supplementary Data

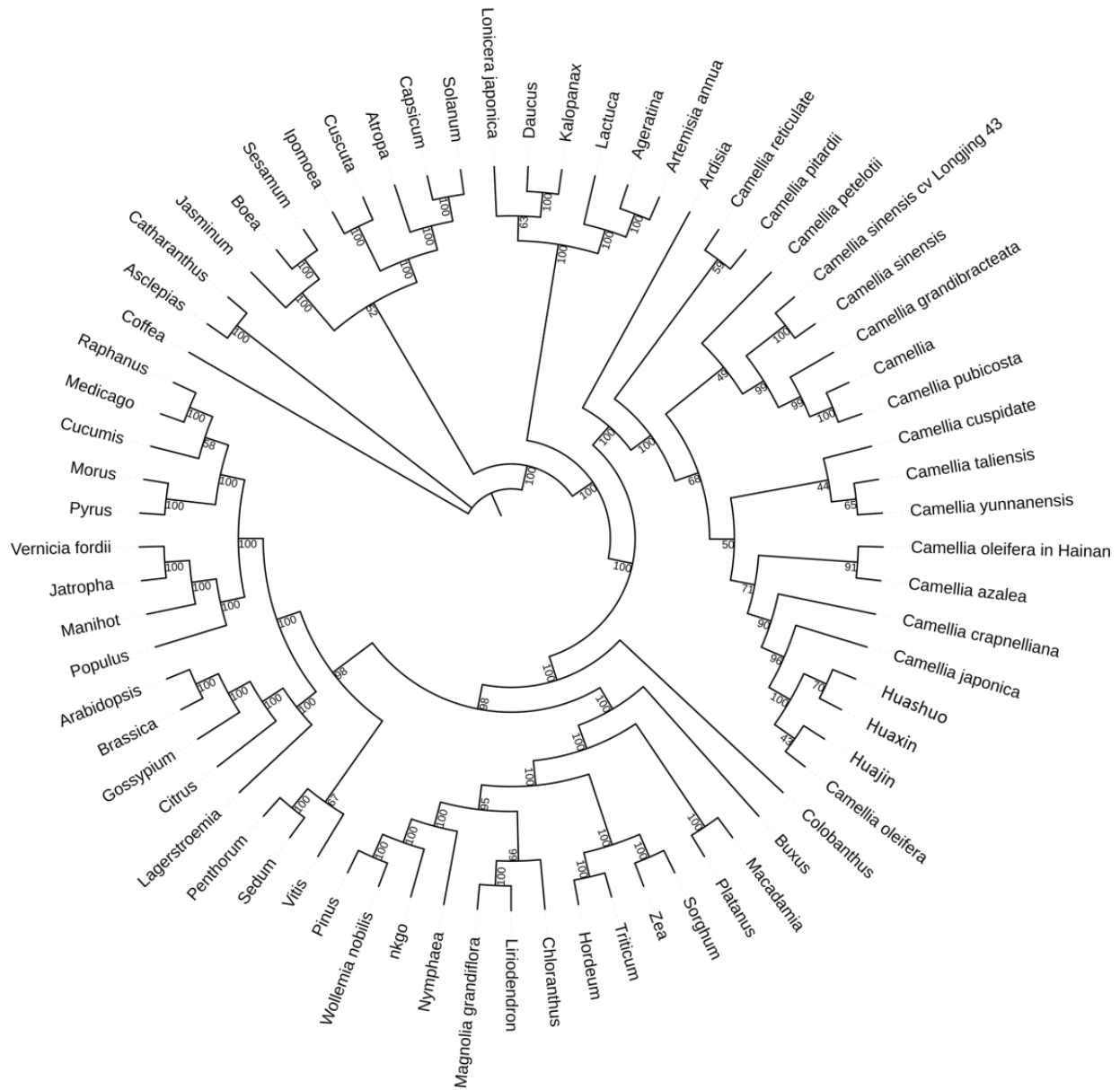


Fig. S1: Phylogenetic tree of 65 taxa based on 50 chloroplast protein-coding genes using maximum likelihood (ML). Bootstrap values (1000 replications) are shown at the nodes

