



The complete chloroplast genome of *Erigeron canadensis* isolated in Korea (Asteraceae): Insight into the genetic diversity of the invasive species

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ABSTRACT: We have determined the complete chloroplast genome of *Erigeron canadensis* isolated in Korea. The circular chloroplast genome of *E. canadensis* is 152,767 bp long and has four subregions: 84,317 bp of large single-copy and 18,446 bp of small single-copy regions are separated by 25,004 bp of inverted repeat regions including 133 genes (88 protein-coding genes, eight rRNAs, and 37 tRNAs). The chloroplast genome isolated in Korea differs from the Chinese isolate by 103 single-nucleotide polymorphisms (SNPs) and 47 insertions and deletion (INDEL) regions, suggesting different invasion sources of *E. canadensis* in Korea and China. A nucleotide diversity analysis revealed that the trend of the nucleotide diversity of *E. canadensis* followed that of 11 *Erigeron* chloroplasts, except for three peaks. The phylogenetic tree showed that our *E. canadensis* chloroplast is clustered with *E. canadensis* reported from China. *Erigeron canadensis* can be a good target when attempting to understand genetic diversity of invasive species.

Keywords: Asteraceae, chloroplast genome, *Erigeron canadensis*, intraspecific variations, invasive plants, Korea, nucleotide diversity

RECEIVED 7 February 2023; **REVISED** 21 March 2023; **ACCEPTED** 23 March 2023

OPEN ACCESS

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INTRODUCTION

Horseweed (*Erigeron canadensis* L.), native to North America, is now widely dispersed throughout the world (Nesom, 1989, 2004). The species was thought to be introduced into Asia in the late 19th century. Since then, it has spread widely to open places, such as roadsides and the margins of farmland and forests as an invasive species, resulting in ecological problems for native plants (Kim, 2005; Kang et al., 2020; Yan et al., 2020). The species has been classified in the genus *Conyza* based on its morphology, specifically *C. canadensis* (L.) Cronquist (Cronquist, 1943; Strother, 2006; Susanna and Garcia-Jacas, 2007), generating taxonomic confusion, as two different names have been used for the same species. However, the most recent taxonomic treatments of Asteraceae recognize the species in *Erigeron* and place *Conyza* under the synonymy of *Erigeron* (Chen and Brouillet, 2011; Keil and Nesom, 2012; POWO, 2023). The morphological features of *Conyza* distinguished from those of

Erigeron include a reduction of the ligule in the ray floret and a decrease in the number of hermaphroditic disc florets relative to female ray florets. However, these characteristics are also found in some species of *Erigeron*, supporting the merge of two genera (Noyes, 2000; Strother, 2006). Molecular data have indicated that *Conyza* is polyphyletic and nested within *Erigeron* (Noyes, 2000; Brouillet et al., 2009). *Erigeron canadensis* has been shown to have medicinal potentials given its antifungal (Curini et al., 2003) and anti-platelet activities (Pawlaczyk et al., 2011). As part of the development of molecular marker for the species, we completed the Korean *E. canadensis* chloroplast genome.

MATERIALS AND METHODS

A plant of the *E. canadensis* was collected in Gangseo-gu, Seoul, Korea (37.529708N, 126.842867E). A voucher specimen was deposited in the Infoboss Cyber Herbarium (IN, voucher number of IB-30034).

The total DNA was extracted from fresh leaves using a DNeasy Plant Mini Kit (QIAGEN, Hilden, Germany). Genome sequencing was performed using NovaSeq6000 at Macrogen Inc., Korea, and *de novo* assembly was done with Velvet v1.2.10 (Zerbino and Birney, 2008) and GapCloser v1.12 (Zhao et al., 2011). Assembled sequences were confirmed by BWA v0.7.17 (Li, 2013) and SAMtools v1.9 (Li et al., 2009) while separating the complete mitochondrial genome of *Uroleucon erigeronense* (Park and Lee, 2022). All bioinformatic analyses were conducted in the Genome Information System (GeIS; <https://geis.infoboss.co.kr/>) as utilized in previous studies (Choi et al., 2021; Kim et al., 2021b; Park et al., 2021a).

Genome annotation was conducted based on another *E. canadensis* chloroplast (NC_046789) (Zhang et al., 2019) with Geneious R11 v11.0.5 (Biomatters Ltd., Auckland, New Zealand). A circular map of the Korean *E. canadensis* chloroplast genome was drawn using OGDRAW v1.31 (Greiner et al., 2019).

Single-nucleotide polymorphisms (SNPs) and insertions and deletions (INDELs) were identified from the pair-wise sequence alignment of the two chloroplast genomes of *E. canadensis* conducted by MAFFT v7.450 (Katoh and Standley, 2013) with the 'Find variations/SNPs' function implemented in Geneious R11 v11.0.5 (Biomatters Ltd., Auckland, New Zealand). The INDEL region was defined as continuous INDELs, as in previous studies. All of these analyses were conducted in the GeIS environment, as used in previous studies (Park et al., 2020d; Park et al., 2021c; Yoo et al., 2021; Park and Xi, 2022).

