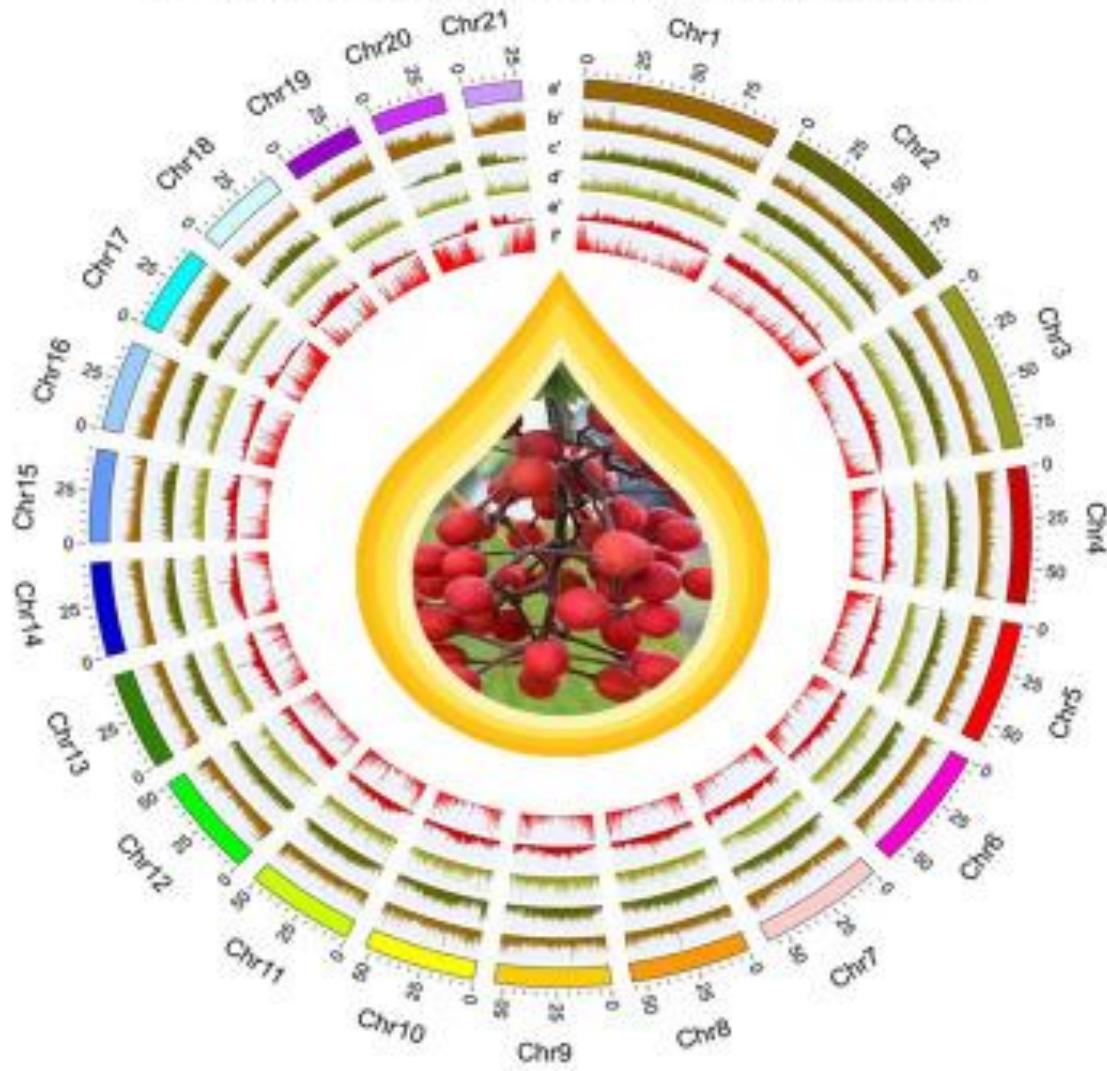


## Genome sequencing of *Idesia polycarpa*



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### Article

The *Idesia polycarpa* genome provides insights into its evolution and oil biosynthesis

**Table S1. Sequence and assembly statistics. Related to Figure 1.**

(A) Summary of sequenced data to assemble the genome of *I. polycarpa*. (B) Quality values of the assembled contigs and scaffolds. (C) The assembly and gene annotation of each pseudo-chromosomes for *I. polycarpa* genomes.

