

Complete chloroplast genome of *Prunus pensylvanica* and its implications for the phylogenetic position within *Prunus sensu lato* (Rosaceae)

Li-Qiu Zhang^a, Peng-He Cao^b, Zhong-Shuai Sun^c and Jun-Lin Yu^a

^aSchool of Medicine and Pharmacy, Tonghua Normal University, Tonghua, China; ^bDepartment of Bioengineering, Enshi Polytechnic, Enshi, China; ^cZhejiang Provincial Key Laboratory of Plant Evolutionary Ecology and Conservation, Taizhou University, Taizhou, China

ABSTRACT

Prunus pensylvanica is one of the two native cherry species of North America. We determined the first complete chloroplast genome of *P. pensylvanica* using genome-skimming approach. The cp genome was 157,953 bp long, with a large single-copy region (LSC) of 86,030 bp and a small single-copy region (SSC) of 19,135 bp separated by a pair of inverted repeats (IRs) of 26,394 bp. It encodes 129 genes, including 84 protein-coding genes, 37 tRNA genes, and 8 ribosomal RNA genes. We also reconstructed the phylogeny of *Prunus sensu lato* using maximum likelihood (ML) method, including our data and previously reported cp genomes of related taxa. The phylogenetic analysis indicated that *P. pensylvanica* is closely related to *P. emarginata*.

ARTICLE HISTORY

Received 14 September 2019
Accepted 25 September 2019

KEYWORDS

Prunus pensylvanica; *Prunus sensu lato*; chloroplast genome; phylogenomics

The classification of the *Prunus sensu lato* (Rosaceae) has long been problematic. Phylogenetic studies using a limited set of markers have often not been able to fully resolve relationships within this genus, indicating that a higher number of molecular characters are required for an improved understanding of relationships within this group (Shi et al. 2013; Chin et al. 2014). By taking advantages of next-generation sequencing technologies that efficiently provide the chloroplast (cp) genomic resources of our interested species, we can rapidly access the abundant genetic information for phylogenetic research and conservation genetics (Li et al. 2017; Liu et al. 2017, 2018). Pin cherry (*Prunus pensylvanica* L.) is one of the two native cherry species of North America (Rohrer 2014). It occurs in many forest types across the northern United States and Canada (Ristau and Horsley 2006, Rohrer 2014). Therefore, we sequenced the whole chloroplast genome of *P. pensylvanica* to elucidate its phylogenetic relationship within *Prunus sensu lato*.

Total genomic DNA was extracted from silica-dried leaves collected from Gill State Forest (west of North Carolina, USA) using a modified CTAB method (Doyle and Doyle 1987). The voucher specimen (LP1007186) was collected and deposited in the Herbarium of Zhejiang University (HZU). DNA libraries preparation and pair-end 125 bp read length sequencing were performed on the Illumina HiSeq 2500 platform. About 5.73 Gb of raw data were trimmed and assembled into contigs using CLC Genomics Workbench 8. All the contigs were then mapped to the

reference cp genome of *Prunus speciosa* (Koidz.) Nakai (MH998233; Sun et al. 2019) using BLAST (NCBI BLAST v2.2.31) search and the draft cp genome of *P. pensylvanica* was constructed by connecting overlapping terminal sequences in Geneious R11 software (Biomatters Ltd., Auckland, New Zealand). Gene annotation was performed via the online programme Dual Organellar Genome Annotator (DOGMA; Wyman et al. 2004).

The complete cp genome of *P. pensylvanica* (GenBank accession MN427872) was 157,953 bp long consisting of a pair of inverted repeat regions (IRs with 26,394 bp) divided by two single-copy regions (LSC with 86,030 bp; SSC with 19,135 bp). The overall GC contents of the total length, LSC, SSC, and IR regions were 36.7%, 34.6%, 30.2%, and 42.5%, respectively. The genome contained a total of 129 genes, including 84 protein-coding genes, 37 tRNA genes, and 8 rRNA genes.

To determine the phylogenetic position of newly sequenced *P. pensylvanica*, phylogenetic analysis was conducted along with 20 representative *Prunus sensu lato* species and two outgroup taxa. We reconstructed a phylogeny employing the GTR + G model and 1000 bootstrap replicates under the maximum-likelihood (ML) inference in RAxML-HPC v.8.2.10 on the CIPRES cluster (Miller et al. 2010). The ML tree (Figure 1) was consistent with the most recent phylogenetic study on *Prunus sensu lato* (Shi et al. 2013; Chin et al. 2014). *Prunus pensylvanica* exhibited the closest relationship with *P. emarginata* (Douglas) Eaton.

