

Nagel J.C., de Oliveira Machado, L., Lemos R.P.M., Barbosa D'Oliveira Matielo C., Poletto T., Poletto I., Stefenon V.M., 2020. Structural, evolutionary and phylogenomic features of the plastid genome of *Carya illinoensis* cv. Imperial. Ann. For. Res. DOI: 10.15287/afr.2019.1413

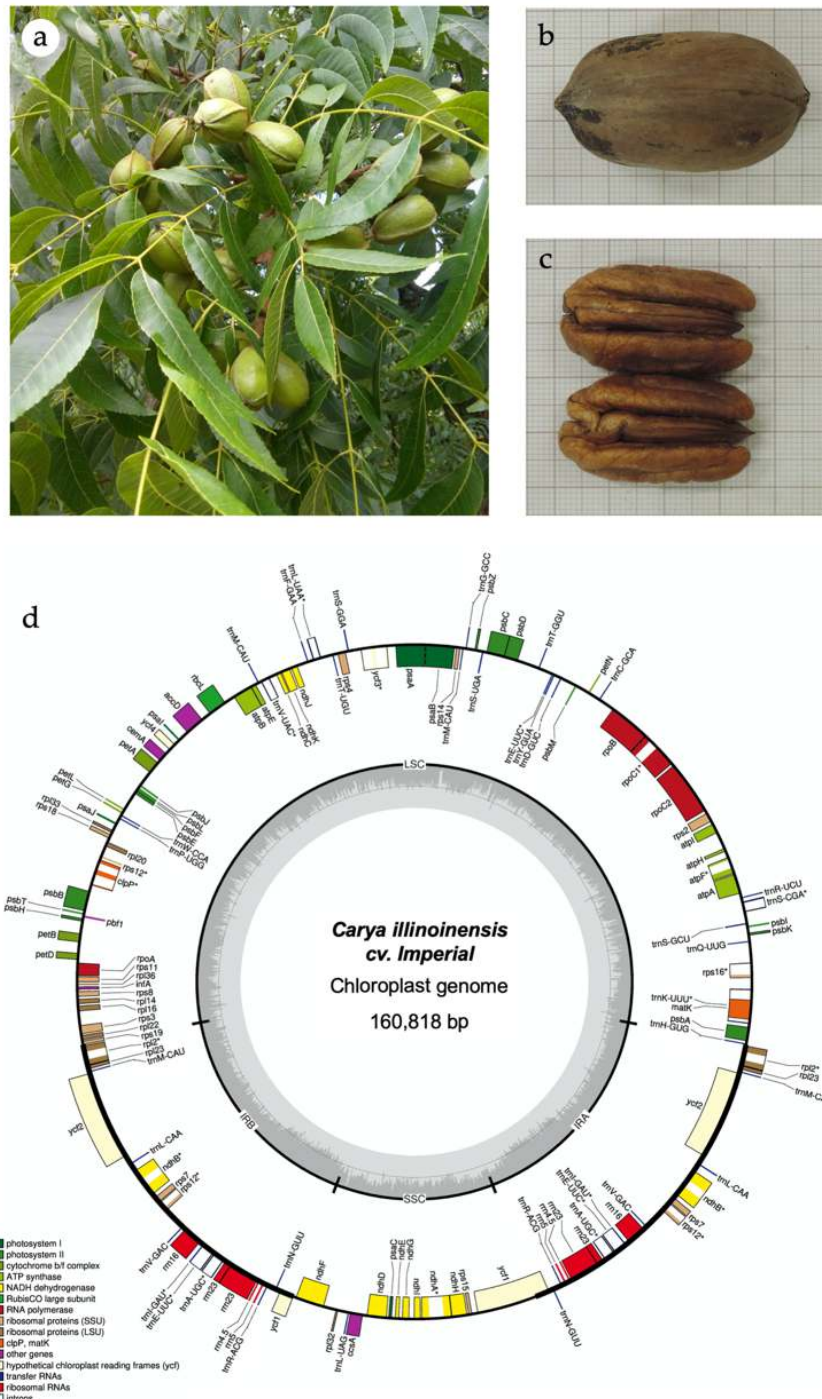


Figure S1 *Carya illinoensis* cv. Imperial. (a) Fruits in intermediate stage of ripening. (b) Ripe nuts and (c) the kernel of the nut. (d) Physical map of the plastid genome of *C. illinoensis* cv. Imperial. The darker gray area in the inner circle represents the GC content, while light gray is the AT content. Coding regions containing introns are marked with one asterisk.