(A)			
Platform	DNB-seq	Hi-C	PacBio (CLR)
Data volume (Gb)	178.30	119.00	111.83
Reads length (bp)	PE150	PE150	17516
Coverage depth (×)	~144.95	~96.75	~90.92

Pseudochromosome	Length(bp)	Gene number	Pseudochromosome	Length(bp)	Gene number
Chr1	93,632,804	3,098	Chr13	47,754,307	1,553
Chr2	92,423,757	3,037	Chr14	45,882,993	1,445
Chr3	84,067,912	2,680	Chr15	45,297,513	1,470
Chr4	67,021,858	2,827	Chr16	44,085,287	1,956
Chr5	60,221,121	2,388	Chr17	41,560,487	2,500
Chr6	59,988,279	1,740	Chr18	41,448,802	1,313
Chr7	59,352,314	1,598	Chr19	35,831,779	1,717
Chr8	56,540,163	1,791	Chr20	34,576,920	2,345
Chr9	54,293,521	1,528	Chr21	27,407,486	1,652
Chr10	52,804,925	1,510	Scaffold	66,697,536	801
Chr11	51,298,384	1,746	Total	1,213,391,197	42,086
Chr12	51,203,049	1,391			

Note: PE, Pair-end.

**Table S2. Repeat sequence content in *I. polycarpa* genome. Related to Figure 2.**

Type	Number of elements	Length occupied (bp)	Percentage of the genome (%)
Class I: Retroelements	501,757	526,447,486	43.39
SINEs	4,137	948,095	0.08
LINEs	13,640	11,713,489	0.97
LTR/Copia	110,298	130,873,371	10.79
LTR/Gypsy	305,157	339,154,986	27.95
Others	183	524201	0.04
Class II: DNA transposons	507,520	179,988,777	14.83
hobo-Activator	19,865	9,632,147	0.79
Tc1-IS630-Pogo	1,136	366,763	0.03
Harbinger	8,602	3,875,169	0.32
RC	57,910	26,192,107	2.16
Unclassified	495,783	138,907,198	11.45
Small RNA	9,953	7,621,447	0.63
Simple repeats	264,951	37,595,353	3.10
Low complexity	41,751	2,039,818	0.17
Total	--	917,844,091	75.64



Figure 1. *I. polycarpa* morphology and genomic landscape  
 (A) General morphology of a representative *I. polycarpa* tree at the fruit stage. Scale bar: 40 cm.  
 (B) A ripe *I. polycarpa* spike. Scale bar: 3 cm.  
 (C) Cross-sections of representative *I. polycarpa* fruit and seeds. Top, fruit cross-section. The region outlined in dashed red is enlarged in the middle. Scale bar: 6 mm. Middle, enlarged image of the pericarp and seeds. Scale bar: 2 mm. Bottom, a coated seed intact (left) and in cross-section (right). Scale bar: 1 mm. P, pericarp; S, seed; F, flesh; Sf, seed film; En, [endosperm](#); Em, embryo.



