



The complete chloroplast genome of Prince Ginseng, *Pseudostellaria heterophylla* (Miq.) Pax (Caryophyllaceae)

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ABSTRACT

We presented complete chloroplast genome of Prince Ginseng, *Pseudostellaria heterophylla* which is 149,795 bp long and has four subregions: 81,460 bp of large single copy (LSC) and 16,983 bp of small single copy (SSC) regions are separated by 25,676 bp of inverted repeat (IR) regions including 126 genes (81 CDS, 8 rRNAs, and 37 tRNAs). The overall GC content of the chloroplast genome is 36.5% and those in the LSC, SSC, and IR regions are 34.3%, 29.4%, and 42.3%, respectively. Phylogenetic trees of 25 Caryophyllaceae species present phylogenetic position of *P. heterophylla* among available *Pseudostellaria* species.

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Pseudostellaria heterophylla (Miq.) Pax (Caryophyllaceae) is a perennial herb widely distributed in north-eastern Asia and its roots are used as medicinal plants in Korea and China. *Pseudostellaria heterophylla* contains many useful chemical compounds or peptides including pseudostellarins (Morita, Kayashita, Takeya, et al. 1994; Morita, Kobata, et al. 1994; Morita, Kayashita, Kobata, et al. 1994a, 1994b; Morita, Kayashita, Takeya, Itokawa 1995; Morita, Kayashita, Takeya, Itokawa, Shira 1995; Han et al. 2007), Kunitz-type trypsin inhibitor, novel lectin (Wang and Ng 2006), and antitumor polysaccharides (Wong et al. 1994). *P. heterophylla* has been studied for floral ontogeny and gene regulatory of dimorphic cleistogamy, which is a mixed mating system having both chasmogamous and cleistogamous flowers (Luo et al. 2012; 2016). *P. heterophylla* belongs to clade I of *Pseudostellaria* genus (Zhang et al. 2017) containing *P. longipedicellata*, *P. palibiniana*, and *P. okamotoi* (Kim et al. 2018; Kim, Heo, Lee, et al. 2019; Kim, Heo, Park 2019; Kim and Park 2019).

We sequenced complete chloroplast genome sequence of *P. heterophylla* collected in Geojedo Island, Geoje-si, Gyeongsangnam-do, Korea (Voucher in InfoBoss Cyber Herbarium; Y. Kim, IB-00063). Total DNA was extracted from fresh leaves of *P. heterophylla* by using a DNeasy Plant Mini Kit (QIAGEN, Hilden, Germany). Genome sequencing was performed using HiSeqX at Macrogen Inc., Korea, and *de novo* assembly and base confirmation were done by Velvet 1.2.10 (Zerbino and Birney 2008), SOAPGapCloser 1.12 (Zhao et al. 2011), BWA 0.7.17 (Li 2013), and SAMtools 1.9 (Li et al. 2009). Geneious R11 11.0.5 (Biomatters Ltd., Auckland,

New Zealand) was used for chloroplast genome annotation based on *P. longipedicellata* (NC_039454; Kim et al. 2018).

The chloroplast genome of *P. heterophylla* (Genbank accession is MK801111) is 149,795 bp long (GC ratio is 36.5%) and has four subregions: 81,460 bp of large single copy (LSC; 34.3%) and 16,983 bp of small single copy (SSC; 29.4%) regions are separated by 25,676 bp of inverted repeat (IR; 42.3%). LSC and SSC are longer than those of three *Pseudostellaria* species; while IR is shorter than those of three *Pseudostellaria* species. It contains 126 genes (81 protein-coding genes, 8 rRNAs, and 37 tRNAs); 18 genes (7 protein-coding genes, 4 rRNAs and 7 tRNAs) are duplicated in IR regions. Its SSC is inverted comparing with other *Pseudostellaria* chloroplast genomes like *Salix koriyanagi* (doi:10.1080/23802359.2019.1602012), *Salix gracilistyla* (Park et al., in submission), and *Hibiscus syriacus* (Kim, Oh, et al. 2019).

