

Supporting Information Figures S1–S8, Tables S1–S4

Article title:

Comparing complete organelle genomes of holoparasitic *Christisonia kwangtungensis* with its close relatives: how different are they?

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The following supporting information is available for this article:

Figure S1. The plastid genome map of holoparasitic *C. kwangtungensis*.

Genes labelled outside the outer circle are transcribed clockwise, while those inside are transcribed counterclockwise. Dashed area in the inner circle indicates the GC content of plastid genome.

Figure S2. Comparison of plastid genome structure among non-parasite

(*Lindenbergia philippensis*), hemi-parasite (*Striga asistrica*), and holoparasite (*Christisonia kwangtungensis*; from top to bottom, respectively). Green lines connect homologous plastid coding genes. Green dotted lines indicate pseudogenized regions. Regions without connecting lines indicate gene loss.

Figure S3. The mitochondrial gene map of holoparasitic *C. kwangtungensis*.

Genes labelled outside the outer circle are transcribed clockwise, while those inside are transcribed counterclockwise. Dashed area in the inner circle indicates the GC content of mitochondrial genome.

Figure S4. Maximum likelihood phylogeny of rpl20 in the mitochondrial genome of *C. kwangtungensis*. Phylogenetic trees show evidence of intracellular gene transfer. The clade length of trees represents the base substitution rate.

Figure S5. Gene expression in the photosynthesis pathway observed in transcriptomes of 10 species. The detected expressed genes are marked as green. Species of the same clade of *C. kwangtungensis* are in the red box. With courtesy of © www.genome.jp/kegg/kegg1.html.

Figure S6. Gene expression in porphyrin and chlorophyll metabolism pathway observed in the transcriptome of *C. kwangtungensis*. Genes with detected expression are in the red boxes. The name and number of gene expression products were marked at each node. With courtesy of © www.genome.jp/kegg/kegg1.html.

Figure S7. Mitochondrial gene content (core genes in blue and variable genes in yellow) of 21 species including *C. kwangtungensis* and *A. indica*. Retained genes are marked in white and lost genes are marked in black.

Figure S8. Maximum likelihood phylogenetic tree of Orobanchaceae based on concatenated sequences of all coding genes present in the plastid genome of *Lindenbergia philippensis*.

Table S1. Statistics of putative plastid transferred genes in mitochondrial genome of *C. kwangtungensis*. Potential donors, transfer types, fragment lengths, and bootstrap of all the putative plastid transferred genes on mitochondrial genome of *C. kwangtungensis*.

Table S2. Comparison of informative characters of the horizontally transferred

fragment *rpl20* of *C. kwangtungensis* and its related species. The alignment site with yellow background is false informative site supports *C. kwangtungensis* nesting into Lamiaceae. Absolute position refers to the position in *rpl20* of *C. kwangtungensis*.

Table S3. Mitochondrial genome sequence of Lamiales used in this study.

Table S4. Plastid genome sequence for plastid phylogeny used in this study.