D

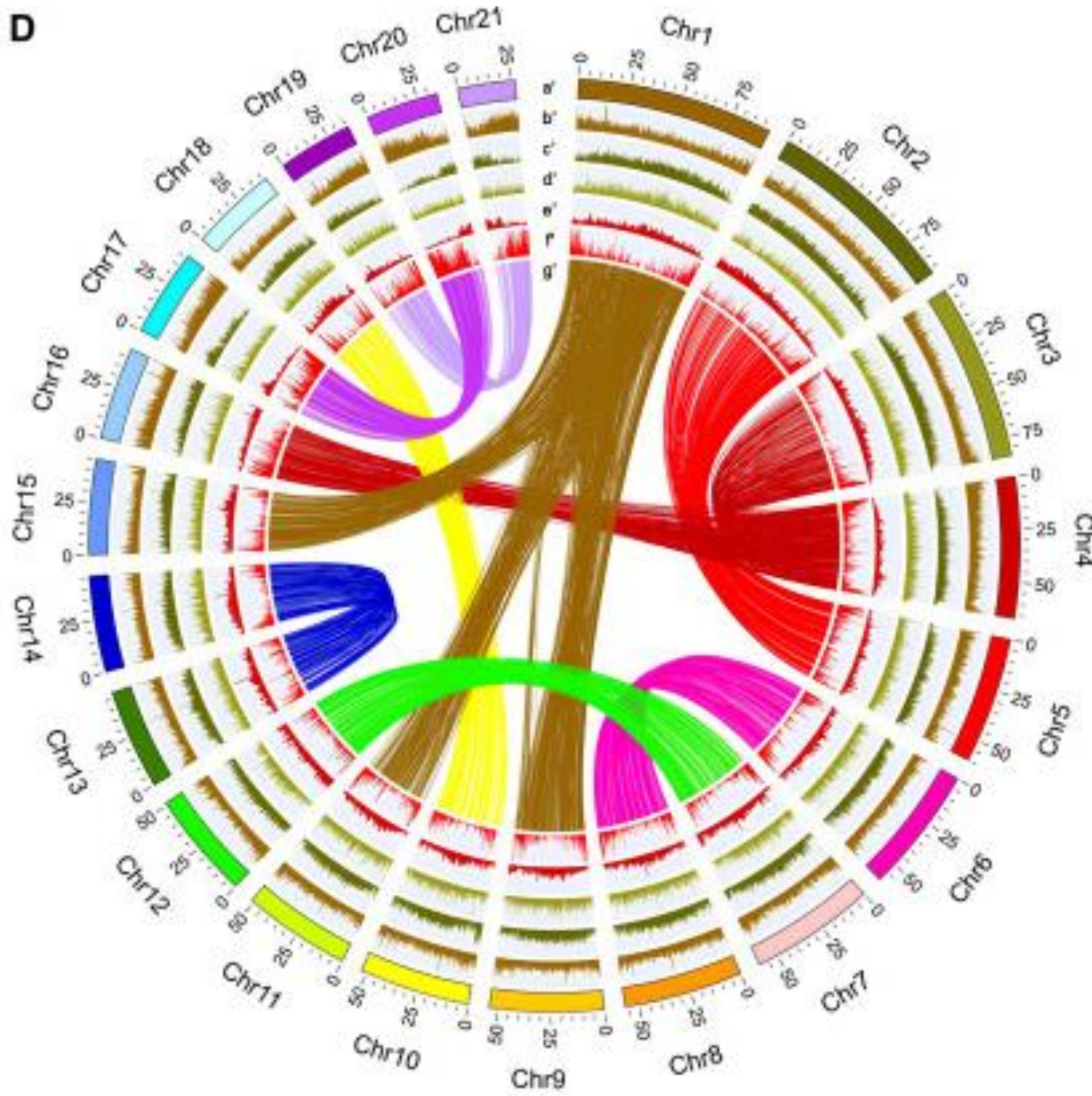
