

Supplementary Material

Table S1. The list of accession numbers of the chloroplast genome sequences used in the phylogenetic analysis.

No.	Taxon	Family	Order	GenBank Accession Number
1	<i>Ananas comosus</i>	Bromeliaceae	Poales	AP014632
2	<i>Elaeis guineensis</i>	Arecaceae	Arecales	JF274081
3	<i>Kingia australis</i>	Dasypogonaceae	Dasypogonales	JX051651
4	<i>Heliconia collinsiana</i>	Heliconiaceae	Zingiberales	JX088660
5	<i>Zingiber spectabile</i>	Zingiberaceae	Zingiberales	JX088661
6	<i>Alpinia zerumbet</i>	Zingiberaceae	Zingiberales	JX088668
7	<i>Xiphidium caeruleum</i>	Haemodoraceae	Commelinales	JX088669
8	<i>Ravenala madagascariensis</i>	Strelitziaceae	Zingiberales	KF601568
9	<i>Orchidantha fimbriata</i>	Lowiaceae	Zingiberales	KF601569
10	<i>Canna indica</i>	Cannaceae	Zingiberales	KF601570
11	<i>Maranta leuconeura</i>	Marantaceae	Zingiberales	KF601571
12	<i>Monocostus uniflorus</i>	Costaceae	Zingiberales	KF601572
13	<i>Costus pulverulentus</i>	Costaceae	Zingiberales	KF601573
14	<i>Thaumatococcus daniellii</i>	Marantaceae	Zingiberales	KF601575
15	<i>Setaria italica</i>	Poaceae	Poales	KJ001642
16	<i>Zizania latifolia</i>	Poaceae	Poales	KM282190
17	<i>Carex siderosticta</i>	Cyperaceae	Poales	KP751906
18	<i>Podococcus barteri</i>	Arecaceae	Arecales	KR347117
19	<i>Mauritia flexuosa</i>	Arecaceae	Arecales	KT312914
20	<i>Hanguana malayana</i>	Hanguanaceae	Commelinales	KT312930

21	<i>Cocos nucifera</i>	Areaceae	Arecales	KX028884
22	<i>Joinvillea ascendens</i>	Joinvilleaceae	Poales	KX035098
23	<i>Tillandsia usneoides</i>	Bromeliaceae	Poales	KY293680
24	<i>Zea mays</i>	Poaceae	Poales	X86563
25	<i>Typha latifolia</i>	Typhaceae	Poales	GU195652
26	<i>Phoenix dactylifera</i>	Areaceae	Arecales	GU811709
27	<i>Magnolia officinalis</i>	Magnoliaceae	Ranunculales	JN867579
28	<i>Triticum monococcum</i>	Poaceae	Poales	KC912690
29	<i>Secale cereale</i>	Poaceae	Poales	KC912691
30	<i>Aegilops tauschii</i>	Poaceae	Poales	JQ754651
31	<i>Musa balbisiana</i>	Musaceae	Zingiberales	KT595228
32	<i>Curcuma flaviflora</i>	Zingiberaceae	Zingiberales	KR967361
33	<i>Syagrus coronata</i>	Areaceae	Arecales	KT896548
34	<i>Aconitum carmichaelii</i>	Ranunculaceae	Ranales	KY407560

Table S2. Genes in the *A. kravanh* chloroplast genome

Gene category	Gene group	Gene names
Self-replication	rRNA	<i>rrn16^a, rrn23^a, rrn5^a, rrn4.5^a</i>
	tRNA	<i>trnA-UGC^{*,a}, trnC-GCA, trnD-GUC, trnE-UUC, trnF-GAA, trnG-GCC[*], trnG-UCC, trnH-GUG^a, trnI-CAU^a, trnI-GAU^{*,a}, trnK-UUU[*], trnL-UAA[*], trnL-UAG, trnL-CAA^a, trnM-CAU, trnM-CAU, trnN-GUU^a, trnP-UGG, trnQ-UUG, trnR-ACG^a, trnR-UCU, trnS-GCU, trnS-UGA, trnS-GGA, trnT-GGU, trnT-UGU, trnV-UAC[*], trnV-GAC^a, trnW-CCA, trnY-GUA</i>
	Small subunit of ribosome	<i>rps2, rps3, rps4, rps7^a, rps8, rps11, rps12^{**,a}, rps14, rps15,</i>

