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Supplementary figures
Chromosome-scale genomes of two commercially important mahogany species



Supplemental Figure 1. Morphological features of *Swietenia macrophylla*

Photos of flower and fruit are obtained from

<https://www.inaturalist.org/observations/63391559>

<https://www.inaturalist.org/observations/24971985>



Supplemental Figure 2. Morphological features of *Khaya senegalensis*

Photos of flower and fruit are obtained from

<https://www.inaturalist.org/observations/69098325>

Table S1 DNA Sequencing statistics of two species

Species	Library construction strategy	Raw reads pair number	Raw base pair number	Raw reads number	Raw base number (bp)	Raw Read length (bp)
<i>Khaya senegalensis</i>	10X	570,609,969	85,591,495,350	1,141,219,938	171,182,990,700	150
	Hi-C	759,897,146	75,989,714,600	1,519,794,292	151,979,429,200	100
<i>Swietenia macrophylla</i>	10X	641,510,428	96,226,564,200	1,283,020,856	192,453,128,400	150
	Hi-C	741,812,693	74,181,269,300	1,483,625,386	148,362,538,600	100

Table S2 RNA sequencing statistics of two species

Species	Tissue	Raw reads pair number	Raw base number	Clean reads pair number	Clean base number	Raw Read length (bp)
<i>Khaya senegalensis</i>	leaf	64,227,120	19,268,136,000	64,143,553	18,425,555,352	150
	xylem1	74,325,184	14,865,036,800	74,150,152	14,082,827,953	100
	xylem2	78,350,807	15,670,161,400	78,223,106	14,857,280,545	100
	xylem3	71,635,114	14,327,022,800	71,527,896	13,585,686,696	100
	phloem1	89,716,011	17,943,202,200	89,540,646	17,006,980,561	100
	phloem2	72,111,286	14,422,257,200	71,972,663	13,670,541,492	100
	phloem3	68,148,636	13,629,727,200	67,934,285	12,901,554,217	100
<i>Swietenia macrophylla</i>	leaf	56,982,281	17,094,684,300	87,583,797	16,629,064,964	150
	xylem	77,568,544	15,513,708,800	77,370,930	14,694,516,379	100
	phloem	76,864,957	15,372,991,400	76,676,834	14,563,059,157	100

Table S3 k-mer analysis of *Khaya senegalensis*, *Swietenia macrophylla*

Species	kmer	raw_peak	genome size	heterozygous ratio	repeat ratio
<i>Khaya senegalensis</i>	21	90	406,501,000	0.73%	42.60%
<i>Swietenia macrophylla</i>	21	123	274,489,000	1.00%	20.14%

Table S4 The genome assembly results of *Khaya senegalensis*, *Swietenia macrophylla*

		<i>Khaya senegalensis</i>				<i>Swietenia macrophylla</i>			
		Contig	Scaffold	Hi-C Contig	Hi-C Scaffold	Contig	Scaffold	Hi-C contig	Hi-C scaffold
Length (bp)	N90	2,705	3,549	2,668	3,429	8,220	9,569	8,149	9,375
	N80	7,782	10,342	7,599	9,898	31,167	1,702,943	29,661	6,790,372
	N70	15,985	374,000	15,000	125,000	57,557	3,044,426	54,962	7,228,676
	N60	29,451	1,328,405	25,728	6,785,394	84,179	5,136,928	81,638	7,881,878
	N50	45,659	2,533,462	40,489	7,098,500	110,842	5,758,776	108,891	8,511,416
	N40	64,779	4,201,832	55,523	8,146,634	139,687	7,125,297	137,783	8,986,794
	N30	86,513	5,447,807	75,871	8,792,228	173,247	7,949,705	171,441	9,504,661
	N20	115,035	7,903,176	102,601	9,309,318	216,783	8,746,502	212,398	9,975,239
Number	N10	163,926	8,986,309	147,164	9,757,406	287,250	9,811,634	280,926	14,894,579
	N90	14,346	7,798	15,102	7,989	3,808	869	3,903	768
	N80	7,257	1,645	7,885	1,734	2,021	42	2,079	26
	N70	4,212	107	4,722	130	1,388	30	1,422	22
	N60	2,685	55	3,058	26	1,001	23	1,020	18
	N50	1,789	34	2,029	21	720	18	731	14
	N40	1,172	23	1,329	16	503	13	510	11
	N30	731	15	822	12	327	9	331	8
	N20	395	9	445	8	185	6	188	5
	N10	151	4	171	4	75	3	76	2
	Maximum length	453,137	11,110,421	377,592	12,119,278	640,644	15,468,293	640,644	15,099,774
	Total length	331,727,067	377,763,054	331,726,582	369,939,925	272,898,649	290,208,927	272,898,173	287,673,742
	Total number>=100bp	62,615	54,771	63,630	54,893	23,653	19,971	23,858	19,920
	Total number>=2000bp	16,772	12,132	17,425	12,062	8,021	5,237	8,116	5,110
	Percentage of N content(%)		12.19		10.33		5.96		5.13

Table S5 Busco assessment of genome assembly of scaffold

BUSCOs	<i>Khaya senegalensis</i>		<i>Swietenia macrophylla</i>	
	NO.	P, %	NO.	P, %
Complete BUSCOs	1,323	96.2	1335	97.0
Complete single copy	1,022	74.3	1080	78.5
Complete duplicated	301	21.9	255	18.5
Fragmented	21	1.5	12	0.9
Missing	31	2.3	28	2.1
Total	1375	100	1375	100

