forests

Article

Comparative Plastome Analyses and Phylogenetic Applications of the *Acer* Section *Platanoidea*

Tao Yu [1], Jian Gao [2], Bing-Hong Huang [3], Buddhi Dayananda [4], Wen-Bao Ma [5], Yu-Yang Zhang [1], Pei-Chun Liao [3,*] and Jun-Qing Li [1,*]

[1] Forestry College, Beijing Forestry University, 35 Qinghua East Road, Haidian District, Beijing 100083, China; yutao123@bjfu.edu.cn (T.Y.); yuyangzhang@bjfu.edu.cn (Y.-Y.Z.)
[2] Faculty of Resources and Environment, Baotou Teachers' College, No.3, Kexue Rd., BaoTou, Inner Mongolia 014030, China; gaojian5688@163.com
[3] School of Life Science, National Taiwan Normal University, No. 88, Sec. 4, TingChow Rd., Wunshan Dist., Taipei 116, Taiwan; sohjiro4321@yahoo.com.tw
[4] School of Agriculture and Food Sciences, The University of Queensland, Brisbane QLD 4072, Australia; buddhi6@gmail.com
[5] Key Laboratory of National Forestry and Grassland Administration on Sichuan Forest Ecology, Resources and Environment Sichuan Academy of Forestry, Chengdu 610081, China; mawenbao_2000@126.com
* Correspondence: pcliao@ntnu.edu.tw (P.-C.L.); lijq@bjfu.edu.cn (J.-Q.L.); Tel.: +886-2-77346330 (P.-C.L.)

Received: 17 March 2020; Accepted: 16 April 2020; Published: 19 April 2020

Abstract: The *Acer* L. (Sapindaceae) is one of the most diverse and widespread genera in the Northern Hemisphere. Section *Platanoidea* harbours high genetic and morphological diversity and shows the phylogenetic conflict between *A. catalpifolium* and *A. amplum*. Chloroplast (cp) genome sequencing is efficient for the enhancement of the understanding of phylogenetic relationships and taxonomic revision. Here, we report complete cp genomes of five species of *Acer* sect. *Platanoidea*. The length of *Acer* sect. *Platanoidea* cp genomes ranged from 156,262 bp to 157,349 bp and detected the structural variation in the inverted repeats (IRs) boundaries. By conducting a sliding window analysis, we found that five relatively high variable regions (*trnH-psbA*, *psbN-trnD*, *psaA-ycf3*, *petA-psbJ* and *ndhA* intron) had a high potential for developing effective genetic markers. Moreover, with an addition of eight plastomes collected from GenBank, we displayed a robust phylogenetic tree of the *Acer* sect. *Platanoidea,* with high resolutions for nearly all identified nodes, suggests a promising opportunity to resolve infrasectional relationships of the most species-rich section *Platanoidea* of *Acer*.

Keywords: *Acer*; sect. *Platanoidea*; chloroplast genome; sequence divergence; structural variation; phylogenetics

---

1. Introduction

Chloroplasts (cp) are essential organelles in plant cells for the processes of photosynthesis and carbon fixation [1]. They possess uniparental inheritance and their genome has a high conservation structure in most land plants [2]. Generally, cp genomes in most angiosperms are circular DNA molecules composed of four parts, namely two inverted repeats (IRs) at approximately 20–28 kb, a vast single-copy region (LSC) at 80–90 kb and a small single-copy region (SSC) at 16–27 kb [3]. The composition of angiosperm cp genomes is relatively conserved and encodes four ribosomal RNAs (rRNAs), roughly 30 transfer RNAs (tRNAs) and approximately 80 single-copy genes [4]. With the rapid development of next-generation sequencing (NGS) and other methods for obtaining the cp genome sequences, the availability of cp genome sequences has increased dramatically for land plants, offering opportunities for the comprehensive structure comparison, improvement of horticultural plant breeding [5,6] and reconstruction of evolutionary relationships [7,8]. In most angiosperms, the cp genome is inherited from the patrilineal lineage and exhibits little or no recombination [9]. Due to its relatively conserved features, cp sequences are commonly used as DNA barcodes for genetic identification, plant systematic studies, and research into plant biodiversity, biogeography, adaptation, etc. [10,11].

Acer L. (Maple), a diverse genus of family Sapindaceae L., contains more than 124 species [12]. Most extant species of the genus are native to Asia, whereas others occur in North America, Europe and North Africa [12–14]. Most *Acer* species are famous ornamental plants [13], and also another usage for pharmaceutical and chemical products [15]. To date, 17 species belonging to the *Acer* section Platanoidea have been recognised in China, in which the section shows high genetics and morphology diversity. [12]. Among them, four species are widespread in various vegetation regions (*A. amplum*, *A. longipes*, *A. mono* and *A. truncatum*) [16], and some are endangered, such as *A. catalpifolium*, *A. miaotaiense*, and *A. yangjuechi.*

However, some species with diversified leaf morphology have taxonomic controversy due to unresolved phylogenetic relationships (for example, *A. longipes* and *A. amplum*) and require further studies and clarification [17]. The comparative plastome analysis allows detailed insights to affirm the phylogenetic placement of these plants and will be useful for species identification, to verify taxonomic levels and identify phylogenetic relationships [8,18]. Recently, cp genomes of *A. miaotaiense* and *A. truncatum* have been reported, but merely the sequence information was provided without further analyses [19,20]. Thus, a comparative study among these two published cp genomes and five newly generated plastomes of sect. *Platanoidea* is conducted and applied to address phylogenetic and taxonomic validity.