Photosynthetic	Large subunit of ribosome	<i>rps16*</i> , <i>rps18</i> , <i>rps19^a</i>
		<i>rpl14</i> , <i>rpl16*</i> , <i>rpl2^{*a}</i> , <i>rpl20</i> , <i>rpl22</i> , <i>rpl23^a</i> , <i>rpl32</i> , <i>rpl33</i> , <i>rpl36</i>
	DNA dependent RNA polymerase	<i>rpoB</i> , <i>rpoC1*</i> , <i>rpoC2</i> , <i>rpoA</i>
	Translational initiation factor	<i>infA</i>
	Subunits of NADH-dehydrogenase	<i>ndhA*</i> , <i>ndhB^{*a}</i> , <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>
		<i>psbA</i> , <i>psaB</i> , <i>psaC</i> , <i>psaI</i> , <i>psaJ</i> , <i>ycf3**</i> , <i>ycf4</i>
	Subunits of photosystem I	<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>
	Subunits of photosystem II	<i>petN</i> , <i>petA</i> , <i>petL</i> , <i>petG</i> , <i>petB*</i> , <i>petD</i>
	Subunits of cytochrome b/f complex	<i>atpI</i> , <i>atpH</i> , <i>atpF*</i> , <i>atpA</i> , <i>atpE</i> , <i>atpB</i>
	Subunits of ATP synthase	<i>rbcL</i>
Other	Large subunit of rubisco	
	Maturase	<i>matK</i>
	Protease	<i>clpP**</i>
	Envelope membrane protein	<i>cemA</i>
	Subunit of Acetyl-CoA-carboxylase	<i>accD</i>
		<i>ccsA</i>
Genes of unknown function	C-type cytochrome synthesis	
	Open Reading Frames (ORF, ycf)	<i>ycf1</i> , <i>ycf15^a</i> , <i>ycf2^a</i>
	Pseudogenes	<i>ycf1</i>

*Genes with one intron; **Genes with two introns; ^aGenes with two copies.

Table S3. Comparison of the sizes of the chloroplast genomes of *A. kravanh* and three other Zingiberaceae species

Species	Length (bp)			
	Total genome	LSC	SSC	IR
<i>Amomum kravanh</i>	162,766	87,728	15,390	29,824
<i>Alpinia zerumbet</i>	159,773	87,644	18,295	26,917
<i>Curcuma flaviflora</i>	160,478	88,008	18,570	26,950
<i>Zingiber spectabile</i>	155,702	85,983	18,611	25,554

