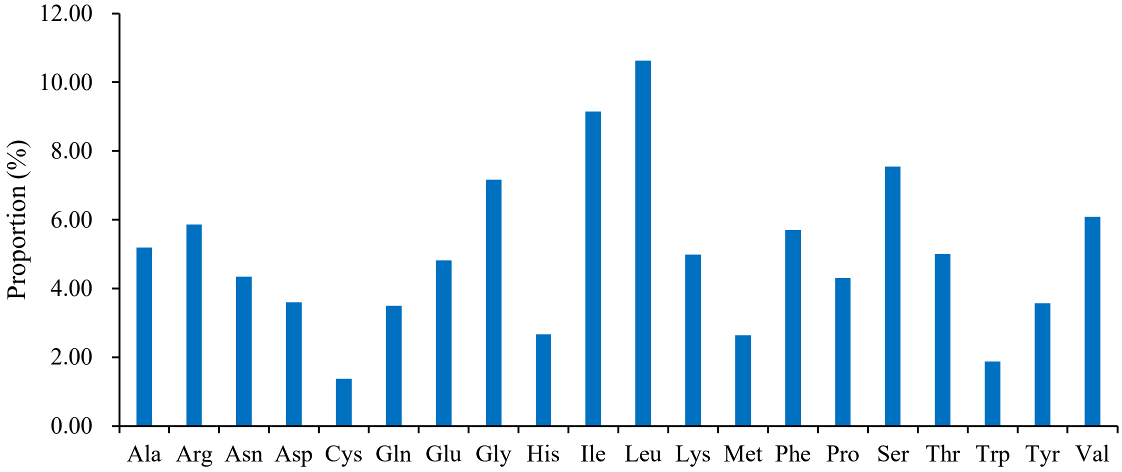

Figure S1. Amino acid frequency among 79 protein-coding genes in the cp genome of *Michelia shiluensis*.

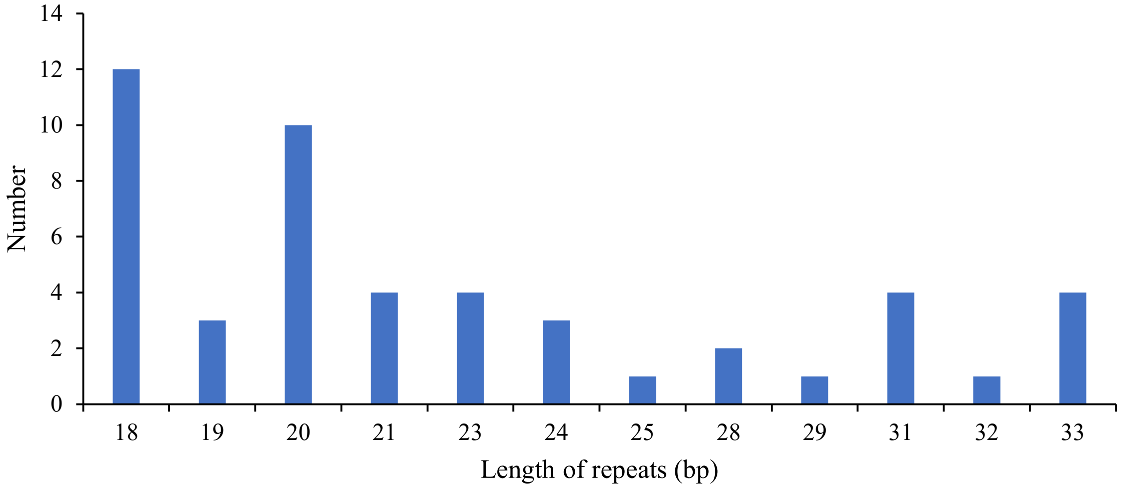

Figure S2. Different lengths of repeats in *Michelia shiluensis* cp genome.

Table S1. Possible RNA editing sites in the chloroplast genome of *Michelia shiluensis*.