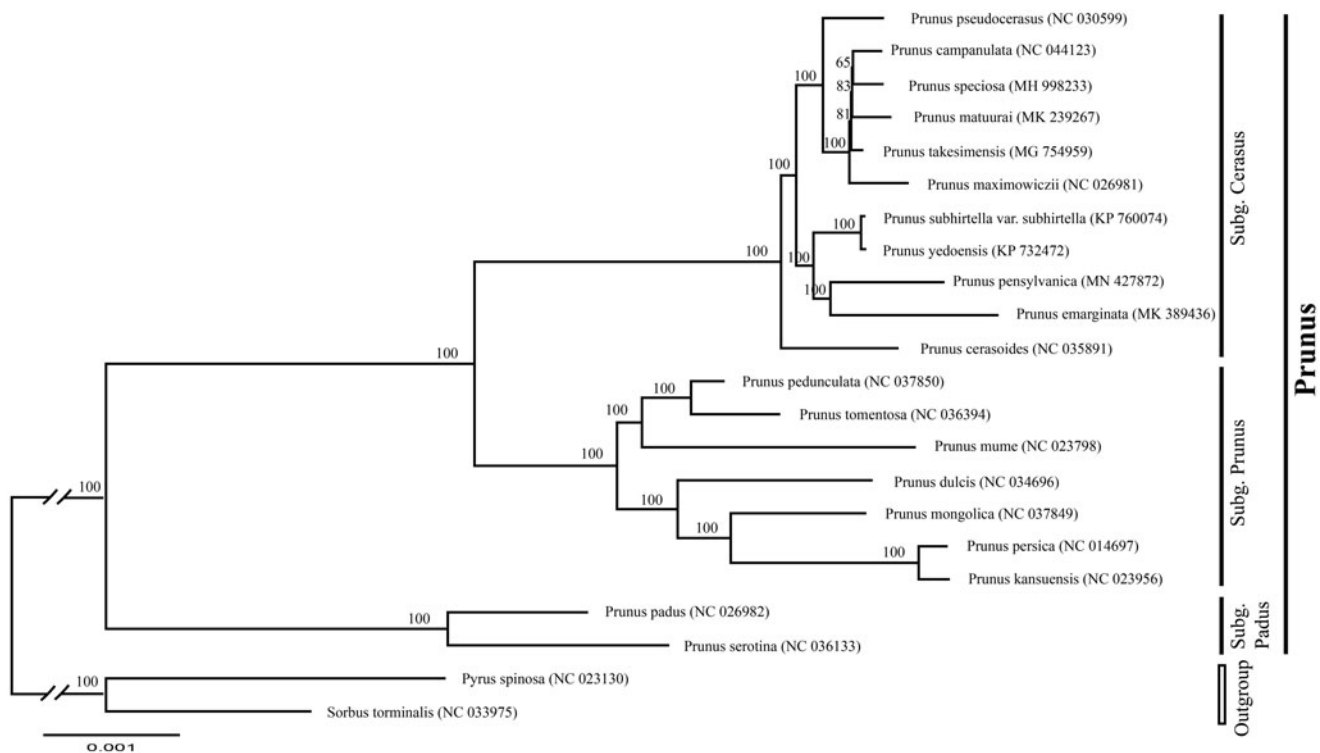


Figure 1. Phylogenetic tree reconstruction of 20 taxa of *Prunus* and two outgroups using ML method. Relative branch lengths are indicated. Numbers near the nodes represent ML bootstrap value. The scientific names of some species are debated.

Disclosure statement

The authors are grateful to the opened raw genome data from public database. The authors report no conflicts of interest and are responsible for the content and writing of the paper.

References

- Chin SW, Shaw J, Haberle R, Wen J, Potter D. 2014. Diversification of almonds, peaches, plums and cherries – molecular systematics and biogeographic history of *Prunus* (Rosaceae). *Molec Phylogen Evol.* 76:34–48.
- Doyle JJ, Doyle JL. 1987. A rapid DNA isolation procedure for small quantities of fresh leaf tissue. *Phytochem Bull.* 19:11–15.
- Li P, Lu RS, Xu WQ, Ohi-Toma T, Cai MQ, Qiu YX, Cameron KM, Fu CX. 2017. Comparative genomics and phylogenomics of East Asian Tulips (*Amana*, Liliaceae). *Front Plant Sci.* 8:451.
- Liu LX, Li R, Worth JRP, Li X, Li P, Cameron KM, Fu CX. 2017. The complete chloroplast genome of Chinese bayberry (*Morella rubra*, Myricaceae): implications for understanding the evolution of Fagales. *Front Plant Sci.* 8:968.
- Liu LX, Li P, Zhang HW, Worth J. 2018. Whole chloroplast genome sequences of the Japanese hemlocks, *Tsuga diversifolia* and *T.sieboldii*, and development of chloroplast microsatellite markers applicable to East Asian *Tsuga*. *J Forest Res.* 23(5):318–323.
- Miller MA, Pfeiffer W, Schwartz T. 2010. Creating the CIPRES Science Gateway for inference of large phylogenetic trees. *Gateway Comput Environ Workshop.* 14:1–8.
- Ristau TE, Horsley SB. 2006. When is pin cherry (*Prunus pensylvanica* L.) a problem in Allegheny Hardwoods? *Northern J Appl Forest.* 23(3): 204–210.
- Rohrer JR. 2014. *Prunus* (Rosaceae). In: *Flora of North America* Editorial Committee, editors. *Flora of North America North of Mexico*. Oxford University Press, New York; p. 352–383, Vol.9.
- Shi S, Li J, Sun J, Yu J, Zhou S. 2013. Phylogeny and classification of *Prunus sensu lato* (Rosaceae). *J Integr Plant Biol.* 55(11):1069–1079.
- Sun ZS, Katsuki T, Liu XH. 2019. Complete chloroplast genome of the wild Oshima Cherry (*Prunus speciosa*, Rosaceae) in Izu islands, Japan. *Mitochondrial DNA Part B.* 4(1):509–510.
- Wyman SK, Jansen RK, Boore JL. 2004. Automatic annotation of organellar genomes with DOGMA. *Bioinformatics.* 20(17):3252–3255.