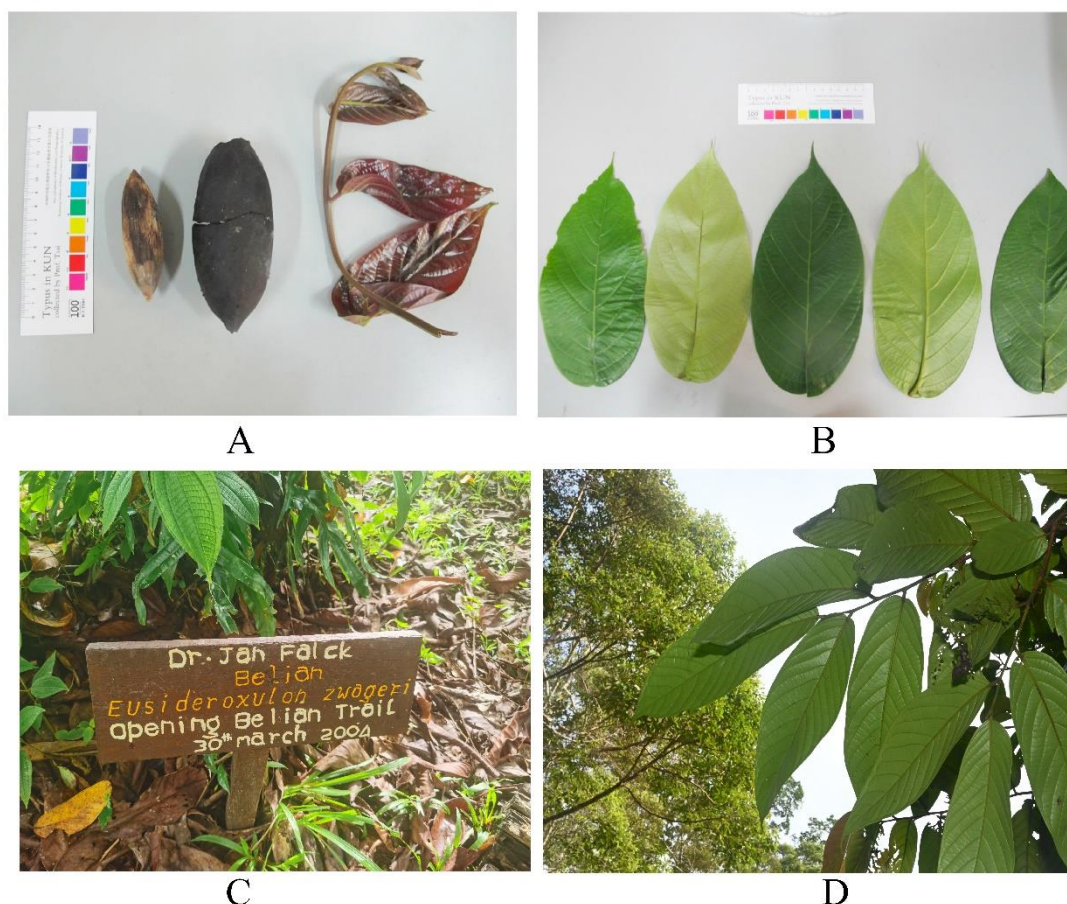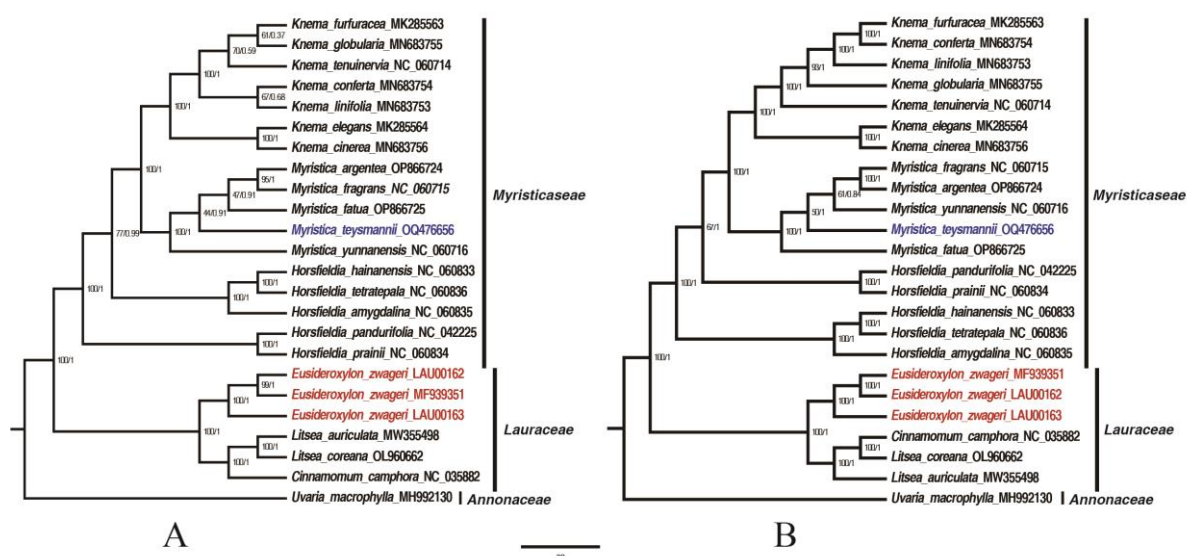# Supplementary Materials

