

Table S1. Information of plastome sequences downloaded from NCBI.

Family	Tribe	Taxon	GenBank accession	Genome size
Cannaceae		<i>Canna indica</i>	KF601570	162,182
Costaceae		<i>Costus pulverulentus</i>	KF601573	163,239
		<i>Hellenia viridis</i>	MK262733	168,966
		<i>Ensete glaucum</i>	LC610748	168,811
Musaceae		<i>Musa itinerans</i>	NC_035723	168,985
		<i>Musella lasiocarpa</i>	NC_035637	169,178
Zingiberaceae	Alpinieae	<i>Alpinia chinensis</i>	NC_050165	163,590
		<i>Alpinia hainanensis</i>	MK262728	162,387
		<i>Amomum krervanh</i>	MF991963	162,766
		<i>Lanxangia tsaoko</i>	MK926774	163,648
		<i>Wurfbainia villosa</i>	MH161416	164,068
	Zingibereae	<i>Boesenbergia kingii</i>	MW326451	163,198
		<i>Cautleya gracilis</i>	NC_046845	164,001
		<i>Curcuma involucrata</i>	MK262725	163,300
		<i>Curcuma longa</i>	MK919702	159,550
		<i>Hedychium coronarium</i>	MK262736	163,949
		<i>Hedychium spicatum</i>	NC_047248	163,531
		<i>Kaempferia elegans</i>	MK209002	163,555
		<i>Kaempferia galanga</i>	MK209001	163,811
		<i>Monolophus coenobialis</i>	MW326458	162,136
		<i>Roscoea alpina</i>	MT012418	163,395
		<i>Roscoea humeana</i>	NC_046582	160,288
		<i>Zingiber corallinum</i>	MW801385	160,957
		<i>Zingiber densissimum</i>	OP869975	163,607
		<i>Zingiber ellipticum</i> 5	OP869976	163,455
		<i>Zingiber flavomaculosum</i>	OP869987	163,298
		<i>Zingiber koshunense</i>	OP869977	163,394
		<i>Zingiber leptorrhizum</i>	OP869984	162,956
		<i>Zingiber mioga</i> 2	MW067011	159,868
		<i>Zingiber montanum</i> 1	OP869985	163,476
		<i>Zingiber montanum</i> 2	MK262727	164,464
		<i>Zingiber montanum</i> 3	MW801386	161,483
		<i>Zingiber neotruncatum</i>	OP869978	162,481
		<i>Zingiber officinale</i> 4	MW602894	162,721
		<i>Zingiber officinale</i> 5	NC_044775	162,621
		<i>Zingiber orbiculatum</i>	OP869979	163,527
		<i>Zingiber purpureum</i> 2	OP869980	163,135
		<i>Zingiber recurvatum</i> 3	MT473712	163,151
		<i>Zingiber smilesianum</i>	OP869981	163,640
		<i>Zingiber spectabile</i>	JX088661	155,890
		<i>Zingiber striolatum</i> 2	ON646165	163,711

<i>Zingiber teres</i>	OM868074	163,428
<i>Zingiber xishuangbannaense</i>	OP869982	163,487
<i>Zingiber yingjiangense</i>	OP869983	163,623
<i>Zingiber zerumbet</i>	MK262726	163,589

Table S2. Gene composition of *Zingiber* species. * Genes including a single intron. ** Genes including two introns. (×2) Genes duplicated in the inverted repeat regions.

Category for genes	Group of genes	Name of genes
Photosynthesis	Subunits of photosystem I	<i>psaA, psaB, psaC, psaI, psaJ</i>
	Subunits of photosystem II	<i>psbA, psbB, psbC, psbD, psbE, psbF, psbH, psbI, psbJ, psbK, psbL, psbM, psbN, psbT, psbZ</i>
	Subunits of cytochrome b/f complex	<i>petA, petB*, petD*, petG, petL, petN</i>
	Subunits of ATP synthase	<i>atpA, atpB, atpE, atpF*, atpH, atpI</i>
	Subunits of NADH dehydrogenase	<i>ndhA*, ndhB*(×2), ndhC, ndhD, ndhE, ndhF, ndhG, ndhH, ndhI, ndhJ, ndhK</i>
Self-replication	Subunit of rubisco	<i>rbcL</i>
	RNA polymerase	<i>rpoA, rpoB, rpoC1*, rpoC2</i>
	Large subunit of ribosomal proteins	<i>rpl2*(×2), rpl14, rpl16a, rpl20, rpl22, rpl23(×2), rpl32, rpl33, rpl36</i>
	Small subunit of ribosomal proteins	<i>rps2, rps3, rps4, rps7(×2), rps8, rps11, rps12**(×2), rps14, rps15, rps16*, rps18, rps19(×2)</i>
	Ribosomal RNAs	<i>rrn4.5(×2), rrn5(×2), rrn16(×2), rrn23(×2)</i>
	Transfer RNAs	<i>trnA-UGC*(×2), trnC-GCA, trnD-GUC, trnE-UUC, trnF-GAA, trnG-M-CAU, trnG-GCC*, trnG-UCC, trnH-GUG(×2), trnI-CAU (×2), trnI-GAU*(×2), trnK-UUU*, trnL-CAA(×2), trnL-UAA*, trnL-UAG, trnM-CAU, 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</i>
Transfer RNAs	Subunit of acetyl-coA-carboxylase	<i>accD</i>
	c-type cytochrome synthesis gene	<i>ccsA</i>
	Envelop membrane protein	<i>cemA</i>
	Protease	<i>clpP**</i>
	Translational initiation factor	<i>infA</i>
	Maturase	<i>matK</i>
Unknown function	Conserved open reading frames	<i>ycf1(×2), ycf2(×2), ycf3**, ycf4</i>

Table S3. Variability of six hyper-variable regions in *Zingiber*.

Marker	Length (bp)	Variable base sites		Informative base sites		Nucleotide diversity (π)	Mean distance	Discrimination success (%)
		Number	Percentage (%)	Number	Percentage (%)			
<i>rpl20</i>	451	60	13.31	41	9.09	0.0199	0.0225	37.93
<i>clpP</i>	2217	91	4.11	47	2.11	0.0128	0.0073	65.52
<i>ycf1</i>	5914	481	8.13	281	4.75	0.0104	0.0146	58.62
<i>rbcL-accD</i>	1269	194	15.29	174	13.71	0.0277	0.0546	65.52
<i>petA-psbJ</i>	922	87	9.44	53	5.75	0.0389	0.0219	41.38
<i>rpl32-trnL</i>	990	111	11.21	63	6.36	0.0184	0.0195	48.28
Combined	11763	1024	8.71	659	5.61	0.0149	0.0175	86.21