Firstly, we reported newly completed cp genomes of five species of the *Acer* sect. *Platanoidea* (*A. catalpifolium*, *A. amplum*, *A. longipes*, *A. yanjuechi* and *A. mono*). Then, we compared the gene contents and the plastomic organisation with two published cp genomes in the sect. *Platanoidea* to identify variable loci that can apply to the species or population-level studies on *Acer*. The aims of this study are: (i) to deepen our understanding of the genetic and structural diversity within the sect. *Platanoidea*, (ii) to increase our understanding of phylogenetic relationships of species within the sect. *Platanoidea*, and (iii) to reconstruct a phylogenetic tree based on these plastomes. Our study also provides genetic resources for future research in this genus.

2. Materials and Methods

2.1. Sampling and DNA Extraction

Young leaves of five *Acer* species (*A. catalpifolium*, *A. amplum*, *A. longipes*, *A. yanjuechi* and *A. mono*) were collected and dried immediately with silica gel for preservation, for each species we collected the leaves from one healthy plant. Collection information of the plant materials is showed in Table S1. Vouchers taxonomical determination was by the Beijing Forestry University herbarium and deposited at the College of Forestry, Beijing Forestry University, China. We isolated total genomic DNA from silica gel-dried leaves according to the modified CTAB method [21].

2.2. Chloroplast Genome Sequencing, Assembling and Annotation

Purified genomic DNA was sequenced using an Illumina MiSeq sequencer at Shanghai OE Biotech. Co., Ltd. A paired-end library was constructed with an insert size of 300 bp, yielding at least 8 GB of 150 bp paired-end reads for each species. Clean reads were obtained with NGS QC Toolkit v2.3.3 (cut-off read length for HQ = 70%, cut-off quality score = 20, trim reads from 5′ = 3, trim reads from 3′ = 7) [22]. We used MITObim v. 1.8 [23] to assemble the five new *Acer* cp sequences with the reference cp genomes, *A. miaotaiense* (KX098452) [19], *A. davidii* (KU977442) [24] and *A. morrisonense* (KT970611) [25]. Gene functions were annotated using DOGMA [26], and the protein-encoding genes (PCG), tRNAs and rRNA were determined and verified using the BLAST searches (https://blast.ncbi.nlm.nih.gov/Blast.cgi).

2.3. Divergence Hotspot Identification

In order to determine the divergence level, a MAFFT: multiple sequence alignment program [27] was used to align cp sequences of seven *Acer* sect. *Platanoidea* species, and then sliding windows of the nucleotide variability (pi) was conducted using DnaSP 5.0 with 600-bp window length and 200-bp step size [28].

2.4. Phylogenomic Reconstruction

To determine the phylogenetic relationship of the *Acer* sect. *Platanoidea*, we performed phylogenetic analyses using 13 cp genome sequences, which comprised five plastome sequences generated in this study, six plastomes of the *Acer* species collected from GenBank, and two of the *Dipteronia* species as an outgroup (Table S2). Consequently, a total length of 160,886 bp was aligned using MAFFT [27]. The best-fitting substitution model (GTR + I + G) was inferred using Modeltest 3.7 [29]. Finally, phylogenomic relationships were reconstructed with Bayesian Inference (BI) and Maximum Likelihood (ML) using MrBayes 3.2 [30] and phyML v3.0 [31], respectively. For the BI tree, 10 million generations were simulated using two parallel Markov Chain Monte Carlo (MCMC) simulations, sampled every 1000 generations. The first 25% of the simulations were discarded (burn-in) to generate a consensus tree. For the ML tree, 1000 bootstrap replicates were conducted to evaluate the supporting values of each node.

3. Results and Discussion

3.1. Chloroplast Genome Organisation of the Acer sect. Platanoidea

The nucleotide sequences of the seven *Acer* sect. *Platanoidea* cp genomes ranged from 156,262 bp to 157,349 bp in length (Figure 1, Table 1), which are similar to other reported cp genomes of *Acer* [19,25]. The variation of chloroplast genome length is mainly caused by the change of LSC region length. The quadripartite structures of these cp genomes were identical to most angiosperms containing a LSC region, SSC region and two inverted repeat regions (IRa and IRb) [32]. The overall GC content of these cp genomes accounts for 37.9% and the GC content of IR regions accounts for 42.8% higher than the LSC (35.9%) and the SSC (32.3%). The new sequences possess 117 genes, including four unique rRNAs, 31 tRNAs, and 82 PCGs, respectively (Table 2). Among them, most cp genes were single copy, while 23 genes exhibited double copies, including four rRNA (*4.5S*, *5S*, *16S* and *23S* rRNA), nine tRNA (*trnA-UGC*, *trnI-CAU*, *trnI-GAU*, *trnL-CAA*, *trnM-CAU*, *trnN-GUU*, *trnR-ACG*, *trnT-GGU* and *trnV-GAC*) and 10 PCGs (*ndhB*, *rpl2*, *rps12*, *rpl23*, *rps19*, *rps7*, *ycf1*, *orf42*, *ycf2* and *ycf15*). Additionally, a total of 18 genes harboured introns, and three genes (*ycf3*, *clpP* and *rps12*) contained two introns.

Table 1. General features of the *Acer* sect. *Platanoidea* chloroplast genomes compared in this study.