Figure S1. Sample images of Belian. (**A**) Belian seeds and young leaves. (**B**) Mature leaves of Belian. (**A**) and (**B**) were collected from Sulawesi. (**C**) Collection site marking. (**D**) Belian III leaves. (**C**) and (**D**) were collected from Kalimantan.

Figure S2. The phylogenetic tree based on complete chloroplast sequences and 75 protein-coding genes with ML and BI methods, including 24 species in the Magnoliids. (**A**) The phylogenetic tree based on complete chloroplast sequences with Maximum Likelihood and Bayesian Inference method, including 24 species in the Magnoliids (Myristicaceae: *Horsfieldia, Knema, Myristica, Endocomia*; Lauraceae: *Cinnamomum, Eusideroxylon, Litsea*; and Annonaceae: *Uvaria* as the outgroup). (**B**)

The phylogenetic tree based on 75 protein-coding genes of complete chloroplast sequences with Maximum Likelihood and Bayesian Inference method, including 24 species in the Magnoliids (Myristicaceae: *Horsfieldia*, *Knema*, *Myristica*, *Endocomia*; Lauraceae: *Cinnamomum*, *Eusideroxylon*, *Litsea*; and Annonaceae: *Uvaria* as the outgroup).

Table S1. Plastome sequences obtained from NCBI and LCGDB for this study.

Species	Accession	Database
Aristolochia contorta	MN132861	NCBI
Aristolochia littoralis	OP950686	NCBI
Aristolochia tubiflora	OP950692	NCBI
Artabotrys pilosus	OK216144	NCBI
Beilschmiedia percoriacea	LAU00120	LCGDB
Beilschmiedia turbinata	LAU00039	LCGDB
Calycanthus chinensis	OP327562	NCBI
Calycanthus fertilis	AJ428413	NCBI
Chimonanthus salicifolius	MW801118	NCBI
Chimonanthus zhejiangensis	MW166219	NCBI
Chloranthus erectus	MH394412	NCBI
Chloranthus henryi	MK922064	NCBI
Chloranthus japonicus	KP256024	NCBI
Chloranthus spicatus	EF380352	NCBI
Cryptocarya densiflora	LAU00050	LCGDB
Drimys granadensis	DQ887676	NCBI
Endiandra dolichocarpa	LAU00053	LCGDB
Eusideroxylon zwageri	LAU00162	LCGDB
Eusideroxylon zwageri	LAU00163	LCGDB
Eusideroxylon zwageri	MF939351	NCBI
Gymnotheca chinensis	MN263889	NCBI
Hernandia nymphaeifolia	MG838431	NCBI
Horsfieldia hainanensis	MN495959	NCBI
Horsfieldia tetratepala	MN495961	NCBI
Houttuynia cordata	MN263890	NCBI
Hypodaphnis zenkeri	OQ621668	NCBI
Idiospermum australiense	MH377056	NCBI
Illigera celebica	LAU00199	LCGDB
Illigera grandiflora	LAU00198	LCGDB
Knema cinerea	MN683756	NCBI
Knema elegans	MK285564	NCBI
Knema linifolia	MN683753	NCBI
Liriodendron chinense	MK887907	NCBI
Liriodendron tulipifera	MN990625	NCBI
Miliusa glochidioides	OM047203	NCBI
Myristica argentea	OP866724	NCBI
Myristica fatua	OP866725	NCBI
Myristica fragrans	NC 060715	NCBI
Myristica teysmannii	OQ476656	NCBI
Piper betle	OM717260	NCBI
Piper boehmeriifolium	OM717256	NCBI
Piper bonii	OM717259	NCBI
Potameia microphylla	MT720950	NCBI
Pseudowintera colorata	MT555077	NCBI
Saururus chinensis	MN263891	NCBI
Stelechocarpus burahol	MN253544	NCBI
Syndiclis chinensis	LAU00155	LCGDB
Tasmannia lanceolata	MT555078	NCBI