Nucleotide diversity was calculated using the method proposed by Nei and Li (Nei and Li, 1979) based on the multiple-sequence alignment of 11 available *Erigeron* chloroplast genomes using a Perl script used in previous studies (Kim et al., 2021a; Kim et al., 2021c; Park et al., 2022). To examine the nucleotide diversity throughout the chloroplast genome, we used a sliding-window analysis with a window size of 500 bp and a step size of 200. Genomic coordination of each window was compared to the gene annotation of the chloroplast genome in GeIS.

Maximum-likelihood (ML), neighbor-joining (NJ), and Bayesian inference (BI) phylogenetic trees were constructed based on the multiple-sequence alignment of twenty chloroplast genomes by MAFFT v7.450 (Katoh and Standley, 2013), including that of the outgroup species, *Praxelis clematidea* (GenBank accession: NC_023833). During the alignment step, chloroplast genomes of *Erigeron philadelphicus* (GenBank accession: MT579972), *Erigeron strigosus* (GenBank accession: MT579973), *Erigeron multiradiatus* (GenBank

accession: NC_056169), and two *Erigeron annuus* types (GenBank accessions: OL350834 and MZ361990) were modified due to the different directions of LSC, SSC, and IRs. The ML and NJ trees were reconstructed in MEGA X (Kumar et al., 2018) with 1,000 and 10,000 bootstrap repeats, respectively. In the ML analysis, a heuristic search was used with nearest-neighbor interchange branch swapping, with the GTR+F+R4 model determined as the best-fit model by jModelTest v2.0.6 (Darriba et al., 2012) and with uniform rates among sites. All other options used the default settings. The posterior probability of each node was estimated by BI using MrBayes v3.2.6 (Huelsenbeck and Ronquist, 2001). The HKY85 model with gamma rates was used as a molecular model. A Markov-chain Monte Carlo algorithm was employed for 1,100,000 generations, sampling trees every 200 generations, with four chains running simultaneously. Trees from the first 100,000 generations were discarded as burn-in.

RESULTS AND DISCUSSION

The *E. canadensis* chloroplast genome isolated in Korea (GenBank accession: MT806101) is 152,767 bp long (GC ratio is 37.1%) with four subregions: 84,317 bp of large single-copy (35.0%) regions, 18,446 bp of small single-copy (30.9%) regions, and 25,004 bp of a pair of inverted repeats (43.0%) (Fig. 1). It is slightly longer than NC_046789 (Zhang et al., 2019). It contains 133 genes (88 protein-coding genes, eight rRNAs, and 37 tRNAs); 18 genes (seven protein-coding genes, four rRNAs and seven tRNAs) are duplicated in the IR regions, identical to that of NC_046789.

There were 103 single-nucleotide polymorphisms (SNPs) and 47 insertions and deletion (INDEL) regions (208 bp in total) against the Chinese *E. canadensis* chloroplast genome (NC_046789). The numbers of intraspecific variations among native populations in closely related species show similar levels. *Erigeron breviscapus* (Vaniot) Hand.-Mazz., distributed in Western China, displays 70 SNPs and 47 INDEL regions (268 bp in total) between two chloroplast genomes (NC_043882 and MK414770) (Meng et al., 2019; Wang and Lanfear, 2019). Two *E. annuus* (L.) Pers. chloroplast genomes (OL350834 and MZ361990) collected in China (Zhou et al., 2022) displayed 30 SNPs and 24 INDEL regions (124 bp in total), the lowest number among the four *Erigeron* species. Thus, the comparison of intraspecific variations suggests that the invasion sources of *E. canadensis* in the China and Korea cases may be different or that multiple invasions in each country have occurred independently due to the relatively high levels of intraspecific variations. Interestingly, the numbers of

