

The complete chloroplast genome of *Potentilla Freyniana* Bornm. (Rosaceae)

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ABSTRACT

Potentilla freyniana Bornm. has radical leaves with petioles and trifoliolate distinguished from *Potentilla fragarioides* and *Duchesnea indica*. In this study, we presented first complete chloroplast genome of *P. freyniana* to understand its phylogenetic position. Its length is 156,381 bp long and has four subregions: 85,724 bp of large single copy (LSC) and 18,617 bp of small single copy (SSC) regions are separated by 26,020 bp of inverted repeat (IR) regions including 129 genes (84 protein-coding genes, 8 rRNAs, and 37 tRNAs). The overall GC content of the chloroplast genome is 36.9% and those in the LSC, SSC, and IR regions are 34.8%, 30.7%, and 42.7%, respectively. Phylogenetic trees show that phylogenetic position of *P. freyniana* disagrees with three phylogenetic studies, showing that more *Potentilla* chloroplast genomes are required for clarifying *Potentilla* phylogeny.

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Genus *Potentilla*, belonging to Rosaceae, covers around 300 species and is distributed in field of mountain from temperate and arctic regions (Rydberg 1898). *Potentilla freyniana* Bornm. has radical leaves with petioles and trifoliolate (Chen and Craven 2007), which is an important key to distinguish from *Potentilla fragarioides* and *Duchesnea indica*.

P. freyniana was clustered with *Potentilla fragarioides* using chloroplast markers (Heo et al. under review), considering that it belongs to Fragarioides/C/P6 clade (Töpel et al. 2011; Feng et al. 2017; Heo et al., under review; Figure 1). Since three phylogenetic studies utilized limited number of molecular markers, complete chloroplast genome of *P. freyniana* will be utilized to understand its phylogenetic position together with available *Potentilla* (Ferrari et al. 2013; Zhang et al. 2017; Park, Heo, Kim, and Kwon under review) and *Duchesnea* chloroplast genomes (Heo et al. under review; Park, Heo et al., under review). Here, we reported completed chloroplast genome of *P. freyniana*.

Total DNA of *P. freyniana* collected in Korea [Voucher in InfoBoss Cyber Herbarium (IN); K-I. Heo, IB-00573] was extracted from fresh leaves by using a DNeasy Plant Mini Kit (QIAGEN, Hilden, Germany). Genome sequencing was performed using HiSeq2000 at Macrogen Inc., Seoul, Korea, and *de novo* assembly was done by Velvet 1.2.10 (Zerbino and Birney 2008), gaps were filled by SOAPGapCloser 1.12 (Zhao et al. 2011). Assembled sequences were confirmed by 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 from that of *Potentilla centigrana* chloroplast genome (MK209637).

The chloroplast genome of *P. freyniana* (Genbank accession is MK209638) is 156,381 bp long and has four subregions: 85,724 bp of large single copy (LSC) and 18,617 bp of small single copy (SSC) regions are separated by 26,020 bp of inverted repeat (IR). It contained 129 genes (84 protein-coding genes, 8 rRNAs, and 37 tRNAs); 17 genes (6 protein-coding genes, 4 rRNAs, and 7 tRNAs) are duplicated in IR regions. The overall GC content of *P. freyniana* chloroplast genome is 36.9% and those in the LSC, SSC, and IR regions are 34.8%, 30.7%, and 42.7%, respectively.