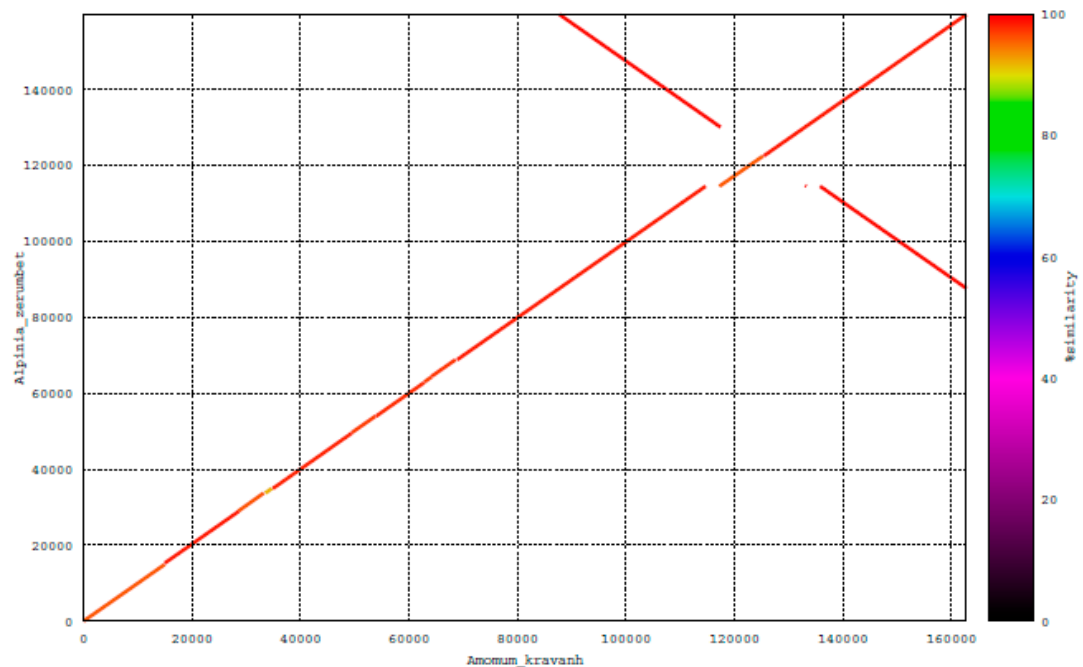


Figure S1. Alignment of the chloroplast genome sequences of *A. kravanh* and *Alpinia zerumbet*.

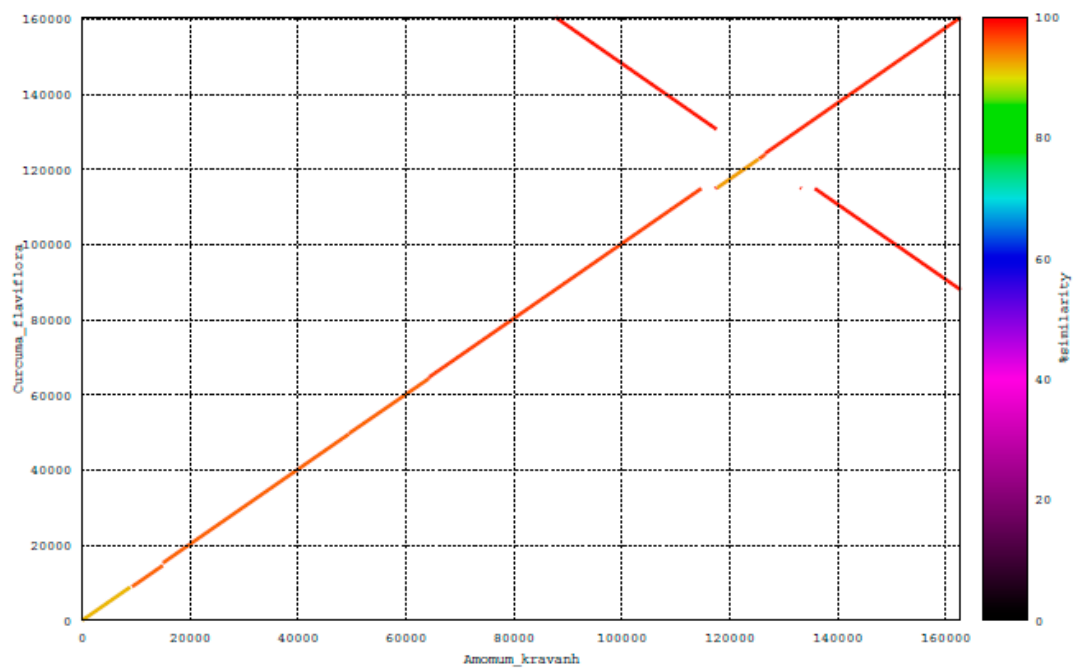


Figure S2. Alignment of the chloroplast genomes of alignment *A. kravanh* and *Curcuma flaviflora*.