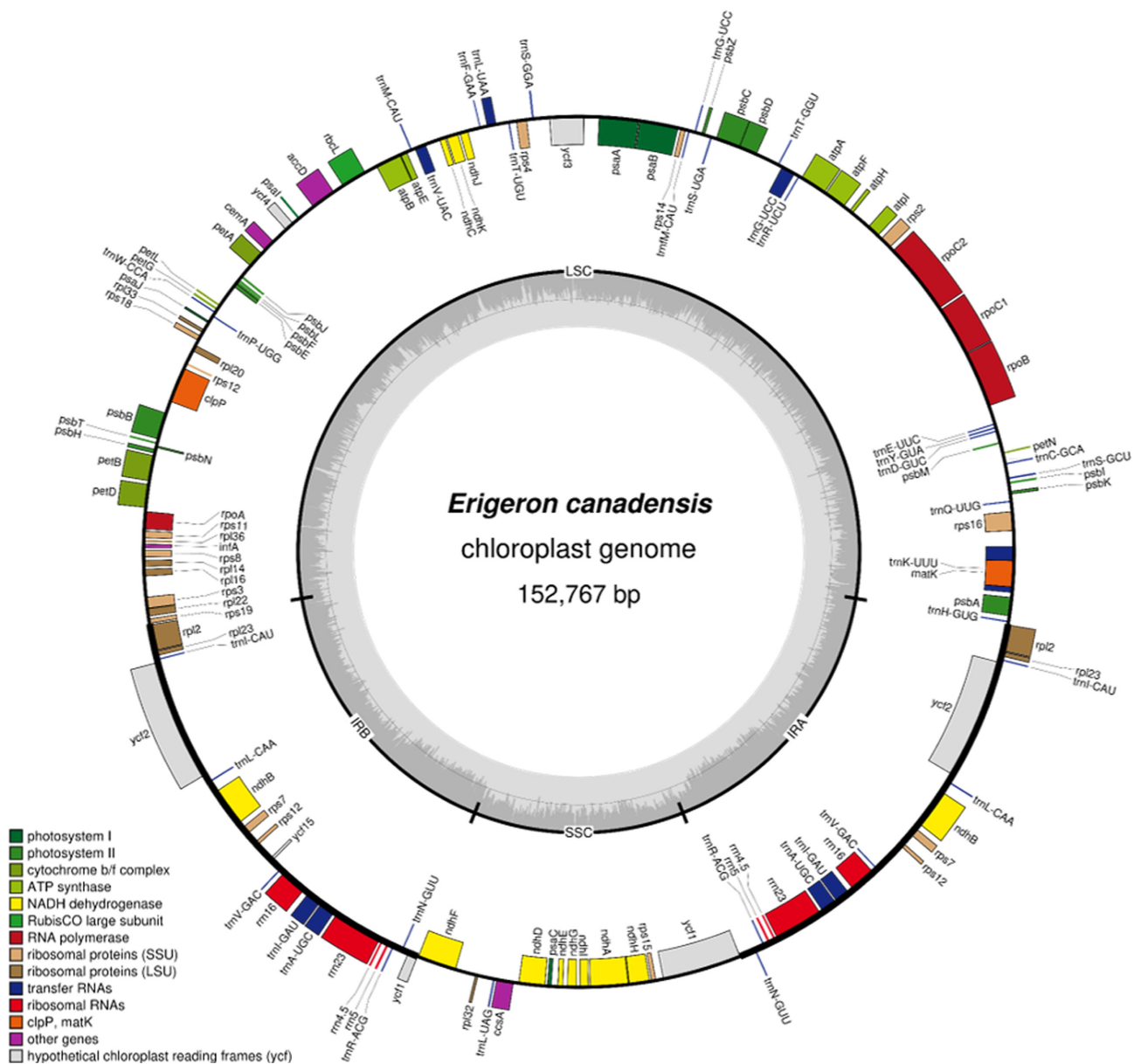


Fig. 1. Circular map of the chloroplast genome of *Erigeron canadensis* isolated in Korea. Genes shown outside are transcribed clockwise and those inside the circle are transcribed in a counter-clockwise arrangement. Genes are color-coded to distinguish different functional groups. The dark grey and light grey plots in the inner circle correspond to the GC content and AT content, respectively.

intraspecific variations of *E. bonariensis* L., native to South America, isolated in Western Australia and in the eastern states of Australia (Hereward et al., 2017; Wang et al., 2018a) amount to 105 SNPs and 87 INDEL regions (1,175 bp in length), also exhibiting similar levels of intraspecific variations among invading populations. These patterns suggest that multiple colonization events of pioneer plants, such as *E. canadensis* and *E. bonariensis*, may have facilitated the invasiveness (Yang et al., 2012).

The numbers of these intraspecific variations are much higher than those of *Artemisia fukudo* Makino (Asteraceae; 7

SNPs and 5 INDEL regions (12 bp)) isolated in Korea (Min et al., 2019) and *Suaeda japonica* Makino (Chenopodiaceae; 3 SNPs and 3 INDEL regions (3 bp in total) isolated in Korea (Kim et al., 2020) as well as those of many plant species of which samples have been isolated in Korea and China (Wang et al., 2018b; Jeon et al., 2019; Kim et al., 2019; Park et al., 2019a; Park et al., 2019b; Choi et al., 2020; Park et al., 2020c). However, they are smaller than those of *Camellia japonica* Wall. (Theaceae; 78 SNPs and 643-bp INDELs) (Park et al., 2019c), *Gastrodia elata* Blume (Orchidaceae; 457 SNPs and 670-bp INDELs) (Park et al., 2020b), *Goodyera schlechtendaliana*

