

Supplementary material for

Evidence of inter-sectional chloroplast capture in *Corymbia* among sections *Torellianae* and *Maculatae*

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Table S1 Summary of *Corymbia* sequencing results and read mappings of the chloroplast genome and external transcribed spacer (ETS) sequence. Each paired-end read library was mapped to the *C. tessellaris* chloroplast genome (GenBank ID: K180803) and ETS sequence (GenBank ID: DQ352522).

Genotype	Paired-end library	Number of reads (post-trim)	Reads mapped to cp genome	% of reads mapped to cp genome	Avg. coverage of the cp genome	Reads mapped to ETS	Avg. coverage of ETS region
CCC2-002	250 bp	169,513,988	4,020,678	2.37	5,846	87089	43631
CCV2-018	250 bp	234,021,522	9,825,502	4.20	14,513	178616	89486
CCV2-019	150 bp	133,333,919	7,032,159	5.27	6,217	45048	13541
CCV2-046	150 bp	137,933,808	5,351,887	3.88	4,678	65101	19569
CH2-009	250 bp	206,959,160	12,208,645	5.90	18,182	122314	61279
CT2-009	150 bp	118,614,348	3,907,488	3.29	3,408	98454	29595
CT2-015	150 bp	123,321,876	4,502,722	3.65	3,960	55330	16632
CT2-019	250 bp	213,411,194	10,145,824	4.75	15,147	144636	72462

CCC, *Corymbia citriodora* subsp. *citriodora* (section *Maculatae*); CCV, *Corymbia citriodora* subsp. *variegata* (section *Maculatae*); CH, *Corymbia henryi* (section *Maculatae*); CT, *Corymbia torelliana* (section *Torellianae*) cp, chloroplast; bp, base pair

Table S2 Description and summary of *Corymbia* genotype chloroplast genomes. CG content (36.8%), gene number (135), coding sequences (85), number of tRNAs (37) and inverted repeat size (24,609 bp) remained constant among genotypes.

Genotype	Chloroplast Size (bp)	LSC (bp)	SSC
CCC2-002	159,995	88,491	18,686
CCV2-018	160,146	88,635	18,693
CCV2-019	160,102	88,592	18,693
CCV2-046	160,119	88,607	18,689
CH2-009	160,095	88,589	18,688
CT2-009	159,994	88,494	18,682
CT2-010	159,994	88,494	18,682
CT2-015	159,994	88,494	18,682
CT2-019	159,976	88,476	18,682

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LSC, long single copy; SSC, short single copy; bp, base pair

Table S3 Summary of chloroplast genome variations within *Corymbia* genotypes relative to *Corymbia maculata* (GenBank ID:KC180801).

Genotype	SNPs	Ts	Tv	Sub	Insert	Del	Ks	Ka	Truncation	Frameshifts
CCC2-002	276	74	193	9	47	54	53	55	1 (<i>rpl32</i>)	1 (<i>ndhF</i>)
CCV2-018	258	65	186	7	42	48	49	58	1 (<i>rpl32</i>)	1 (<i>ndhF</i>)
CCV2-019	267	66	195	6	45	59	46	67	2 (<i>rpl32</i> ; <i>rpl2</i>)	1 (<i>ndhF</i>)
CCV2-046	231	73	149	9	34	47	42	56	0	1 (<i>ndhF</i>)
CH2-009	265	67	192	6	41	57	46	60	1 (<i>rpl32</i>)	1 (<i>ndhF</i>)
CT2-009	283	72	201	10	46	55	56	54	1 (<i>rpl32</i>)	1 (<i>ndhF</i>)
CT2-015	283	71	202	10	47	54	56	54	1 (<i>rpl32</i>)	1 (<i>ndhF</i>)
CT2-019	283	72	202	9	45	54	55	54	1 (<i>rpl32</i>)	1 (<i>ndhF</i>)

CCC, *Corymbia citriodora* subsp. *citriodora* (section *Maculatae*); CCV, *Corymbia citriodora* subsp. *variegata* (section *Maculatae*); CH, *Corymbia henryi* (section *Maculatae*); CT, *Corymbia torelliana* (section *Torellianae*); SNP, single nucleotide polymorphism; Ts, transition; Tv, transversion; Sub, multiple nucleotide substitution; Insert, insertion; Del, deletion; Ks, synonymous mutation; Ka, non-synonymous mutation

Table S4 Matrix of total number of differences between eucalypt chloroplasts (after removal of inverted repeat B). Matrix was created using Geneious (v 7.05) and alignment using MAFFT (Kato et al. 2002). Below diagonal represents the total summed differences among chloroplast genomes; above diagonal represents the approximate percentage of differences across the alignment.

	A. costata	A. floribunda	C. maculata	CCC2-002	CCV2-018	CCV2-019	CCV2-046	CH2-009	CT2-009	CT2-015	CT2-019	E. camaldulensis
A. costata		0.08	1	1.16	0.95	0.97	0.87	0.96	1.16	1.16	1.15	3.42
A. floribunda	111		0.92	1.08	0.87	0.89	0.79	0.88	1.08	1.08	1.07	3.34
C. maculata	1301	1196		0.63	0.53	0.53	0.41	0.53	0.64	0.64	0.62	3.29
CCC2-002	1515	1408	823		0.3	0.36	0.56	0.35	0.06	0.06	0.04	3.4
CCV2-018	1246	1139	689	388		0.16	0.37	0.15	0.31	0.31	0.29	3.22
CCV2-019	1264	1157	693	467	205		0.38	0.05	0.36	0.36	0.35	3.22
CCV2-046	1132	1027	540	736	480	502		0.37	0.58	0.57	0.56	3.19
CH2-009	1257	1150	691	460	199	68	490		0.36	0.36	0.35	3.21
CT2-009	1521	1414	831	72	399	470	752	468		0	0.03	3.4
CT2-015	1521	1414	830	73	400	471	751	469	1		0.03	3.4
CT2-019	1504	1397	814	55	381	454	734	452	33	34		3.39
E. camaldulensis	4469	4362	4296	4438	4208	4211	4170	4194	4444	4444	4431	

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Figure S1 Variable length gap within the *Corymbia* chloroplast genome. Alignment of chloroplast genomes with submitted GenBank *Corymbia maculata* (KC180801) reference was completed using MAFFT (Kato et al., 2002) and visualized in Geneious (v 7.05).