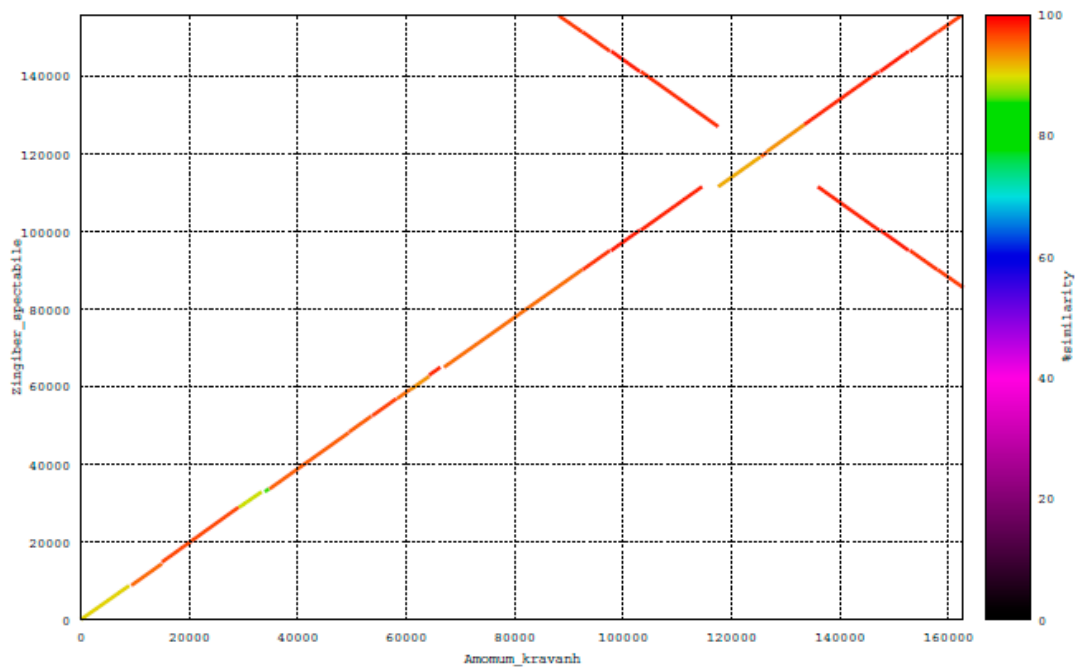
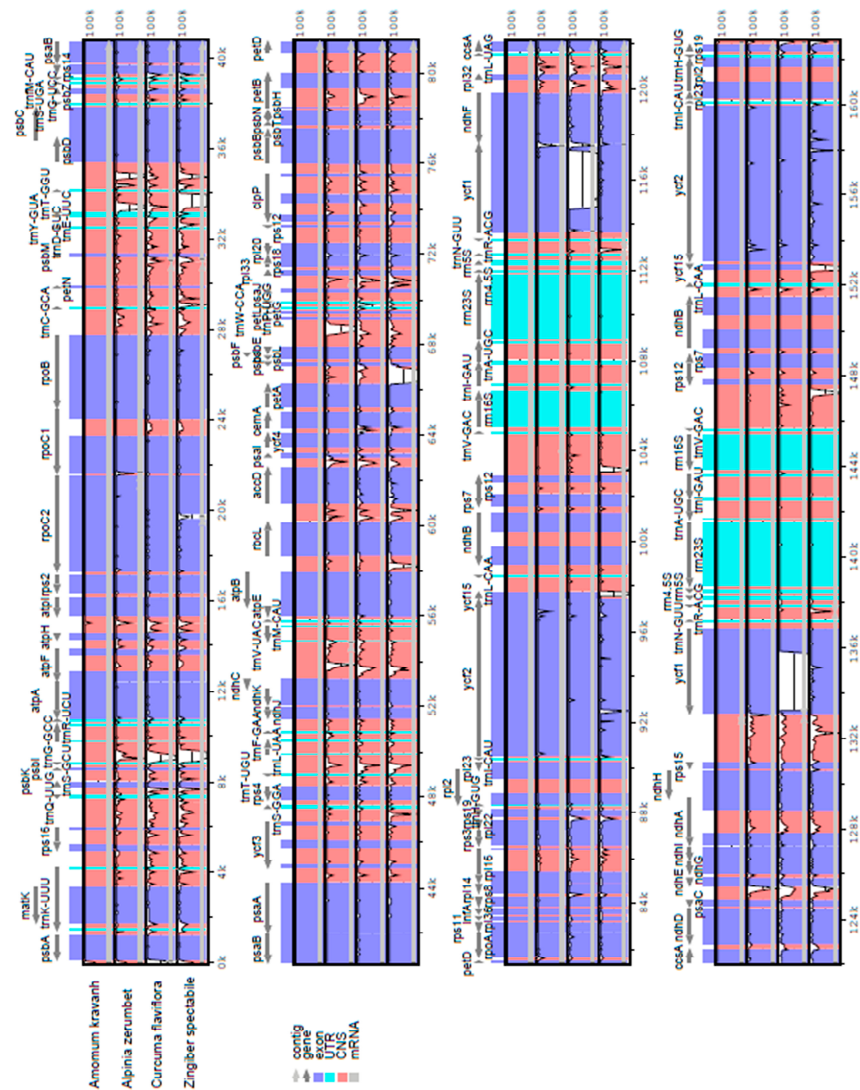