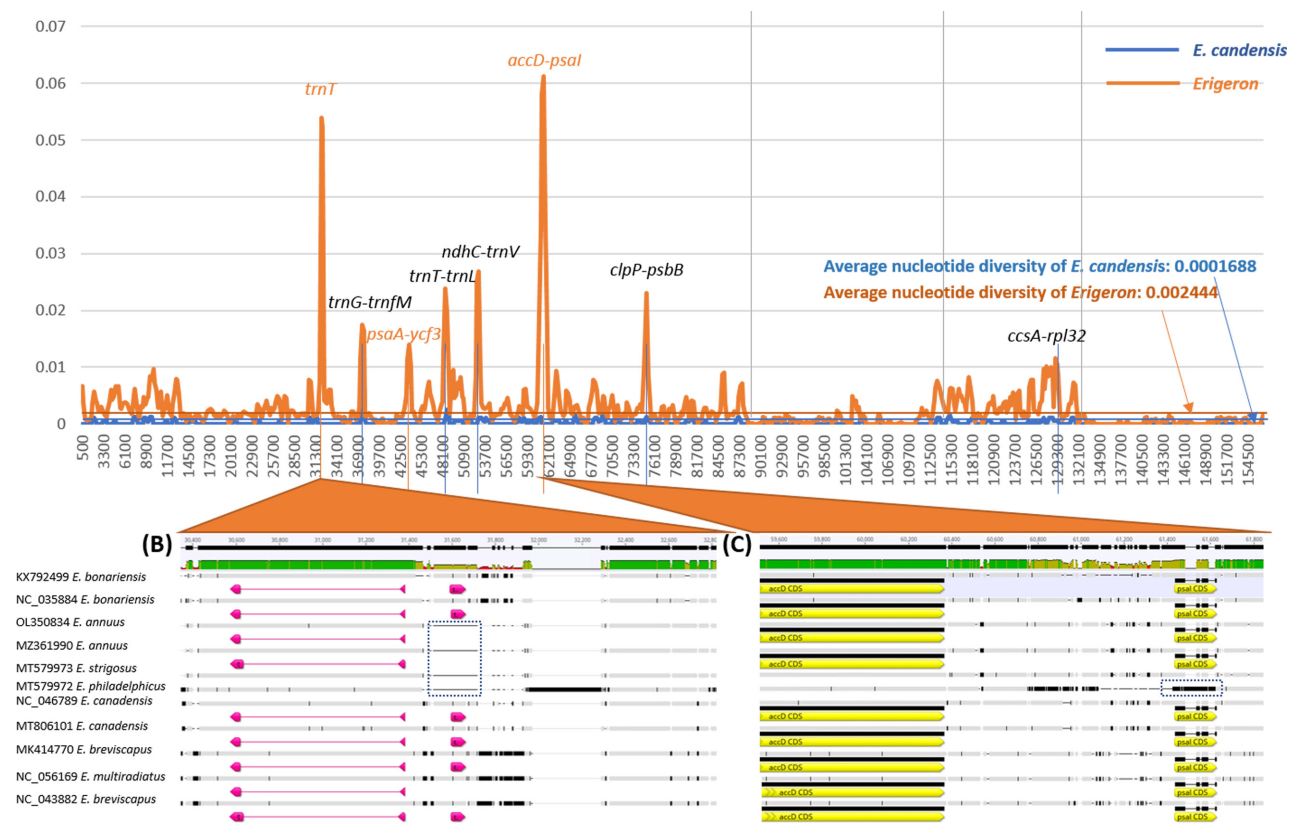


Fig. 2. Nucleotide diversity of two *E. canadensis* and 11 *Erigeron* chloroplast genomes. (A) displays nucleotide diversities along with the chloroplast genomic coordination of *E. canadensis* (blue line) and *Erigeron* (orange line). Labels on the peaks are gene names in the corresponding positions. (B) and (C) show multiple sequence alignments of two regions, the *trnT* and *accD-psal* peaks. The GenBank accessions of 11 *Erigeron* chloroplast genomes and species names are displayed on the left. Blue dotted boxes indicate different configurations in the alignments.

Rchb. f. (Orchidaceae; 163 to 827 SNPs and 1,060-bp to 1,794-bp INDELs) (Oh et al., 2019a, 2019b), and *Selaginella tamariscina* (P.Beauv.) Spring (1,213 SNPs and 1,641-bp INDELs) (Park et al., 2020a) isolated in Korea and China. The level of intraspecific variation of the chloroplast genomes can be determined by the rate of molecular evolution, the generation times, and the evolutionary history of each species, and this factor should be investigated with more populations to cover the entire range of variation.