Name	Total (bp)	LSC (bp)	SSC (bp)	IR (bp)	GC%
A. catalpifolium	157,349	85,745	18,066	26,769	37.9
A. miaotaiense	156,595	86,327	18,068	26,100	37.9
A. longipes	157,137	85,531	18,068	26,769	37.9
A. amplum	156,995	85,386	18,077	26,766	37.9
A. mono	156,985	85,378	18,069	26,769	37.9
A. yangjuechi	157,088	85,483	18,069	26,768	37.9
A. truncatum	156,262	86,019	18,073	26,085	37.9

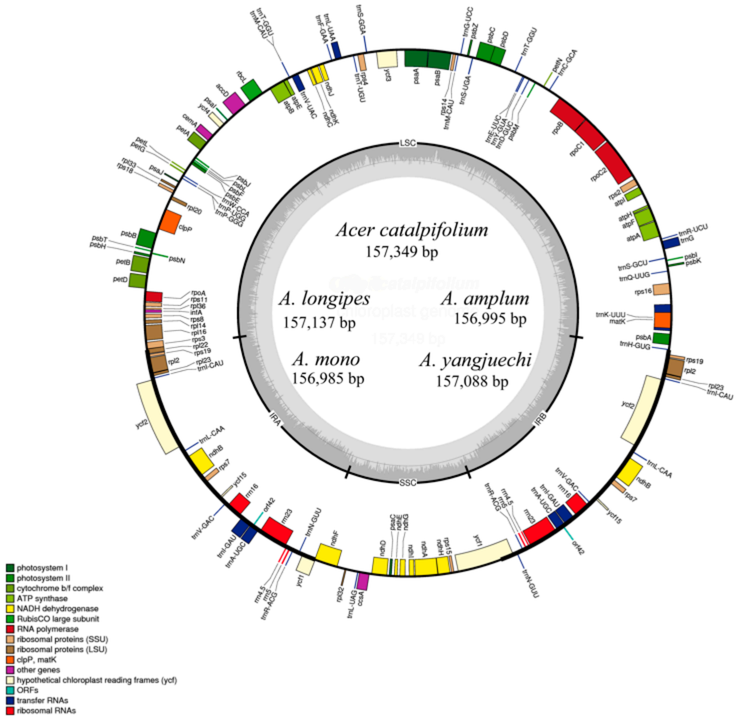

Figure 1. Merged gene map of the complete chloroplast genomes of five *Acer* sect. *Platanoidea* species. Genes belonging to different functional groups are colour-coded. The genes drawn inside the circle are transcribed clockwise, while those outside are transcribed counter-clockwise. Darker grey in the inner circle corresponds to the GC content of the chloroplast genome.

Table 2. Genes presented in the *Acer* sect. *Platanoidea* chloroplast genome.

	Group of Gene	Genes Name
1	Photostsyem I	*psaA, psaB, psaC, psaI, psaJ*
2	Photostsyem II	*psbA, psbB, psbC, psbD, psbE, psbF, psbh, psbI, psbJ, psbK, psbL, psbM, psbN, psbT, psbZ*
3	Cytochrome b/f complex	*petA, petB*, petD*, petG, petL, petN*
4	ATP synthase	*atpA, atpB, atpE, atpF*, atpH, atpI*
5	NADH dehydrogenase	*ndhA*, ndhB*, ndhC, ndhD, ndhE, ndhF, ndhG, ndhH, ndhI, ndhJ, ndhK*
6	RubisCO large subunit	*rbcL*
7	RNA polymerase	*ropA, ropB, ropC1*, ropC2*
8	Ribosomal proteins(SSU)	*rps2, rps3, rps4, rps7, rps8, rps11, rps12**, rps14, rps15, rps16*, rps18, rps19*
9	Ribosomal proteins (LSU)	*rpl2*, rpl14, rpl16*, rpl20, rpl22, rpl23*(×2)*, rpl32, rpl33, rpl36*
10	Other gene	*clpP **, matK, accD, ccsA, infA, cemA*
11	Proteins of unknown function	*ycf1, ycf2, ycf3**, ycf4, ycf15*
12	ORFs	*Orf42*
13	Transfer RNAs	31 tRNAs(six contain a single intron)
14	Ribosomal RNAs	rrn4.5, rrn5, rrn16, rrn23

Note: a single asterisk (*) following after gene names indicate intron-containing genes, and double asterisks (**) following after gene names indicate two introns in the gene.

3.2. Comparative Analysis of the Genomic Structure

Contraction and expansion of the IRs, LSC and SSC are important to the evolution of cp genomes [33,34], which is the leading cause of gene order and the size changes of the cp genome [35]. Detailed structure comparisons among the 13 cp genomes of the *Acer* species were presented in Figure 2. *rpl22* in the LSC/IR boundary and *rps19* was the last gene in most *Acer* sect. *Platanoidea* cp genomes included *A. mono*, *A. amplum*, *A. catalpifolium*, *A. yangjuechi*, *A. longipes*, *A. morrisonense*, *A. davidii* and *A. griseum*. However, the different structures of *rps19* in the LSC/IR boundary and the last gene *rpl2* were found in *A. truncatum*, *A. miaotaiense* and *A. buergerianum*. Among the Arecoideae species, *rpl22* and *rps19* gene order changes in the IRA/LSC borders were also observed and has become the most varied rearrangement in this section [36]. Similarly, the rearrangement has been reported in the Apiales species, which also has two structure types of *rpl23* and *rps19* in the LSC/IR boundary [37]. Length variations of the *Acer* cp genomes were found by contraction and expansion of the LSC and IRs, the length of the LSC varies from 85,379 bp to 86,327 bp, and the length of the IR varies from 26,085 bp to 26,769 bp (Figure 2). Moreover, the type of unique structural borders of the cp genome (*A. truncatum*, *A. miaotaiense*, and *A. buergerianum*) also show a contraction of IRs, which indicates variations in boundary genes may be caused by variations in length.