Table S1: Repeat sequences in the *Camellia* 'Huashuo' chloroplast genome

No.	Repeat size (bp)	Repeat 1 start	Repeat 2 start	Repeat type	Repeat 1 location	Repeat 2 location
1	42	100969	122811	F	.	.
2	42	122811	142603	P	.	.
3	38	93926	93944	F	ycf2	ycf2
4	38	93926	149632	P	ycf2	ycf2-D2
5	38	93944	149650	P	ycf2	ycf2-D2
6	38	149632	149650	F	ycf2-D2	ycf2-D2
7	30	9044	47319	P	tRNA004	tRNA015
8	26	90268	153320	F	ycf2	ycf2-D2
9	24	4773	4785	F	.	.
10	23	10610	10641	P	.	.
11	22	96356	96382	P	.	.
12	22	96356	147210	F	.	.
13	22	96382	147236	F	.	.
14	22	147210	147236	P	.	.
15	21	9050	37392	F	tRNA004	tRNA012
16	21	37392	47322	P	tRNA012	tRNA015
17	21	38531	69118	F	tRNA014	tRNA022
18	20	32601	115307	P	.	.
19	20	33236	73270	F	.	.
20	20	48914	69301	C	.	.
21	20	49017	61239	P	.	.
22	20	93926	93962	F	ycf2	ycf2
23	20	93926	149632	P	ycf2	ycf2-D2
24	20	93962	149668	P	ycf2	ycf2-D2
25	20	128481	128992	F	ycf1	ycf1
26	20	149632	149668	F	ycf2-D2	ycf2-D2
27	19	10546	38339	F	tRNA005	tRNA013
28	19	15278	101337	F	.	.
29	19	15278	142258	P	.	.
30	19	31379	73807	P	.	.
31	19	31825	130243	F	.	ycf1
32	19	31829	65886	F	.	.
33	19	69362	101317	C	.	.
34	19	69362	142278	R	.	.
35	19	110783	127267	F	.	ycf1
36	19	127267	132812	P	ycf1	.
37	18	8089	127534	F	.	ycf1

C: complement repeats, F: forward repeats, R: reverse repeats, P: palindrome repeats

Table S2: Repeat sequences in the *Camellia* 'Huajin' chloroplast genome

No.	Repeat size (bp)	Repeat 1 start	Repeat 2 start	Repeat type	Repeat 1 location	Repeat 2 location
1	42	100979	122821	F	.	.
2	42	122821	142613	P	.	.
3	38	93936	93954	F	ycf2	ycf2
4	38	93936	149642	P	ycf2	ycf2-D2
5	38	93954	149660	P	ycf2	ycf2-D2
6	38	149642	149660	F	ycf2-D2	ycf2-D2
7	30	9043	47326	P	tRNA004	tRNA015
8	26	90278	153330	F	ycf2	ycf2-D2
9	24	4773	4785	F	.	.
10	23	10609	10640	P	.	.
11	22	96366	96392	P	.	.
12	22	96366	147220	F	.	.
13	22	96392	147246	F	.	.
14	22	147220	147246	P	.	.
15	21	9049	37398	F	tRNA004	tRNA012
16	21	37398	47329	P	tRNA012	tRNA015
17	21	38538	69128	F	tRNA014	tRNA022
18	20	32607	115318	P	.	.
19	20	33242	73280	F	.	.
20	20	48921	69311	C	.	.
21	20	49023	61248	P	.	.
22	20	53392	115319	F	.	.
23	20	93936	93972	F	ycf2	ycf2
24	20	93936	149642	P	ycf2	ycf2-D2
25	20	93972	149678	P	ycf2	ycf2-D2
26	20	128491	129002	F	ycf1	ycf1
27	20	149642	149678	F	ycf2-D2	ycf2-D2
28	19	10545	38345	F	tRNA005	tRNA013
29	19	15279	101347	F	.	.
30	19	15279	142268	P	.	.
31	19	31385	73817	P	.	.
32	19	31831	130253	F	.	ycf1
33	19	31835	65896	F	.	.
34	19	32607	53392	P	.	.
35	19	53395	83103	R	.	.
36	19	69372	101327	C	.	.
37	19	69372	142288	R	.	.