Table S1 Mean number of base substitutions per site (below diagonal) and the corresponding standard errors (above diagonal) per site of the *rps16* gene (mean overall distance = 0.003)

<i>C. illinoensis</i> cv. Imperial		0.00000	0.00496	0.00000	0.00330	0.00729	0.00398	0.00692	0.00314	0.00765	0.00492
<i>C. illinoensis</i> MH909599.1	0.00000		0.00496	0.00000	0.00330	0.00729	0.00398	0.00692	0.00314	0.00765	0.00492
<i>C. sinensis</i>	0.00747	0.00747		0.00542	0.00359	0.00759	0.00342	0.00780	0.00342	0.00553	0.00557
<i>Cy. paliurus</i>	0.00000	0.00000	0.00817		0.00341	0.00677	0.00341	0.00619	0.00341	0.00534	0.00534
<i>J. cathayensis</i>	0.00392	0.00392	0.00393	0.00406		0.00560	0.00000	0.00515	0.00000	0.00396	0.00396
<i>J. cinerea</i>	0.01513	0.01513	0.01515	0.01233	0.00790		0.00667	0.00505	0.00667	0.00792	0.00679
<i>J. hopeiensis</i>	0.00817	0.00817	0.00372	0.00406	0.00000	0.01131		0.00642	0.00000	0.00375	0.00378
<i>J. major</i>	0.01515	0.01515	0.01518	0.01235	0.00791	0.00747	0.01133		0.00642	0.00751	0.00624
<i>J. mandshurica</i>	0.00372	0.00372	0.00372	0.00406	0.00000	0.01131	0.00000	0.01133		0.00375	0.00378
<i>J. regia</i>	0.01873	0.01873	0.00750	0.00819	0.00394	0.01520	0.00373	0.01522	0.00373		0.00000
<i>J. sigilata</i>	0.00754	0.00754	0.00755	0.00819	0.00394	0.01140	0.00376	0.01141	0.00376	0.00000	

Table S2 Mean number of base substitutions per site (below diagonal) and the corresponding standard errors (above diagonal) per site of the *trnQ-UUG - psbK* region (mean overall distance = 0.5143)

<i>C. illinoensis</i> cv. Imperial		0.00000	9.40250	8.75936	8.98291	0.00450	8.31387	0.00441	8.31387	10.46610	10.46610
<i>C. illinoensis</i> MH909599.1	0.00000		9.40250	8.75936	8.98291	0.00450	8.31387	0.00441	8.31387	10.46610	10.46610
<i>C. sinensis</i>	0.58852	0.58852		4.50475	4.37666	9.41907	10.17579	9.41239	10.17579	11.21316	11.21316
<i>Cy. paliurus</i>	0.57243	0.57243	0.25536		0.00544	8.76642	10.49037	8.76553	10.49037	10.97471	10.97471
<i>J. cathayensis</i>	0.58538	0.58538	0.25169	0.01041		8.95387	10.30488	8.95298	10.30488	10.83186	10.83186
<i>J. cinerea</i>	0.00885	0.00885	0.59310	0.56537	0.56833		8.28891	0.00235	8.28891	10.42431	10.42431
<i>J. hopeiensis</i>	0.54763	0.54763	0.54992	0.61433	0.60043	0.54070		8.29303	0.00000	11.60489	11.60489
<i>J. major</i>	0.00887	0.00887	0.58771	0.56202	0.56496	0.00292	0.54215		8.29303	10.42431	10.42431
<i>J. mandshurica</i>	0.54763	0.54763	0.54992	0.61433	0.60043	0.54070	0.00000	0.54215		11.60489	11.60489
<i>J. regia</i>	0.73818	0.73818	0.67651	0.73196	0.72998	0.71124	0.69945	0.71124	0.69945		0.00000
<i>J. sigilata</i>	0.73818	0.73818	0.67651	0.73196	0.72998	0.71124	0.69945	0.71124	0.69945	0.00000	

Table S3 Mean number of base substitutions per site (below diagonal) and the corresponding standard errors (above diagonal) per site of the *trnV-UAC – trnM-CAU* region (mean overall distance = 0.004)