Gene	Nucleotide Position	Amino Acid Position	Codon Conversion	Amino Acid Conversion	Score
accD	758	253	TCG=>TTG	S=>L	0.8
accD	1325	442	TCA=>TTA	S=>L	1
accD	1367	456	CCT=>CTT	P=>L	1
atpA	773	258	TCA=>TTA	S=>L	1
atpA	914	305	TCA=>TTA	S=>L	1
atpB	1184	395	TCA=>TTA	S=>L	1
atpF	263	88	GCG=>GTG	A=>V	1
atpF	479	160	TCG=>TTG	S=>L	1
atpI	349	117	CGG=>TGG	R=>W	1
atpI	428	143	CCC=>CTC	P=>L	1
atpI	629	210	TCA=>TTA	S=>L	1
ccsA	118	40	CCG=>TCG	P=>S	1
ccsA	628	210	CAC=>TAC	H=>Y	0.86
ccsA	644	215	ACT=>ATT	T=>I	0.86

clpP	556	186	CAT=>TAT	H=>Y	1
matK	202	68	CAT=>TAT	H=>Y	0.86
matK	383	128	TCA=>TTA	S=>L	0.86
matK	439	147	CAT=>TAT	H=>Y	0.86
matK	463	155	CAT=>TAT	H=>Y	1
matK	649	217	CAT=>TAT	H=>Y	1
matK	904	302	CAC=>TAC	H=>Y	1
matK	1183	395	CGG=>TGG	R=>W	1
matK	1193	398	TCG=>TTG	S=>L	0.86
matK	1252	418	CAC=>TAC	H=>Y	1
ndhA	50	17	TCG=>TTG	S=>L	1
ndhA	107	36	CCT=>CTT	P=>L	1
ndhA	341	114	TCA=>TTA	S=>L	1
ndhA	476	159	TCA=>TTA	S=>L	1
ndhA	566	189	TCA=>TTA	S=>L	1
ndhA	1073	358	TCC=>TTC	S=>F	1
ndhB	149	50	TCA=>TTA	S=>L	1
ndhB	446	149	TCA=>TTA	S=>L	1
ndhB	467	156	CCA=>CTA	P=>L	1
ndhB	542	181	ACG=>ATG	T=>M	1
ndhB	586	196	CAT=>TAT	H=>Y	1
ndhB	611	204	TCA=>TTA	S=>L	0.8
ndhB	737	246	CCA=>CTA	P=>L	1
ndhB	830	277	TCA=>TTA	S=>L	1
ndhB	836	279	TCA=>TTA	S=>L	1
ndhB	1102	368	CGC=>TGC	R=>C	1
ndhB	1112	371	TCA=>TTA	S=>L	1
ndhB	1193	398	TCA=>TTA	S=>L	1
ndhB	1255	419	CAT=>TAT	H=>Y	1
ndhB	1481	494	CCA=>CTA	P=>L	1
ndhD	20	7	TCT=>TTT	S=>F	0.8
ndhD	32	11	TCA=>TTA	S=>L	1
ndhD	286	96	CGG=>TGG	R=>W	0.8
ndhD	356	119	TCA=>TTA	S=>L	1
ndhD	521	174	CCA=>CTA	P=>L	1
ndhD	572	191	TCA=>TTA	S=>L	1
ndhD	851	284	TCA=>TTA	S=>L	1
ndhD	920	307	ACA=>ATA	T=>I	1
ndhD	1166	389	TCG=>TTG	S=>L	0.8
ndhD	1271	424	TCA=>TTA	S=>L	0.8
ndhD	1283	428	TCA=>TTA	S=>L	0.8
ndhF	62	21	TCA=>TTA	S=>L	1
ndhF	137	46	TCA=>TTA	S=>L	0.8
ndhF	259	87	CAC=>TAC	H=>Y	1
ndhF	290	97	TCA=>TTA	S=>L	1
ndhF	392	131	TCC=>TTC	S=>F	1
ndhF	442	148	CAT=>TAT	H=>Y	1
ndhF	1001	334	CCA=>CTA	P=>L	1
ndhF	1510	504	CTT=>TTT	L=>F	1
ndhG	148	50	CAT=>TAT	H=>Y	1