Figure S1

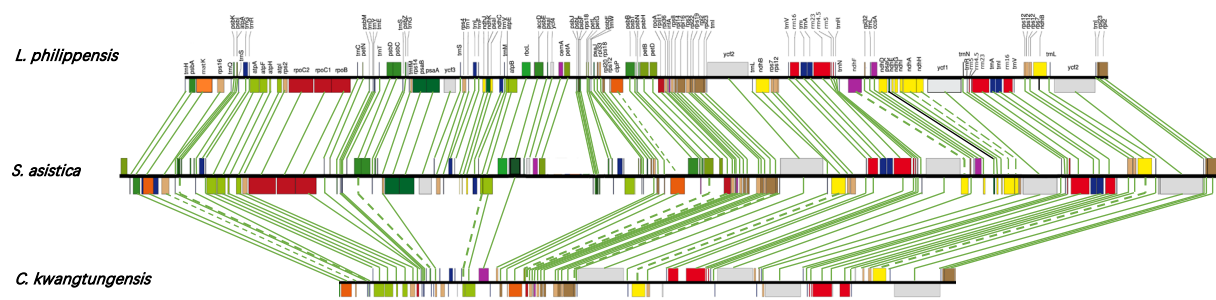


Figure S2

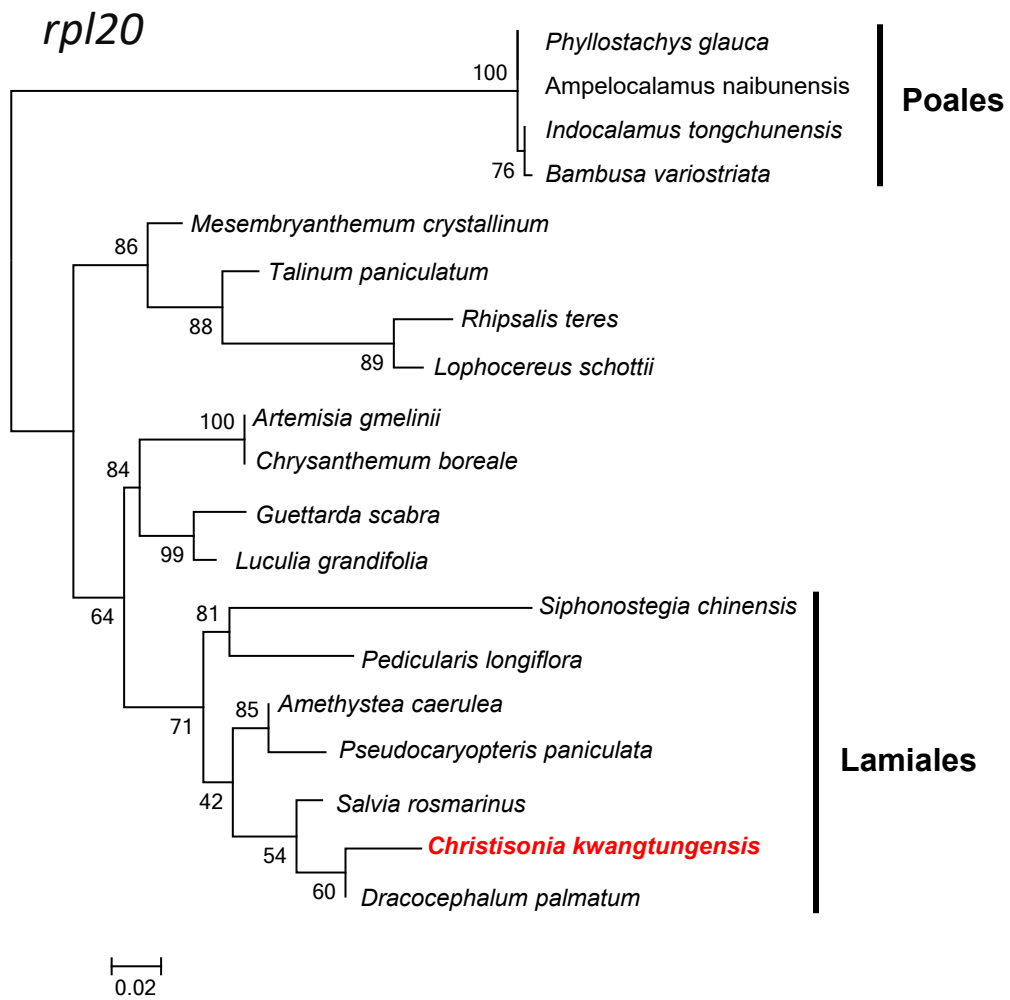


Figure S4



Figure S5

[illegible]

