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The complete chloroplast genome of *Leucobryum juniperoideum* (brid.) C. Müll. (Leucobryaceae, Bryophyta)

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ABSTRACT
We presented complete chloroplast genome of *Leucobryum juniperoideum* which is 124,649 bp long and has four subregions: 86,309 bp of large single copy (LSC) and 18,696 bp of small single copy (SSC) regions are separated by 9,882 bp of inverted repeat (IR) regions including 127 genes (82 protein-coding genes, eight rRNAs, and 37 tRNAs). The overall GC content is 30.5% and those in the LSC, SSC, and IR regions are 28.1%, 26.8%, and 44.5%, respectively. Phylogenetic trees show that phylogenetic position of *L. juniperoideum* is congruent with the previous phylogenetic study of moss species.

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Genus *Leucobryum* is one of 14 major genera in the Leucobryaceae. (Santos and Stech 2017). The Greek word, *Leuko*, means white color explaining that pale leaf color is a main characteristic of this genus (Santos and Stech 2017). Leaves are composed of two kinds of cells: leucocyst, external hyaline layers, and chlorocyst, central single layer of green cell (Smith 2004). Leucocyst is major reason for pale leaf color of this genus. *Leucobryum juniperoideum* (Brid.) C. Müll, known as small white moss, is distributed worldwide (Blackstock 1987). *L. juniperoideum* is distinguished with allied species by sporophytes rarely produced due to difficulties of distinguishing with gametophytic characters. Recently, molecular characteristics are used for alternate solution for its identification (Crundwell 1972; Patterson et al. 1998; Vanderpoorten et al. 2003). To acquire more molecular characteristics of *L. juniperoideum* we completed its whole chloroplast genome sequence.

L. juniperoideum was collected in a Seojung stream, Seogwipo, Republic of Korea (33.342995 N, 126.669843E; Voucher in InfoBoss Cyber Herbarium (IN); W. Kwon, IB-50006). Its DNA was extracted by using DNeasy Plant Mini Kit (QIAGEN, Hilden, Germany). Genome sequencing was performed using HiSeqX at Macrogen Inc., Korea, and *de novo* assembly and conformation 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 *Fissidens nobilis* chloroplast genome (MK876184; Kwon et al. 2019)

L. juniperoideum chloroplast genome (Genbank accession is MK952779), the first chloroplast genome of family Leucobryaceae, is 124,649 bp long (GC ratio is 30.5%) and has four subregions: 86,309 bp of large single copy (28.1%) and 18,696 bp of small single copy (26.8%) regions are separated by 9,882 bp of inverted repeat (IR; 44.5%). It is shorter than that of neighbor species, *Fissidens nobilis,* by 184 bp (Kwon et al. 2019). It contains 127 genes (82 protein-coding genes, eight rRNAs, and 37 tRNAs); nine genes (four rRNAs and five tRNAs) are duplicated in IR regions.

Ten complete chloroplast genomes including *L. juniperoideum* were used for constructing neighbor joining (bootstrap repeat is 10,000) and maximum likelihood (bootstrap repeat is 1,000) phylogenic trees using MEGA X (Kumar et al. 2018) and IQ-TREE (Nguyen et al. 2015), respectively, after aligning whole chloroplast genome sequences using MAFFT 7.388 (Katoh and Standley 2013). Phylogenetic trees present genus *Leucobryum* is clustered with genus *Fissidens*, which is incongruent of phylogenetic relationship among three genera, *Leucobryum*, *Fissidens*, and *Syntrichia* (Liu et al. 2019; Kwon et al. 2019; Figure 1). In addition, two basal moss species, *Sphagnum palustre* (Jonathan Shaw et al. 2016) and *Takakia lepidozioides,* are clustered (Figure 1), which is same to the result of previous study (Kwon et al. 2019) but incongruent with another phylogentic study (Liu et al. 2019). Taken together, it indicates additional moss chloroplast genomes are required to clarify phylogenetic relationship of these species. With the aid of next generation sequencing technologies, more moss chloroplast genomes sequenced in near future will contribute understanding its phylogenetic relationship.

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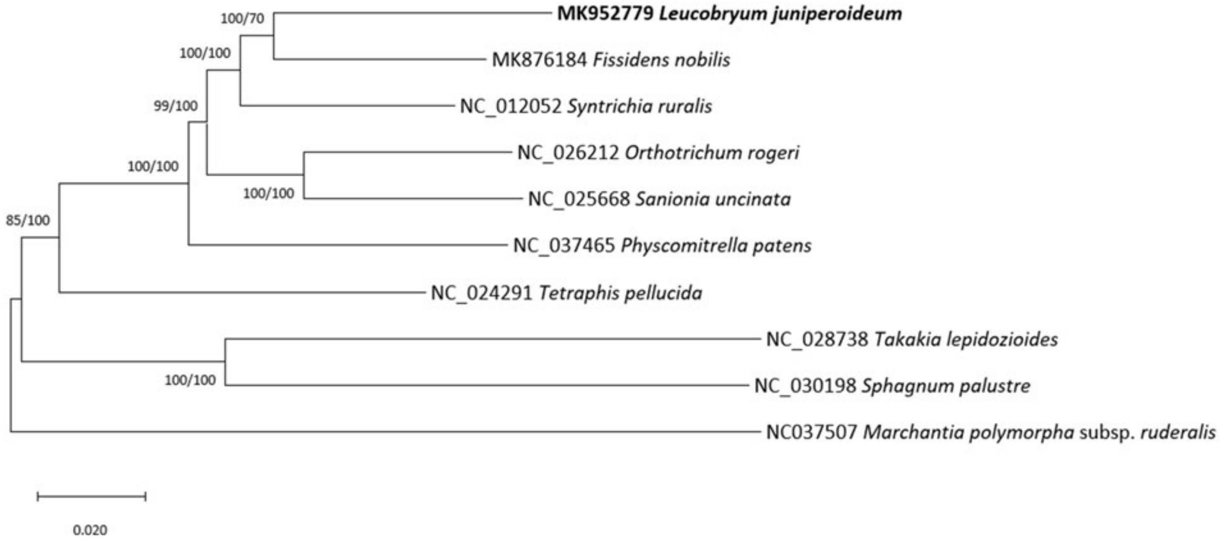

Figure 1. Neighbor joining (bootstrap repeat is 10,000) and maximum likelihood (bootstrap repeat is 1,000) phylogenetic tree of ten complete chloroplast genomes: *Fissidens nobilis* (MK876184 in this study), *Syntrichia ruralis* (NC_012052), *Orthotrichum rogeri* (NC_026212), *Sanionia uncinata* (NC_025668), *Physcomitrella patens* (NC_037465), *Tetraphis pellucida* (NC_024291), *Sphagnum palustre* (NC_030198), *Takakia lepidozioides* (NC_028738) and *Marchantia polymorpha* subsp. *ruderalis* (NC_037507) as an outgroup. 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.

Disclosure statement

The authors declare that they have no competing interests.

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