ndhG	155	52	CCA=>CTA	P=>L	1
ndhG	314	105	ACA=>ATA	T=>I	0.8
ndhG	413	138	ACA=>ATA	T=>I	0.8
petL	5	2	CCT=>CTT	P=>L	0.86
psaB	1919	640	ACG=>ATG	T=>M	1
psaI	80	27	TCT=>TTT	S=>F	0.86
psbE	214	72	CCT=>TCT	P=>S	1
psbF	77	26	TCT=>TTT	S=>F	1
rpl2	209	70	ACA=>ATA	T=>I	1
rpl20	290	97	CCT=>CTT	P=>L	1
rpl20	308	103	TCA=>TTA	S=>L	0.86
rpoA	368	123	CCA=>CTA	P=>L	1
rpoA	830	277	TCA=>TTA	S=>L	1
rpoB	365	122	TCT=>TTT	S=>F	1
rpoB	500	167	TCA=>TTA	S=>L	0.86
rpoB	578	193	TCA=>TTA	S=>L	1
rpoB	593	198	TCG=>TTG	S=>L	1
rpoB	650	217	CCG=>CTG	P=>L	0.86
rpoB	2027	676	TCT=>TTT	S=>F	1
rpoB	2453	818	TCA=>TTA	S=>L	0.86
rpoC1	41	14	TCA=>TTA	S=>L	1
rpoC1	629	210	CCG=>CTG	P=>L	1
rpoC1	802	268	CGG=>TGG	R=>W	1
rpoC1	941	314	CCA=>CTA	P=>L	1
rpoC1	974	325	TCA=>TTA	S=>L	0.86
rpoC2	1594	532	CCT=>TTT	P=>F	1
rpoC2	1783	595	CGT=>TGT	R=>C	0.86
rpoC2	2296	766	CGG=>TGG	R=>W	1
rpoC2	2330	777	TCG=>TTG	S=>L	1
rpoC2	3100	1034	CGC=>TGC	R=>C	0.8
rpoC2	3301	1101	CAT=>TAT	H=>Y	1
rpoC2	3713	1238	TCA=>TTA	S=>L	0.86
rps2	248	83	TCA=>TTA	S=>L	1
rps8	182	61	TCA=>TTA	S=>L	0.86
rps14	80	27	TCA=>TTA	S=>L	1
rps14	149	50	CCA=>CTA	P=>L	1
rps16	143	48	TCA=>TTA	S=>L	1
rps16	212	71	TCA=>TTA	S=>L	0.83
ycf3	44	15	TCT=>TTT	S=>F	1
ycf3	185	62	ACG=>ATG	T=>M	1
ycf3	191	64	CCA=>CTA	P=>L	1
ycf3	407	136	TCC=>TTC	S=>F	1

Table S2. Repeats in the chloroplast genome of *Michelia shiluensis* (F: forward, R: reverse, C: complement and P: palindromic).

S/N	Repeat Size	Repeat Position 1	Repeat Type	Repeat Location 1	Repeat Position 2	Repeat Location 2	E-Value
1	33	95290	F	*ycf2*	95314	*ycf2*	9.77e-11
2	33	95280	P	*ycf2*	152833	*ycf2*	9.77e-11
3	33	95314	P	*ycf2*	152857	*ycf2*	9.77e-11
4	33	152833	F	*ycf2*	152857	*ycf2*	9.77e-11
5	32	132787	F	*ycf1*	132805	*ycf1*	3.91e-10
6	31	92856	F	*ycf2*	92877	*ycf2*	1.56e-09
7	31	92856	P	*ycf2*	155272	*ycf2*	1.56e-09
8	31	9287	P	*trnS-GCU*	155293	*ycf2*	1.56e-09
9	31	155272	F	*ycf2*	155293	*ycf2*	1.56e-09
10	29	67813	P	IGS	67854	IGS	2.50e-08
11	28	9399	F	IGS	9426	IGS	1.00e-07
12	28	38930	P	IGS	38930	IGS	1.00e-07
13	25	9258	F	*trnS-GCU*	38089	*trnS-UGA*	1.00e-07
14	24	9262	P	*trnS-GCU*	47538	*trnS-GGA*	1.00e-07
15	24	118449	P	IGS	118476	IGS	1.00e-07
16	24	120707	P	IGS	120740	IGS	1.00e-07
17	23	113262	F	IGS	113303	IGS	1.02e-04
18	23	113262	P	IGS	134854	IGS	1.02e-04
19	23	113303	P	IGS	134895	IGS	1.02e-04
20	23	134854	F	IGS	134895	IGS	1.02e-04
21	21	33837	R	IGS	33837	IGS	1.64e-03
22	21	38093	P	*trnS-UGA*	47541	*trnS-GGA*	1.00e-03
23	21	39240	F	*trnM-CAU*	70618	*trnP-UGG*	1.00e-03
24	21	45027	F	IGS	45048	IGS	1.00e-03
25	20	385	P	IGS	411	IGS	6.55e-03
26	20	4671	P	IGS	4671	IGS	6.55e-03
27	20	15814	P	IGS	15839	IGS	6.55e-03
28	20	38161	P	*trnS-UGA*	47480	IGS-*trnS-GGA*	6.55e-03
29	20	50743	F	IGS	50763	IGS	6.55e-03
30	20	52858	R	*ndhC*	52858	*ndhC*	6.55e-03
31	20	60607	R	IGS	60607	IGS	6.55e-03
32	20	67349	P	IGS	67465	IGS	6.55e-03
33	20	124214	R	IGS	124214	IGS	6.55e-03
34	20	130346	P	*ycf1*	130368	*ycf1*	6.55e-03
35	19	4392	R	IGS	4392	IGS	2.62e-02
36	19	25211	R	*rpoB*	25211	*rpoB*	2.62e-02
37	19	118593	F	IGS	118613	IGS	2.62e-02
38	18	17858	F	*rpoC2*	88603	*rpl2* Intron	1.05e-01
39	18	17858	P	*rpoC2*	159559	*rpl2* Intron	1.05e-01
40	18	28333	F	IGS	123484	IGS	1.05e-01
41	18	31355	R	IGS	31355	IGS	1.05e-01
42	18	41271	F	*psaB*	43495	*psaA*	1.05e-01