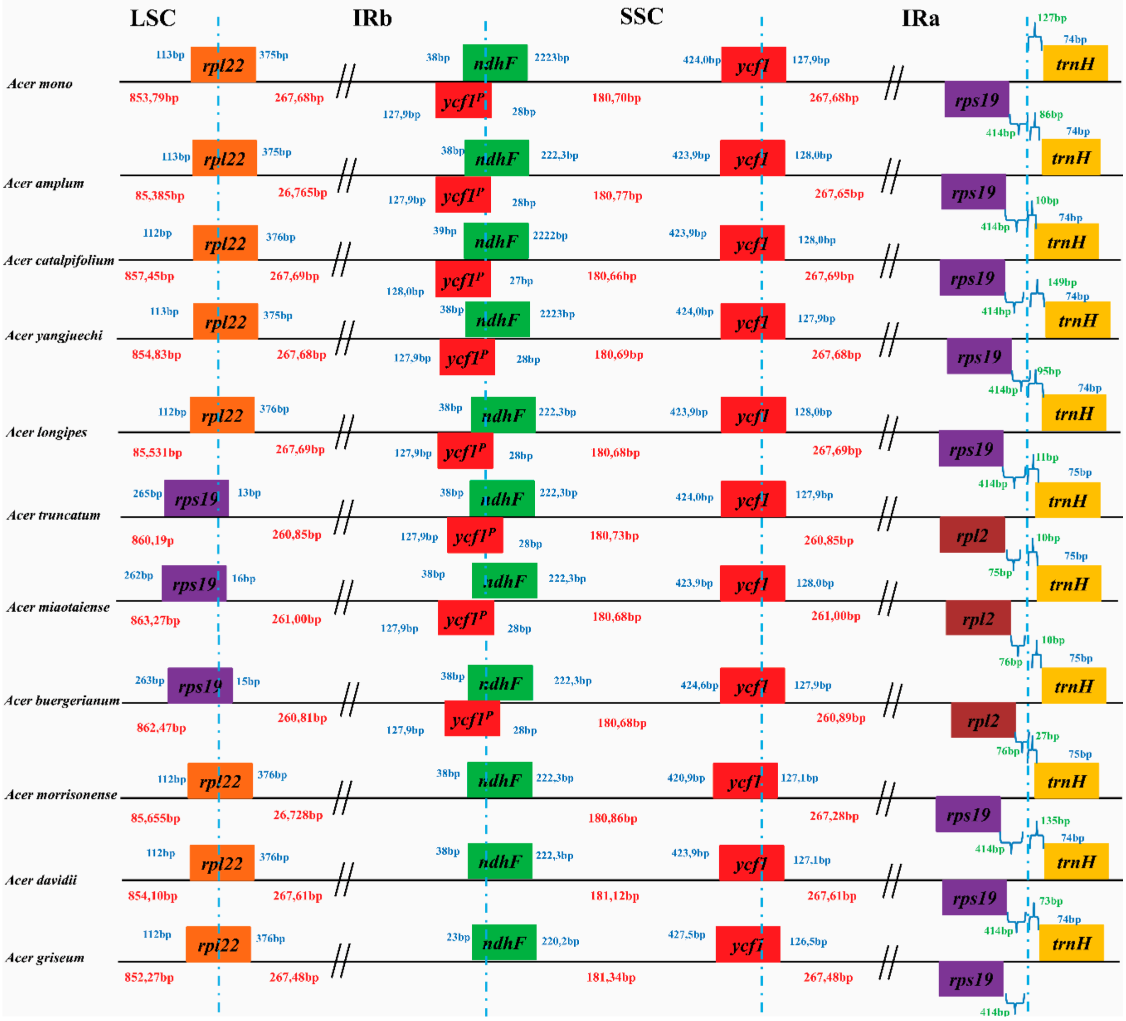

Figure 2. Comparison of the junction sites of the LSC, IRs and SSC regions among 13 Acer sect. Platanoidea species chloroplast genomes. Different colour boxes indicate specific genes and those above the genome lines indicate their transcriptions in a forward direction, while the under-line boxes are in the reverse direction. The length of the LSC, SSC, and IR regions is shown in red, the length of the gene distance from the boundary is shown in green, the length of the gene is shown in blue, and the P represents the pseudogene.

3.3. Divergence Hotspot of the Acer sect. Platanoidea Species

Sliding window analysis of the whole cp genome was performed to identify hotspots of the *Acer* sect. *Platanoidea* species. In Figure 3, it is apparent that the *trnH-psbA*, *psbN-trnD*, *psaA-ycf3*, *petA-psbJ* and *ndhA* intron nucleotide variability was higher than other regions. Most divergent hotspot loci are located in the LSC region, which allows for the proper design of the genetic markers. Only one hotspot *ndhA* intron was located in the SSC region. The IR regions were much more conserved. This result was similar to other cp genomes [37,38]. The general barcode *trnH-psbA* has demonstrated extreme variation in plant groups [39,40]. Thus, the highest variation *trnH-psbA* has the potential to be used in DNA barcoding in the *Acer* sect. *Platanoidea*. Additionally, the evolutionary history of *A. mono* has been inferred by using *psbA-trnH*, *trnL-trnF* and an intron of *rpl16* [16]. The regions of the *psaA-ycf3*, *petA-psbJ* and *ndhA* intron have been indicated as high variations in previous studies. In witch-hazel (genus *Hamamelis* L., Hamamelidaceae), appropriate variations of *psaA-ycf3* were used to reconstruct phylogenetic relationships [41]. In *Scutellaria*, *petA-psbJ* was one of six fast-evolving DNA sequences in the cp genome [42], while a systematic study shows that Muhlenbergiinae has high variation at the *ndhA* intron [43].