Note: LCGDB=Lauraceae Chloroplast Genome Database.

Table S2. Genes present in the Belian chloroplast genome.

Gene funcction	Group of genes	Name of genes
Photosynthesis gene	Photosystem I	*psaA, psaB, psaC, psaI, psaJ*
	Photosystem II	*psbA, psbB, psbC, psbD, psbE, psbF, psbH, psbI, psbJ, psbK, psbL, psbM, psbN, psbT, psbZ, ycf3***
	Cytochrome b/f complex	*petA, petB*, petD*, petG, petL, petN*
	ATP synthase	*atpA, atpB, atpE, atpF*, atpH, atpI*
	NADH-dehydrogenase	*ndhA*, ndhB* (2), ndhC, ndhD, ndhE, ndhF, ndhG, ndhH, ndhI, ndhJ, ndhK*
	Rubisco Large subunit	*rbcL*
Self-replication gene	RNA polymerase	*rpoA, rpoB, rpoC1*, rpoC2*
	Ribosomal proteins (LSU)	*rpl2*, rpl14, rpl16*, rpl20, rpl22, rpl23 (2), rpl32, rpl33, rpl36*
	Ribosomal proteins (SSU)	*rps2, rps3, rps4, rps7 (2), rps8, rps11, rps12 (2), rps14, rps15, rps16*, rps18, rps19*
	Transfer RNAs	*trnA-UGC**(2), trnC-GCA, trnD-GUC, trnE-UUC, trnF-GAA, trnG-GCC, trnG-UCC*, trnH-GUG, trnI-CAU(2), trnI-GAU*(2), trnK-UUU**, trnL-CAA(2), trnL-UAA, trnL-UAG*, trnM-CAU(2), trnN-GUU(2), trnP-UGG, trnQ-UUG, trnR-ACG(2), trnR-UCU, trnS-GCU, trnS-GGA, trnS-UGA, trnT-GGU, trnT-UGU, trnV-GAC(2), trnV-UAC*, trnW-CCA, trnY-GUA*
	Ribosomal RNAs	*rrn4.5(2), rrn5(2), rrn16(2), rrn23(2)*
Other genes	Subunit of Acetyl-CoA-carboxylase	*accD*
	C-type cytochrom synthesis gene	*ccsA*
	Envelop membrane protein	*cemA*
	Protease	*clpP***
	Translational initiation factor	*infA*
	Maturase	*matK*
Functions unknown	Hypothetical chloroplast reading frames (*ycf*)	*ycf1(2), ycf2(2), ycf4*

Note: "*" means gene with one intron; "**" means gene with two introns; (2) means number of copies of multi-copy genes.

Table S3. Mutation present in the Belian chloroplast genome.