The nucleotide diversity rates between the two chloroplast genomes of *E. canadensis* and among all 11 *Erigeron* chloroplast genomes were calculated. The average nucleotide diversity of the two *E. canadensis* chloroplast genome is 0.0001688, nearly identical to that of *Arabidopsis thaliana* (L.) Heynh. (Park et al., 2020c), smaller than that of *Zoysia japonica* Steud. (0.000217) (Lee and Park, 2021), and larger than that of *Chenopodium album* L. (0.0000625) (Park et al., 2021b), while that of 11 *Erigeron* chloroplast genomes is 0.002444 (Fig. 2). Eight peaks presenting high nucleotide diversity among the 11 *Erigeron* chloroplast genomes included

three peaks, *trnT*, *psaA-ycf3*, and *accD-psal*, with no peak of the nucleotide diversity of *E. canadensis* but with 11 *Erigeron* chloroplast genomes (Fig. 2A). Among the three peaks, the *trnT* peak showed that four chloroplast genomes (GenBank accession numbers OL350834, MZ361990, MT579973, and MT579972) lost *trnT* regions (Fig. 2B) with the *accD-psal* peak indicating that MT579972 (*E. philadelphicus* Willd.) has different sequences in *psal* CDS (Fig. 2C). This finding shows that except for these three peaks, the *E. canadensis* chloroplast genomes follow a trend of nucleotide diversity similar to that found in *Erigeron* chloroplast genomes.

Twenty Asteraceae chloroplast genomes including one outgroup, *Praxelis clematidea* (Hieron. ex Kuntze) R. M. King & H. Rob., were used to reconstruct the ML, NJ, and BI phylogenetic trees. All phylogenetic trees indicate that the *E. canadensis* chloroplast genome assembled in this study is strongly clustered with that of the previously sequenced *E. canadensis* (Fig. 3). Our phylogenetic analysis of chloroplast genomes also shows that species previously classified in the genus *Conyza* (i.e., *E. bonariensis* and *E. canadensis*) are

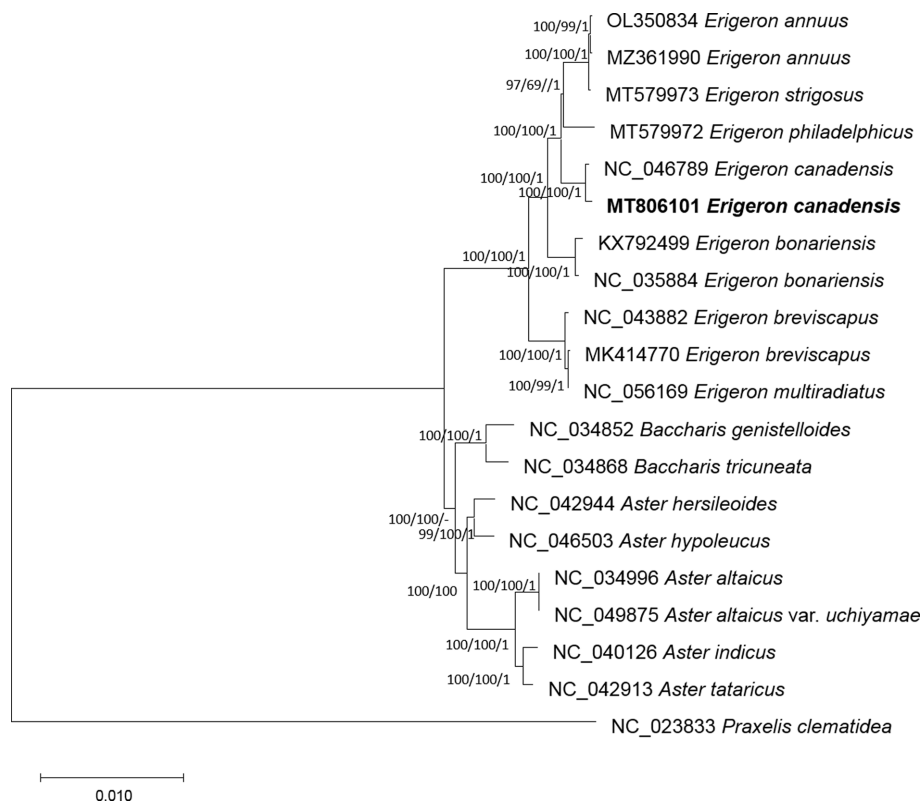


Fig. 3. Maximum-likelihood (ML) and Bayesian inference (BI) phylogenetic trees of fifteen chloroplast genomes. Phylogenetic tree was drawn based on the ML tree. The numbers above the branches are the bootstrap support values of the ML and NJ trees and the posterior probabilities from the BI tree.

nested within *Erigeron*, supporting the broad circumscription of *Erigeron* (Chen and Brouillet, 2011; Keil and Nesom, 2012; POWO, 2023). The new chloroplast genome data obtained in this study will contribute to a better understand of the genetic diversity of invasive species, which in turn will inform those involved in the management of invasive plants.

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ACKNOWLEDGMENTS

This study was carried out with the support of an InfoBoss Research Grant (IBG-0008) and a research grant from the National Research Foundation of Korea [NRF-2020R111A3068464].