Figure S6

	<i>C. kwangtungensis</i>	<i>A. indica</i>	<i>Castilleja paramensis</i>	<i>Mimulus guttatus</i>	<i>Salvia miltiorrhiza</i>	<i>Rotheca serrata</i>	<i>Ajuga reptans</i>	<i>Hesperelaea palmeri</i>	<i>Nicotiana tabacumgensis</i>	<i>Solanum pennellii</i>	<i>Rhazya stricta</i>	<i>Arabidopsis thaliana</i>	<i>Silene latifolia</i>	<i>Glycine max</i>	<i>Medicago truncatula</i>	<i>Senna tora</i>	<i>Lactuca sativa</i>	<i>Vitis vinifera</i>	<i>Oryza sativa</i>	<i>Triticum aestivum</i>	<i>Liriodendron tulipifera</i>
<i>atp1</i>																					
<i>atp4</i>																					
<i>atp6</i>																					
<i>atp8</i>																					
<i>atp9</i>																					
<i>ccmB</i>																					
<i>ccmC</i>																					
<i>ccmFc</i>																					
<i>ccmFn</i>																					
<i>cob</i>																					
<i>cox1</i>																					
<i>cox2</i>																					
<i>cox3</i>																					
<i>matR</i>																					
<i>mttB</i>																					
<i>nad1</i>																					
<i>nad2</i>																					
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<i>nad4</i>																					
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<i>nad5</i>																					
<i>nad6</i>																					
<i>nad7</i>																					
<i>nad9</i>																					
<i>rpl2</i>																					
<i>rpl5</i>																					
<i>rpl10</i>																					
<i>rpl16</i>																					
<i>rps1</i>																					
<i>rps2</i>																					
<i>rps3</i>																					
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<i>rps13</i>																					
<i>rps14</i>																					
<i>rps19</i>																					
<i>sdh3</i>																					
<i>sdh4</i>																					

