

The complete chloroplast genome sequence of a narrow alpine endemic, *Taraxacum hallaisanense* (Asteraceae), on Jeju Island, Korea

Woong Lee^a, Young-Soo Kim^{a,b}, Seung-Chul Kim^c and Jae-Hong Pak^{a,b}

^aResearch Institute for Dok-do and Ulleung-do Island, Kyungpook National University, Daegu, Republic of Korea; ^bDepartment of Biology, School of Life Sciences, Kyungpook National University, Daegu, Republic of Korea; ^cDepartment of Biological Sciences, Sungkyunkwan University, Suwon, Republic of Korea

ABSTRACT

The first complete chloroplast genome sequence of Jeju Island endemic diploid dandelion, *Taraxacum hallaisanense*, is reported in this study. The plastome size is 151,554 bp in total length, with one large single copy (LSC; 84,066 bp), one small single copy (SSC; 18,524 bp), and two inverted repeat (IR) regions (IR_a and IR_b, each with 24,482 bp). The overall GC content is 37.7% and the genome contained 129 genes, including 84 protein-coding with 2 pseudogenes (*ycf1* and *accD*), 37 transfer RNA, and 8 ribosomal RNA genes. Phylogenetic analysis of 19 representative plastomes of the Asteraceae suggests that *Taraxacum* is monophyletic with strong bootstrap support and also that *T. hallaisanense* is closely related to *T. mongolicum*.

ARTICLE HISTORY

Received 1 November 2020
Accepted 24 February 2021

KEYWORDS

Chloroplast genome; alpine endemic; *Taraxacum hallaisanense*; Jeju Island

The genus *Taraxacum* (Cichorieae, Asteraceae) includes approximately 2500 species, distributing mainly in the northern hemisphere with main diversity in mountains of Eurasia (Richards 1973; Ge et al. 2007). A few species also occur in the temperate regions of the southern hemisphere (Ge et al. 2007). *Taraxacum* represents an example of evolutionary and taxonomic complexity due to agamosperous reproduction, complex multiple hybridity, and frequent polyploidy (Asker and Jerling 1992; Kirschner et al. 2003, 2015; Závěská Drábková et al. 2009). In East Asia, approximately 50 species in two sections (*Mongolica* and *Ceratophora*) can be found with one center of diversity in Japan (22 species) (Kitamura 1957; Morita 1980). Six species of *Taraxacum* occur in the Korean Peninsula: native *T. coreanum* and introduced *T. officinale* distribute widely throughout all provinces, while two natives *T. ohwianum* and *T. platycedum* rather narrowly occur in central and northeastern parts of the Korean Peninsula. *Taraxacum hallaisanense* is very narrowly restricted to Jeju Island, whereas *T. mongolicum* occurs disjunctly in North and South Korea. While a baseline phylogenetic framework of *Taraxacum* was hypothesized based on the internal transcribed spacer of nuclear ribosomal DNA (nrDNA ITS) and chloroplast DNA sequences (Kirschner et al. 2003, 2015), we know very little about overall phylogenetic relationships among species in East Asia. With regard to complete plastid genome sequences of *Taraxacum* in Korea, two traditional medicinal herbs, *T. platycarpum* and *T. mongolicum*, were reported (Kim et al. 2016). However, little is known for

complete plastid genome sequences of congeneric species in Korea, such as *T. coreanum*, *T. ohwianum*, *T. platycedum*, etc. Therefore, the aim of this study is to characterize the plastid genome of *T. hallaisanense*, which is endemic to Jeju Island, Korea, and determine its phylogenetic position among congeneric species.

Total DNA (Voucher specimen: 33°21'31"N, 126°30'11"E; 1600 m elevation) was isolated using the DNeasy plant Mini Kit (Qiagen, Carlsbad, CA) and sequenced by the Illumina platform (Macrogen, Seoul, Korea). The specimen was deposited at Kyungpook National University Herbarium (KNU; <http://bio.knu.ac.kr/PhD/profile/lst.do?seq=6>, Jae-Hong Pak, jhpak@knu.ac.kr) under the voucher specimen of 'Lee180531-001'. A total of 30,937,892 paired-end reads were obtained and assembled *de novo* with Velvet v. 1.2.10 using multiple *k*-mers (Zerbino and Birney 2008). The tRNAs were confirmed using tRNAsacn-SE (Lowe and Eddy 1997). The complete plastome length of *T. hallaisanense* (MW067130) was 151,554 bp, with one large single-copy region (LSC; 84,066 bp), one small single-copy region (SSC; 18,524 bp), and two inverted repeat regions (IR_a and IR_b; 24,482 bp each). The overall GC content was 37.7% and the plastome contained 129 genes, including 84 protein-coding genes with 2 pseudogenes (*ycf1* and *accD*), 8 rRNA, and 37 tRNA genes. A total of 14 genes were duplicated in the inverted repeat regions, including 7 tRNA, 4 rRNA, and 3 protein-coding genes.