<i>C. illinoensis</i> cv. Imperial		0.00188	0.00225	0.00238	0.00240	0.00257	0.00238	0.00257	0.00238	0.00238
<i>C. illinoensis</i> MH909599.1	0.00324		0.00311	0.00312	0.00312	0.00323	0.00312	0.00323	0.00312	0.00312
<i>C. sinensis</i>	0.00647	0.00982		0.00145	0.00146	0.00185	0.00145	0.00185	0.00145	0.00145
<i>Cy. paliurus</i>	0.00647	0.00982	0.00214		0.00000	0.00101	0.00000	0.00101	0.00000	0.00000
<i>J. cathayensis</i>	0.00654	0.00984	0.00217	0.00000		0.00102	0.00000	0.00102	0.00000	0.00000
<i>J. cinerea</i>	0.00757	0.01094	0.00323	0.00107	0.00108		0.00101	0.00000	0.00101	0.00101
<i>J. hopeiensis</i>	0.00647	0.00982	0.00215	0.00000	0.00000	0.00107		0.00101	0.00000	0.00000
<i>J. major</i>	0.00757	0.01094	0.00323	0.00107	0.00108	0.00000	0.00107		0.00101	0.00101
<i>J. mandshurica</i>	0.00647	0.00982	0.00214	0.00000	0.00000	0.00107	0.00000	0.00107		0.00000
<i>J. regia</i>	0.00647	0.00982	0.00214	0.00000	0.00000	0.00107	0.00000	0.00107	0.00000	

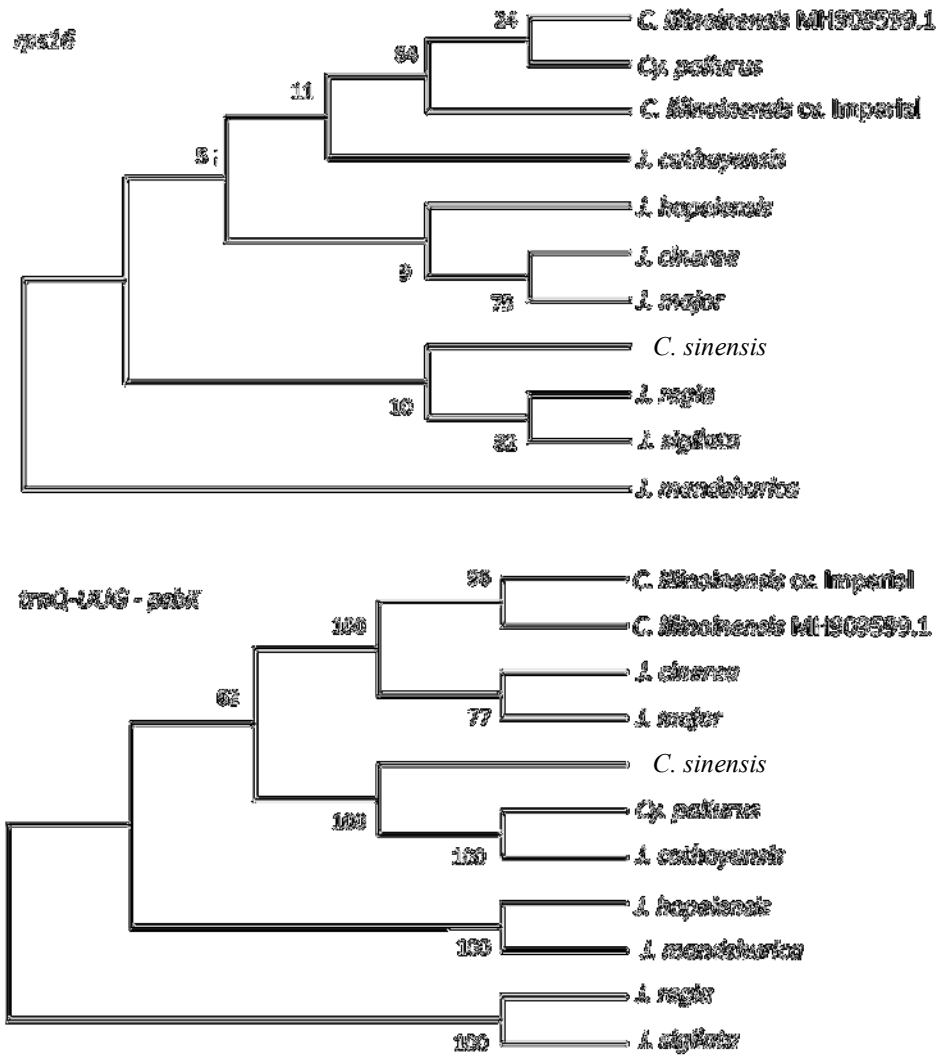
Table S4 Mean number of base substitutions per site (below diagonal) and the corresponding standard errors (above diagonal) per site of the *ndhG* gene (mean overall distance = 0.009)