Table S6 The repaeat annotation

Repeat Type	<i>Khaya senegalensis</i>		<i>Swietenia macrophylla</i>	
	% in genome	Length (bp)	%in genome	Length (bp)
SINE	0.03	147,284	0.08	263,198
LINE	0.54	2,083,942	0.48	1,416,342
LTR Copia	9.04	34,812,994	6.24	18,385,381
LTR Gypsy	4.87	18,776,751	5.19	15,295,668
LTR total	16.13	62,173,775	13.15	38,788,013
DNA	4.77	18,398,988	2.93	8,654,436
Satellite	0.03	149,272	0.06	177,417
Simple repeat	0.86	3,317,974	0.12	377,442
Unknown	9.56	36,852,027	6.36	18,761,431
Total	29.5	113,634,213	21.83	64,340,915

Table S7 Model plant or related species in gene annotation

Organism	Annotation version	Downloaded database	Paper URL
<i>Arabidopsis thaliana</i>	TAIR10	https://www.ncbi.nlm.nih.gov/datasets/taxonomy/3702/	—
<i>Anacardium occidentale</i>	v0.9	https://www.ncbi.nlm.nih.gov/datasets/taxonomy/171929/	https://www.nature.com/articles/s41598-022-22600-7
<i>Citrus sinensis</i>	v1.1	https://www.ncbi.nlm.nih.gov/datasets/taxonomy/2711/	https://academic.oup.com/hr/article/10/1/uhac247/6794931
<i>Citrus maxima</i>	—	https://ngdc.cncb.ac.cn/bioproject/browse/insdc/PRJNA796621	https://academic.oup.com/hr/article/doi/10.1093/hr/uhac175/6655783
<i>Dimocarpus longan</i>	—	https://ngdc.cncb.ac.cn/gwh/Assembly/21447/show	https://academic.oup.com/hr/article/doi/10.1093/hr/uhac021/6532241
<i>Eucalyptus grandis</i>	v1.0	https://jgi.doe.gov/	—

Table S8 The result and busco assessment of gene annotation

Table S8-1 The result of gene annotation

	<i>Khaya senegalensis</i>	<i>Swietenia macrophylla</i>
Protein-coding gene number	32,914	34,129
Mean gene length (bp)	3,068.00	3,052.92
Mean cds length (bp)	1,217.50	1,204.82
Mean exons per gene	5.29	5.58
Mean exon length (bp)	230.06	215.60
Mean intron length (bp)	431.15	402.79

Table S8-2 Busco assessment of gene annotation

BUSCOs	<i>Khaya senegalensis</i>		<i>Swietenia macrophylla</i>	
	NO.	P,%	NO.	P,%
Complete BUSCOs	1,268	92.2	1,284	93.4
Complete single copy	1,034	75.2	1,055	76.7
Complete duplicated	234	17	229	16.7
Fragmented	46	3.3	29	2.1
Missing	61	4.5	62	4.5
Total	1375	100	1375	100

Table S9 The functional annotation

	<i>Swietenia macrophylla</i>		<i>Khaya senegalensis</i>	
	Number of genes	Percentage (%)	Number of genes	Percentage (%)
Nr-Annotated	33,193	97.26	31,386	98.36
Swissprot-Annotated	27,014	79.15	26,004	81.50
KEGG-Annotated	24,807	72.69	23,855	74.76
COG-Annotated	12,664	37.11	12,568	39.39
TrEMBL-Annotated	32,924	96.47	31,309	98.12
Interpro-Annotated	26,063	76.37	25,304	79.30
Overall	33,255	97.44	31,426	98.49
Unannotated	874	2.56	482	1.51

**Table S10 The Annotation of non-coding RNA genes in the genomes of
Swietenia macrophylla, *Khaya senegalensis***

Species		miRNA	tRNA	rRNA					snRNA			
				Total rRNA	18S	28S	5.8S	5S	Total snRNA	CD-box	HACA-box	splicing
<i>Khaya senegalensis</i>	Copy(w)	189	844	630	390	154	24	62	381	225	64	92
	Average length (bp)	123	76	186	238	98	120	97	113	96	125	147
	Total length (bp)	23,156	63,790	116,988	92,966	15,154	2,868	6,000	43,138	21,681	7,970	13,487
	% of genome	0.61%	1.69%	3.10%	2.46%	0.40%	0.08%	0.16%	1.14%	0.57%	0.21%	0.36%
<i>Swietenia macrophylla</i>	Copy (w)	187	648	249	54	119	6	70	324	182	50	92
	Average length (bp)	123	75	142	293	96	118	105	116	95	127	152
	Total length (bp)	22,946	48,817	35,343	15,808	11,456	708	7,371	37,570	17,206	6,348	14,016
	% of genome	0.79%	1.68%	1.22%	0.54%	0.39%	0.02%	0.25%	1.29%	0.59%	0.22%	0.48%

Table S11 DNA reads mapped to the genome

Species	mapped reads rate	properly mapped paired reads
<i>Khaya senegalensis</i>	97.68%	82.72%
<i>Swietenia macrophylla</i>	97.43%	90.55%