

The complete chloroplast genome of *Hemerocallis fulva*

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ABSTRACT

We have sequenced the complete chloroplast genome of *Hemerocallis fulva*, a species of the Asphodelaceae family, through Illumina HiSeq paired-end sequencing. The total size of chloroplast genome of *Hemerocallis fulva* was 155,855 bp with a large single-copy (LSC) region of 84,607 bp, a small single-copy (SSC) region of 18,508 bp, and a pair of identical inverted repeat regions (IRs) of 26,370 bp. The genome contained a total of 112 genes, including 79 protein-coding genes, 29 transfer RNA (tRNA) genes, and 4 ribosomal RNA (rRNA) genes. The phylogenetic analysis of *Hemerocallis fulva* with 10 related species exhibited the closest taxonomical relationship with Aloe species in the Asphodelaceae family.

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Main text

Hemerocallis fulva, with common name of daylily, belongs to the genus *Hemerocallis* which consists of approximately 19 perennial flowering plants and is a part of the Asphodelaceae

family which habitats throughout the Northern and Southern Hemispheres. *Hemerocallis fulva* has been known for effective on antihemorrhagic, lumbar pain, and stomachache and used as medicinal plant in Korea. The leaves of *Hemerocallis fulva*

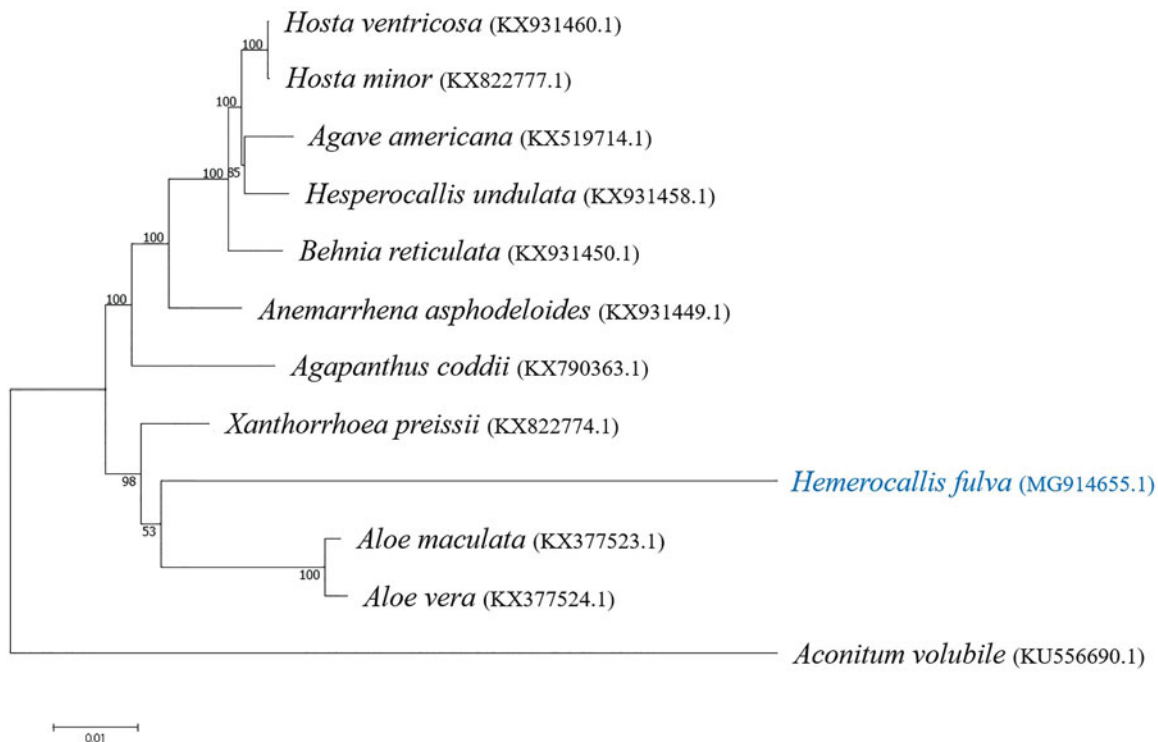




Figure 1. Phylogenetic analysis of *H. fulva* with 11 species by neighbor-joining (NJ) methods. Phylogenetic tree was generated using complete chloroplast genome sequences, including outgroup species of *Aconitum volubile*. Numbers in the nodes are the bootstrap values from 1000 replicates.

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were provided from Hantaek botanical garden (www.hantaek.co.kr) in Yongin-si, Korea (37° 05'40.4"N, 127°24'23.7"E) and used to construct the genomic library for Illumina paired-end (PE) sequencing. The high-quality PE reads were assembled by CLC Assembly Cell (ver. 4.010, CLC QIAGEN, Hilden, Germany), followed by manual curation through PE reads mapping (Kim et al. 2015). Annotation of the complete chloroplast genome was performed with GeSeq and manual corrections (Tillich et al. 2017). The complete chloroplast genome sequence of *H. fulva* was submitted to GenBank with the accession number of MG914655.

The complete chloroplast genome of *H. fulva* was 155,855 bp in length with 37.38% of G + C content, comprising a large single copy (LSC) region of 84,607 bp, a small single copy (SSC) region of 18,508 bp, and a pair of inverted repeat (IRa and IRb) regions of 26,370 bp. The genome contained 112 genes, including 79 protein-coding genes, 29 tRNA genes, and 4 rRNA genes. In addition, 58 simple sequence repeats (SSR) were detected using SSR-identification program (Beier et al. 2017).

In order to investigate the evolutionary relationship, the complete chloroplast genome sequences of *H. fulva* in this analysis and 10 related species from GenBank with *Aconitum volubile* as an outgroup were aligned using MAFFT (ver. 7.271) (Katoh et al. 2002), followed by phylogenetic tree construction obtained from a maximum likelihood (ML) analysis with 1000 bootstraps using MEGA 7.0 (Kumar et al. 2016). The phylogenetic tree exhibited the close relationship of genus *Hemerocallis* and genus *Aloe* in the family of Asphodelaceae (Figure 1).

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Disclosure statement

No potential conflict of interest was reported by the authors.

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