Figure S7

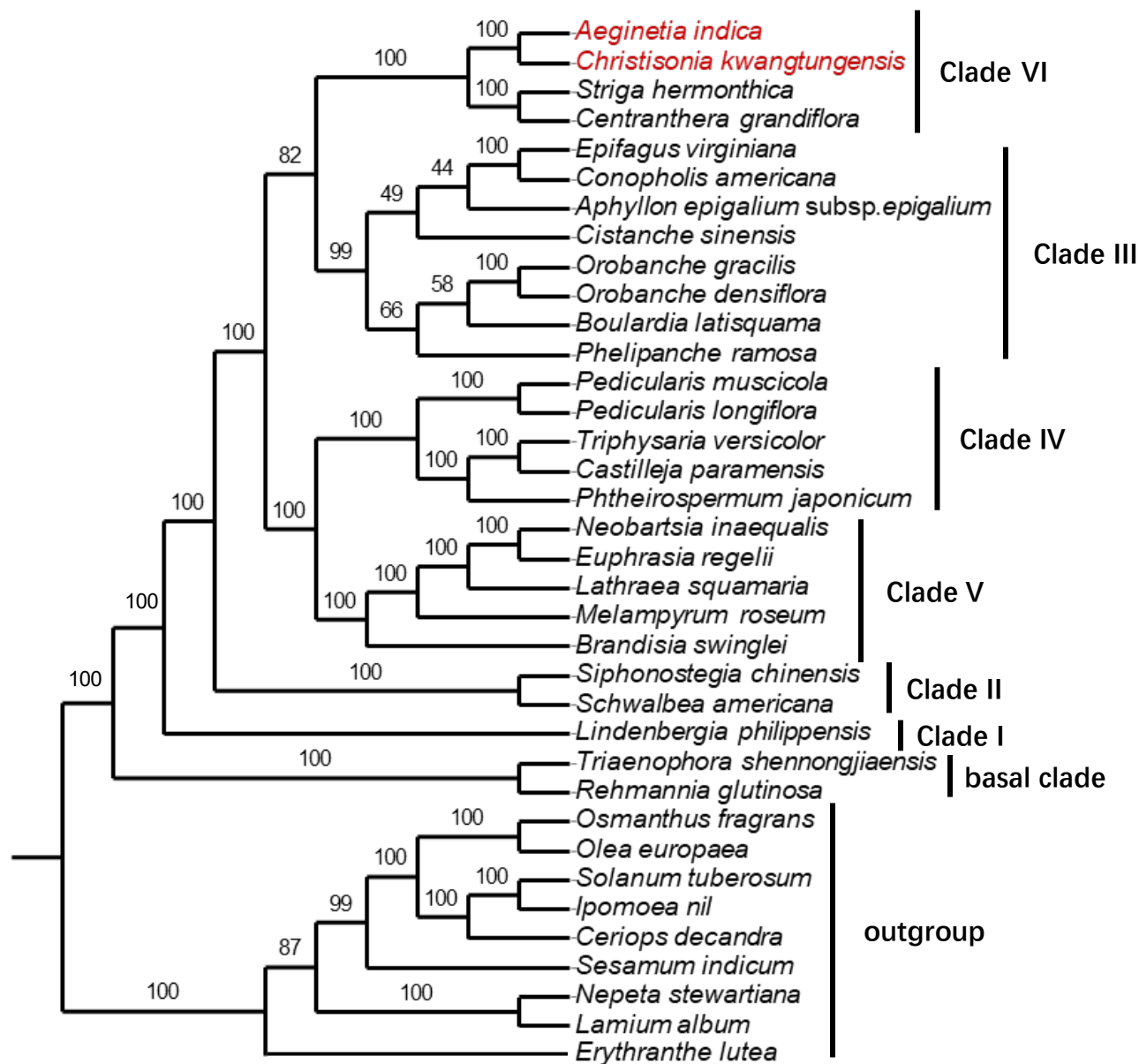


Table S1. Statistics of putative plastid transferred genes in mitochondrial genome of *C. kwangtungensis*. Potential donors, transfer types, fragment lengths, and bootstrap of all the putative plastid transferred genes on mitochondrial genome of *C. kwangtungensis*.

Gene	Potential donors	Type	Length (bp)	Bootstrap (%)
<i>ycf2</i>	Asparagales (Orchidaceae)	HGT	72	85
<i>rpl16</i>	Gentianales (Rubiaceae)	HGT	209	100
<i>rpl14</i>	Gentianales (Rubiaceae)	HGT	305	90
<i>rpoB</i>	Lamiales	IGT	570	100
<i>ndhB</i>	Lamiales	IGT	1130	93
<i>rpl20</i>	Lamiales	IGT	69	71
<i>petB</i>	Lamiales	IGT	576	100

Table S2. Comparison of informative characters of the horizontally transferred fragment *rpl20* of *C. kwangtungensis* and its related species. Alignment site with yellow background is false informative site supports *C. kwangtungensis* nesting into Lamiaceae. Absolute position refers to the position in *rpl20* of *C. kwangtungensis*.

Absolute position	153	156	158	164	166	175	187	192	203	211
<i>Christisonia kwangtungensis</i>	T	G	C	G	G	C	A	G	T	A
<i>Dracocephalum palmatum</i>	T	G	A	G	G	C	A	G	T	G
<i>Salvia rosmarinus</i>	T	G	A	G	A	C	A	G	T	G
<i>Pedicularis longiflora</i>	C	T	A	G	A	C	G	C	T	G
<i>Siphonostegia chinensis</i>	T	G	A	T	A	G	G	G	G	G

Table S3. Mitochondrial genome sequence of Lamiales used in this study.

Lineage	Species	Parasitic lifestyle	Data type	GenBank Accession No.
Orobanchaceae	<i>Castilleja paramensis</i>	hemi-parasitic	complete	KT959112
	<i>Neobartsia pedicularoides</i>	hemi-parasitic	partial	KP940485-KP940493
	<i>Orobanche densiflora</i>	holoparasitic	partial	KT367291-KT367292
	<i>O. austrohispanica</i>	holoparasitic	partial	KT366929, KT366933, KT366957-KT366958 KT366955
	<i>O. rapum-genistae</i>	holoparasitic	partial	KT367470, KT367476, KT367509-KT367510, KT367489
	<i>Aphyllon epigalium</i>	holoparasitic	partial	MH129026
	<i>A. notocalifornicum</i>	holoparasitic	partial	MG987142
	<i>Aeginetia indica</i>	holoparasitic	complete	MW851294
	<i>Christisonia kwangtungensis</i>	holoparasitic	complete	OM219025-OM219027
Oleaceae	<i>Chionanthus rupicola</i>	non-parasitic	complete	MG372115
	<i>Hesperelaea palmeri</i>	non-parasitic	complete	KX545367
	<i>Olea cuspidata</i>	non-parasitic	complete	MG372116
	<i>Ol. europaea</i>	non-parasitic	complete	MG372117
	<i>Ol. guanchica</i>	non-parasitic	complete	MG372120
	<i>Ol. laperrinei</i>	non-parasitic	complete	MG372121
Lamiaceae	<i>Ajuga reptans</i>	non-parasitic	complete	KF709392
	<i>Salvia miltiorrhiza</i>	non-parasitic	complete	KF177345
Gesneriaceae	<i>Boea hygrometrica</i>	non-parasitic	complete	JN107812
	<i>Haberlea rhodopensis</i>	non-parasitic	complete	MH757117
Phrymaceae	<i>Mimulus guttatus</i>	non-parasitic	complete	JN098455
Lentibulariaceae	<i>Utricularia reniformis</i>	non-parasitic	complete	KY774314

