

MITOGENOME ANNOUNCEMENT



Complete chloroplast genome of Ulleung Island endemic, *Epilobium ulleungensis* (Onagraceae), in Korea

Ji Young Yang^a, Jae-Min Chung^b and Seung-Chul Kim^c

^aResearch Institute for Dok-do and Ulleung-do Island, Kyungpook National University, Daegu, Republic of Korea; ^bKorea National Arboretum, Pocheon, Republic of Korea; ^cDepartment of Biological Sciences, Sungkyunkwan University, Suwon, Republic of Korea

ABSTRACT

The first complete chloroplast genome sequences of Korean endemic *Epilobium* in Ulleung Island, *Epilobium ulleungensis*, were reported in this study. The *E. ulleungensis* plastome was 160,912 bp long, with the large single copy (LSC) region of 88,915 bp, the small single copy (SSC) region of 17,327 bp, and two inverted repeat (IR) regions of 27,335 bp. The plastome contained 131 genes, including 84 protein-coding, eight ribosomal RNA, and 37 transfer RNA genes. The overall GC content was 36.5%. Phylogenetic analysis of nine representative plastomes within the family Onagraceae suggests strongly that *E. ulleungensis* is sister to the clade containing species of *Oenothera* in tribe Onagreae.

ARTICLE HISTORY

Received 7 May 2018
Accepted 9 May 2018

KEYWORDS

Chloroplast genome; Korean endemic; *Epilobium ulleungensis*; Ulleung Island; Onagraceae

Owing to its remarkable diversity in morphology, ecology, and cytology, the genus *Epilobium* L., with approximately 175 species, represents the largest group in Onagraceae and is mainly distributed in temperate regions (Raven 1988; Hoch and Raven 1992; Baum et al. 1994). As for infrageneric classification system, eight highly distinctive sections have been proposed and recent molecular phylogenetic study recognized two main clades, i.e. sect. *Epilobium* and the 'xerophytic' clade (six sections included), and sect. *Chamaenerion* being the earliest diverged lineage within the genus (Raven 1976, 1988; Baum et al. 1994). Of eight sections delimited based on morphological and cytological characters (Raven 1976), sect. *Epilobium* is the largest one (ca. 150 spp.) with major radiation in Australasia and smaller ones in temperate South America and southern Africa (Raven and Raven 1976; Baum et al. 1994). Although preliminary nrDNA ITS phylogeny within the genus was performed and infrageneric classification system was evaluated (Baum et al. 1994), several questions (e.g. relationship within the 'xerophytic' clade and sectional relationship among *Boisduvalia*, *Zauschneria*, and *Currantia*) require additional study based on extensive sampling within the genus and additional plastid and independent nuclear markers. In Korea, a total of 12 species of *Epilobium* are currently recognized (National List of Species of Korea 2018), including one recently described insular endemic *E. ulleungensis* on Ulleung Island (Chung et al. 2017). Neither phylogenetic relationships nor complete chloroplast genome sequences is available among species of *Epilobium* in Korea. Therefore, in this study, we sequenced the plastome of

E. ulleungensis and compared it to other plastomes in the family Onagraceae.

Total DNA (Voucher specimen: JMC15101, KH) was isolated using the DNeasy plant Mini Kit (Quiagen, Carlsbad, CA) and sequenced by the Illumina HiSeq 4000 (Illumina Inc., San Diego, CA). A total of 11,439,577 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 tRNAscan-SE (Lowe and Eddy 1997). The total plastome length of *E. ulleungensis* (MH198310) was 160,912 bp, with large single copy (LSC; 88,915 bp), small single copy (SSC; 17,327 bp), and two inverted repeats (IRa and IRb; 27,335 bp each). The overall GC content was 38.2% (LSC, 36.3%; SSC, 33.2%; IRs, 42.8%) and the plastome contained 131 genes, including 84 protein-coding, eight rRNA, and 37 tRNA genes. A total of 18 genes were duplicated in the inverted repeat regions, including seven tRNA, four rRNA, and seven protein coding genes including *ndhF* gene. The complete *ycf1* gene was located in SSC and the *infA* gene located in LSC became a pseudogene.

To confirm the phylogenetic position of *E. ulleungensis*, nine representative plastomes of Onagraceae and two out-group species from Lythraceae were aligned using MAFFT v.7 (Katoh and Standley 2013) and maximum likelihood (ML) analysis was conducted based on the concatenated 77 coding genes using IQ-TREE v.1.4.2 (Nguyen et al. 2015). The ML tree (Figure 1) strongly suggested that *E. ulleungensis* (tribe Epilobieae) is sister to the clade containing species of *Oenothera* (tribe Onagreae).

CONTACT Seung-Chul Kim ✉ sonchus96@skku.edu Department of Biological Sciences, Sungkyunkwan University, 2066 Seobu-ro, Suwon, 16419, Republic of Korea

© 2018 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.