C: complement repeats, F: forward repeats, R: reverse repeats, P: palindrome repeats

Table S3: Repeat sequences in the *Camellia* 'Huaxin' chloroplast genome

No.	Repeat size (bp)	Repeat 1 start	Repeat 2 start	Repeat type	Repeat 1 location	Repeat 2 location
1	42	100979	122821	F	.	.
2	42	122821	142613	P	.	.
3	38	93936	93954	F	ycf2	ycf2
4	38	93936	149642	P	ycf2	ycf2-D2
5	38	93954	149660	P	ycf2	ycf2-D2
6	38	149642	149660	F	ycf2-D2	ycf2-D2
7	30	9049	47327	P	tRNA004	tRNA015
8	26	90278	153330	F	ycf2	ycf2-D2
9	24	4773	4785	F	.	.
10	23	10615	10646	P	.	.
11	22	96366	96392	P	.	.
12	22	96366	147220	F	.	.
13	22	96392	147246	F	.	.
14	22	147220	147246	P	.	.
15	21	9055	37399	F	tRNA004	tRNA012
16	21	37399	47330	P	tRNA012	tRNA015
17	21	38539	69128	F	tRNA014	tRNA022
18	20	32608	115318	P	.	.
19	20	33243	73280	F	.	.
20	20	48922	69311	C	.	.
21	20	53394	115319	F	.	.
22	20	93936	93972	F	ycf2	ycf2
23	20	93936	149642	P	ycf2	ycf2-D2
24	20	93972	149678	P	ycf2	ycf2-D2
25	20	128491	129002	F	ycf1	ycf1
26	20	149642	149678	F	ycf2-D2	ycf2-D2
27	19	10551	38346	F	tRNA005	tRNA013
28	19	15284	101347	F	.	.
29	19	15284	142268	P	.	.
30	19	31386	73817	P	.	.
31	19	31832	130253	F	.	ycf1
32	19	31836	65896	F	.	.
33	19	32608	53394	P	.	.
34	19	53397	83103	R	.	.
35	19	69372	101327	C	.	.
36	19	69372	142288	R	.	.
37	19	110793	127277	F	.	ycf1

C: complement repeats, F: forward repeats, R: reverse repeats, P: palindrome repeats

Table S4: Distribution of simple sequence repeats (SSR) in the *Camellia* 'Huashuo' chloroplast genome

No.	SSR_type	SSR_repeat_motif	Length	SSR_start	SSR_end	Location	Region
1	p1	(A)11	11	349	359	.	LSC
2	p1	(A)10	10	3782	3791	.	LSC
3	p1	(T)12	12	8757	8768	.	LSC
4	p1	(A)13	13	8901	8913	psbI	LSC
5	p1	(A)11	11	9427	9437	.	LSC
6	p1	(A)11	11	12556	12566	.	LSC
7	p1	(T)12	12	13928	13939	.	LSC
8	p1	(T)11	11	15060	15070	.	LSC
9	p1	(T)13	13	15459	15471	.	LSC
10	p1	(A)11	11	17280	17290	.	LSC
11	p1	(T)11	11	19486	19496	rpoC2	LSC
12	p1	(T)10	10	27186	27195	rpoB	LSC
13	p1	(A)15	15	32601	32615	.	LSC
14	p1	(A)13	13	32938	32950	.	LSC
15	p1	(T)13	13	33244	33256	.	LSC
16	p1	(A)13	13	37638	37650	.	LSC
17	p1	(A)11	11	38277	38287	.	LSC
18	p1	(A)11	11	38510	38520	.	LSC
19	p1	(A)12	12	44195	44206	.	LSC
20	p1	(A)12	12	46247	46258	.	LSC
21	p1	(A)10	10	46503	46512	.	LSC
22	p1	(T)10	10	48940	48949	.	LSC
23	p1	(A)10	10	49352	49361	.	LSC
24	p1	(T)10	10	52654	52663	ndhK	LSC
25	p1	(T)13	13	53391	53403	.	LSC
26	p1	(T)10	10	56352	56361	atpB	LSC
27	p1	(T)14	14	56786	56799	.	LSC
28	p1	(T)12	12	59002	59013	.	LSC
29	c	(T)10ggtgacataagatctaattgt agaaagaatcaaaagtgcggataa ttc(T)17	76	60723	60798	.	LSC
30	p1	(T)10	10	63162	63171	.	LSC
31	p1	(A)10	10	65323	65332	.	LSC
32	p1	(T)13	13	73278	73290	.	LSC
33	p1	(T)10	10	80650	80659	rpoA	LSC
34	p1	(T)10	10	82572	82581	.	LSC
35	p1	(T)14	14	83097	83110	.	LSC
36	p1	(A)12	12	83624	83635	.	LSC
37	p1	(T)11	11	85075	85085	.	LSC
38	p1	(T)10	10	105333	105342	.	IRA
39	p1	(A)11	11	110391	110401	.	IRA
40	p1	(T)14	14	115314	115327	.	SSC
41	p1	(T)10	10	116841	116850	.	SSC
42	p1	(A)11	11	117127	117137	ccsA	SSC
43	p1	(T)12	12	121326	121337	.	SSC
44	p1	(T)12	12	127303	127314	ycfI	SSC
45	p1	(T)12	12	128918	128929	ycfI	SSC
46	p1	(A)12	12	129222	129233	ycfI	SSC
47	p1	(A)10	10	129755	129764	ycfI	SSC
48	p1	(T)17	17	130136	130152	ycfI	SSC
49	p1	(T)11	11	133214	133224	.	IRB
50	p1	(A)10	10	138273	138282	.	IRB

