The complete chloroplast genome of Castanopsis sieboldii (Makino) Hatus (Fagaceae)

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ABSTRACT
Castanopsis sieboldii (Makino) Hatus is an evergreen tree that distributes in Eastern Asia including Islands of Korea and Japan. The chloroplast genome of C. sieboldii was successfully sequenced. Its length is 160,705 bp long (GC ratio is 36.8%) and has four subregions: 90,821 bp of large single copy (34.6%) and 19,014 bp of small single copy (30.8%) regions are separated by 25,075 bp of inverted repeat (42.8%) regions including 134 genes (89 protein-coding genes, eight rRNAs, and 37 tRNAs). Interspecific variations of Castanopsis are at a moderate level in comparison to those of the other genera. Phylogenetic trees show that C. sieboldii chloroplast genome was clustered with the other two Castanopsis species.

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and Potentilla chinensis (1236 SNPs and 2295-bp INDELs; Park et al. 2019; Dang et al. 2020). Moreover, they are similar or higher than the numbers of intraspecific variations identified from the samples between Korea and China (Heo et al. 2019; Oh et al. 2019a, 2019b; Park, Kim, Xi, Oh, et al. 2019; Park, Suh, et al. 2020; Heo et al. 2020; Oh and Park 2020). These results indicate that the numbers of interspecific variations identified from the three Castanopsis species are at a moderate level.

Thirteen Fagaceae chloroplast genomes including one outgroup species, Betula platyphylla, were used for constructing bootstrapped Maximum-Likelihood (ML), Neighbor-joining (NJ), and Bayesian Inference (BI) phylogenetic trees using MEGA X (Kumar et al. 2018) and MrBayes v3.2.6 (Ronquist et al. 2012), respectively, 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 ML and NJ phylogenetic trees with default values for other options using MEGA X. Bootstrap analyses with 1000 and 10,000 pseudoreplicates were conducted for ML and NJ trees, respectively. The GTR model with gamma rates was used as a molecular model and Markov-chain Monte Carlo algorithm was employed for 1,100,000 generations, sampling trees every 200 generations, with four chains running simultaneously for BI tree. Three phylogenetic trees display that three Castanopsis species are clustered in one clade and are congruent to each other with high supportive values of ML, NJ, and BI (Figure 1). In addition, the topology of Castanopsis, Castanea, Quercus, and Fagus genera in the phylogenetic tree is congruent to the previous phylogenetic and morphological study (Manos et al. 2008). Taken together, our chloroplast genome is useful to investigate phylogenetic relationships of C. sieboldii as well as its genetic diversities along with geographical distribution.

Disclosure statement
The authors declare that they have no competing interests.

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Data availability statement
Chloroplast genome sequence can be accessed via accession number of MZ028444 in GenBank of NCBI at https://www.ncbi.nlm.nih.gov. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA724746, SAMN18857600, and SRR14316975, respectively.

References
Aoki K, Ueno S, Kamijo T, Setoguchi H, Murakami N, Kato M, Tsumura Y. 2014. Genetic differentiation and genetic diversity of Castanopsis...
(Fagaceae), the dominant tree species in Japanese broadleaved evergreen forests, revealed by analysis of EST-associated microsatellites. PloS One. 9(1):e87429.

Dang H, Xu J, Jin Z. 2020. The complete chloroplast genome of *Potentilla chinensis*. Mitochondrial DNA Part B. 5(2):1180–1181.

Daniel Hinsinger D, Sergej Strijk J. 2017. Complete chloroplast genome sequence of *Castanopsis coccinea* (Fagaceae), a threatened species from Hong Kong and South-Eastern China. Mitochondrial DNA A DNA Mapp Seq Anal. 28(1):65–66.

Del Valle JC, Casimiro-Soriguer I, Buide M, Narbona E, Whittall JB. 2019. Whole plastome sequencing within *Silene* section Psammophilae reveals mainland hybridization and divergence with the Balearic Island populations. Front Plant Sci. 10:1466.

Ferrarini M, Moretto M, Ward JA, Heo K-I, Park J, Xi H, Min J. 2020. The complete chloroplast genome of *Euscaphis chinensis* (Campanulaceae). Mitochondrial DNA B Resour. 5(4):3845–3847.

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 M, Xi H, Park J. 2021. Genome-wide comparative analyses of GATA transcription factors among 19 Arabidopsis ecotype genomes: intraspecific characteristics of GATA transcription factors. PloS One. 16(5):e0252181.

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.

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. 1000 Genome Project Data Processing Subgroup. 2009. The sequence alignment/map format and SAMtools. Bioinformatics. 25(16):2078–2079.

Manos PS, Cannon CH, Oh S-H. 2008. Phylogenetic relationships and taxonomic status of the paleoenemic Fagaceae of western North America: recognition of a new genus. Notholithocarpus. Madroño. 55(3):181–190.

Nock CJ, Hardner CM, Montenegro JD, Ahmad Termizi AA, Hayashi S, Playford J, Edwards D, Batley J. 2019. Wild origins of macadamia domestication identified through intraspecific chloroplast genome sequencing. Front Plant Sci. 10:334.