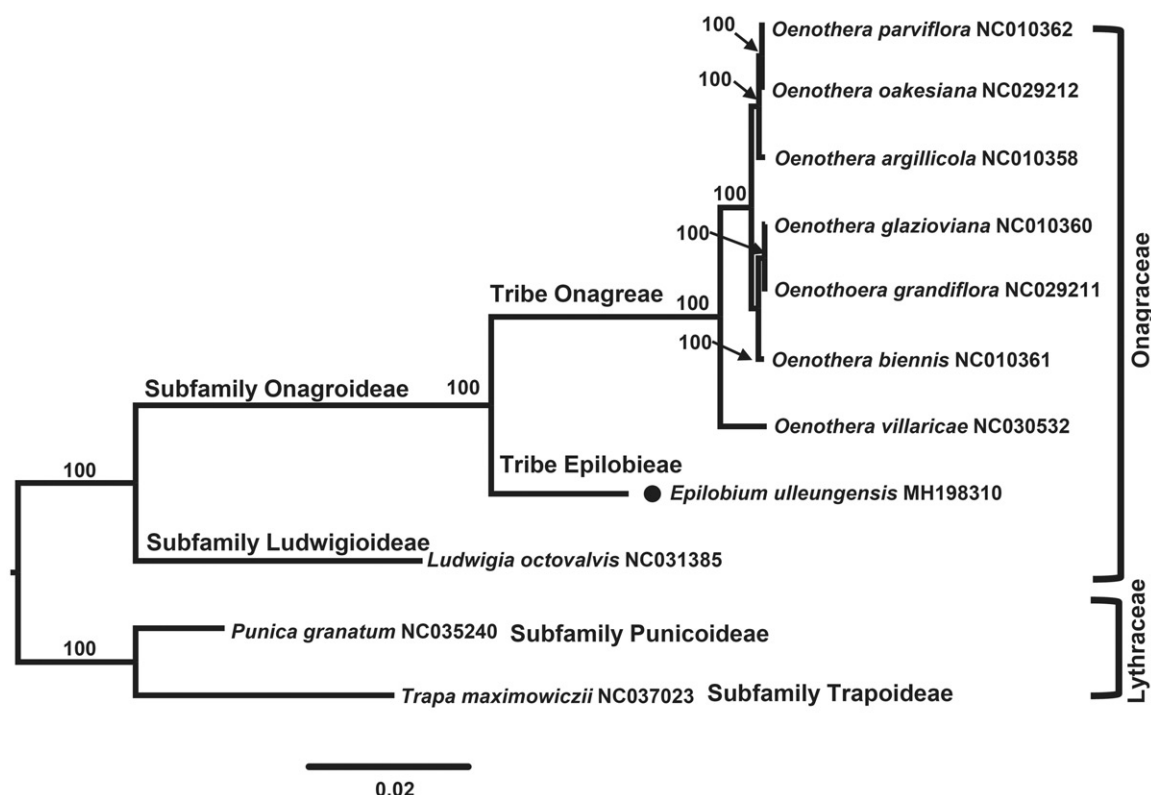


Figure 1. Maximum-likelihood (ML) tree based on 77 protein-coding genes in the nine representative plastomes of Onagraceae. The bootstrap value based on 1000 replicates is shown on each node.

Disclosure statement

No potential conflict of interest was reported by the authors.

Funding

This work was supported by Basic Science Research Program through the National Research Foundation of Korea (NRF) funded by the Ministry of Education (2016R1A5A1A05011910 and 2017RID1A3B03034296) to JYY and Korea National Arboretum (KNA1-2-5, 08-05) to JMC.

References

- Baum DA, Sytsma KJ, Hoch PC. 1994. A phylogenetic analysis of *Epilobium* (Onagraceae) based on nuclear ribosomal DNA sequences. *Syst Bot.* 19:363–388.
- Chung J-M, Shin J-K, Sun E-M, Kim H-W. 2017. A new species of *Epilobium* (Onagraceae) from Ulleungdo Island, Korea, *Epilobium ulleungensis*. *Korean J Pl Taxon.* 47:100–105.
- Hoch PC, Raven PH. 1992. *Boisduvalia*, a coma-less *Epilobium* (Onagraceae). *Phytologia.* 73:456–459.
- Katoh K, Standley DM. 2013. MAFFT multiple sequence alignment software version 7: improvements in performance and usability. *Mol Biol Evol.* 30:772–780.
- Lowe TM, Eddy SR. 1997. tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence. *Nucleic Acids Res.* 25:955–964.
- National List of Species of Korea. 2018. National Institute of Biological Resources. [accessed 2018 May 2]. <http://kbr.go.kr>
- Nguyen L-T, Schmidt HA, von Haeseler A, Minh BQ. 2015. IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. *Mol Biol Evol.* 32:268–274.
- Watts GB, Gard M. Md. 1937. Generic and sectional delimitation in Onagraceae, tribe Epilobieae. *Ann Mo Bot Gard.* 11:326–340.
- Raven PH. 1988. Onagraceae as a model of plant evolution. In: Gottlieb LD, Jain SK, editors. *Plant evolutionary biology*. New York (NY): Chapman and Hall Press; p. 85–107.
- Raven PH, Raven TE. 1976. The genus *Epilobium* in Australia: a systematic and evolutionary study. *Dept Sci Industr Res Bull.* 216:1–321.
- Zerbino DR, Birney E. 2008. Velvet: algorithms for de novo short read assembly using de Bruijn graphs. *Genome Res.* 18:821–829.