Table S5: Distribution of simple sequence repeats (SSR) in the *Camellia* 'HuaJin' chloroplast genome

No.	SSR_type	SSR_repeat_motif	Length (bp)	SSR_start	SSR_end	Location	Region
1	p1	(A)11	11	349	359	.	LSC
2	p1	(A)10	10	3782	3791	.	LSC
3	p1	(T)12	12	8756	8767	.	LSC
4	p1	(A)13	13	8900	8912	psbI	LSC
5	p1	(A)11	11	9426	9436	.	LSC
6	p1	(T)10	10	10978	10987	.	LSC
7	p1	(A)11	11	12557	12567	.	LSC
8	p1	(T)12	12	13929	13940	.	LSC
9	p1	(T)11	11	15061	15071	.	LSC
10	p1	(T)13	13	15460	15472	.	LSC
11	p1	(A)16	16	17281	17296	.	LSC
12	p1	(T)11	11	19492	19502	rpoC2	LSC
13	p1	(T)10	10	27192	27201	rpoB	LSC
14	p1	(A)15	15	32607	32621	.	LSC
15	p1	(A)13	13	32944	32956	.	LSC
16	p1	(T)13	13	33250	33262	.	LSC
17	p1	(A)13	13	37644	37656	.	LSC
18	p1	(A)11	11	38283	38293	.	LSC
19	p1	(A)12	12	38516	38527	.	LSC
20	p1	(A)12	12	44202	44213	.	LSC
21	p1	(A)12	12	46254	46265	.	LSC
22	p1	(A)10	10	46510	46519	.	LSC
23	p1	(A)10	10	49358	49367	.	LSC
24	p1	(T)11	11	52660	52670	ndhK	LSC
25	p1	(T)14	14	53398	53411	.	LSC
26	p1	(T)10	10	56360	56369	atpB	LSC
27	p1	(T)14	14	56794	56807	.	LSC
28	p1	(T)12	12	59010	59021	.	LSC
29	p1	(T)17	17	60790	60806	.	LSC
30	p1	(T)10	10	61528	61537	.	LSC
31	p1	(T)10	10	63172	63181	.	LSC
32	p1	(A)10	10	65333	65342	.	LSC
33	p1	(T)13	13	73288	73300	.	LSC
34	p1	(T)10	10	80660	80669	rpoA	LSC
35	p1	(T)10	10	82582	82591	.	LSC
36	p1	(T)14	14	83107	83120	.	LSC
37	p1	(A)12	12	83634	83645	.	LSC
38	p1	(T)11	11	85085	85095	.	LSC
39	p1	(T)10	10	105343	105352	.	IRA
40	p1	(A)11	11	110401	110411	.	IRA
41	p1	(T)14	14	115325	115338	.	SSC
42	p1	(T)10	10	116852	116861	.	SSC
43	p1	(A)11	11	117138	117148	ccsA	SSC
44	p1	(T)11	11	121337	121347	.	SSC
45	p1	(T)12	12	127313	127324	ycf1	SSC
46	p1	(T)12	12	128928	128939	ycf1	SSC
47	p1	(A)12	12	129232	129243	ycf1	SSC
48	p1	(A)10	10	129765	129774	ycf1	SSC
49	p1	(T)17	17	130146	130162	ycf1	SSC
50	p1	(T)11	11	133224	133234	.	IRB
51	p1	(A)10	10	138283	138292	.	IRB

