

Table S1: Plastome sequences used for phylogenomic analysis. Species included in the comparative analysis are highlighted in green. The plastome generated in this study is in bold.

Subgenera	Section & subsection	Species	GenBank accession number
<i>Ficus</i> subg. <i>Ficus</i>	Sect. <i>Ficus</i>		
	Subsect. <i>Ficus</i>	<i>Ficus carica</i>	KY635880.1
	Subsect. <i>Frutescentiae</i>	<i>Ficus erecta</i>	MT093220.1
		<i>Ficus formosana</i>	MW648426.1
		<i>Ficus heteromorpha</i>	MW039145.1
		<i>Ficus tikoua</i>	MT075555.1
		<i>Ficus ischnopoda</i>	ON711004.1
		<i>Ficus pandurata</i>	OL639015.1
	Subsect. <i>Eriosycea</i>	<i>Ficus hirta</i>	MN364706.1
		<i>Ficus langkokensis</i>	ON711005.1
<i>Ficus</i> subg. <i>Sycidium</i>	Sect. <i>Palaeomorphe</i>	<i>Ficus tinctoria</i>	ON711012.1
<i>Ficus</i> subg. <i>Sycomorus</i>	Sect. <i>Hemicardia</i>	<i>Ficus heterostyla</i>	OK077762.1
	Sect. <i>Sycocarpus</i>		
	Subsect. <i>Macrostyla</i>	<i>Ficus squamosa</i>	OK077764.1
	Subsect. <i>Neomorphe</i>	<i>Ficus auriculata</i>	OK078618
		<i>Ficus beipeiensis</i>	MT611420.1
		<i>Ficus oligodon</i>	OK077763.1
	Subsect. <i>Sycomorus</i>	<i>Ficus racemosa</i>	KT368151.1
<i>Ficus</i> subg. <i>Synoecia</i>	Sect. <i>Rhizocladus</i>		
	Subsect. <i>Plagiostigma</i>	<i>Ficus dinganensis</i>	OK375500.1
		<i>Ficus pumila</i>	MZ351203.1
		<i>Ficus sarmentosa</i>	OL415083.1
<i>Ficus</i> subg. <i>Urostigma</i>	Sect. <i>Galoglychia</i>		
	Subsect. <i>Cyathistipulae</i>	<i>Ficus lyrata</i>	MW039148.1
	Subsect. <i>Platyphyllae</i>	<i>Ficus populifolia</i>	OP132395.1
	Sect. <i>Urostigma</i>		
	Subsect. <i>Conosycea</i>	<i>Ficus altissima</i>	MW043478.1
		<i>Ficus benamina</i>	MW039146.1
		<i>Ficus curtipes</i>	NC_053833.1
		<i>Ficus microcarpa</i>	NC_053834.1
	Subsect. <i>Urostigma</i>	<i>Ficus concinna</i>	MZ128521.1
		<i>Ficus religiosa</i>	NC_033979
		<i>Ficus virens</i>	MW039142.1
Outgroup family Flacourtiaceae		<i>Flacourtia indica</i>	MN078145.1
		<i>Homalium ceylanicum</i>	NC_045235.1
		<i>Poliothyrsis sinensis</i>	NC_037412.1

Table S2: List of genes encoded by *Ficus populifolia* plastome.