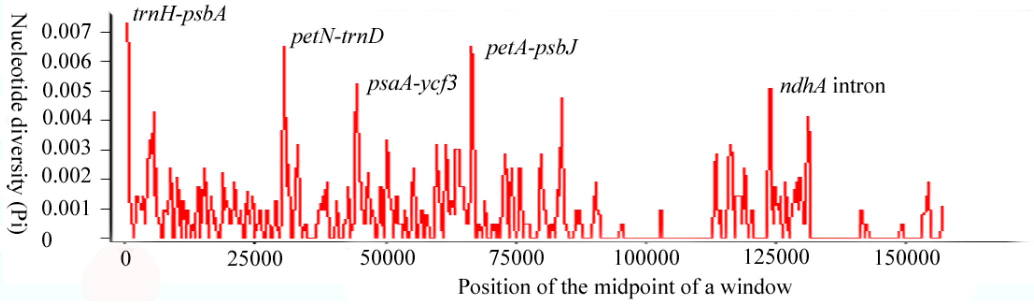

Figure 3. Sliding-window analysis on the cp genomes for seven *Acer* sect. *Platanoidea* species.

The endangered plants, *A. catalpifolium*, *A. yangjuechi* and *A. miaotaiense* in the *Acer* sect. *Platanoidea*, have small population sizes [44]. Population genetics studies of these species are relatively weak, and with limited conservation goals [45,46]. These high variability regions can provide alternative sites for subsequent studies and will contribute to the conservation of endangered plants.

3.4. Phylogenetic Analysis

The phylogenomic inference based on cp genomes shows high bootstrap supports in most nodes that provided robust evolutionary placement and relationship of the *Acer* species (Figure 4). The results showed that seven sampled species of the *Acer* sect. *Platanoidea* formed a single clade, which is consistent with previous studies of the *Acer* phylogeny [14,47]. In this clade, *A. catalpifolium*, *A. mono*, *A. miaotaiense and A. yangjuechi* had the closest phylogenetic relationship and formed a subclade, while *A. truncatum*, *A. longipes*, *A. amplum* formed another one. Previous phylogenetic inference of the *Acer* did not contain species with a small population size in the sect. *Platanoidea* (such as *A. catalpifolium* and *A. yangjuechi*) [14,47]. Phylogenetic analysis exhibited in this study for the issue of *A. longipes A. amplum* complex in the sect. Platanoidea raised earlier [17], and the phylogenetic position of *A. catalpifolium* was also redefined.

It is somewhat surprising that *A. mono* is not a sister with *A. truncatum* but with *A. yangjuechi*, which differs from some published studies [13]. Since *A. mono* is widespread in Asia and comprised of multiple local varieties, we cannot rule out that the possibility of the grouping of *A. mono* and *A. yangjuechi* due to adjacent sampling localities of *A. mono* and *A. yangjuechi* in Lin'an, Zhejiang province of China, the only extant habitat of *A. yangjuechi* [48]. Liu et al. [49] showed that the population composition of the Lin'an population is significantly different from the neighbouring populations of *A. mono*. The clustering of *A. mono* and *A. yangjuechi* inferred in this study may not only reflect the truth of geographic divergence in the genetics of *A. mono* but also implies the chloroplast capture by ancient hybridisation events between the two species in Lin'an.

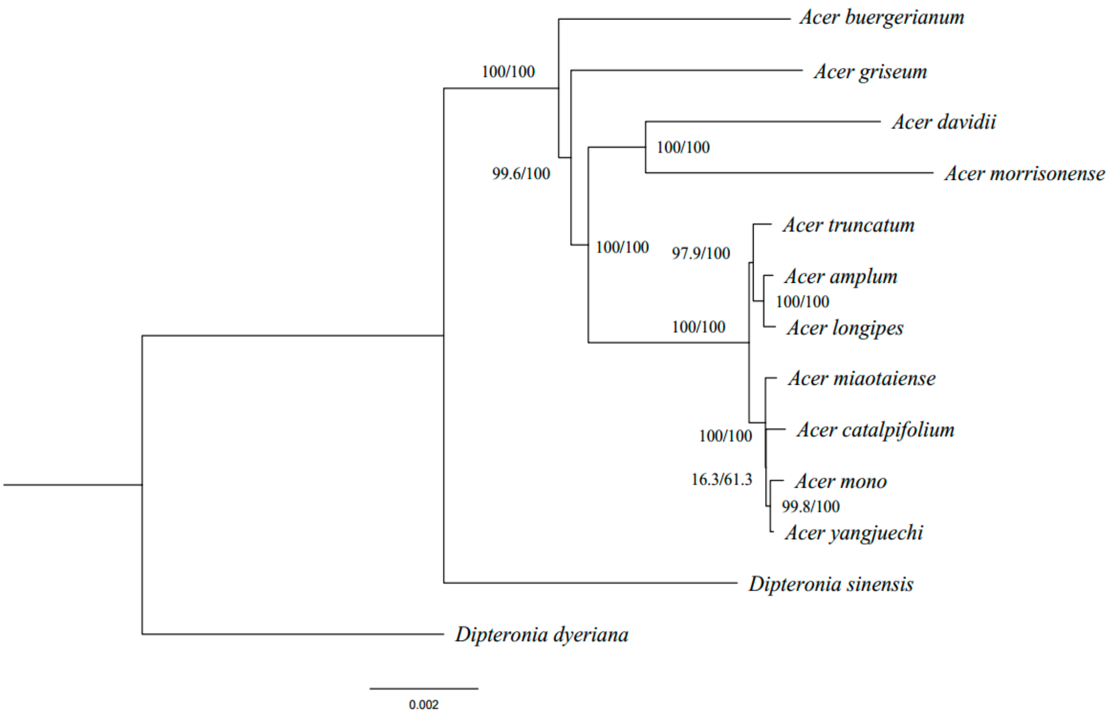

Figure 4. Phylogenetic tree of 13 *Acer* species inferred by Maximum Likelihood (ML) and Bayesian Inference (BI) methods, based on the whole cp genome sequences. The numbers above the branches are the bootstrap values of ML methods and the posterior probabilities of BI.