43	18	43373	P	*psaA*	43373	*psaA*	1.05e-01
44	18	49935	P	*trnL-UAA* Intron	49935	*trnL-UAA* Intron	1.05e-01
45	18	87289	R	IGS	128842	*IGS*	1.05e-01
46	18	93481	P	*ycf2*	93481	*ycf2*	1.05e-01
47	18	93481	F	*ycf2*	154681	*ycf2*	1.05e-01
48	18	106615	P	*trnI-GAU*	113035	*trnN-GUU*	1.05e-01
49	18	106615	F	*trnI-GAU*	135127	*trnN-GUU*	1.05e-01

Table S3. Single sequence repeats in the chloroplast genome of *Michelia shiluensis.*

Repeat	Length (bp)	Number	Start position
A	8	21	4,748;9,767;13,440;19,888;23,549;29,214;31,815;39,220;39,898;47,159;69,840;72,351;74,237;81,793;92,206;114,724;118,583;121,178;135,671;141,097;143,974
	9	12	1,726;3,938;13,859;32,779;33,393;34,070;50,239;58,364;67,339;93,480;117,903;130,358
	10	4	211;30,578;63,302;132,580
	11	1	12,772
	12	2	49,370;126,152
	13	3	5,389;15,836;112,100
	14	2	38,855;46,897
	15	1	64,741
C	8	2	7,183;48,455
	9	1	118,574
	10	1	71,232
G	8	1	37,005
T	8	26	2,040;4,976;5,371;10,698;15,515;27,415;34,448;49,169;53,497;54,952;55,879;63,549;64,156;67,453;69,697;87,292;88,083;104,200;107,077;112,503;118,593;119,671;128,851;129,617;131,353;155,968
	9	23	4,581;13,470;14,149;15,826;30,814;33,502;33,580;34,794;38,748;45,369;53,506;55,823;62,532;64,354;71,242;86,420;87,062;119,684;122,856;130,369;131,665;131,962;154,693
	10	6	10,377;34,847;55,663;70,271;77,926;84,472
	11	4	7,758;10,272;74,504;84,969
	12	6	17,544;19,744;31,359;51,198;72,381;75,488
	13	1	136,069
	14	1	124,218
AT	10	2	21,118;33,344
TA	10	2	9,454;60,205
	12	2	34,971;71,854
TC	10	2	64,948;128,841
AAT	12	1	128,895
ATA	12	1	57,878
TTC	12	1	71,546
AAAT	12	2	117,050;4,393
AATC	12	1	126,465
AATG	12	1	65,558
AATT	12	1	115,077
ACAT	12	1	87,684
ATAA	12	1	73,123
CATT	12	1	131,010
TAAA	12	1	46,888
AACCGA	18	1	7,029
ACTAAT	18	1	144,538
TATTAG	18	1	103,625