Category	Group of genes	Name of genes	Number
Self-replication	ribosomal RNA genes (rRNA)	<i>rrn5</i> ^(X2) , <i>rrn4.5</i> ^(X2) , <i>rrn16</i> ^(X2) , <i>rrn23</i> ^(X2)	8 (4)
	Transfer RNA genes (tRNA)	<i>trnH</i> -GUG, <i>trnK</i> -UUU ⁺ , <i>trnQ</i> -UUG, <i>trnS</i> -GCU, <i>trnG</i> -UCC ⁺ , <i>trnR</i> -UCU, <i>trnC</i> -GCA, <i>trnD</i> -GUC, <i>trnY</i> -GUA, <i>trnE</i> -UUC, <i>trnT</i> -GGU, <i>trnS</i> -UGA, <i>trnG</i> -GCC, <i>trnM</i> -CAU, <i>trnfm</i> -CAU, <i>trnS</i> -GGA, <i>trnT</i> -UGU, <i>trnL</i> -UAA ⁺ , <i>trnF</i> -GAA, <i>trnV</i> -UAC ⁺ , <i>trnW</i> -CCA, <i>trnP</i> -UGG, <i>trnI</i> -CAU ^(X2) , <i>trnL</i> - CAA ^(X2) , <i>trnV</i> -GAC ^(X2) , <i>trnI</i> -GAU ^{+,(X2)} , <i>trnA</i> -UGC ^{+,(X2)} , <i>trnR</i> -ACG ^(X2) , <i>trnN</i> - GUU ^(X2) , <i>trnL</i> -UAG	37 (7)
	Small subunit of ribosome	<i>rps2</i> , <i>rps3</i> , <i>rps4</i> , <i>rps7</i> ^(X2) , <i>rps8</i> , <i>rps11</i> , <i>rps12</i> ^{+,(X2)} , <i>rps14</i> , <i>rps15</i> , <i>rps16</i> ⁺ , <i>rps18</i> , <i>rps19</i>	14 (2)
	Large subunit of ribosome	<i>rpl2</i> ^{+,(X2)} , <i>rpl14</i> , <i>rpl16</i> ⁺ , <i>rpl20</i> , <i>rpl22</i> , <i>rpl23</i> ^(X2) , <i>rpl32</i> , <i>rpl33</i> , <i>rpl36</i>	11 (2)
	DNA-dependent RNA polymerase	<i>rpoA</i> , <i>rpoB</i> , <i>rpoC1</i> ⁺ , <i>rpoC2</i>	4
Genes for photosynthesis	Photosystem I	<i>psaA</i> , <i>psaB</i> , <i>psaC</i> , <i>psaI</i> , <i>psaJ</i> , <i>ycf3</i> ⁺⁺	6
	Photosystem II	<i>psbA</i> , <i>psbB</i> , <i>psbC</i> , <i>psbD</i> , <i>psbE</i> , <i>psbF</i> , <i>psbH</i> , <i>psbI</i> , <i>psbJ</i> , <i>psbK</i> , <i>psbL</i> , <i>psbM</i> , <i>psbN</i> , <i>psbT</i> , <i>psbZ</i> ,	15
	Subunits of cytochrome b/f complex	<i>petA</i> , <i>petB</i> ⁺ , <i>petD</i> ⁺ , <i>petG</i> , <i>petL</i> , <i>petN</i>	6
	Subunits of ATP synthase	<i>atpA</i> , <i>atpB</i> , <i>atpE</i> , <i>atpF</i> ⁺ , <i>atpH</i> , <i>atpI</i>	6
	Subunits of rubisco	<i>rbcL</i>	1
	Subunits of NADH-dehydrogenase	<i>ndhA</i> ⁺ , <i>ndhB</i> ^{+(X2)} , <i>ndhC</i> , <i>ndhD</i> , <i>ndhE</i> , <i>ndhF</i> , <i>ndhG</i> , <i>ndhH</i> , <i>ndhI</i> , <i>ndhJ</i> , <i>ndhK</i> ⁺	12 (1)
Other genes	Chloroplast envelope membrane protein	<i>cemA</i>	1
	Maturase	<i>matK</i>	1

	Protease	<i>clpP</i> ⁺⁺	1
	Subunit acetyl-coA carboxylase	<i>accD</i>	1
	C-type cytochrome synthesis	<i>ccsA</i>	1
	Translational initiation factor	<i>infA</i>	1
Genes of unknown function	Conserved open reading frames	<i>ycf1, ycf2</i> ^(X2) , <i>ycf4</i>	4 (1)
Total			130 (17)

+ Gene with one intron, ++ gene with two introns, (×2) indicates that the number of the repeat unit is 2, parentheses indicate the number of duplicated genes

Table S3: Codon-anticodon recognition patterns and codon usage of the *F. populifolia* plastome.

