

Comparison of the complete plastomes and the phylogenetic analysis of *Paulownia* species

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Supplementary Table 1. Genes in the chloroplast genomes of the six *Paulownia* species

Category of genes	Group of genes	Names of genes				
Photosynthesis-related genes	Photosystem I	<i>psaA</i>	<i>psaB</i>	<i>psaC</i>	<i>psaI</i>	<i>psaJ</i>
		<i>ycf3**</i>	<i>ycf4</i>			
	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>
	NADPH dehydrogenase	<i>ndhA*</i>	<i>ndhB*</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>				
	ATP synthase	<i>atpA</i>	<i>atpB</i>	<i>atpE</i>	<i>atpF*</i>	<i>atpH</i>
		<i>atpI</i>				
	Rubisco	<i>rbcL</i>				
	cytochrome b/f complex	<i>petA</i>	<i>petB*</i>	<i>petD*</i>	<i>petG</i>	<i>petL</i>
		<i>petN</i>				
Transcription- and translation-related genes	ribosomal proteins	<i>rps2</i>	<i>rps3</i>	<i>rps4</i>	<i>rps7</i>	<i>rps8</i>
		<i>rps11</i>	<i>rps12**</i>	<i>rps14</i>	<i>rps15</i>	<i>rps16</i>
		<i>rps18</i>	<i>rps19</i>	<i>rpl2*</i>	<i>rpl14</i>	<i>rpl16*</i>
		<i>rpl20</i>	<i>rpl22</i>	<i>rpl23</i>	<i>rpl32</i>	<i>rpl33</i>
		<i>rpl36</i>				
	transcription	<i>rpoA</i>	<i>rpoB</i>	<i>rpoC1*</i>	<i>rpoC2</i>	
	translation	<i>infA*</i>				
	initiation factor					
RNA genes	transfer RNA	<i>trnA-UGC*</i>	<i>trnC-GCA</i>	<i>trnD-GUC</i>	<i>trnE-UUC</i>	<i>trnF-GAA</i>
		<i>trnG-GCC</i>	<i>trnG-UCC</i>	<i>trnH-GUG</i>	<i>trnI-CAU</i>	<i>trnI-GAU*</i>
		<i>trnK-UUU*</i>	<i>trnL-UAG</i>	<i>trnL-UAA*</i>	<i>trnL-CAA</i>	<i>trnM-CAU</i>
		<i>trnM-CAU</i>	<i>trnN-GUU</i>	<i>trnP-UGG</i>	<i>trnP-GGG</i>	<i>trnQ-UUG</i>
		<i>trnR-ACG</i>	<i>trnR-UCU</i>	<i>trnS-GCU</i>	<i>trnS-UGA</i>	<i>trnS-GGA</i>
		<i>trnT-UGU</i>	<i>trnT-GGU</i>	<i>trnV-UAC*</i>	<i>trnV-GAC</i>	<i>trnW-CCA</i>
		<i>trnY-GUA</i>				
	ribosomal RNA	<i>rrn5</i>	<i>rrn4.5</i>	<i>rrn16</i>	<i>rrn23</i>	

Supplementary Table 1. (Continued)

Other genes	RNA processing	<i>matK</i>		
	fatty acid synthesis	<i>accD</i>		
	carbon metabolism	<i>cemA</i>		
	proteolysis	<i>clpP</i> **		
Genes of unknown function	conserved reading	<i>ycf1</i>	<i>ycf2</i>	<i>ycf15</i>
	frames			

* Gene containing a single intron, ** Gene containing tow introns.

Supplementary Table 2. Type of SSRs in the chloroplast genomes of the eight *Paulownia* species

