

MITOGENOME ANNOUNCEMENT



The multipartite mitochondrial genome of *Fallopia multiflora* (Caryophyllales: Polygonaceae)

Chang-Kug Kim^a  and Yong-Kab Kim^b

^aGenomics Division, National Institute of Agricultural Sciences, Jeonju, Korea; ^bSchool of Electrical Information Communication Engineering, Wonkwang University, Iksan, Korea

ABSTRACT

Fallopia multiflora is an important Oriental herb belonging to the family Polygonaceae. The *F. multiflora* mitochondrial genome consists of two circular chromosomes that were 200,352- and 112,098-nucleotides long. The mitochondrial genome encodes 57 genes, including 34 protein-coding genes, 20 transfer RNA (tRNA) genes, and three ribosomal RNA (rRNA) genes. When accounting for 3 overlapping genes, 38 genes were found in chromosome I, and 22 in chromosome II. The phylogenetic analysis suggests that *F. multiflora* is closely related to *Beta macrocarpa* and *Silene latifolia*.

ARTICLE HISTORY

Received 7 December 2017
Accepted 18 January 2018

KEYWORDS

Fallopia multiflora;
Polygonaceae family;
mitochondrial genome

Fallopia multiflora (Hashuoh in Korean) is an important herb in Korea, Japan, and China (Han et al. 2016). We extracted genomic DNA from fresh leaves collected from the Oriental Medicine Resource Center of Wonkwang University (geographic coordinate: N 35°56'38", E 126°57'16"). The whole body specimen was registered to the National Agrobiodiversity Center (<http://genebank.rda.go.kr/>) under the voucher number IT 272664. A total of 4.76 Gbp of data was obtained using the Illumina MiSeq platform (San Diego, CA). DNA libraries were constructed from the Illumina paired-end (PE) library using the Illumina platform.

The mitochondrial genome of *F. multiflora* consists of two circular chromosomes, I (GenBank accession number: MF611850), and II (MF611851). The chromosomes were numbered based on the genome size, and the lengths of the chromosomes were 200,352 and 112,098 nucleotides. *Fallopia multiflora* had two mitochondrial genomes.

Multipartite mitochondrial genomes have been reported in some plants, animals, and fungi (Wei et al. 2012).

The mitochondrial genome of *F. multiflora* encoded 57 genes, including 34 protein-coding genes, 20 transfer RNA (tRNA) genes, and three ribosomal RNA (rRNA) genes. Of these 57 genes, 38 were found in chromosome I, and 22 in chromosome II. Three genes overlapped. In addition, we identified 15 open reading frames (ORFs) and splicing variants of the *nad1*, *nad2*, and *nad5* genes. Interestingly, the *nad1* and *nad5* splicing genes were located at exons 1, 2, 3 in chromosome II and exons 4, 5 in chromosome I. Phylogenetic relationships of 15 common *F. multiflora* protein-coding sequences were revealed by comparing data with the genomes of eight other reported species in the Pentapetalae subdivision. The phylogenetic analysis suggested that *F. multiflora* is closely related to the *Beta macrocarpa* and *Silene latifolia* groups (Figure 1).

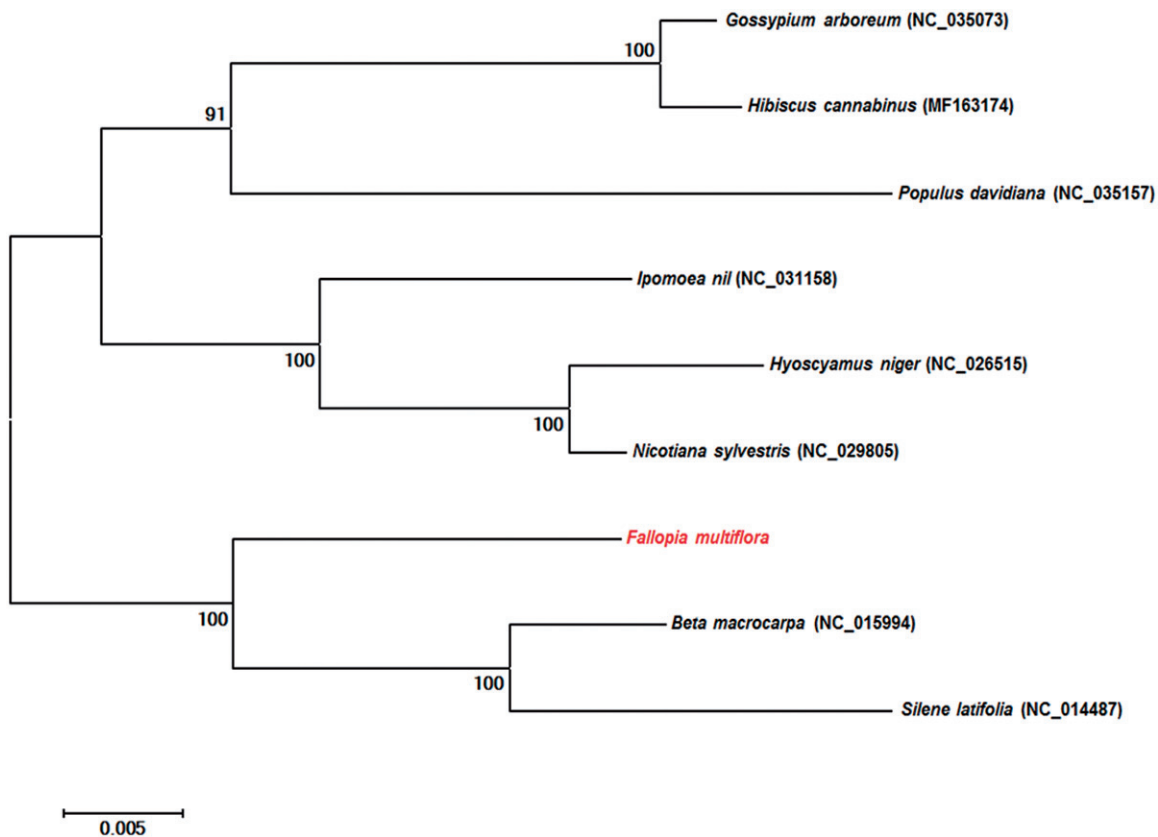


Figure 1. Phylogeny of *F. multiflora* and eight related species based on mitochondrial genome sequences. The phylogenetic tree was constructed using maximum likelihood analysis with 1000 bootstrap replicates based on the full mitochondrial genomes of nine species from the Pentapetalae subdivision.

Disclosure statement

The authors declare no conflict of interest.

Funding

This paper was supported by Wonkwang University in 2017 (Wonkwang 2017).

ORCID

Chang-Kug Kim  <http://orcid.org/0000-0002-8770-1736>

References

- Han EH, Cho K, Goo Y, Kim M, Shin YW, Kim YH, Lee SW. 2016. Development of molecular markers, based on chloroplast and ribosomal DNA regions, to discriminate three popular medicinal plant species, *Cynanchum wilfordii*, *Cynanchum auriculatum*, and *Polygonum multiflorum*. *Mol Biol Rep.* 43:323–332.
- Wei DD, Shao R, Yuan ML, Dou W, Barker SC, Wang JJ. 2012. The multipartite mitochondrial genome of *Liposcelis bostrychophila*: insights into the evolution of mitochondrial genomes in bilateral animals. *PLoS One.* 7:e33973.