The complete chloroplast genome of *Atriplex gmelinii* C. A. Mey. ex Bong. (Amaranthaceae)

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ABSTRACT

*Atriplex gmelinii* C. A. Mey. Ex Bong., 1838 is an annual halophytic herb found in East Asia and North America. The chloroplast genome of *A. gmelinii* was successfully sequenced. The assembled genome (151,852 bp; GC ratio, 37.3%) is composed of four subregions, with the large single copy (LSC; 83,872 bp; 35.4%) and small single copy (SSC; 17,812 bp; 30.9%) regions separated by two regions of inverted repeat regions (25,084 bp; 42.8%). A total of 130 genes were predicted with 85 protein-coding genes, 8 rRNAs, and 37 tRNAs. The phylogenetic analyses inferred from whole chloroplast genomes of 35 species, including 34 species in Amaranthaceae and one outgroup species, suggest a close relationship between *A. gmelinii* and *A. centralasiatica*.

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and Huelsenbeck 2003) to carry out Bayesian Inference (BI) after aligning whole chloroplast genomes by MAFFT v7.450 (Katoh and Standley 2013). A heuristic search was used with nearest-neighbor interchange branch swapping, the Tamura-Nei model, and uniform rates among sites to construct an ML phylogenetic tree with default values for other options. To estimate the node confidences, bootstrap analysis with 1,000 pseudoreplicates was conducted. For the Bayesian inferences, the GTR model with gamma rates was used as a molecular model and a Markov-Chain Monte Carlo algorithm was employed for 1,000,000 generations with four chains running simultaneously. To build the consensus tree of BI we sampled trees every 200 generations after removing 100 K generations as a ‘burn-in.’ All phylogenetic trees inferred from ML and BI methods showed that *A. gmelinii* is strongly grouped with *A. centralasiatica* (Figure 1). The *Atriplex* group is a sister to the group composed of three species (*C. album, C. ficifolium, and Chenopodium quinoa* Willd._1798) in the genus *Chenopodium*.

**Ethical statements**

Authors declare that there is no ethical or legal violation in obtaining the study materials and preforming research. The species used in this study is not listed in the IUCN Red List and plant materials were collected in the location that was not designated as a protective area in Korea. Authors confirmed that the plant materials for this study were not subjected to be approved from Institutional Review Board (IRB) in the Catholic University of Korea.
Author contributions

JP and STK conceptualized the project and designed the experiment. JP, YK generated sequencing data. JP, JM and STK analyzed the data. JP and STK wrote the manuscript with input from all other authors. All authors have read and agreed to the published version of the manuscript.

Disclosure statement

No potential conflict of interest was reported by the authors.

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Data availability statement

Chloroplast genome sequence can be accessed via accession number of MT810472 in GenBank of NCBI at https://www.ncbi.nlm.nih.gov. The associated BioProject, BioSample, and SRA study numbers are PRJNA692662, SAMN17360090 (SRS8042657), and SRP302073(SRR13449797), respectively.

References

Bae J, Yoon H, Choo Y, Song S. 2003. The responses of antioxidative enzymes and salt tolerance of Atriplex gmelinii. Korean J Ecol. 26: 273–280.
Bassett I, Crompton C. 1973. The genus Atriplex (Chenopodiaceae) in Canada and Alaska. III. Three hexaploid annuals: A. subspicata, A. gmelinii, and A. alaskensis. Can J Bot. 51(10):1715–1723.
Chen Y, Yang Z. 2018. Characterization of the complete plastome of Dysphania botrys, a candidate plant for cancer treatment. Mitochondrial DNA B Resour. 3(2):1214–1215.
Hong S-Y, Cheon K-S, Yoo K-O, Lee H-O, Cho K-S, Suh J-T, Kim S-J, Nam H-J, Sohn H-B, Kang K-K, Na Y-E, Bang H-S. 2011. Effects of climate change on C 4 plant list and distribution in South Korea: a review. Korean J Agric Forest Meteorol. 13(3):123–139.
Kim Y, Park, Jung Y. 2019b. The complete chloroplast genome of Limonium tetragonum (Plumbaginaceae) isolated in Korea. Korean J PI Taxon. 51(3):337–344.
Kumar S, Stecher G, Li M, Knyaz C, Tamura K. 2018. MEGA X: Molecular evolutionary genetics analysis across computing platforms. Mol Biol Evol. 35(6):1547–1549. doi:10.1093/molbev/mss127.
Li H. 2013. Aligning sequence reads, clone sequences and assembly contigs with BWA-MEM. arXiv preprint arXiv:13033997.
Li H, Handsaker B, Wysoker A, Fennell T, Ruan J, Homer N, Marth G, Abecasis G, Durbin R. 2009. The sequence alignment/map format and SAMtools. Bioinformatics. 25(16):2078–2079.
Oh S-H, Park J. 2020. The complete chloroplast genome of Eusacapsis japonica (Thunb.) Kanitz (Staphyleaceae) isolated in Korea. Mitochondrial DNA B Resour. 5(3):3751–3753.
Park J, An J-H, Kim Y, Kim D, Yang B-G, Kim T. 2020. Database of National Species List of Korea: the taxonomical systematics platform for managing scientific names of Korean native species. J Species Res. 9(3):233–246.
Park J, Kim Y. 2019. The second complete chloroplast genome of Dysphania pumilio (R. Br.) mosyakin & clemants (Amranthaceae): intra-species variation of invasive weeds, Mitochondrial DNA B Resour. 4(1): 1428–1429.
Park MJ, Kim J, Kong C-S, Seo Y. 2019. Inhibition of MMP-2 and-9 by crude extracts and their solvent-partitioned fractions from the halophyte Atriplex gmelinii. Ocean Polar Res. 41(2):79–88.
Park J, Min J, Kim Y, Chung Y. 2021. The Comparative Analyses of Six Complete Chloroplast Genomes of Morphologically Diverse Chenopodium album (L.) (Amaranthaceae) isolated in Korea. Int J Genomics. 2021:6643444–6643415.
Park J, Xi H, Kim Y. 2021. The complete mitochondrial genome of Arabidopsis thaliana (Brassicaceae) isolated in Korea. Korean J PI Taxon. 51(2):176–180.
Park J, Xi H, Oh S-h. 2020. Comparative chloroplast genomics and phylogenetic analysis of the Viburnum dilatatum complex (Adoxaceae) in Korea. Korean J PI Taxon. 50(1):8–16.
Ronquist F, Huelsembeck JP. 2003. MrBayes 3: Bayesian phylogenetic inference under mixed models. Bioinformatics. 19(12):1572–1574. doi: 10.1093/bioinformatics/btg180.
Zerbo IR, Birney E. 2008. Velvet: algorithms for de novo short read assembly using de Bruijn graphs. Genome Res. 18(5):821–829.
Zhang X-J, Wang N, Zhang L-Y, Fan S-J, Qu X-J. 2019. Characterization of the complete plastome of Atriplex centralasiatica (Chenopodiaceae), an annual halophytic herb. Mitochondrial DNA B Resour. 4(2): 2475–2476.
Zhao Q-Y, Wang Y, Kong Y-M, Luo D, Li X, Hao P. 2011. Optimizing de novo transcriptome assembly from short-read RNA-Seq data: a comparative study. BMC Bioinf. 12(514):S2.