Nineteen representative species of Asteraceae (18 from tribe Cichorieae and one outgroup from tribe Astereae),

CONTACT Seung-Chul Kim ✉ sonchus96@skku.edu Department of Biological Sciences, Sungkyunkwan University, 2066, Seobu-ro, Suwon 16419, Republic of Korea; Jae-Hong Pak ✉ jhpak@knu.ac.kr Department of Biology, School of Life Sciences, Kyungpook National University, 80, Daehak-ro, Buk-gu, Daegu 41566, Republic of Korea

© 2021 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group.

This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0/>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

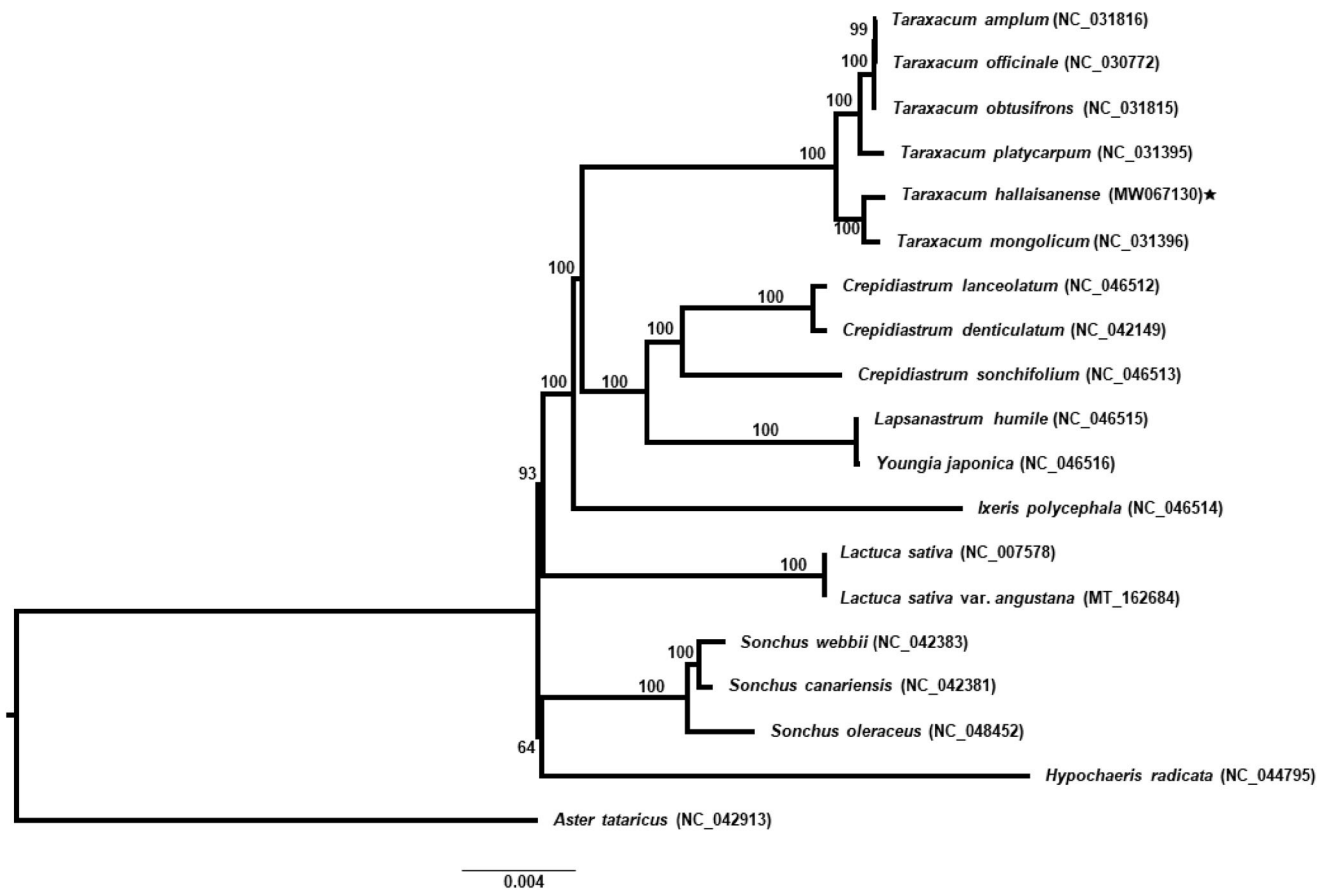


Figure 1. The maximum-likelihood (ML) tree based on 18 representatives of Asteraceae (tribe Cichorieae) and one outgroup taxon, *Aster tataricus* (tribe Astereae). The bootstrap support value based on 1000 replicates is shown on each node.