Codon	Amino acid	count	RSCU	tRNA	Codon	Amino acid	count	RSCU	tRNA
UUU	Phe	2376	1.31	<i>trnF</i> -GAA	UAU	Tyr	1659	1.62	<i>trnY</i> -GUA
UUC	Phe	1407	0.69		UAC	Tyr	783	0.38	
UUA	Leu	1366	1.79	<i>trnL</i> -UAA	UAA	Stop	1421	0	
UUG	Leu	1062	1.23	<i>trnL</i> -CAA	UAG	Stop	831	0	
CUU	Leu	1234	1.31	<i>trnL</i> -UAG	CAU	His	959	1.54	<i>trnH</i> -GUG
CUC	Leu	696	0.43		CAC	His	389	0.46	
CUA	Leu	891	0.84		CAA	Gln	1077	1.56	<i>trnQ</i> -UUG
CUG	Leu	499	0.4		CAG	Gln	475	0.44	
AUU	Ile	1940	1.42		AAU	Asn	1911	1.53	<i>trnN</i> -GUU
AUC	Ile	1159	0.59		AAC	Asn	744	0.47	
AUA	Ile	1734	0.99	<i>trnI</i> -CAU	AAA	Lys	2329	1.47	
AUG	Met	869	1	<i>trnM</i> -CAU	AAG	Lys	1037	0.53	
GUU	Val	859	1.45	<i>trnV</i> -GAC	GAU	Asp	1030	1.61	<i>trnD</i> -GUC
GUC	Val	424	0.48		GAC	Asp	419	0.39	
GUA	Val	801	1.53		GAA	Glu	1341	1.5	<i>trnE</i> -UUC
GUG	Val	437	0.55		GAG	Glu	612	0.5	
UCU	Ser	1145	1.7	<i>trnS</i> -GGA	UGU	Cys	707	1.5	<i>trnC</i> -GCA
UCC	Ser	824	0.97		UGC	Cys	436	0.5	
UCA	Ser	952	1.28		UGA	Stop	1040	0	
UCG	Ser	563	0.56	<i>trnS</i> -UGA	UGG	Trp	677	1	<i>trnW</i> -CCA
CCU	Pro	623	1.56	<i>trnP</i> -UGG	CGU	Arg	361	1.18	<i>trnR</i> -ACG
CCC	Pro	539	0.69		CGC	Arg	222	0.36	<i>trnR</i> -UCU
CCA	Pro	743	1.18		CGA	Arg	505	1.39	
CCG	Pro	386	0.57		CGG	Arg	369	0.38	
ACU	Thr	666	1.62		AGA	Arg	656	2	
ACC	Thr	537	0.72		AGG	Arg	418	0.69	
ACA	Thr	716	1.22	<i>trnT</i> -GGU	AGU	Ser	1050	1.13	<i>trnS</i> -GCU
ACG	Thr	361	0.44	<i>trnT</i> -UGU	AGC	Ser	584	0.36	
GCU	Ala	461	1.86	<i>trnA</i> -UGC	GGU	Gly	523	1.27	
GCC	Ala	369	0.58		GGC	Gly	336	0.4	<i>trnG</i> -GCC
GCA	Ala	473	1.15		GGA	Gly	752	1.67	
GCG	Ala	235	0.41		GGG	Gly	535	0.66	

Table S4: Predicted RNA editing site in the *F. populifolia* plastome.