<i>C. illinoensis</i> cv. Imperial		0.00000	0.00362	0.00570	0.00395	0.00506	0.00395	0.00549	0.0039	0.0043	0.0043
<i>C. illinoensis</i> MH909599.1	0.00000		0.00362	0.00570	0.00395	0.00506	0.00395	0.00549	0.0039	0.0043	0.0043
<i>C. sinensis</i>	0.00765	0.00765		0.00580	0.00416	0.00497	0.00416	0.00553	0.0042	0.0047	0.0047
<i>Cy. paliurus</i>	0.01955	0.01955	0.01947		0.00339	0.00434	0.00339	0.00500	0.0034	0.0040	0.0040
<i>J. cathayensis</i>	0.01154	0.01154	0.01149	0.00766		0.00231	0.00000	0.00298	0.0000	0.0017	0.0017
<i>J. cinerea</i>	0.01551	0.01551	0.01545	0.01158	0.00380		0.00231	0.00158	0.0023	0.0028	0.0028
<i>J. hopeiensis</i>	0.01154	0.01154	0.01149	0.00766	0.00000	0.00380		0.00298	0.0000	0.0017	0.0017
<i>J. major</i>	0.01762	0.01762	0.01755	0.01364	0.00575	0.00190	0.00575		0.0029	0.0034	0.0034
<i>J. mandshurica</i>	0.01154	0.01154	0.01149	0.00766	0.00000	0.00380	0.00000	0.00575		0.0017	0.0017
<i>J. regia</i>	0.01349	0.01349	0.01344	0.00959	0.00189	0.00571	0.00189	0.00768	0.0019		0.0000
<i>J. sigilata</i>	0.01349	0.01349	0.01344	0.00959	0.00189	0.00571	0.00189	0.00768	0.0019	0.0000	

Table S5 Mean number of base substitutions per site (below diagonal) and the corresponding standard errors (above diagonal) of the *rrn23 - trnA-UGC* (mean overall distance = 0.418)

<i>C. illinoensis</i> cv. Imperial		0.00155	0.00157	0.12549	0.12549	0.12549	0.12549	0.12549	0.12549	0.12549	0.12549
<i>C. illinoensis</i> MH909599.1	0.00676		0.00187	0.12439	0.12439	0.12439	0.12439	0.12439	0.12439	0.12439	0.12439
<i>C. sinensis</i>	0.01077	0.01224		0.10247	0.10247	0.10247	0.10247	0.10247	0.10247	0.10247	0.10247
<i>Cy. paliurus</i>	1.01607	1.04102	0.81596		0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000
<i>J. cathayensis</i>	1.01607	1.04102	0.81596	0.00000		0.00000	0.00000	0.00000	0.00000	0.00000	0.00000
<i>J. cinerea</i>	1.01607	1.04102	0.81596	0.00000	0.00000		0.00000	0.00000	0.00000	0.00000	0.00000
<i>J. hopeiensis</i>	1.01607	1.04102	0.81596	0.00000	0.00000	0.00000		0.00000	0.00000	0.00000	0.00000
<i>J. major</i>	1.01607	1.04102	0.81596	0.00000	0.00000	0.00000	0.00000		0.00000	0.00000	0.00000
<i>J. mandshurica</i>	1.01607	1.04102	0.81596	0.00000	0.00000	0.00000	0.00000	0.00000		0.00000	0.00000
<i>J. regia</i>	1.01607	1.04102	0.81596	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000		0.00000
<i>J. sigilata</i>	1.01607	1.04102	0.81596	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	

Figure S2 Maximum Parsimony analysis of 11 species of tribe Juglandae, using the hotspot regions of nucleotide divergence, determined through a sliding window analysis. The evolutionary history was inferred using the Maximum Parsimony method with the Subtree-Pruning-Regrafting (SPR) algorithm with search level 1 in which the initial trees were obtained by the random addition of sequences. The bootstrap consensus tree was inferred from 100 replicates.



