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MITOGENOME ANNOUNCEMENT

The complete chloroplast genome of *Fissidens nobilis* Griff. (Fissidentaceae, Bryophyta)

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ABSTRACT

We presented a complete chloroplast genome of *Fissidens nobilis* which is 124,962 bp long and has four subregions: 86,122 bp of large single-copy (LSC) and 18,708 bp of small single-copy (SSC) regions are separated by 10,066 bp of inverted repeat (IR) regions including 127 genes (82 protein-coding genes, 8 rRNAs, and 37 tRNAs). The overall GC content is 29.2% and those in the LSC, SSC, and IR regions are 26.6%, 26.0%, and 43.5%, respectively. Phylogenetic trees show that the phylogenetic position of *F. nobilis* is congruent with the previous phylogenetic study of moss species.

Genus *Fissidens* is one of the most diversified genera in Bryophyta covering around 450 species (Crosby et al. 2000). It is the only genus in Family Fissidentaceae (Pursell and Bruggeman-Nannenga 2004), characterized by two vaginant laminae in each leaf forming a pocket-shaped structure. Recent molecular phylogeny study presented that *Fissidens nobilis* Griff. is a basal group of subgenus *Pachyfissidens* (Suzuki et al. 2018), which is one of the four subgenera in the genus *Fissidens* (Pursell and Bruggeman-Nannenga 2004). Due to morphological varieties of *Fissidens*, it is a good target to decipher chloroplast genomes for understanding the relationship between morphological and genetic diversity. Here, we completed chloroplast genome of *F. nobilis* as a first chloroplast genome of *Fissidens* as well as order Dicranales.

F. nobilis was collected in a Seojung stream, Seogwipo, Republic of Korea (33.342995N, 126.669843E; Voucher in InfoBoss Cyber Herbarium (IN); W. Kwon, IB-50005). Its DNA was extracted 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 sequence 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 *Physcomitrella patens* chloroplast genome (NC_037465; Sugiura et al. 2003).

The chloroplast genome of *Fissidens nobilis* (Genbank accession is MK876184) is 124,962 bp long (GC ratio is 29.2%) and has four subregions: 86,122 bp of large single-copy (LSC; 26.6%) and 18,708 bp of small single-copy (SSC; 26.0%) regions are separated by 10,066 bp of inverted repeats (IRs; 43.5%). It is longer than that of one of the neighbor species, *Syntrichia ruralis* by 2,332 bp (Oliver et al. 2010). It contains 127 genes (82 protein-coding genes, 8 rRNAs, and 37 tRNAs), in which nine genes (four rRNAs and five tRNAs) are duplicated in IR regions.

Nine complete chloroplast genomes including *F. nobilis* were used for constructing neighbor joining (bootstrap repeat is 10,000) and maximum likelihood (bootstrap repeat is 1,000) phylogenetic trees using MEGA X (Kumar et al. 2018) after aligning whole chloroplast genomes using MAFFT 7.388 (Katoh and Standley 2013) with correcting direction of SSC and LSC of *Physcomitrella patens* (NC_037465). Phylogenetic trees present rigid phylogenetic position of *F. nobilis*, which is congruent with the recent study of moss species based on organelle and nuclear loci (Liu et al. 2019). In addition, two basal moss species, *Sphagnum palustre* (Jonathan Shaw et al. 2016), and *Takakia lepidozioides*, are clustered in the tree (Figure 1). It is incongruent with the previous study (Liu et al. 2019), requiring additional chloroplast genome sequences of basal moss species. Complete chloroplast genomes of moss species in the trees present their phylogenetic relation with high bootstrap values and congruent between neighbor joining and maximum likelihood trees (Figure 1), reflecting that moss chloroplast genome sequences can provide rigid phylogenetic relationship. Additional chloroplast genomes sequenced in near future will contribute to construct a detailed phylogenetic relationship of moss species.
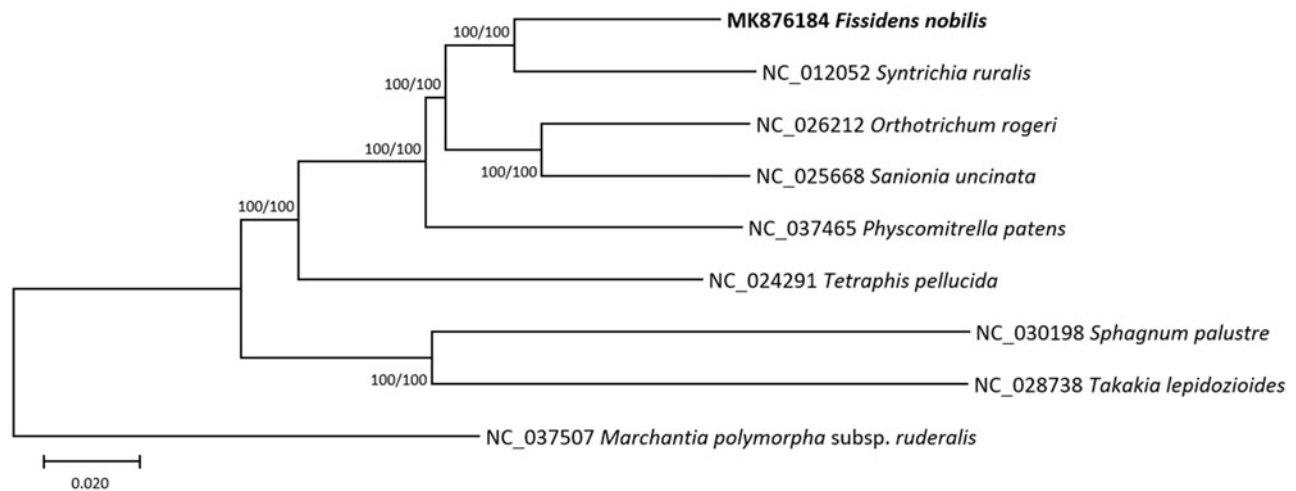
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Figure 1. Neighbor joining (bootstrap repeat is 10,000) and maximum likelihood (bootstrap repeat is 1,000) phylogenetic tree of 10 complete chloroplast genomes: *Fissidens nobilis* (MK876184 in this study), *Syntrichia ruralis* (NC_012052), *Orthotrichum 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, respectively.