Table S4. Plastid genome sequence for plastid phylogeny used in this study.

Species Name	Taxonomic Groups	Life Style	GenBank Accession No.
<i>Rehmannia glutinosa</i>	basal clade	autotrophs	NC_034308
<i>Triaenophora shennongjiaensis</i>	basal clade	autotrophs	NC_039781
<i>Lindenbergia philippensis</i>	Clade I	autotrophs	NC_022859
<i>Schwalbea americana</i>	Clade II	hemi-parasites	NC_023115
<i>Siphonostegia chinensis</i>	Clade II	hemi-parasites	NC_046038
<i>Aphyllon epigaliumsubsp.epigalium</i>	Clade III	holoparasites	MH050785
<i>Boulardia latisquama</i>	Clade III	holoparasites	NC_025641
<i>Cistanche sinensis</i>	Clade III	holoparasites	MN614129
<i>Conopholis americana</i>	Clade III	holoparasites	NC_023131
<i>Epifagus virginiana</i>	Clade III	holoparasites	NC_001568
<i>Orobanche densiflora</i>	Clade III	holoparasites	NC_031442
<i>Orobanche gracilis</i>	Clade III	holoparasites	NC_023464
<i>Phelipanche ramosa</i>	Clade III	holoparasites	NC_023465
<i>Triphysaria versicolor</i>	Clade IV	hemi-parasites	NC_053793
<i>Castilleja paramensis</i>	Clade IV	hemi-parasites	NC_031805
<i>Pedicularis longiflora</i>	Clade IV	hemi-parasites	NC_046852
<i>Pedicularis muscicola</i>	Clade IV	hemi-parasites	NC_046853
<i>Phtheirospermum japonicum</i>	Clade IV	hemi-parasites	NC_053792
<i>Brandisia swinglei</i>	Clade V	hemi-parasites	NC_042954
<i>Euphrasia regelii</i>	Clade V	hemi-parasites	NC_045041
<i>Lathraea squamaria</i>	Clade V	holoparasites	NC_027838
<i>Melampyrum roseum</i>	Clade V	hemi-parasites	NC_053791
<i>Neobartsia inaequalis</i>	Clade V	hemi-parasites	KF922718
<i>Aeginetia indica</i>	Clade VI	holoparasites	MN529629
<i>Christisonia kwangtungensis</i>	Clade VI	holoparasites	OL362208
<i>Centranthera grandiflora</i>	Clade VI	hemi-parasites	NC_059747
<i>Striga hermonthica</i>	Clade VI	hemi-parasites	KU212372
<i>Ceriops decandra</i>	outgroup	autotrophs	NC_061406
<i>Olea europaea</i>	outgroup	autotrophs	NC_013707
<i>Ipomoea nil</i>	outgroup	autotrophs	NC_031159
<i>Solanum tuberosum</i>	outgroup	autotrophs	NC_008096
<i>Erythranthe lutea</i>	outgroup	autotrophs	NC_030212
<i>Lamium album</i>	outgroup	autotrophs	NC_036971
<i>Nepeta stewartiana</i>	outgroup	autotrophs	NC_057283
<i>Osmanthus fragrans</i>	outgroup	autotrophs	NC_042377
<i>Sesamum indicum</i>	outgroup	autotrophs	NC_016433