Figure S3. Alignment of the chloroplast genomes of *A. kravanh* and *Zingiber spectabile*.



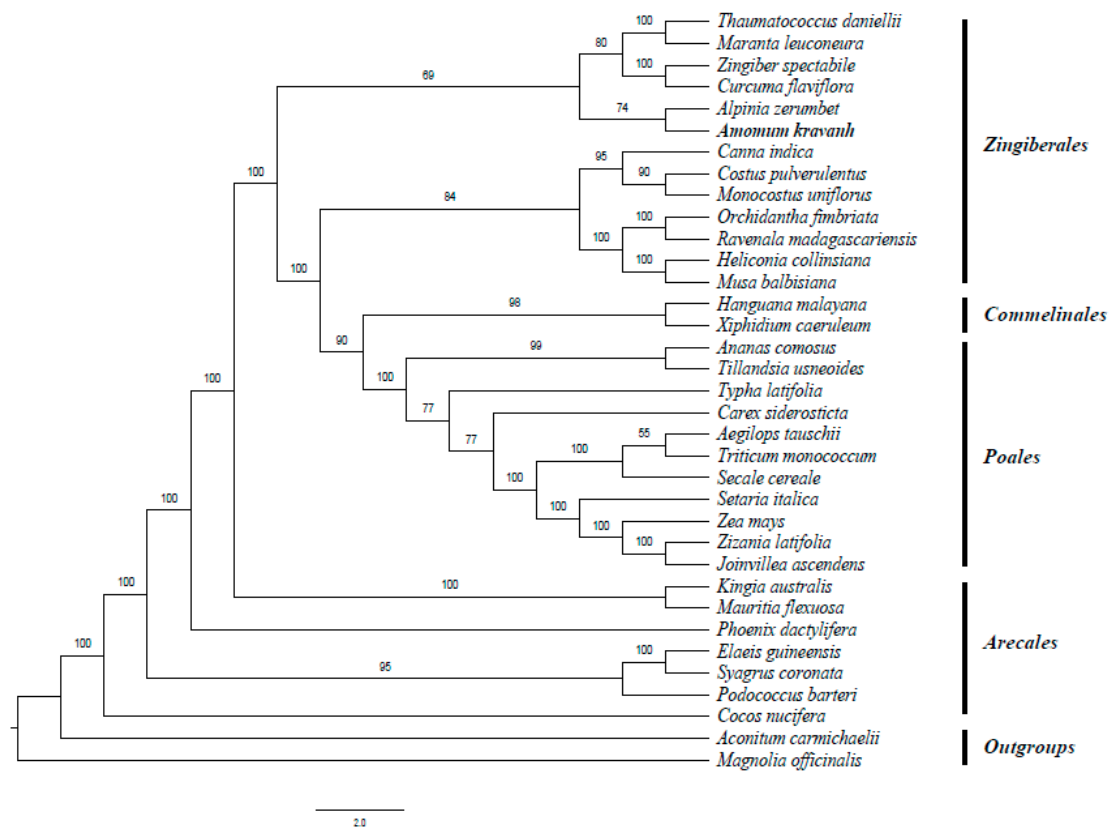


Figure S5. MP phylogenetic tree of 33 taxa in the commelinids clade based on the concatenated sequences of 58 shared chloroplast protein-coding genes. Numbers above each node are MP bootstrap values > 50%. *Magnolia officinalis* and *Aconitum carmichaelii* was used as outgroups.