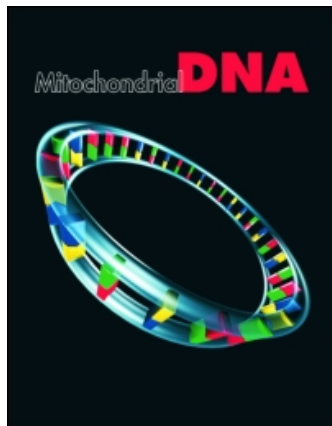


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The complete chloroplast genome sequence of *Fagopyrum cymosum*

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MITOGENOME ANNOUNCEMENT

The complete chloroplast genome sequence of *Fagopyrum cymosum*Jun Yang¹, Chaolong Lu^{1,2}, Qi Shen^{1,3}, Yuying Yan^{1,4}, Changjiang Xu^{1,4}, and Chi Song¹¹Institute of Chinese Materia Medica, China Academy of Chinese Medical Sciences, Beijing, China, ²Maize Research Institute, Sichuan Agricultural University, Wenjiang, China, ³Guizhou Rapeseed Institute, Guizhou Province of Academy of Agricultural Sciences, Guiyang, China, and ⁴Research Center of Buckwheat Industry Technology, Guizhou Normal University, Guiyang, China**Abstract**

Fagopyrum cymosum is a traditional medicinal plant. In this study, the complete chloroplast genome of *Fagopyrum cymosum* is presented. The total genome size is 160,546 bp in length, containing a pair of inverted repeats (IRs) of 32,598 bp, separated by large single copy (LSC) and small single copy (SSC) of 84,237 bp and 11,014 bp, respectively. Overall GC contents of the genome were 36.9%. The chloroplast genome harbors 126 annotated genes, including 91 protein coding genes, 29 tRNA genes, and six rRNA genes. Eighteen genes contain one or two introns. Phylogenetic analyses indicated a clear evolutionary relationship among species of Caryophyllales.

KeywordsChloroplast, *Fagopyrum cymosum*, genome sequence, medicinal plant**History**

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Buckwheat is an important nutrient-rich pseudo-cereal crop. The crop is rich in carbohydrates, flavonoids, and other desirable physiological products, such as rutin, which has anti-oxidant, anti-inflammatory, and anti-hypertensive functions, and cannot be found in other grains (Thwe et al., 2013). Hence, buckwheat has been produced as healthy grain, medicinal tea, or health-care drugs (Demidenko et al., 2011). *Fagopyrum cymosum* is one of the wild-type species of buckwheat (Yamane et al., 2003). Buckwheat belongs to Polygonaceae family, however, remains uncertain regarding the taxonomy relationship to other species within the Caryophyllales and the asterids. In the past years, chloroplast is viewed as important research resources in plant phylogenetic analysis and evolution studies for their uniparental inheritance mode and relatively conservative sequences (Huang et al., 2014; Zeng et al., 2014). Logacheva et al. (2008) reported a complete chloroplast genome sequence from *Fagopyrum esculentum* ssp. *ancestrale*, a wild ancestor of cultivated common buckwheat, has elucidated the sister relationship between Caryophyllales (including Polygonaceae) and asterids (Logacheva et al., 2008). In the article, complete chloroplast genome of *Fagopyrum cymosum* is presented to provide useful data for the phylogenetic research of buckwheat.

Total genome DNA of *Fagopyrum cymosum* was extracted to construct 180 bp small-size-fractionated libraries according to NEBNext Ultra DNA library Prep Kit for Illumina (Illumina Inc., San Diego, CA). Whole genome sequencing was executed using

Illumina Hiseq 1500 Genome Analyzer (Illumina Inc., San Diego, CA) (rapid run model configuration for pair-end 100 reads) at the Institute of Chinese Materia Medica in China. Raw reads were filtered by the standard method (Patel & Jain, 2012). Then 3,113,101 filtered reads were assembled into the complete chloroplast genome using SOAPdenovo software (Algorithmic Biology Lab, San Diego, CA) (Luo et al., 2012). *Fagopyrum esculentum* ssp. *ancestrale* chloroplast genome sequence was used as a reference genome (Qian et al., 2013). Chloroplast genome annotation is described according to methods of Liu et al. (2012). From them, the most homologous clusters of protein, cDNA, and rRNA from GenBank were allocated on *Fagopyrum cymosum* chloroplast genome with the combination of Blastx, Blastn, protein2genome, and est2genome programs (Liu et al., 2012). And the inverted repeats were identified using the vmatch software tool (vmatch software tool) (Abouelhoda et al., 2004). tRNAs were identified using tRNAscan (Lowe Lab, Los Angeles CA) (Lowe & Eddy, 1997). The complete chloroplast genome sequence together with gene annotations was submitted to the GenBank under the accession number of KP404630.