4. Conclusions

In this study, we firstly reported complete cp genomes of five *Acer* sect. *Platanoidea* species (*A. catalpifolium*, *A. amplum*, *A. longipes*, *A. yanjuechi* and *A. mono*) using the NGS technology. In comparison with other published *Acer* species from NCBI, we found that the *Acer* species have similar cp genome structure and gene content. The divergence hotspots identified in the cp genome of the *Acer* sect. *Platanoidea* could be applied to develop molecular markers for further population genetics studies. The high variation at the IR/LSC and IR/SSC boundaries were also reported. The phylogenetic analysis strongly supported that *A. catalpifolium* has the closest relationship with *A. miaotaiense*, followed by *A. mono*, and *A. yanjuechi*, which confirms the species-complex relationship of *A. longipes* and *A. amplum*. The available genomic data presented in this paper provides a basis for further research on the evolutionary history and conservation genetics of endangered species of genus *Acer*.

Supplementary Materials: The following are available online at http://www.mdpi.com/1999-4907/11/4/462/s1, Table S1: General features of the *Acer* sect. *Platanoidea* chloroplast genomes compared in this study. Table S2: Acer taxa sampled in this study.

Author Contributions: T.Y. and J.G. conceived and designed the work; J.G. and Y.-Y.Z. collected samples; T.Y., J.G. and B.-H.H. performed the experiments and analysed the data; T.Y. and J.G. wrote the manuscript; P.-C.L., W.-B.M., B.D. and J.-Q.L. critically reviewed the manuscript. All authors have read and agreed to the published version of the manuscript.

Funding: This research was financially supported by the program "Reintroduction Technologies and Demonstration of Extremely Rare Wild Plant Population" of National Key Research and Development Program (2016YFC0503106) to J.Q.L., the Ministry of Science and Technology of Taiwan (grant number: 108-2628-B-003-001) and National Taiwan Normal University (NTNU) to P.C.L. and "The biogeographical feature and competitive hybridization of Maple (*Acer* L.) in East Asia" of National Natural Science Foundation of China (41901063) to J.G.

Conflicts of Interest: The authors declare no conflict of interest.