Min (original sequence)	Length	Change	Polymorphism Type	Amino Acid Change	CDS	CDS Position	Codon Change	gene
502	1	C -> A	SNP (transversion)					
791	1	A -> G	SNP (transition)					
1538	1	(T)10 -> (T)9	Deletion (tandem repeat)					
1538	0	(T)10 -> (T)11	Insertion (tandem repeat)					
1779	5	AAATG	Deletion					
3449	1	C -> A	SNP (transversion)					
4000	1	C -> T	SNP (transition)	D -> N	matK CDS	1183	GAT -> AAT	matK
4334	1	G -> T	SNP (transversion)		matK CDS	849	TCC -> TCA	matK
5554	1	C -> A	SNP (transversion)					
5998	1	A -> C	SNP (transversion)					
6176	1	G -> T	SNP (transversion)					
6177	1	G -> T	SNP (transversion)					
6197	1	(T)10 -> (T)9	Deletion (tandem repeat)					
7007	1	A -> G	SNP (transition)					
7148	1	(A)10 -> (A)9	Deletion (tandem repeat)					
7242	1	-C	Deletion					
7398	1	A -> G	SNP (transition)					
7825	1	C -> T	SNP (transition)	V -> I	rps16 CDS	4	GTA -> ATA	rps16
8666	0	CACAG	Insertion					
8812	1	C -> A	SNP (transversion)					
9731	1	C -> A	SNP (transversion)					
11378	1	G -> C	SNP (transversion)					
12100	1	A -> C	SNP (transversion)					
13416	1	T -> C	SNP (transition)		atpA CDS	1224	CAA -> CAG	atpA
16067	15	TTAATATGAATTTCC	Deletion (tandem repeat)					
16074	1	G -> T	SNP (transversion)					
17259	1	T -> C	SNP (transition)					
17917	1	C -> A	SNP (transversion)	V -> F	atpI CDS	133	GTT -> TTT	atpI
18360	1	C -> G	SNP (transversion)		rps2 CDS	618	GCG -> GCC	rps2
19001	0	(T)10 -> (T)11	Insertion (tandem repeat)					
19668	1	T -> C	SNP (transition)	I -> V	rpoC2 CDS	3661	ATT -> GTT	rpoC2
22029	1	G -> T	SNP (transversion)	H -> N	rpoC2 CDS	1300	CAT -> AAT	rpoC2
25375	1	T -> G	SNP (transversion)					
25385	1	C -> T	SNP (transition)					
25596	1	(T)10 -> (T)9	Deletion (tandem repeat)					
26245	0	ATAGAA	Insertion					
26423	1	T -> C	SNP (transition)		rpoB CDS	3057	GGA -> GGG	rpoB
27194	1	T -> G	SNP (transversion)		rpoB CDS	2286	GGA -> GGC	rpoB
29960	0	GATAT	Insertion					
30399	1	G -> T	SNP (transversion)					
31241	1	A -> G	SNP (transition)					
31874	1	T -> G	SNP (transversion)					
31898	0	TTCATAAA	Insertion					
32123	1	C -> G	SNP (transversion)					
32490	1	A -> C	SNP (transversion)					
32852	1	A -> C	SNP (transversion)					
32853	1	A -> C	SNP (transversion)					
32910	1	C -> T	SNP (transition)					
33016	1	(A)7 -> (A)6	Deletion (tandem repeat)					
33339	1	T -> C	SNP (transition)					
34139	0	(CTATG)2 -> (CTATG)3	Insertion (tandem repeat)					