CONFLICT OF INTEREST

Sang-Hun OH, the Editor-in-Chief of the Korean Journal of Plant Taxonomy, was not involved in the editorial evaluation or decision to publish this article. The authors declare that there are no conflicts of interest.

DATA AVAILABILITY STATEMENT

The chloroplast genome sequence can be accessed via accession number of MT806101 in GenBank of NCBI at <https://www.ncbi.nlm.nih.gov>. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA688747, SAMN17188058, and SRR13333571, respectively.

LITERATURE CITED

- Brouillet, L., T. Lowrey, L. Urbatsch, V. Karaman-Castro, G. Sancho, S. Wagstaff and J. Semple. 2009. Astereae. Systematics, Evolution and Biogeography of the Compositae.
- Chen, Y. and L. Brouillet. 2011. Wu ZY, Raven PH, Hong DY, editors. *Erigeron*. In Flora of China Vol. 20. Beijing St. Louis: Science Press Missouri Botanical Garden Press.
- Choi, N. J., H. Xi and J. Park. 2021. A Comparative Analyses of the Complete Mitochondrial Genomes of Fungal Endosymbionts in *Sogatella furcifera*, White-Backed Planthoppers. *International Journal of Genomics* 2021: 6652508.
- Choi, Y. G., N. Yun, J. Park, H. Xi, J. Min, Y. Kim and S.-H. Oh. 2020. The second complete chloroplast genome sequence of the *Viburnum erosum* (Adoxaceae) showed a low level of intra-spe-

- cies variations. *Mitochondrial DNA Part B* 5: 271-272.
- Cronquist, A. 1943. The separation of *Erigeron* from *Comyza*. *Bulletin of the Torrey Botanical Club* 629-632.
- Curini, M., A. Bianchi, F. Epifano, R. Bruni, L. Torta and A. Zambonelli. 2003. Composition and in vitro antifungal activity of essential oils of *Erigeron canadensis* and *Myrtus communis* from France. *Chemistry of Natural Compounds* 39: 191-194.
- Darriba, D., G. L. Taboada, R. Doallo and D. Posada. 2012. jModelTest 2: More models, new heuristics and parallel computing. *Nature Methods* 9: 772-772.
- Greiner, S., P. Lehwark and R. Bock. 2019. OrganellarGenomeDRAW (OGDRAW) version 1.3. 1: Expanded toolkit for the graphical visualization of organellar genomes. *Nucleic Acids Research* 47: W59-W64.
- Hereward, J. P., J. A. Werth, D. F. Thornby, M. Keenan, B. S. Chauhan and G. H. Walter. 2017. Complete chloroplast genome of glyphosate resistant *Comyza bonariensis* (L.) Cronquist from Australia. *Mitochondrial DNA Part B* 2: 444-445.
- Jeon, J.-H., H.-S. Park, J. Y. Park, T. S. Kang, K. Kwon, Y. B. Kim, J.-W. Han, S. H. Kim, S. H. Sung and T.-J. Yang. 2019. Two complete chloroplast genome sequences and intra-species diversity for *Rehmannia glutinosa* (Orobanchaceae). *Mitochondrial DNA Part B* 4: 176-177.
- Kang, E. S., S.-R. Lee, S. H. Oh, D.-K. Kim, S.-Y. Jung and D. C. Son. 2020. Comprehensive review about alien plants in Korea. *Korean Journal of Plant Taxonomy* 50: 89-119.
- Keil, D. J. and G. L. Nesom. 2012. Baldwin BG, Goldman DH, Keil DJ, Patterson R, Rosatti TJ, Wilken DH, editors. *Erigeron*. In *Jepson Manual, Vascular Plants of California*. 2nd ed. University of California Press.
- Kim, K. D. 2005. Invasive plants on disturbed Korean sand dunes. *Estuarine, Coastal and Shelf Science* 62: 353-364.
- Kim, M.-H., S. Park, J. Lee, J. Baek, J. Park and G. W. Lee. 2021a. The complete chloroplast genome of *Glycyrrhiza uralensis* Fisch. isolated in Korea (Fabaceae). *Korean Journal of Plant Taxonomy* 51: 353-362.