Nine partial or complete *Potentilla* (Ferrari et al. 2013; Zhang et al. 2017), two *Duchesnea* (Heo et al., under review; Park et al., under review), and five Rosaceae chloroplast genomes were used for constructing phylogenetic trees. Whole chloroplast genome sequences were aligned by MAFFT 7.388 (Katoh and Standley 2013) for constructing neighborjoining (bootstrap repeat is 10,000) and maximum likelihood (bootstrap repeat is 1,000) trees using MEGA X (Kumar et al. 2018). Phylogenetic trees show that *P. freyniana* shows independent lineage (Figure 1), supported by three phylogenetic studies (Töpel et al. 2011; Feng et al. 2017; Heo et al., under review). In addition, trees support that Fragarioides/C/P6 clade is clustered with Argentea/F and E/P7 clades; while three phylogenetic studies indicated that Reptans/D/P4 clades were clustered with Argentea/F and E/P7 clades (Töpel et al. 2011; Feng et al. 2017; Heo et al. under review). It reflects that phylogenetic relationship of *Potentilla* species should be analyzed with more samples with complete chloroplast genome for better resolution.

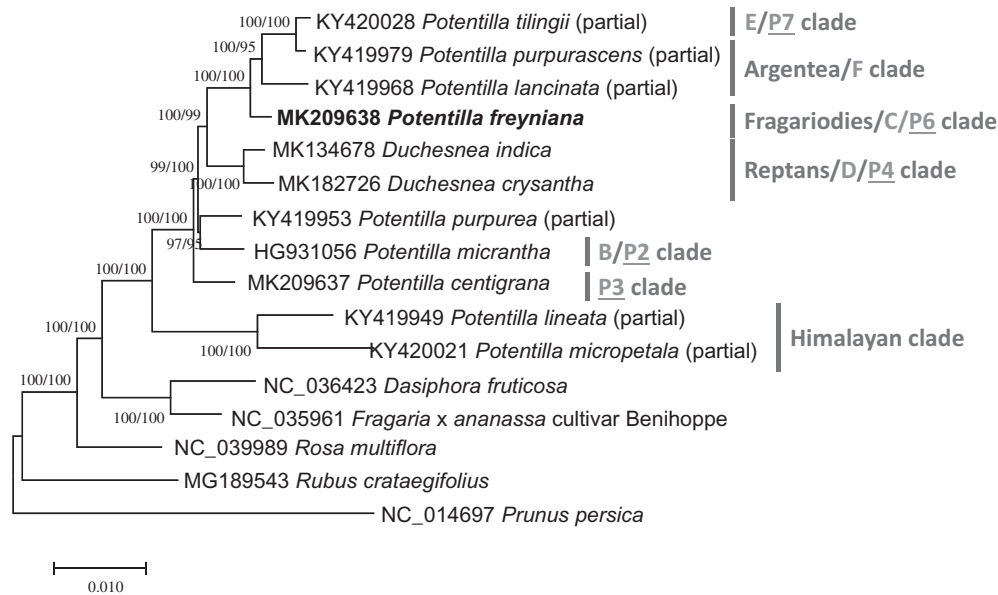


Figure 1. Neighbor joining (bootstrap repeat is 10,000) and maximum likelihood (bootstrap repeat is 1,000) phylogenetic tree of sixteen Rosaceae partial or complete chloroplast genomes: *Potentilla freyniana* (MK209638; in this study), *Potentilla centigrana* (MK209637), *Duchesnea chrysantha* (MK182726), *Duchesnea indica* (MK134678), *Potentilla tilingii* (KY420028; partial genome), *Potentilla lancinata* (KY419968; partial genome), *Potentilla purpurea* (KY419953; partial genome), *Potentilla purpurascens* (KY419979; partial genome), *Potentilla micropetala* (KY420021; partial genome), *Potentilla micrantha* (HG931056), *Potentilla lineata* (KY419949; partial genome), *Dasiphora fruticosa* (NC 036423), *Fragaria x ananassa* cultivar Benihoppe (NC_035961), *Rubus crataegifolius* (MG189543), and *Rosa multiflora* (NC_039989), and *Prunus persica* (NC_014697). The numbers above branches indicate bootstrap support values of maximum likelihood and neighbor joining phylogenetic tree, respectively. Clade names were presented as dark grey, light grey, and underlined characters, defined by Töpel et al. (2011), Feng et al. (2017), Heo et al. (under review), respectively.

Disclosure statement

The authors declare that they have no competing interests.

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