Gene	Nucleotide Position	Amino Acid Position	Codon Conversion	Amino Acid Conversion	Score
<i>accD</i>	13	5	CGG => TGG	R => W	1
	344	115	CCA => CTA	P => L	1
	1421	474	CCT => CTT	P => L	1
<i>atpA</i>	779	260	TCA => TTA	S => L	1
	797	266	CCT => CTT	P => L	1
	920	307	TCA => TTA	S => L	1
<i>atpB</i>	37	13	CCC => TCC	P => S	1
<i>atpF</i>	19	7	CCT => TCT	P => S	0.86
<i>atpI</i>	76	26	CTC => TTC	L => F	0.86
<i>clpP</i>	559	187	CAC => TAC	H => Y	1
	52	18	CTC => TTC	L => F	1
	640	214	CAT => TAT	H => Y	1
<i>matK</i>	1187	396	TCA => TTA	S => L	0.86
	107	36	CCT => CTT	P => L	1
	341	114	TCA => TTA	S => L	1
<i>ndhA</i>	566	189	TCA => TTA	S => L	1
	1073	358	TCC => TTC	S => F	1
	149	50	TCA => TTA	S => L	1
<i>ndhB</i>	467	156	CCA => CTA	P => L	1
	542	181	ACG => ATG	T => M	1
	586	196	CAT => TAT	H => Y	1
<i>ndhD</i>	611	204	TCA => TTA	S => L	0.8
	737	246	CCA => CTA	P => L	1
	746	249	TCT => TTT	S => F	1
<i>rpoB</i>	830	277	TCA => TTA	S => L	1
	836	279	TCA => TTA	S => L	1
	1112	371	TCA => TTA	S => L	1
<i>rpoCI</i>	1255	419	CAT => TAT	H => Y	1
	1291	431	CTC => TTC	L => F	1
	1481	494	CCA => CTA	P => L	1
<i>rpoD</i>	20	7	ACG => ATG	T => M	1
	331	111	CGG => TGG	R => W	0.8
	401	134	CCA => CTA	P => L	1
<i>rpoE</i>	617	206	TCA => TTA	S => L	1
	692	231	TCG => TTG	S => L	1
	896	299	TCA => TTA	S => L	1
<i>rpoF</i>	905	302	CCT => CTT	P => L	1
	1094	365	GCT => GTT	A => V	1
	1316	439	TCA => TTA	S => L	0.8
<i>rpoH</i>	1423	475	CTT => TTT	L => F	0.8
	338	113	TCT => TTT	S => F	1
	2426	809	TCA => TTA	S => L	0.86
<i>rpoI</i>	41	14	TCA => TTA	S => L	1

	1562	521	ACG => ATG	T => M	0.86
	1505	502	ACG => ATG	T => M	0.86
<i>rpoC2</i>	1612	538	CTT => TTT	L => F	1
	1807	603	CGT => TGT	R => C	0.86
	1987	663	CTT => TTT	L => F	0.83
<i>rps14</i>	80	27	TCA => TTA	S => L	1
<i>rps16</i>	212	71	TCA => TTA	S => L	0.83
<i>rps2</i>	248	83	TCA => TTA	S => L	1

Table S5: Repeat sequences present in the *F. populifolia* plastome.