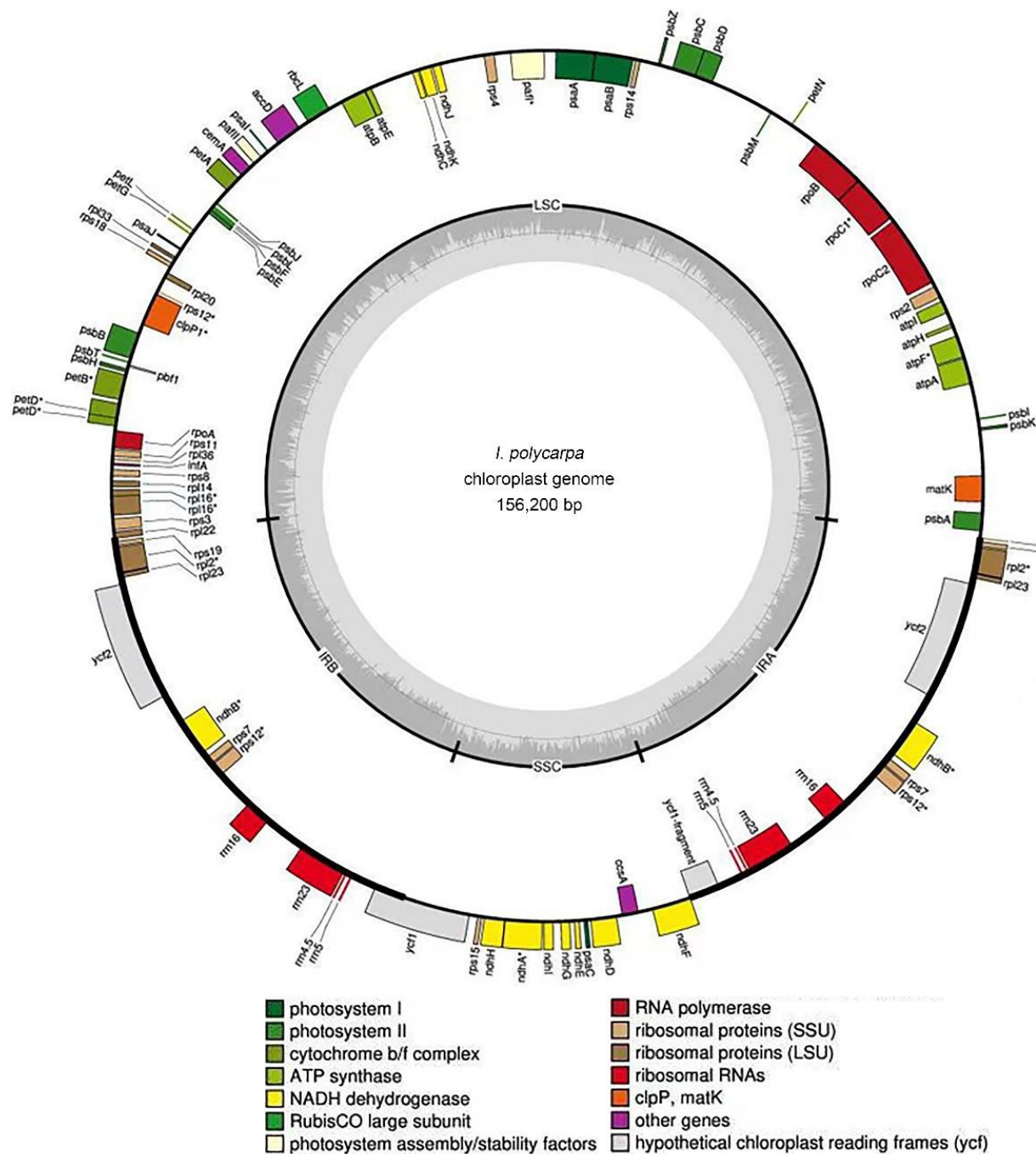