- Kim, M., H. Xi and J. Park. 2021b. Genome-wide comparative analyses of GATA transcription factors among 19 *Arabidopsis* ecotype genomes: Intraspecific characteristics of GATA transcription factors. *PLoS one* 16: e0252181.
- Kim, S.-T., S.-H. Oh and J. Park. 2021c. The complete chloroplast genome of *Diarthron linifolium* (Thymelaeaceae), a species found on a limestone outcrop in eastern Asia. *Korean Journal of Plant Taxonomy* 51: 345-352.
- Kim, Y., K.-I. Heo and J. Park. 2019. The second complete chloroplast genome sequence of *Pseudostellaria palibiniana* (Takeda) Ohwi (Caryophyllaceae): Intraspecific variations based on geographical distribution. *Mitochondrial DNA Part B* 4: 1310-1311.
- Kim, Y., J. Park and Y. Chung. 2020. The comparison of the complete chloroplast genome of *Suaeda japonica* Makino presenting different external morphology (Amaranthaceae). *Mitochondrial DNA Part B* 5: 1616-1618.
- Kumar, S., G. Stecher, M. Li, C. Knyaz and K. Tamura. 2018. MEGA X: Molecular Evolutionary Genetics Analysis across Computing Platforms. *Molecular Biology and Evolution* 35: 1547-1549.
- Lee, B. and J. Park. 2021. The complete chloroplast genome of *Zoysia japonica* Steud. isolated in Korea (Poaceae): Investigation of potential molecular markers on *Z. japonica* chloroplast genomes. *Plant Biotechnology Reports* 15: 707-715.
- Li, H. 2013. Aligning sequence reads, clone sequences and assembly contigs with BWA-MEM. arXiv preprint arXiv:13033997.
- Li, H., B. Handsaker, A. Wysoker, T. Fennell, J. Ruan, N. Homer, G. Marth, G. Abecasis and R. Durbin. 2009. The sequence alignment/map format and SAMtools. *Bioinformatics* 25: 2078-2079.
- Meng, J., L. Zhang, Z. Dong and J. He. 2019. Complete plastid genome sequence of *Erigeron breviscapus* (Asteraceae), an endemic traditional Chinese herbal medicine. *Mitochondrial DNA Part B* 4: 4077-4078.
- Min, J., J. Park, Y. Kim and W. Kwon. 2019. The complete chloroplast genome of *Artemisia fukudo* Makino (Asteraceae): Providing insight of intraspecific variations. *Mitochondrial DNA Part B* 4: 1510-1512.
- Nei, M. and W.-H. Li. 1979. Mathematical model for studying genetic variation in terms of restriction endonucleases. *Proceedings of the National Academy of Sciences* 76: 5269-5273.
- Nesom, G. L. 1989. Infrageneric taxonomy of New World *Erigeron* (Compositae: Astereae). *Phytologia*.
- Nesom, G. L. 2004. Taxonomic reevaluations in North American *Erigeron* (Asteraceae: Astereae). *SIDA, Contributions to Botany* 19-39.
- Noyes, R. D. 2000. Biogeographical and evolutionary insights on *Erigeron* and allies (Asteraceae) from ITS sequence data. *Plant Systematics and Evolution* 220: 93-114.
- Oh, S.-H., H. J. Suh, J. Park, Y. Kim and S. Kim. 2019a. The complete chloroplast genome sequence of a morphotype of *Goodyera schlechtendaliana* (Orchidaceae) with the column appendages. *Mitochondrial DNA Part B* 4: 626-627.
- Oh, S.-H., H. J. Suh, J. Park, Y. Kim and S. Kim. 2019b. The complete chloroplast genome sequence of *Goodyera schlechtendaliana* in Korea (Orchidaceae). *Mitochondrial DNA Part B* 4: 2692-2693.
- Park, J., Y. Kim, G.-H. Lee and C.-H. Park. 2020a. The complete chloroplast genome of *Selaginella tamariscina* (Beauv.) Spring (Selaginellaceae) isolated in Korea. *Mitochondrial DNA Part B* 5: 1654-1656.