including *T. hallaisanense*, were aligned using MAFFT v.7 (Katoh and Standley 2013) and based on complete plastid genome sequences, maximum likelihood (ML) analysis with 1000 bootstrap replications was conducted using IQ-TREE v.1.6.7 (Nguyen et al. 2015). *Aster tataricus* (tribe Astereae) was used as an outgroup. The ML tree suggested that the genus *Taraxacum* is monophyletic (100% bootstrap support, BS) (Figure 1). *Taraxacum* is sister to the clade containing closely related genera, such as *Crepidiastrum*, *Lapsanastrum*, and *Youngia* (100% BS). Within the genus *Taraxacum*, two major lineages can be identified; one lineage includes *T. hallaisanense* and *T. mongolicum* and the other includes *T. amplum*, *T. officinale*, *T. obtusifrons*, and *T. platycarpum* (Figure 1). The plastid genome suggested that *T. hallaisanense*, which is a narrow Jeju Island endemic and diploid ($2n=2X=16$) species in Korea, is closely related to *T. mongolicum*, which is triploid ($2n=3X=24$) occurring in the mainland. However, species relationships among diploid species in Korea and Japan based on 15 capitulum traits suggested that Korean species, *T. hallaisanense* and *T. ohiwanum* (diploid and triploid) are related to *T. japonicum*, which occurs in southern-central part of Honshu, Japan (Lee et al. 2004). To infer accurate phylogenetic relationships among species of diploid and polyploid *Taraxacum* species in East Asia, it is necessary to sample broadly and apply highly variable nuclear and chloroplast markers. The complete plastid genome assembled in this study will provide valuable information for identifying useful plastid markers for DNA

barcoding and elucidating phylogenetic among species within the genus.

Disclosure statement

No potential competing interest was reported by the author(s).

Funding

This work was supported by Basic Science Research Program through the National Research Foundation of Korea (NRF) funded by the Ministry of Education [2016R1A6A1A05011910].

Data availability statement

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at <https://www.ncbi.nlm.nih.gov/> under the accession no. MW067130. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA697908, SRR13590697, and SAMN17676085, respectively.

References

- Asker S, Jerling L. 1992. Apomixis in plants. Boca Raton (FL); London (UK): CRC press. p. 320.
- Ge X, Kirschner J, Štěpánek J. 2007. *Taraxacum*. In: Wu ZY, Raven PH, Hong DY, editors. Flora of China. Beijing (China): Science Press; St. Louis (MO): Botanical Garden Press; p. 20–21.
- Katoh K, Standley DM. 2013. MAFFT multiple sequence alignment software version 7: improvements in performance and usability. *Mol Biol Evol.* 30(4):772–780.

- Kim J-K, Park JY, Lee YS, Woo SM, Park H-S, Lee S-C, et al. 2016. The complete chloroplast genomes of two *Taraxacum* species, *T. platycarpum* Dahlst. and *T. mongolicum* Hand.-Mazz. (Asteraceae). Mitochondrial DNA. Part B. 1:412–413.
- Kirschner J, Štěpánek J, Mes THM, Nijss JCMd, Oosterveld P, Štorchová H, Kuperus P. 2003. Principal features of the cpDNA evolution in *Taraxacum* (Asteraceae, Lactuceae): a conflict with taxonomy. *Plant Syst Evol.* 239(3–4):231–255.
- Kirschner J, Závěská Drábková L, Štěpánek J, Uhlemann I. 2015. Towards a better understanding of the *Taraxacum* evolution (Compositae-Cichorieae) on the basis of nrDNA of sexually reproducing species. *Plant Syst Evol.* 301(4):1135–1156.
- Kitamura S. 1957. Compositae Japonicae, pars sexta. *Mem. Coll Sci Univ Kyoto Ser B.* 24:1–42.
- Lee KH, Yang JY, Pak JH, Morita T, Ito M, Pak JH. 2004. Relationship of diploid East Asian *Taraxacum* Wiggers using the capitulum morphological character. *Korean J Pl Taxon.* 34(2):153–166.
- Lowe TM, Eddy SR. 1997. tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence. *Nucleic Acids Res.* 25(5):955–964.
- Morita T. 1980. A search for diploid *Taraxacum* in Korea and eastern China, by means of pollen observations on herbarium specimens. *J Jap Bot.* 55:1–12.
- Nguyen LT, Schmidt HA, von Haeseler A, Minh BQ. 2015. IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. *Mol Biol Evol.* 32(1):268–274.
- Richards AJ. 1973. The origin of *Taraxacum* agamospecies. *Bot J Linn Soc.* 66(3):189–211.
- Závěská Drábková L, Kirschner J, Štěpánek J, Závěský L, Vlček Č. 2009. Analysis of nrDNA polymorphism in closely related diploid sexual, tetraploid sexual and polyploid agamosperous species. *Plant Syst Evol.* 278(1–2):67–85.
- Zerbino DR, Birney E. 2008. Velvet: algorithms for de novo short read assembly using de Bruijn graphs. *Genome Res.* 18(5):821–829.