Figure 1. *I. polycarpa* morphology and genomic landscape

(D) Summary of the *I. polycarpa* genomic landscape. (a') Length of each pseudochromosome in megabases (Mb). (b') CG content (28%–35%). (c') Number of repeat element (100–500). (d') Number of *Copia* elements (0–72). (e') Number of *Gypsy* elements (0–221). (f') Number of genes (30–500). (g') Syntenic blocks in [homologous chromosomes](#). Each line represents a block longer than 2 kb. All data were based on 200-kb windows.



**Figure S2. Chloroplast reference genome of *I. polycarpa*. Related to Figure 1.**

The localization and function of the annotated genes are illustrated in the outer circle.

GC content is graphed around the inner circle with the line indicating 36.79% GC content. The map was generated using OrganellarGenomeDraw.

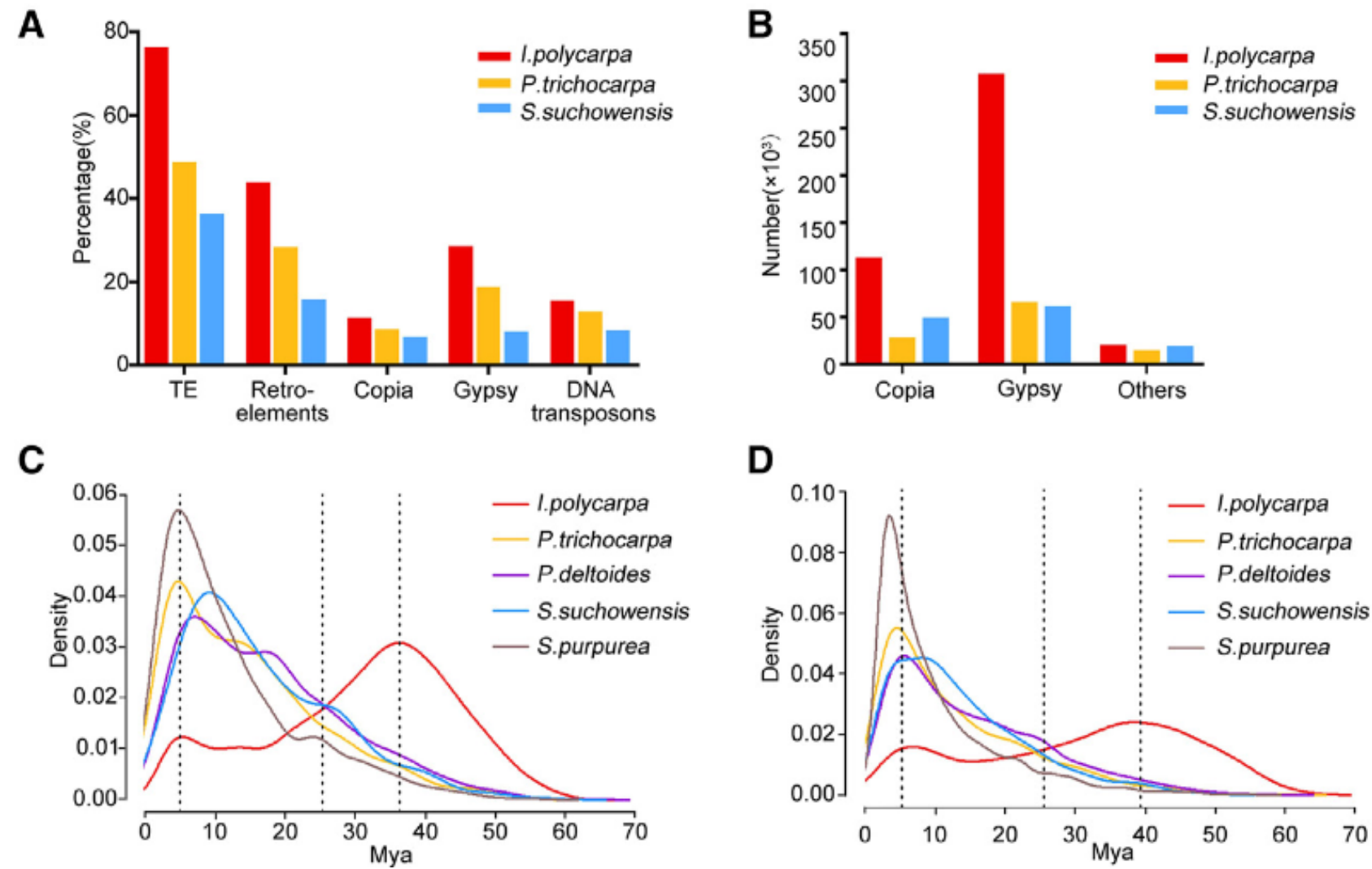


Figure 2. Characteristics of *Copia* and *Gypsy* [retroelements](#) in *I. polycarpa* and other woody plants in the family *Salicaceae*

(A) Distribution of repeat element types in *I. polycarpa* (red), [Populus trichocarpa](#) (yellow), and *Salix suchowensis* (blue).

(B) The number of intact [retroelements](#) in *I. polycarpa*, *P. trichocarpa*, and *S. suchowensis*.

(C and D) Expansion of *Copia* (C) and *Gypia* (D) retroelements in *I. polycarpa* and other species in the family *Salicaceae* (*P. trichocarpa*, *S. suchowensis*, *P. deltoides*, and *S. purpurea*).