Disclosure statement

No potential conflict of interest was reported by the authors.

Funding

This work was supported by InfoBoss Research Grant [IBG-0027].

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References

Crosby MR, Magill RE, Allen B, He S. 2000. A checklist of the mosses. St. Louis: Missouri Botanical Garden.

Jonathan Shaw A, Devos N, Liu Y, Cox CJ, Goffinet B, Flatberg KI, Shaw B. 2016. Organellar phylogenomics of an emerging model system: *Sphagnum* (peatmoss). Ann Bot. 118:185–196.

Katoh K, Standley DM. 2013. MAFFT multiple sequence alignment software version 7: improvements in performance and usability. Mol Biol Evol. 30:772–780.

Kumar S, Stecher G, Li M, Knyaz C, Tamura K. 2018. MEGA X: molecular evolutionary genetics analysis across computing platforms. Mol Biol Evol. 35:1547–1549.

Li H. 2013. Aligning sequence reads, clone sequences and assembly contigs with BWA-MEM. Quantit Biol. arXiv preprint arXiv:13033997.

Li H, Handsaker B, Wysoker A, Fennell T, Ruan J, Homer N, Marth G, Abecasis G, Durbin R. 2009. The sequence alignment/map format and SAMtools. Bioinformatics. 25:2078–2079.

Liu Y, Johnson MG, Cox CJ, Medina R, Devos N, Vanderpoorten A, Hedenäs L, Bell NE, Shevock JR, Aguero B, et al. 2019. Resolution of the ordinal phylogeny of mosses using targeted exons from organellar and nuclear genomes. Nature Commun. 10:1485.

Oliver MJ, Murdock AG, Mishler BD, Kuehl JV, Boore JL, Mandoli DF, Everett KD, Wolf PG, Duffy AM, Karol KG. 2010. Chloroplast genome sequence of the moss *Tortula ruralis*: gene content, polymorphism, and structural arrangement relative to other green plant chloroplast genomes. BMC Genom. 11:143.

Pursell RA, Bruggeman-Nannenga MA. 2004. A revision of the infrageneric taxa of *Fissidens*. Bryologist. 107:1–20.2.0.CO;2.

Sugiura C, Kobayashi Y, Aoki S, Sugita C, Sugita M. 2003. Complete chloroplast DNA sequence of the moss *Physcomitrella patens*: evidence for the loss and relocation of rpoA from the chloroplast to the nucleus. Nucleic Acids Res. 31:5324–5331.

Suzuki T, Inoue Y, Tsubota H. 2018. Molecular phylogeny of the genus *Fissidens* (Fissidentaceae, Bryophyta) and a refinement of the infrageneric classification. Mol Phylogenet Evol. 127:190–202.

Zerbino DR, Birney E. 2008. Velvet: algorithms for *de novo* short read assembly using de Bruijn graphs. Genome Res. 18:821–829.

Zhao Q, Wang Y, Kong YM, Luo D, Li X, Hao P. 2011. Optimizing *de novo* transcriptome assembly from short-read RNA-Seq data: a comparative study. BMC Bioinformatics. 12:S2.