	Mono	Di	Tri	Tetra	Penta	Hexa	Imperfect repeat
<i>P. elongata</i>				(ATTG) ₃ = 1			
	(A) ₁₀₋₁₃ = 24			(GTCT) ₃ = 1			
	(T) ₁₀₋₁₂ = 23	(TA) ₅₋₇ = 4	(TTA) ₄ = 1	(TCTA) ₃ = 1	(TATTT) ₃ = 1		
	(G) ₁₁ = 1	(AT) ₅ = 2	(TTC) ₄ = 1	(GAAA) ₃ = 1			
	(C) ₁₁ = 1		(ATA) ₄ = 1	(AAAC) ₃ = 1			
<i>P. australis</i>				(AATA) ₃ = 1			
				(ATTG) ₃ = 1			
	(A) ₁₀₋₁₃ = 23			(GTCT) ₃ = 1			
	(T) ₁₀₋₁₃ = 23	(TA) ₅₋₇ = 4	(TTC) ₄ = 1	(TCTA) ₃ = 1	(TATTT) ₃ = 1		
	(G) ₁₀₋₁₁ = 2	(AT) ₅ = 2	(ATA) ₄ = 1	(AAAC) ₃ = 1			
<i>P. kawakamii</i>	(C) ₁₁ = 1			(GAAA) ₃ = 2			
				(AATA) ₃ = 1			
				(ATTG) ₃ = 1			
				(GTCT) ₃ = 1			
	(A) ₁₀₋₁₄ = 23			(ATA) ₄ = 1			
<i>P. fargesii</i>	(T) ₁₀₋₁₃ = 26	(TA) ₅₋₆ = 4	(TTA) ₄ = 1	(AAAC) ₃ = 1			
	(G) ₁₁ = 1	(AT) ₅ = 1	(TTC) ₄ = 1	(GAAA) ₃ = 1	(TATTT) ₃ = 1		(GAAA) ₃ tttctc(T) ₁₀ = 1
	(C) ₁₁ = 1			(TCTA) ₃ = 1			(T) ₁₀ c(T) ₁₀ = 1
				(TTTC) ₃ = 1			
				(AATA) ₃ = 1			
<i>P. catalpifolia</i>				(ATTG) ₃ = 1			
				(GTCT) ₃ = 1			
	(A) ₁₀₋₁₃ = 23			(ATA) ₄ = 1			
	(T) ₁₀₋₁₂ = 24	(TA) ₅₋₆ = 4	(TTA) ₄ = 1	(AATA) ₃ = 1			
	(G) ₁₁ = 1	(AT) ₅ = 2	(ATA) ₄ = 1	(TCTA) ₃ = 1	(TATTT) ₃ = 1		
<i>P. fortunei</i>	(C) ₁₁ = 1			(TTC) ₄ = 1			
				(GAAA) ₃ = 2			
				(AAAC) ₃ = 1			
				(ATTG) ₃ = 1			
				(GTCT) ₃ = 1			
<i>P. fortunei</i>				(TCTA) ₃ = 1			
	(A) ₁₀₋₁₃ = 23			(ATA) ₄ = 1			
	(T) ₁₀₋₁₃ = 22	(TA) ₅₋₇ = 4	(TTA) ₄ = 1	(TCTA) ₃ = 1	(TATTT) ₃ = 1	(TTCAAT) ₃	
	(G) ₁₁ = 1	(AT) ₅ = 2	(ATA) ₄ = 1	(GAAA) ₃ = 2		= 1	
	(C) ₁₁ = 1			(AATA) ₃ = 1			
<i>P. fortunei</i>				(AAAC) ₃ = 1			
				(ATTG) ₃ = 1			
				(GTCT) ₃ = 1			
	(A) ₁₀₋₁₃ = 23			(ATA) ₄ = 1			
	(T) ₁₀₋₁₄ = 23	(TA) ₅₋₇ = 4	(TTA) ₄ = 1	(AAAC) ₃ = 1			
<i>P. fortunei</i>	(G) ₁₁ = 1	(AT) ₅ = 2	(TTC) ₄ = 1	(AATA) ₃ = 1	(TATTT) ₃ = 1		
	(C) ₁₁ = 1		(ATA) ₄ = 1	(TCTA) ₃ = 1			
				(GAAA) ₃ = 2			

Supplementary Table 2. (Continued)

				(ATTG) ₃ = 1		
				(GTCT) ₃ = 1		
	(A) ₁₀₋₁₄ = 24		(TTA) ₄ = 1	(TCTA) ₃ = 1		
<i>P. tomentosa</i>	(T) ₁₀₋₁₃ = 26	(TA) ₅₋₈ = 4	(TTC) ₄ = 1	(AAAC) ₃ = 1	(TATTT) ₃ = 1	(GAAA) ₃ tttctc(T) ₁₂ = 1
	(G) ₁₀ = 1	(AT) ₅ = 1	(ATA) ₄ = 1	(GAAA) ₃ = 1		
	(C) ₁₀ = 1			(AATA) ₃ = 1		
				(TTTC) ₃ = 1		
				(ATTG) ₃ = 1		
	(A) ₁₀₋₁₄ = 24		(TTA) ₄ = 1	(GTCT) ₃ = 1		
<i>P. coreana</i>	(T) ₁₀₋₁₃ = 26	(TA) ₅₋₈ = 4	(TTC) ₄ = 1	(TCTA) ₃ = 1	(TATAT) ₃ = 1	(GAAA) ₃ tttctc(T) ₁₂
	(G) ₁₀ = 1	(AT) ₅ = 1	(ATA) ₄ = 1	(AAAC) ₃ = 1	(TATTT) ₃ = 1	= 1
	(C) ₁₀ = 1			(AATA) ₃ = 1		
				(GAAA) ₃ = 1		

Supplementary Table 3. Sample information about the six *Paulownia* species

No.	Species	Locality	Longitude (°E)	Latitude (°N)	Altitude	Habitat
1	<i>Paulownia australis</i>	Nanping, Fujian, China	118°32′	26°41′	512.00 m	Natural forest
2	<i>Paulownia fargesii</i>	Wuhan, Hubei, China	114°18′	30°28′	46.00 m	Natural forest
3	<i>Paulownia fortunei</i>	Zhengzhou, Henan, China	113°34′	34°42′	83.00 m	Paulownia germplasm resource nursery
4	<i>Paulownia kawakamii</i>	Zhengzhou, Henan, China	113°34′	34°42′	83.00 m	Paulownia germplasm resource nursery
5	<i>Paulownia elongata</i>	Zhengzhou, Henan, China	113°34′	34°42′	83.00 m	Paulownia germplasm resource nursery
6	<i>Paulownia catalpifolia</i>	Zhengzhou, Henan, China	113°34′	34°42′	83.00 m	Paulownia germplasm resource nursery