References

1. Neuhaus, H.E.; Emes, M.J. Nonphotosynthetic metabolism in plastids. *Annu. Rev. Plant Biol.* **2000**, *51*, 111–140. [CrossRef] [PubMed]
2. Armbrust, E.V. Uniparental inheritance of chloroplast genomes. *Adv. Photosynth. Respir.* **1998**, *7*, 93–113.
3. Choi, K.S.; Chung, M.G.; Park, S.J. The complete chloroplast genome sequences of three veroniceae species (plantaginaceae): Comparative analysis and highly divergent regions. *Front. Plant Sci.* **2016**, *7*. [CrossRef] [PubMed]
4. Yu, T.; Lv, J.; Li, J.; Du, F.K.; Yin, K. The complete chloroplast genome of the dove tree Davidia involucrata (Nyssaceae), a relict species endemic to China. *Conserv. Genet. Resour.* **2016**, *8*, 1–4. [CrossRef]
5. Sonah, H.; Deshmukh, R.K.; Singh, V.P.; Gupta, D.K.; Singh, N.K.; Sharma, T.R. Genomic resources in horticultural crops: Status, utility and challenges. *Biotechnol. Adv.* **2011**, *29*, 199–209. [CrossRef]
6. Xiong, J.S.; Ding, J.; Li, Y. Genome-editing technologies and their potential application in horticultural crop breeding. *Hortic. Res.* **2015**, *2*. [CrossRef]
7. Cai, J.; Ma, P.F.; Li, H.T.; Li, D.Z. Complete plastid genome sequencing of fourtiliaspecies (malvaceae): A comparative analysis and phylogenetic implications. *PLoS ONE* **2015**, *10*. [CrossRef]
8. Ruhsam, M.; Rai, H.S.; Mathews, S.; Ross, T.G.; Graham, S.W.; Raubeson, L.A.; Mei, W.; Thomas, P.I.; Gardner, M.F.; Ennos, R.A.; et al. Does complete plastid genome sequencing improve species discrimination and phylogenetic resolution in Araucaria? *Mol. Ecol. Resour.* **2015**, *15*, 1067–1078. [CrossRef]
9. Yi, X.; Gao, L.; Wang, B.; Su, Y.J.; Wang, T. The complete chloroplast genome sequence of Cephalotaxus oliveri (Cephalotaxaceae): Evolutionary comparison of cephalotaxus chloroplast DNAs and insights into the loss of inverted repeat copies in gymnosperms. *Genome Biol. Evol.* **2013**, *5*, 688–698. [CrossRef]
10. Wambugu, P.W.; Brozynska, M.; Furtado, A.; Waters, D.L.; Henry, R.J. Relationships of wild and domesticated rices (Oryza AA genome species) based upon whole chloroplast genome sequences. *Sci. Rep.* **2015**, *5*. [CrossRef]
11. Brozynska, M.; Furtado, A.; Henry, R.J. Genomics of crop wild relatives: Expanding the gene pool for crop improvement. *Plant Biotechnol. J.* **2016**, *14*, 1070–1085. [CrossRef] [PubMed]
12. Xu, T.Z.; Chen, Y.S.; de Jong, P.C.; Oterdoom, H.J. Aceraceae. In *Flora of China*; Wu, Z.Y., Raven, P.H., Hong, D.Y., Eds.; Science press: Beijing, China, 2008; Volume 11, pp. 515–553.
13. Van Gelderen, D.M.; De Jong, P.C.; Oterdoom, H.J. *Maples of the World*; Timber Press: Portland, OR, USA, 1994; ISBN 0881920002.
14. Renner, S.S.; Grimm, G.W.; Schneeweiss, G.M.; Stuessy, T.F.; Ricklefs, R.E. Rooting and dating maples (Acer) with an uncorrelated-rates molecular clock: Implications for north American/Asian disjunctions. *Syst. Biol.* **2008**, *57*, 795–808. [CrossRef] [PubMed]
15. Rosado, A.; Vera-Vélez, R.; Cota-Sánchez, J.H. Floral morphology and reproductive biology in selected maple (Acer, L.) species (Sapindaceae). *Braz. J. Bot.* **2018**, *41*, 1–14. [CrossRef]
16. Guo, X.; Wang, H.; Bao, L.; Wang, T.; Bai, W.; Ye, J.; Ge, J. Evolutionary history of a widespread tree species Acer mono in East Asia. *Ecol. Evol.* **2014**, *4*, 4332–4345. [PubMed]
17. Grimm, G.W.; Denk, T. The Colchic region as refuge for relict tree lineages: Cryptic speciation in field maples. *Turk. J. Bot.* **2014**, *38*, 1050–1066. [CrossRef]
18. Kumar, S.; Hahn, F.M.; McMahan, C.M.; Cornish, K.; Whalen, M.C. Comparative analysis of the complete sequence of the plastid genome of Parthenium argentatum and identification of DNA barcodes to differentiate Parthenium species and lines. *BMC Plant Biol.* **2009**, *9*, 131. [CrossRef]
19. Zhang, Y.; Li, B.; Chen, H.; Wang, Y. Characterization of the complete chloroplast genome of Acer miaotaiense (Sapindales: Aceraceae), a rare and vulnerable tree species endemic to China. *Conserv. Genet. Resour.* **2016**, *8*, 1–3. [CrossRef]
20. Wang, R.; Fan, J.; Chang, P.; Zhu, L.; Zhao, M.; Li, L. Genome survey sequencing of acer truncatum bunge to identify genomic information, simple sequence repeat (ssr) markers and complete chloroplast genome. *Forests* **2019**, *10*, 87. [CrossRef]
21. Doyle, J.J. A rapid DNA isolation procedure for small amounts of fresh leaf tissue. *Phytochem. Bull.* **1987**, *19*, 11–15.