- Park, J., Y. Kim and K. Lee. 2019a. The complete chloroplast genome of Korean mock strawberry, *Duchesnea chrysantha* (Zoll. & Moritz) Miq. (Rosaceae). *Mitochondrial DNA Part B* 4: 864-865.
- Park, J., Y. Kim, H. Xi, T. Jang and J.-H. Park. 2019b. The complete chloroplast genome of *Abeliophyllum distichum* Nakai (Oleaceae), cultivar Ok Hwang 1ho: Insights of cultivar specific variations of *A. distichum*. *Mitochondrial DNA Part B* 4: 1640-1642.
- Park, J., Y. Kim, H. Xi, Y. J. Oh, K. M. Hahm and J. Ko. 2019c. The complete chloroplast genome of common camellia tree in Jeju island, Korea, *Camellia japonica* L. (Theaceae): Intraspecific variations on common camellia chloroplast genomes. *Mitochondrial DNA Part B* 4: 1292-1293.
- Park, J., J. Lee and J. Park. 2022. The investigation of intraspecific characteristics and comparative analyses of the complete mitochondrial genome of *Stegobium paniceum* (Linnaeus, 1758) (Coleoptera: Ptinidae) assembled from public NGS raw reads of the black truffle, *Tuber melanosporum*. *Science Progress* 105: 00368504211072355.
- Park, J., S. H. Lee and J. H. Kim. 2021a. Complete genome sequence of the endosymbiotic bacterium “*Candidatus Riesia pediculicola*”. *Microbiology Resource Announcements*. 10.
- Park, J. and W. Lee. 2022. The complete mitochondrial genome of *Uroleucon erigeronense* (Thomas, 1878) (Hemiptera: Aphididae). *Mitochondrial DNA Part B* 7: 84-86.
- Park, J., J. Min, Y. Kim and Y. Chung. 2021b. The comparative analyses of six complete chloroplast genomes of morphologically diverse *Chenopodium album* L. (Amaranthaceae) collected in Korea. *International Journal of Genomics* 2021.
- Park, J., Y. Suh and S. Kim. 2020b. A complete chloroplast genome sequence of *Gastrodia elata* (Orchidaceae) represents high sequence variation in the species. *Mitochondrial DNA Part B* 5: 517-519.
- Park, J. and H. Xi. 2022. The complete chloroplast genome of *Campsis grandiflora* (Bignoniaceae). *Korean Journal of Plant Taxonomy* 52: 156-172.
- Park, J., H. Xi and Y. Kim. 2020c. The Complete Chloroplast Genome of *Arabidopsis thaliana* Isolated in Korea (Brassicaceae): An Investigation of Intraspecific Variations of the Chloroplast Genome of Korean *A. thaliana*. *International Journal of Genomics* 2020.
- Park, J., H. Xi and Y. Kim. 2021c. The complete mitochondrial genome of *Arabidopsis thaliana* (Brassicaceae) isolated in Korea. *Korean Journal of Plant Taxonomy* 51: 176-180.
- Park, J., H. Xi and S.-H. Oh. 2020d. Comparative chloroplast genomics and phylogenetic analysis of the *Viburnum dilatatum* complex (Adoxaceae) in Korea. *Korean Journal of Plant Taxonomy* 50: 8-16.
- Pawlaczyk, I., L. Czerchawski, W. Kuliczowski, B. Karolko, W. Pilecki, W. Witkiewicz and R. Gancarz. 2011. Anticoagulant and anti-platelet activity of polyphenolic-polysaccharide preparation isolated from the medicinal plant *Erigeron canadensis* L. *Thrombosis Research* 127: 328-340.
- POWO. 2023. Plants of the World Online. Royal Botanic Gardens, Kew; [accessed 2023 January 31]. <http://www.plantsoftheworldonline.org/>.
- Strother, J. L. 2006. Committee FoNAE, editor. *Coryza*. In *Flora of North America North of Mexico*. Vol. 20. New York and Oxford.
- Susanna, A. and N. Garcia-Jacas. 2007. The families and genera of vascular plants, vol 8, Flowering plants, Eudicots. Asterales, Berlin: Springer pp. 284–342.
- Wang, A., H. Wu, X. Zhu and J. Lin. 2018a. Species identification of *Coryza bonariensis* assisted by chloroplast genome sequencing. *Frontiers in Genetics* 9: 374.
- Wang, W., S. Chen and X. Zhang. 2018b. Whole-genome comparison reveals heterogeneous divergence and mutation hotspots in chloroplast genome of *Eucommia ulmoides* Oliver. *International Journal of Molecular Sciences* 19: 1037.
- Wang, W. and R. Lanfear. 2019. Stable and widespread structural heteroplasmy in chloroplast genomes revealed by a new long-read quantification method. *BioRxiv*. 692798.
- Yan, H., L. Feng, Y. Zhao, L. Feng, C. Zhu, Y. Qu and H. Wang. 2020. Predicting the potential distribution of an invasive species, *Erigeron canadensis* L., in China with a maximum entropy model. *Global Ecology and Conservation* 21: e00822.
- Yang, J., L. Tang, Y.-L. Guan and W.-B. Sun. 2012. Genetic diversity of an alien invasive plant Mexican sunflower (*Tithonia diversifolia*) in China. *Weed Science* 60: 552-557.
- Yoo, S.-C., S.-H. Oh and J. Park. 2021. Phylogenetic position of *Daphne genkwa* (Thymelaeaceae) inferred from complete chloroplast data. *Korean Journal of Plant Taxonomy* 51: 171-175.
- Zerbino, D. R. and E. Birney. 2008. Velvet: Algorithms for *de novo* short read assembly using de Bruijn graphs. *Genome Research* 18: 821-829.
- Zhang, Z., X. Jiang, Y. Chen, P. Zhu, L. Li, Y. Zeng and T. Tang. 2019. Characterization of the complete chloroplast genome sequence of *Coryza canadensis* and its phylogenetic implications. *Mitochondrial DNA Part B* 4: 2028-2030.
- Zhao, Q.-Y., Y. Wang, Y.-M. Kong, D. Luo, X. Li and P. Hao. 2011. Optimizing *de novo* transcriptome assembly from short-read RNA-Seq data: A comparative study. *BMC Bioinformatics* 12: S2.
- Zhou, J., J. Li, S. Peng and X. An. 2022. Characterization of the complete chloroplast genome of the invasive plant *Erigeron annuus* (L.) Pers. (Asterales: Asteraceae). *Mitochondrial DNA Part B* 7: 188-190.