

## Mitochondrial DNA Part B Resources

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## The complete chloroplast genome of *Allium fistulosum*

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### ABSTRACT

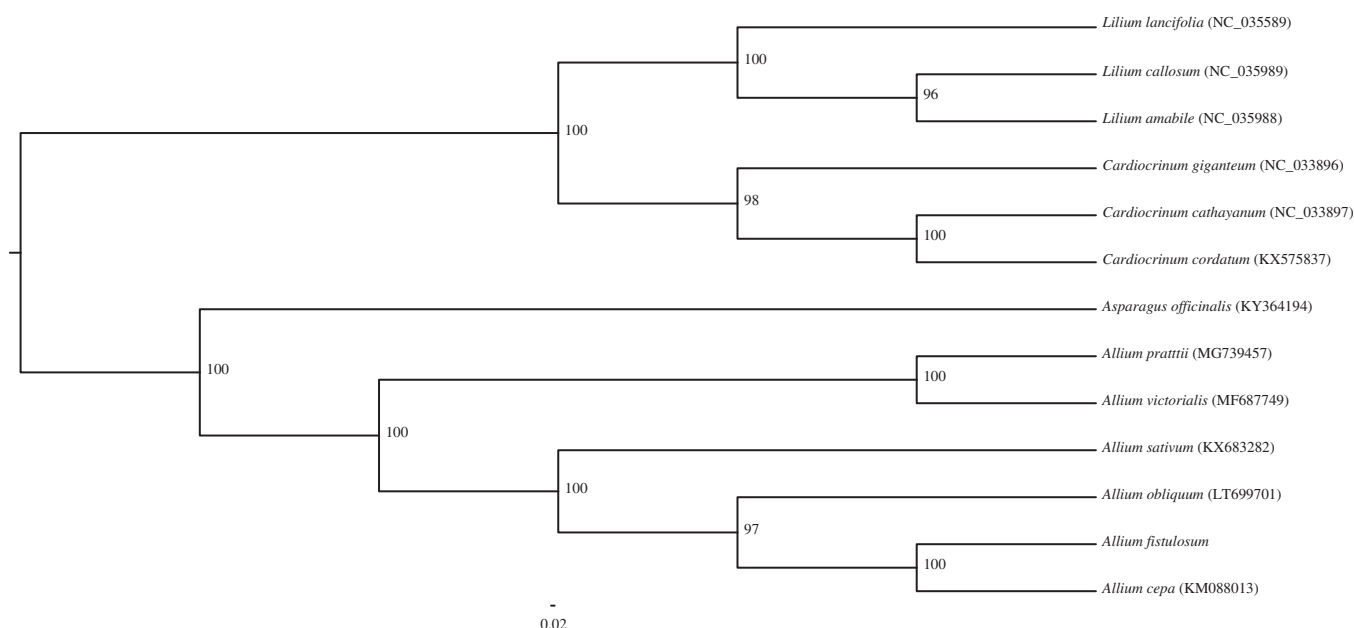
The complete chloroplast genome of *Allium fistulosum* (Bunching onion) was determined. The length of the complete chloroplast genome is 153,164 bp. The whole chloroplast genome consists of 82,237 bp long single copy (LSC) and 17,907 bp small single copy (SSC) regions, separated by a pair of 26,510 bp inverted repeat (IR) regions. The *Allium fistulosum* chloroplast genome encodes 114 annotated known unique genes including 80 protein-coding genes, 30 tRNA genes, and four rRNA genes.

### ARTICLE HISTORY

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### KEYWORDS

*Cepa*; chloroplast genome; phylogenetic analysis



**Figure 1.** Phylogenetic analysis of *A. fistulosum* with 12 related species. Numbers in the nodes are the bootstrap values from 1000.

Species of *Allium* L. section *Cepa* (Mill.) Prokh. (Amaryllidaceae) are endangered and economical important plants in the world. *Allium* sect. *Cepa* consists of 12 species (Gurushidze et al. 2007). Two most economically important cultivated species are *Allium cepa* L. and *Allium fistulosum* L. *A. fistulosum* is possibly native to West China and widely cultivated elsewhere (Xu and Kamelin 2000). Up to now all phylogenetic analyses on *Allium* sect. *Cepa* were based upon a few genes, it is prudent and necessary to examine further evidence before adopting this taxonomic treatment. We

assembled the complete cp genome of *A. fistulosum* to provide genomic and genetic sources for further research on economical important species of section *Cepa*. The fresh leaves of *A. fistulosum* were provided by Kunming Botanical Garden, section of Sino-Uzbekistan Global Allium Garden, Yunnan province, China. Voucher specimen was deposited in the Herbarium of Kunming Institute of Botany, Chinese Academy of Sciences (KUN, ZY087). Total DNA was extracted from 100 mg of fresh leaves using the modified CTAB method (Doyle and Doyle 1987). Genomic DNA was fragmented into

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500 bp to construct pair-end library. Illumina libraries were prepared according to the manufacturer's protocol and then sequenced using an Illumina HiSeq 2500 system at BGI (Shenzhen, Guangdong, China). We assembled the cp genome following the approach described in Jin et al. (2018). The plastome of *A. cepa* was used as reference genome for assembly (Genbank accession: KM088013). The cp genome of *A. fistulosum* was annotated using Geneious v10.2 (Kearse et al. 2012), then start and stop codons and intron/exon boundaries were manual proofread. The annotated chloroplast genome of *A. fistulosum* has been deposited into the GenBank with the Accession number MH926357. Phylogenetic analysis was performed using RAXML-HP BlackBox v8.1.24 software (Stamatakis 2006) with the GTRGAMMAI model as suggested (RAXML manual). The phylogenetic analysis of 12 chloroplast genomes showed that *A. fistulosum* is closely related to *A. cepa* (Figure 1).

The complete cp genome sequence of *A. fistulosum* is 153,164 bp and shows a characteristic circular structure, including a pair of IRs (26,510 bp, GC – 42.7% for each) that divide the genome into two single-copy regions (LSC 82,237 bp, GC – 34.6%; SSC 17,907 bp, GC – 29.7%), whereas coding regions (92,124 bp, GC – 39.5%) and non-coding regions (92,124 bp, GC – 32.8%). There are a total of 134 genes in the genome, including 80 protein-coding genes, 30 tRNA genes, four ribosomal RNA genes, and 20 duplicated genes. Among these, 13 genes (*atpF*, *rps16*, *rpoC1*, *petB*, *petD*, *rpl16*, two *rpl2*, two *rps12*, two *ndhB* and *ndhA*) contain a single intron and two genes (*ycf3* and *clpP*) contain double intron. The two (*ycf15* and *rps2*) genes are putative pseudogenes in the complete cp genome of *A. fistulosum*. This complete cp genome can be further used for population genomic studies, phylogenetic analyses, genetic engineering studies of genus *Allium*.

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## Disclosure statement

The authors declare no conflicts of interest and are responsible for the content.

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