Oh S-H, Park J. 2020. The complete chloroplast genome of *Eucaphis japonica* (Thunb.) Kanitz (Staphyleaceae) isolated in Korea. Mitochondrial DNA B Resour. 5(3):3753–3769.

Oh S-H, Suh HJ, Park J, Kim Y, Kim S. 2019b. The complete chloroplast genome sequence of a morphotype of *Goodyera schelchtendaliana* (Orchidaceae) with the column appendages. Mitochondrial DNA Part B. 4(1):626–627.

Oh S-H, Suh HJ, Park J, Kim Y, Kim S. 2019a. The complete chloroplast genome sequence of *Goodyera schelchtendaliana* in Korea (Orchidaceae). Mitochondrial DNA B Resour. 4(2):2692–2693.

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, Bae Y, Kim B-Y, Nam G-H, Park J-M, Lee BY, Suh H-J, Oh S-H. 2021. The complete chloroplast genome of *Campanula takesimana* Nakai from Dokdo Island in Korea (Campanulaceae). Mitochondrial DNA B Resour. 6(1):135–137.

Park J, Heo K-I, Kim Y, Kwon W. 2019. The complete chloroplast genome of *Potentilla centigrana* Maxim. (Rosaceae). Mitochondrial DNA Part B. 4(1):688–689.

Park J, Heo K-I, Kim Y, Kwon W. 2019. The complete chloroplast genome of *Potentilla freyniana* Bormm. (Rosaceae). Mitochondrial DNA B Resour. 4(2):2420–2421.

Park J, Kim Y, Xi H, Nho M, Woo J, Seo Y. 2019. The complete chloroplast genome of high production individual tree of *Coffea arabica* L. (Rubiaceae). Mitochondrial DNA Part B. 4(1):1541–1542.

Park J, Kim Y, Xi H, Oh YJ, Hahm KM, Ko J. 2019. The complete chloroplast genome of common camellia tree, *Camellia japonica* L. (Theaceae), adapted to cold environment in Korea. Mitochondrial DNA Part B. 4(1):1038–1040.

Park J, Lee J, Lee W. 2021. The complete mitochondrial genome of *Aphis gossypii* Glover, 1877 (Hemiptera: Aphididae) isolated from *Lenurus japonicus* in Korea. Mitochondrial DNA B Resour. 6(1):62–65.

Park J, Min J, Kim Y, Chung Y. 2021. The comparative analyses of six complete chloroplast genomes of morphologically diverse *Chenopodium album* L. (Amaranthaceae) collected in Korea. Int J Genomics. 2021:6643444.

Park J, Oh S-H. 2020. A second complete chloroplast genome sequence of *Fagus multirnervis* Nakai (Fagaceae): intraspecific variations on chloroplast genome. Mitochondrial DNA Part B. 5(2):1868–1869.

Park J, Park J, Kim J-H, Cho JR, Kim Y, Seo BY. 2019. The complete mitochondrial genome of *Micromus angulatus* (Stephens, 1836)(Neuroptera: Hemerobiidae). Mitochondrial DNA Part B. 4(1):1467–1469.

Park J, Suh Y, Kim S. 2020. A complete chloroplast genome sequence of *Gastrodia elata* (Orchidaceae) represents high sequence variation in the species. Mitochondrial DNA B Resour. 5(1):517–519.

Park J, Xi H, Oh S-h. 2020. Comparative chloroplast genomics and phylogenetic analysis of the *Viburnum dilatatum* complex (Adoxaceae) in Korea. Korean J Pl Taxon. 50(1):8–16.

Park J, Yun N, Oh S-H. 2019. The complete chloroplast genome of an endangered species in Korea, *Halenia corniculata* (L.) Cornaz (Gentianaceae). Mitochondrial DNA Part B. 4(1):1539–1540.

Ronquist F, Teslenko M, Van Der Mark P, Ayres DL, Darling A, Ho H, Larget B, Liu L, Suchard MA, Huelsenbeck JP. 2012. MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. Syst Biol. 61(3):539–542.

Sun Y, Hu H, Huang H, Vargas-Mendoza CF, 2014. Chloroplast diversity and population differentiation of *Castanopsis fargesii* (Fagaceae): a dominant tree species in evergreen broad-leaved forest of subtropical China. Tree Genet Genomes. 10(6):1531–1539.

Yamakawa T. 1966. Problem of *Castanopsis cuspidata* Schottky. Bull Fac Educ Kochi Univ. 18:65–73.

Yamazaki H. 1987. A taxonomical revision of *Castanopsis cuspidata* (Thunb) Schottky and the allies in Japan and Taiwan 1. J Jpn Bot. 62:289–298.

Yang JY, Pak J-H, Kim S-C. 2018. The complete plastome sequence of *Rubus takesimensis* endemic to Ulleung Island, Korea: insights into molecular evolution of anagenetically derived species in *Rubus* (Rosaceae). Gene. 668:221–228.

Ye X-M, Guo Y-P, Lei X-G, Sun R-X. 2019. The complete chloroplast genome of *Castanopsis fargesii* Franch.(Fagaceae). Mitochondrial DNA Part B. 4(1):1656–1657.