Position	Count	Change	Type	AA change	Region	Pos	Codon change	Gene
34429	0	(T)9 -> (T)10	Insertion (tandem repeat)					
35272	1	A -> G	SNP (transition)					
35299	1	G -> A	SNP (transition)					
35551	1	A -> G	SNP (transition)					
38690	1	T -> C	SNP (transition)		psbC CDS	1287	TCT -> TCC	psbC
38966	7	TCCCACC -> GGTGGGA	Microinversion					psbC-trnS
39389	0	TTTCAATTT	Insertion					
40086	1	C -> A	SNP (transversion)					
44049	1	A -> G	SNP (transition)		psaA CDS	1254	ACT -> ACC	psaA
44374	1	C -> T	SNP (transition)	R -> K	psaA CDS	929	AGG -> AAG	psaA
44382	1	A -> G	SNP (transition)		psaA CDS	921	CAT -> CAC	psaA
45273	1	T -> G	SNP (transversion)		psaA CDS	30	GTA -> GTC	psaA
47188	1	T -> G	SNP (transversion)					
47389	1	G -> A	SNP (transition)					
48103	1	A -> G	SNP (transition)					
48996	1	(A)8 -> (A)7	Deletion (tandem repeat)					
48996	0	(A)8 -> (A)9	Insertion (tandem repeat)					
49907	1	G -> A	SNP (transition)					
50215	5	AACTT	Deletion					
50220	0	(A)2 -> (A)3	Insertion (tandem repeat)					
50392	0	(A)9 -> (A)10	Insertion (tandem repeat)					
51498	1	A -> G	SNP (transition)					
51894	1	G -> A	SNP (transition)					
51983	1	G -> T	SNP (transversion)					
52914	0	TATGGATAT	Insertion					
53683	1	(T)12 -> (T)11	Deletion (tandem repeat)					
53683	0	(T)12 -> (T)13	Insertion (tandem repeat)					
53790	1	T -> G	SNP (transversion)	L -> F	ndhC CDS	294	TTA -> TTC	ndhC
54302	1	A -> C	SNP (transversion)					
54410	1	T -> G	SNP (transversion)					
55159	1	A -> T	SNP (transversion)					
55394	1	G -> A	SNP (transition)					
56881	1	T -> C	SNP (transition)					
56883	1	T -> AC	Insertion					
56954	1	(T)10 -> (T)9	Deletion (tandem repeat)					
57060	1	C -> A	SNP (transversion)		atpE CDS	399	TCG -> TCT	atpE
57671	1	C -> A	SNP (transversion)	M -> I	atpB CDS	1281	ATG -> ATT	atpB
59330	1	A -> C	SNP (transversion)					
59460	1	A -> G	SNP (transition)					
59528	10	GATGTATTTG	Deletion					
60135	1	G -> T	SNP (transversion)		rbcL CDS	414	CTG -> CTT	rbcL
60417	1	G -> A	SNP (transition)		rbcL CDS	696	ACG -> ACA	rbcL
61296	1	C -> A	SNP (transversion)					
61692	0	TTTCT	Insertion					
61713	0	TATTAG	Insertion					
62177	1	G -> A	SNP (transition)	S -> N	accD CDS	338	AGT -> AAT	accD
62360	1	C -> ACATTTATAGTTA	Insertion	P -> HIYSY	accD CDS	521	CCC -> CAC,ATT,TAT,AGT,TAC	accD
63603	1	A -> T	SNP (transversion)					
63850	1	A -> G	SNP (transition)					
64888	1	C -> G	SNP (transversion)	P -> R	ycf4 CDS	458	CCC -> CGC	ycf4
65302	1	A -> C	SNP (transversion)					
66074	1	A -> G	SNP (transition)		cemA CDS	177	AGA -> AGG	cemA
68310	1	A -> G	SNP (transition)					
68311	0	(G)8 -> (G)9	Insertion (tandem repeat)					
68544	1	G -> A	SNP (transition)					
68852	12	GAATCAGACAAA -> TTTGTCTGATTC	Microinversion					petA-psbJ
70567	1	(A)10 -> (A)9	Deletion (tandem repeat)					
71578	5	CCGAT	Deletion					
72527	1	C -> A	SNP (transversion)					
72861	1	G -> A	SNP (transition)		rpl33 CDS	189	GAG -> GAA	rpl33
73321	1	A -> C	SNP (transversion)					
75509	1	(T)13 -> (T)12	Deletion (tandem repeat)					
75510	1	(T)13 -> (T)12	Deletion (tandem repeat)					
75672	1	(A)9 -> (A)8	Deletion (tandem repeat)					
76659	1	G -> A	SNP (transition)					
77290	1	A -> C	SNP (transversion)					
77647	1	A -> G	SNP (transition)	E -> G	psbB CDS	248	GAA -> GGA	psbB
79116	1	G -> A	SNP (transition)	A -> T	psbT CDS	7	GCA -> ACA	psbT
79731	1	G -> A	SNP (transition)	S -> N	psbH CDS	218	AGT -> AAT	psbH
80042	1	C -> A	SNP (transversion)					
80477	1	C -> T	SNP (transition)					
82038	1	C -> A	SNP (transversion)					
84749	1	T -> G	SNP (transversion)		infA CDS	183	TCA -> TCC	infA
85919	1	C -> A	SNP (transversion)	R -> L	rpl14 CDS	92	CGA -> CTA	rpl14
86177	2	GA -> TC	Microinversion	S -> E	rpl16 CDS	355	TCA -> GAA	rpl16
87465	1	(T)14 -> (T)13	Deletion (tandem repeat)					
87593	0	(TT)7 -> (TT)8	Insertion (tandem repeat)					
87593	0	(T)14 -> (T)15	Insertion (tandem repeat)					
88786	1	C -> T	SNP (transition)	R -> K	rpl22 CDS	8	AGG -> AAG	rpl22
91078	6	ATCGAT	Deletion	RSI -> S	ycf2 CDS	1275	AGA, TCG, ATT -> AGT	ycf2
92734	1	T -> G	SNP (transversion)	D -> E	ycf2 CDS	2931	GAT -> GAG	ycf2
93606	1	C -> A	SNP (transversion)	P -> Q	ycf2 CDS	3803	CCA -> CAA	ycf2
95656	1	C -> A	SNP (transversion)	F -> L	ycf2 CDS	5853	TTC -> TTA	ycf2
96970	5	AAGAC	Deletion					
114060	1	C -> A	SNP (transversion)	L -> F	ndhF CDS	2220	TTG -> TTT	ndhF
114074	1	T -> G	SNP (transversion)	I -> L	ndhF CDS	2206	ATA -> CTA	ndhF
115152	1	A -> C	SNP (transversion)	D -> E	ndhF CDS	1128	GAT -> GAG	ndhF
116340	1	T -> C	SNP (transition)					
116376	1	G -> T	SNP (transversion)					
116395	1	A -> C	SNP (transversion)					
116440	1	(A)11 -> (A)10	Deletion (tandem repeat)					
117212	2	(AA)5 -> (AA)4	Deletion (tandem repeat)					
117212	0	(A)10 -> (A)11	Insertion (tandem repeat)					
117337	1	C -> T	SNP (transition)					
117731	3	TTC -> GAA	Microinversion					rrn5S-trnR
117768	0	(T)10 -> (T)11	Insertion (tandem repeat)					
118156	1	C -> T	SNP (transition)					
118175	1	G -> T	SNP (transversion)					
118447	1	(A)14 -> (A)13	Deletion (tandem repeat)					
118448	1	(A)14 -> (A)13	Deletion (tandem repeat)					
118556	0	ATGAC	Insertion					
119104	1	C -> A	SNP (transversion)	F -> L	ccsA CDS	225	TTC -> TTA	ccsA