Repeat Size	Repeat Position 1	Repeat Type	Repeat Location	Repeat Position 2	Repeat Location	E-value
39	46581	F	<i>ycf3</i>	103014	IGS	2.40E-14
39	46581	P	<i>ycf3</i>	146234	IGS	2.40E-14
33	353	P	IGS	392	IGS	9.83E-11
31	93636	F	<i>ycf2</i>	93657	<i>ycf2</i>	1.57E-09
31	93636	P	<i>ycf2</i>	155599	<i>ycf2</i>	1.57E-09
31	93657	P	<i>ycf2</i>	155620	<i>ycf2</i>	1.57E-09
31	155599	F	<i>ycf2</i>	155620	<i>ycf2</i>	1.57E-09
30	9061	P	IGS	48392	<i>trnS</i> -GGA	6.29E-09
30	31819	P	IGS	31819	IGS	6.29E-09
29	49494	R	IGS	49494	IGS	2.52E-08
27	29135	P	IGS	29166	IGS	4.03E-07
26	10726	P	IGS	10756	IGS	1.61E-06
26	50037	P	IGS	50037	IGS	1.61E-06
26	60776	P	IGS	60776	IGS	1.61E-06
25	34106	P	IGS	34132	IGS	6.44E-06
25	60211	F	<i>rbcL</i>	60236	<i>rbcL</i>	6.44E-06
25	78886	P	IGS	78912	IGS	6.44E-06
25	112280	P	IGS	112308	IGS	6.44E-06
25	112280	F	IGS	136954	IGS	6.44E-06
25	112308	F	IGS	136982	IGS	6.44E-06
25	136954	P	IGS	136982	IGS	6.44E-06
24	7559	P	IGS	7559	IGS	2.58E-05
23	46581	F	<i>ycf3</i>	126352	<i>ndhA</i>	1.03E-04
23	103014	F	IGS	126352	<i>ndhA</i>	1.03E-04
23	126352	P	<i>ndhA</i>	146250	IGS	1.03E-04
22	3875	P	<i>trnK</i> -UUU	3875	<i>trnK</i> -UUU	4.12E-04
22	5892	P	<i>rps16</i>	95589	<i>ycf2</i>	4.12E-04
22	5892	F	<i>rps16</i>	153676	<i>ycf2</i>	4.12E-04
22	6901	P	IGS	6901	IGS	4.12E-04
22	10651	F	<i>trnG</i> -UCC	39272	<i>trnG</i> -GCC	4.12E-04
22	33358	P	IGS	33358	IGS	4.12E-04
22	38071	P	<i>trnS</i> -UGA	48334	IGS	4.12E-04
22	64904	P	IGS	64904	IGS	4.12E-04
22	126520	P	<i>ndhA</i>	126520	<i>ndhA</i>	4.12E-04
21	4712	F	IGS	4725	IGS	1.65E-03
21	9067	F	<i>trnS</i> -GCU	38005	<i>trnS</i> -UGA	1.65E-03
21	38005	P	<i>trnS</i> -UGA	48395	<i>trnS</i> -GGA	1.65E-03
21	67629	F	IGS	67647	IGS	1.65E-03
21	74780	F	<i>clpP1</i>	74799	<i>clpP1</i>	1.65E-03
21	84069	R	IGS	84069	IGS	1.65E-03
21	117645	R	IGS	117645	IGS	1.65E-03

21	123071	P	IGS	123093	IGS	1.65E-03
20	33449	P	IGS	33449	IGS	6.60E-03
20	39056	R	IGS	75828	<i>clpP1</i>	6.60E-03
20	52638	P	IGS	69574	IGS	6.60E-03
20	54254	R	<i>ndhC</i>	54254	<i>ndhC</i>	6.60E-03
20	58367	P	IGS	114585	<i>ycf1,ndhF</i>	6.60E-03
20	69763	P	IGS	69763	IGS	6.60E-03
20	84706	P	<i>rps8</i>	84706	<i>rps8</i>	6.60E-03

Table S6 : SSRs detected in five *Ficus* plastomes.

SSR type	Repeat Unit	<i>F. populifolia</i>	<i>F. concinna</i>	<i>F. hirta</i>	<i>F. racemosa</i>	<i>F. sarmentosa</i>
Mono	A	63	63	61	58	56
	C	2	1	2	1	3
	G	2	1	1	1	2
	T	89	90	81	88	79
Di	AG/CT	1	1	1	1	1
	AT/AT	17	18	21	18	20
Tri	AAG/CTT	1	1	1	1	1
	AAT/ATT	2	3	4	3	3
	AAAG/CTTT	2	2	2	2	2
Tetra	AAAT/ATTT	4	7	5	4	7
	AATT/AATT	1	1	1	1	1
	AGAT/ATCT	1	1	1	1	1
	AAAC/GTTT	0	1	0	0	0
	AAAGG/CCTTT	1	1	1	1	1
Penta	AATTC/AATTG	0	1	1	1	1
	AAAAT/ATTTT	0	0	1	1	1
Hexa	AAGGAG/CCTTCT	0	0	2	0	0
total		186	192	186	182	179