Table S6: Distribution of simple sequence repeat (SSR) in *Camellia* 'Huaxin' chloroplast genome

No.	SSR type	SSR repeat motif	Length (bp)	SSR start	SSR end	Location	Region
1	p1	(A)11	11	349	359	.	LSC
2	p1	(A)10	10	3782	3791	.	LSC
3	p1	(T)12	12	8762	8773	.	LSC
4	p1	(A)13	13	8906	8918	psbI	LSC
5	p1	(A)11	11	9432	9442	.	LSC
6	p1	(A)11	11	12562	12572	.	LSC
7	p1	(T)12	12	13934	13945	.	LSC
8	p1	(T)11	11	15066	15076	.	LSC
9	p1	(T)13	13	15465	15477	.	LSC
10	p1	(A)12	12	17286	17297	.	LSC
11	p1	(T)11	11	19493	19503	rpoC2	LSC
12	p1	(T)10	10	27193	27202	rpoB	LSC
13	p1	(A)15	15	32608	32622	.	LSC
14	p1	(A)13	13	32945	32957	.	LSC
15	p1	(T)13	13	33251	33263	.	LSC
16	p1	(A)13	13	37645	37657	.	LSC
17	p1	(A)11	11	38284	38294	.	LSC
18	p1	(A)12	12	38517	38528	.	LSC
19	p1	(A)12	12	44203	44214	.	LSC
20	p1	(A)12	12	46255	46266	.	LSC
21	p1	(A)10	10	46511	46520	.	LSC
22	p1	(T)10	10	48948	48957	.	LSC
23	p1	(A)10	10	49360	49369	.	LSC
24	p1	(T)11	11	52662	52672	ndhK	LSC
25	p1	(T)14	14	53400	53413	.	LSC
26	p1	(T)10	10	56362	56371	atpB	LSC
27	p1	(T)14	14	56796	56809	.	LSC
28	p1	(T)12	12	59012	59023	.	LSC
29	p1	(T)17	17	60792	60808	.	LSC
30	p1	(T)10	10	63172	63181	.	LSC
31	p1	(A)10	10	65333	65342	.	LSC
32	p1	(T)13	13	73288	73300	.	LSC
33	p1	(T)10	10	80660	80669	rpoA	LSC
34	p1	(T)10	10	82582	82591	.	LSC
35	p1	(T)14	14	83107	83120	.	LSC
36	p1	(A)12	12	83634	83645	.	LSC
37	p1	(T)11	11	85085	85095	.	LSC
38	p1	(T)10	10	105343	105352	.	IRA
39	p1	(A)11	11	110401	110411	.	IRA
40	p1	(T)14	14	115325	115338	.	SSC
41	p1	(T)10	10	116852	116861	.	SSC
42	p1	(A)11	11	117138	117148	ccsA	SSC
43	p1	(T)11	11	121337	121347	.	SSC
44	p1	(T)12	12	127313	127324	ycfI	SSC
45	p1	(T)12	12	128928	128939	ycfI	SSC
46	p1	(A)12	12	129232	129243	ycfI	SSC
47	p1	(A)10	10	129765	129774	ycfI	SSC
48	p1	(T)17	17	130146	130162	ycfI	SSC
49	p1	(T)11	11	133224	133234	.	IRB
50	p1	(A)10	10	138283	138292	.	IRB