119884	5	CTACT -> AGTAG	Microinversion					ccsA-ndhD
121968	1	T -> G	SNP (transversion)					
123325	0	(T)9 -> (T)10	Insertion (tandem repeat)					
125016	1	G -> T	SNP (transversion)					
125508	0	T	Insertion					
125912	1	C -> T	SNP (transition)		ndhA CDS	456	TCG -> TCA	ndhA
127851	1	T -> C	SNP (transition)	I -> V	rps15 CDS	70	ATA -> GTA	rps15
128484	1	G -> T	SNP (transversion)	P -> Q	ycf1 CDS	4700	CCA -> CAA	ycf1
129296	3	AAA -> TTT	Microinversion	F -> K	ycf1 CDS	3886	TTT -> AAA	ycf1
129657	1	G -> C	SNP (transversion)	T -> R	ycf1 CDS	3527	ACA -> AGA	ycf1
132180	1	C -> T	SNP (transition)	S -> N	ycf1 CDS	1004	AGT -> AAT	ycf1
132644	1	T -> C	SNP (transition)	I -> M	ycf1 CDS	540	ATA -> ATG	ycf1
149751	5	GTCTT	Deletion					
151069	1	G -> T	SNP (transversion)	F -> L	ycf2 CDS	5853	TTC -> TTA	ycf2
153119	1	G -> T	SNP (transversion)	P -> Q	ycf2 CDS	3803	CCA -> CAA	ycf2
153991	1	A -> C	SNP (transversion)	D -> E	ycf2 CDS	2931	GAT -> GAG	ycf2
155642	6	ATCGAT	Deletion	RSI -> S	ycf2 CDS	1275	AGA, TCG, ATT -> AGT	ycf2