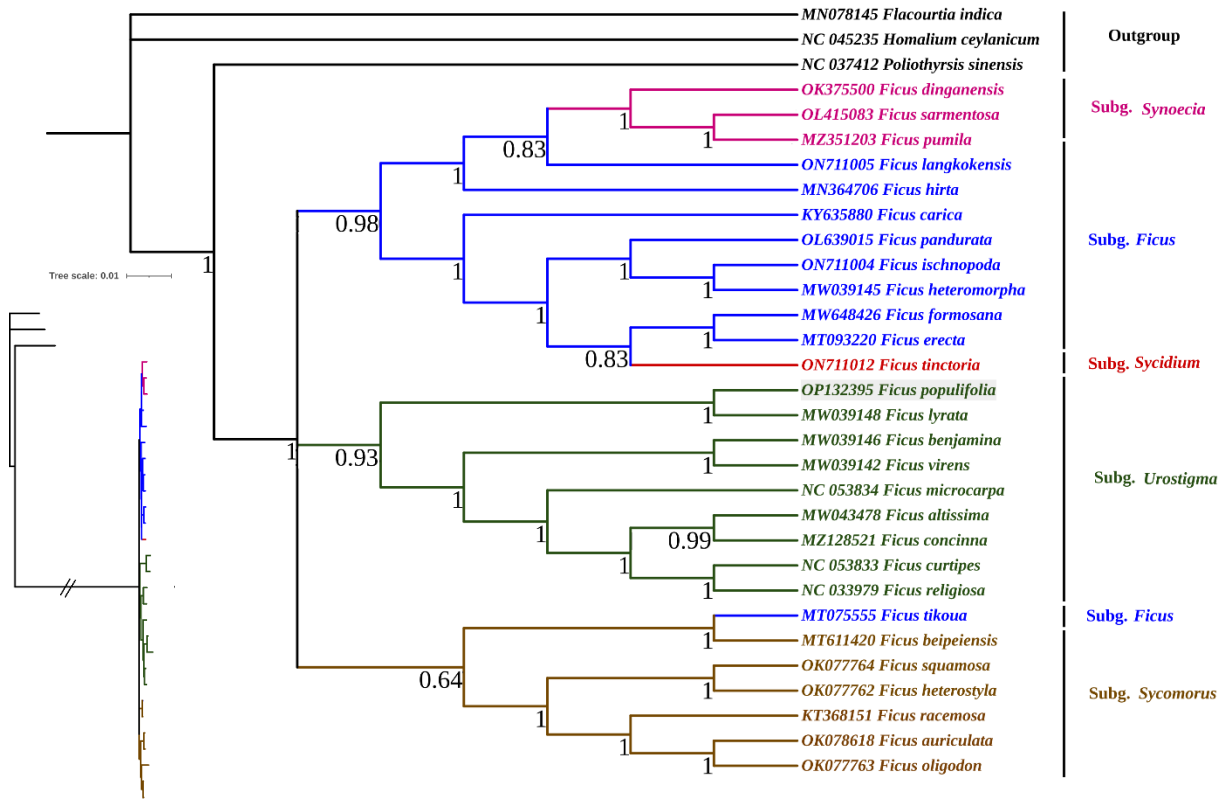


Figure S1. Phylogenomic relationship of 28 *Ficus* species based on 78 coding genes inferred from BI analysis. Bayesian posterior probabilities are present below the lines.