To sum, the complete chloroplast genome of *Fagopyrum cymosum* has a total length of 160,546 bp. Similar to typical chloroplast genome structure in higher plants, it has a large single copy (LSC) region of 84,237 bp and a small single copy (SSC) region of 11,014 bp, and separated by a pair of inverted repeats IRs of 32,598 bp. The GC content of the whole chloroplast genome is 36.9%. The gene coding regions account for 58.3% of the genome. It includes 126 unique genes, composed of 91 protein-coding genes and six rRNA genes. Among these genes, 18 genes contain one or two introns. The chloroplast genome contains 29 different tRNA genes, and 10 are present in the IRs regions. Phylogenetic analyses indicated clear evolutionary relationship between *Fagopyrum cymosum* and species of Caryophyllales (Figure 1).

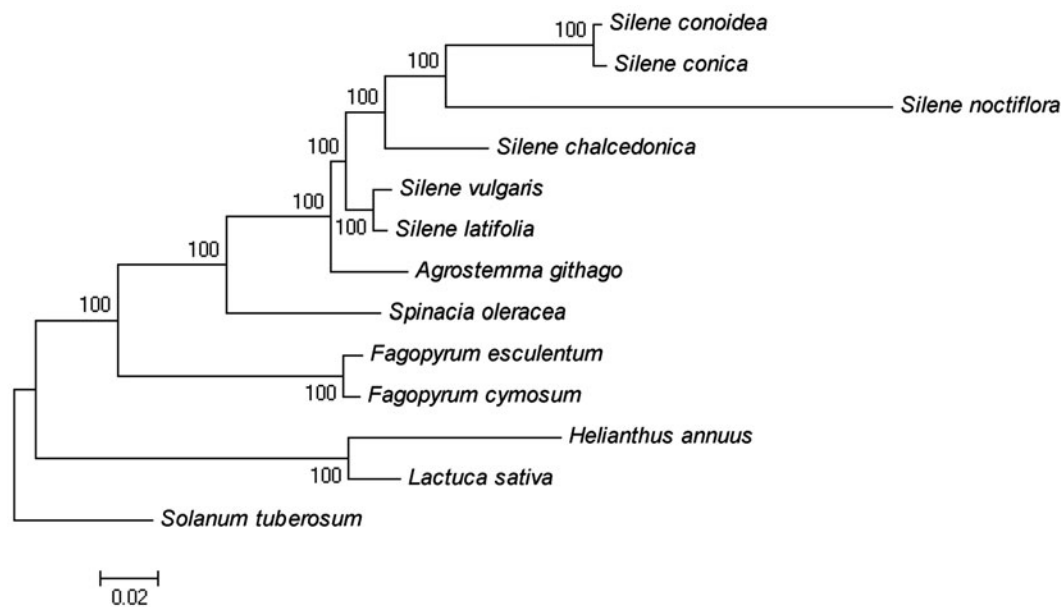


Figure 1. Phylogenetic tree of 13 species. For phylogenetic analyses of *Fagopyrum cymosum*, additional 12 species were selected and their complete chloroplast genome sequences were retrieved from NCBI. The chloroplast genome sequences were aligned using CLUSTALW 2 (Lowe Lab, Los Angeles CA) (Larkin et al., 2007). The phylogenetic tree was constructed by the neighbor-joining (NJ) method with MEGA 5 (MEGA Inc., Englewood, NJ) (Tamura et al., 2011). *Solanum tuberosum* was used as outgroup species (Qin et al., 2014). The phylogenetic tree is notable that *Fagopyrum cymosum* share closest relatives with *Fagopyrum esculentum* ssp. *ancestrale*. Both of them belong to Polygonaceae family. Similar to Logacheva et al. (2008), it also give us the important clue is that Polygonaceae belongs to Caryophyllales, only earlier separated with other Caryophyllales species, and remain closer relatives with asterids.

Declaration of interest

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