Sixteen Caryophyllaceae complete chloroplast genomes were aligned by MAFFT 7.388 (Kato and Standley 2013) with rearranging SSC sequences of *Colobanthus apetalus* (Androsiuk et al. 2018) and *P. heterophylla* for constructing bootstrapped neighbor joining and maximum likelihood trees using MEGA X (Kumar et al. 2018). Phylogenetic trees show that *P. heterophylla* is located outside of four *Pseudostellaria* chloroplast genomes, congruent with previous phylogeny (Zhang et al. 2017; Figure 1). Moreover, *Cerastium* was also positioned outside of *Pseudostellaria* clade with a relatively long branch (Figure 1), presenting a lack of taxa between *Cerastium* and *Pseudostellaria*. With additional chloroplast genomes of the species between *Cerastium* and *Pseudostellaria*, such as *Stellaria*, it contributes understanding of *Pseudostellaria* phylogeny in detail.

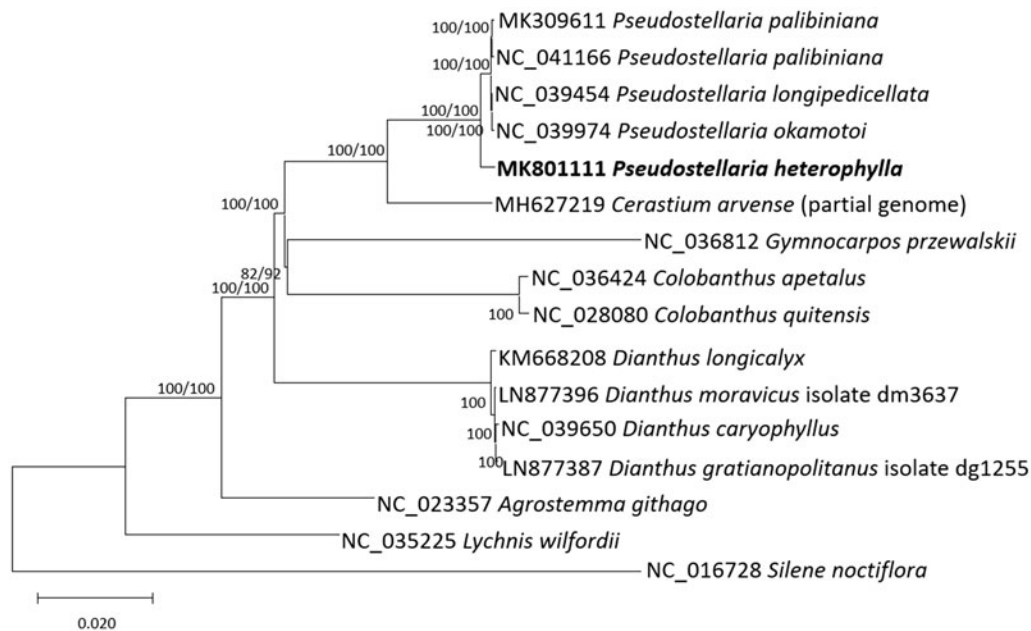


Figure 1. Neighbor joining (bootstrap repeat is 10,000) and maximum likelihood (bootstrap repeat is 1,000) phylogenetic trees of sixteen Caryophyllaceae complete chloroplast genomes: *Pseudostellaria heterophylla* (MK801111, in this study), *Pseudostellaria longipedicellata* (NC_039454), *Pseudostellaria okamotoi* (NC_039974), *Pseudostellaria palibiniana* (NC_041166 and MK309611), *Cerastium arvense* (MH627219; partial genome), *Gymnocarpus przewalskii* (NC_036812), *Colobanthus apetalus* (NC_036424), *Colobanthus quitensis* (NC_028080), *Dianthus longicalyx* (KM668208), *Dianthus moravicus* isolate dm3637 (LN877396), *Dianthus caryophyllus* (NC_039650), *Dianthus grantianopolitanus* (LN877387), *Agrostemma githago* (NC_023357), *Lychnis wilfordii* (NC_035225), and *Silene noctiflora* (NC_016728). Phylogenetic tree was drawn based on neighbor joining tree. The numbers above branches indicate bootstrap support values of neighbor joining and maximum likelihood phylogenetic trees, respectively.

Disclosure statement

The authors declare that they have no competing interests.

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