22. Dai, M.; Thompson, R.C.; Maher, C.; Contrerasgalindo, R.; Kaplan, M.H.; Markovitz, D.M.; Omenn, G.; Meng, F. NGSQC: Cross-platform quality analysis pipeline for deep sequencing data. *BMC Genom.* **2010**, *11*. [CrossRef]
23. Hahn, C.; Bachmann, L.; Chevreux, B. Reconstructing mitochondrial genomes directly from genomic next-generation sequencing reads–A baiting and iterative mapping approach. *Nucleic Acids Res.* **2013**, *41*, e129. [CrossRef] [PubMed]
24. Jia, Y.; Yang, J.; He, Y.L.; He, Y.; Niu, C.; Gong, L.L.; Li, Z.H. Characterization of the whole chloroplast genome sequence of Acer davidii Franch (Aceraceae). *Conserv. Genet. Resour.* **2016**, *8*, 1–3. [CrossRef]
25. Li, Z.-H.; Xie, Y.-S.; Zhou, T.; Jia, Y.; He, Y.-L.; Yang, J. The complete chloroplast genome sequence of Acer morrisonense (Aceraceae). *Mitochondrial DNA Part A* **2015**, *28*, 309–310. [CrossRef] [PubMed]
26. Wyman, S.K.; Jansen, R.K.; Boore, J.L. Automatic annotation of organellar genomes with DOGMA. *Bioinformatics* **2004**, *20*, 3252–3255. [CrossRef]
27. Katoh, K.; Kuma, K.; Toh, H.; Miyata, T. MAFFT version 5: Improvement in accuracy of multiple sequence alignment. *Nucleic Acids Res.* **2005**, *33*, 511–518. [CrossRef]
28. Librado, P.; Rozas, J. DnaSP v5: A software for comprehensive analysis of DNA polymorphism data. *Bioinformatics* **2009**, *25*, 1451–1452. [CrossRef]
29. Posada, D.; Buckley, T.R. Model selection and model averaging in phylogenetics: Advantages of akaike information criterion and bayesian approaches over likelihood ratio tests. *Syst. Biol.* **2004**, *53*, 793–808. [CrossRef]
30. Huelsenbeck, J.P.; Ronquist, F. MRBAYES: Bayesian inference of phylogenetic trees. *Bioinformatics* **2001**, *17*, 754–755. [CrossRef]
31. Guindon, S.; Lethiec, F.; Duroux, P.; Gascuel, O. PHYML Online–A web server for fast maximum likelihood-based phylogenetic inference. *Nucleic Acids Res.* **2005**, *33*, 557–559. [CrossRef]
32. Daniell, H.; Lin, C.-S.; Yu, M.; Chang, W.-J. Chloroplast genomes: Diversity, evolution, and applications in genetic engineering. *Genome Biol.* **2016**, *17*, 134. [CrossRef]
33. Guo, H.; Liul, J.; Luo, L.; Wei, X.; Zhang, J.; Qi, Y.; Zhang, B.; Liu, H.; Xiao, P. Complete chloroplast genome sequences of Schisandra chinensis: Genome structure, comparative analysis, and phylogenetic relationship of basal angiosperms. *Sci. China Life Sci.* **2017**, *60*, 1286–1290. [CrossRef] [PubMed]
34. Curci, P.L.; Paola, D.D.; Danzi, D.; Vendramin, G.G.; Sonnante, G. Complete chloroplast genome of the multifunctional crop globe artichoke and comparison with other asteraceae. *PLoS ONE* **2015**, *10*. [CrossRef] [PubMed]
35. Qian, J.; Song, J.; Gao, H.; Zhu, Y.; Xu, J.; Pang, X.; Yao, H. The complete chloroplast genome sequence of the medicinal plant salvia miltiorrhiza. *PLoS ONE* **2013**, *8*. [CrossRef] [PubMed]
36. Xie, D.-F.; Yu, Y.; Deng, Y.-Q.; Li, J.; Liu, H.-Y.; Zhou, S.-D.; He, X.-J. Comparative analysis of the chloroplast genomes of the Chinese endemic genus Urophysa and their contribution to chloroplast phylogeny and adaptive evolution. *Int. J. Mol. Sci.* **2018**, *19*, 1847. [CrossRef]
37. He, L.; Qian, J.; Li, X.; Sun, Z.; Xu, X.; Chen, S. Complete chloroplast genome of medicinal plant Lonicera japonica: Genome rearrangement, intron gain and loss, and implications for phylogenetic studies. *Molecules* **2017**, *22*, 249. [CrossRef]
38. Han, Y.W.; Duan, D.; Ma, X.F.; Jia, Y.; Liu, Z.L.; Zhao, G.F.; Li, Z.H. Efficient identification of the forest tree species in aceraceae using DNA barcodes. *Front. Plant Sci.* **2016**, *7*. [CrossRef]
39. Kress, W.J.; Erickson, D.L. A two-locus global DNA barcode for land plants: The coding rbcL gene complements the non-coding trnH-psbA spacer region. *PLoS ONE* **2007**, *2*. [CrossRef]
40. Pang, X.; Chang, L.; Shi, L.; Rui, L.; Dong, L.; Li, H.; Cherny, S.S.; Chen, S. Utility of the trnh–Psba intergenic spacer region and its combinations as plant dna barcodes: a meta-analysis. *PLoS ONE* **2012**, *7*. [CrossRef]
41. Lahaye, R.R.Y.; Savolainen, V.; Duthoit, S.; Maurin, O.; Bank, M. A test of psbK-psbI and atpF-atpH as potential plant DNA barcodes using the flora of the Kruger National Park (South Africa) as a model system. *Nat. Preced.* **2008**. [CrossRef]
42. Timme, R.E.; Kuehl, J.V.; Boore, J.L.; Jansen, R.K. A comparative analysis of the Lactuca and Helianthus (Asteraceae) plastid genomes: Identification of divergent regions and categorization of shared repeats. *Am. J. Bot.* **2007**, *94*, 302–312. [CrossRef]

43. Falchi, A.; Paolini, J.; Desjobert, J.M.; Melis, A.; Costa, J.; Varesi, L. Phylogeography of Cistus creticus L. on Corsica and Sardinia inferred by the TRNL-F and RPL32-TRNL sequences of cpDNA. *Mol. Phylogenetics Evol.* **2009**, *52*, 538–543. [CrossRef] [PubMed]
44. Baillie, J.E.M.; Hilton, C.; Stuart, S.N. *IUCN Red List of Threatened Species: A Global Species Assessment*; IUCN-The World Conservation Union: Grand, Switzerland, 2004.
45. Zhang, Y.; Yu, T.; Ma, W.; Tian, C.; Sha, Z.; Li, J. Morphological and physiological response of Acer catalpifolium Rehd. Seedlings to water and light stresses. *Glob. Ecol. Conserv.* **2019**, *19*, 10. [CrossRef]
46. Zhao, J.; Yao, X.; Xi, L.; Yang, J.; Chen, H.; Zhang, J. Characterization of the chloroplast genome sequence of acer miaotaiense: comparative and phylogenetic analyses. *Molecules* **2018**, *23*, 1740. [CrossRef] [PubMed]
47. Li, J.H.; Yue, J.P.; Shoup, S. Phylogenetics of Acer (Aceroideae, Sapindaceae) based on nucleotide sequences of two chloroplast non-coding regions. *Harv. Pap. Bot.* **2006**, *11*, 101–115. [CrossRef]
48. Li, Q.; Liu, X.; Su, J.; Cong, Y. Extraction of genomic DNA from Acer yangjuechi and system optimization of SRAP-PCR. *Jiangsu J. Agric. Sci.* **2009**, *25*, 538–541.
49. Liu, C.; Tsuda, Y.; Shen, H.; Hu, L.; Saito, Y.; Ide, Y. Genetic structure and hierarchical population divergence history of Acer mono var. mono in South and Northeast China. *PLoS ONE* **2014**, *9*. [CrossRef]