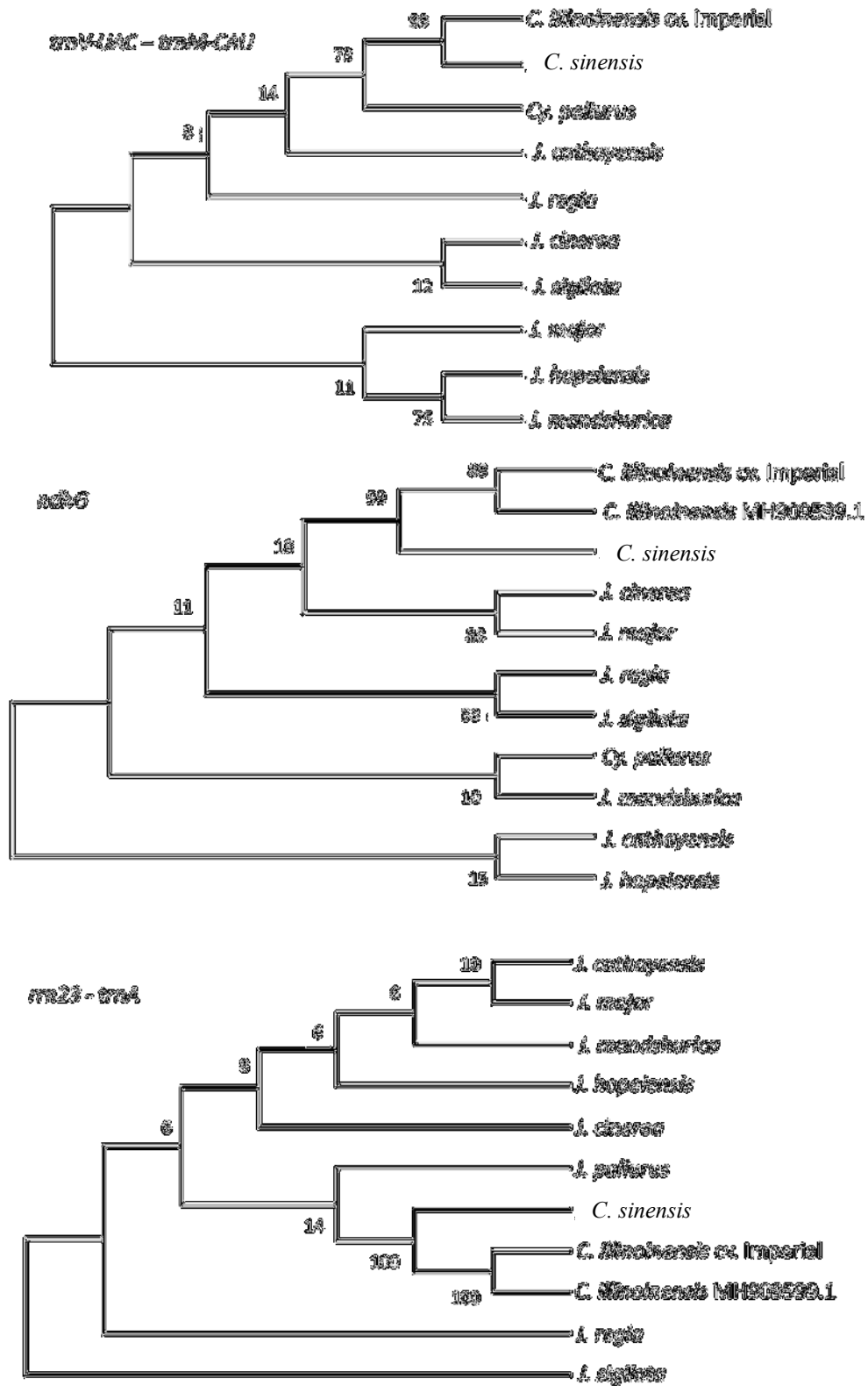


Table S6. Examples of homologous SSR loci in *Carya illinoniensis* cv. Imperial and *Carya illinoensis* MH909599.1. Loci 1 and 2 have the same motif, size and position in the plastid genome of both individuals. Loci 3 and 4 differ in the start and end position due to the one base deletion in *C. illinoniensis* cv. Imperial. Loci 5 to 7 have differences concerning the number of repeats of the motif, representing putatively polymorphic markers.

Locus	<i>C. illinoniensis</i> cv. Imperial				<i>C. illinoensis</i> MH909599.1			
	Motif	Size	Start	End	Motif	Size	Start	End
1	(T) ₁₁	11	3996	4006	(T) ₁₁	11	3996	4006
2	(A) ₁₁ ...(A) ₁₀	74	4499	4572	(A) ₁₁ ...(A) ₁₀	74	4499	4572
3	(AT) ₆	12	73572	73583	(AT) ₆	12	73573	73584
4	(T) ₁₀ ...(T) ₁₂	116	76205	76320	(T) ₁₀ ...(T) ₁₂	116	76206	76321
5	(A) ₂₆ ...(A) ₁₁	128	9858	9985	(A) ₁₆ ...(A) ₁₁	125	9861	9985
6	(A) ₂₃	23	70941	70963	(A) ₁₂	12	70953	70964
7	(A) ₂₁	21	126737	126757	(A) ₁₄	14	126745	126758

Loci 2, 4 and 5 are interrupted SSRs and the reticence within the repeat motifs represent the sequence within the repeated sequence that does not match the motif sequence.