

## The complete chloroplast genome sequence of garden cress (*Lepidium sativum* L.) and its phylogenetic analysis in Brassicaceae family

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### ABSTRACT

Garden cress, *Lepidium sativum* L., is not only an important vegetable which is cultivated in the entire world, but also a widely used folk medicine for the treatment of hyperactive airways disorders. However, as a member of Brassicaceae, few studies have been carried out on its phylogenetic relationship with other Brassicaceae members. Herein, the complete chloroplast (cp) genome of garden cress was deciphered by the combination of Illumina HiSeq and PacBio HiSeq Platform after extracting of its cp DNA. The cp genome showed a typically quadripartite cycle with 154997 bp, including a pair of inverted repeats (IRa and IRb) of 26491 bp intersected by a large single copy (LSC) region of 84007 bp and a small single copy (SSC) region of 18008 bp. Totally, 128 unique genes were assembled in this cp genome, including 83 protein genes, 37 tRNAs and 8 rRNAs. A total of 73 simple sequence repeats (SSRs) with a length of at least 10 bp were detected. Phylogenetic analysis based on 30 cp genome of Brassicaceae family showed that the *L. sativum* was closely related to *L. virginicum*. This study provides important information for future evolution, genetic and molecular biology studies of *L. sativum*.

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### KEYWORDS

Garden cress; chloroplast genome; phylogenetic analysis; PacBio HiSeq



As a member of Brassicaceae family, garden cress (*Lepidium sativum* L.), a fast growing annual, glabrous, erect herb is cultivated as a culinary vegetable in the entire world (Diwakar et al. 2010). Furthermore, cress seeds which are rich in health promoting phytochemical constituents are widely used as a folk medicine for the treatment hypertension and renal diseases (Patel et al. 2009). The aqueous extract of garden cress seeds is also demonstrated to be effective to induce apoptosis and necrosis in the human breast cancer cells (Doke and Guha 2014). Because garden cress can be harvested several times throughout the year, its seed oil is taken as potential industrial oil for biodiesel production (Nehdi et al. 2012). Although garden cress has received very many of attention, few studies have been carried out on its phylogenetic.

The cp genome DNA was isolated from 5 g fresh leaves which were collected from Wanquan County, Hebei Province, China (40°45'56"N, 114°38'47"E) using chloroplast DNA extraction kit and stored in School of Life Science, Guizhou Normal University (No. ZB1044). Then two libraries with insert of 20 kb and 400 bp DNA fragments were constructed and sequenced by the platform of PacBio Sequel and Illumina HiSeq 4000, respectively. The cp genome of garden cress was assembled based on cp-related reads by the Canu programme using MHAP (MinHash Alignment Process) (Koren et al. 2017). For further correction and refinement, Then BLASR was used to map PacBio reads back to the assembly to refine the initial assembly. After that, Illumina reads were

mapped to the assembly using BWA-MEM (Li 2014) with default parameters to further correct the assembly. The complete cp genome was submitted to GenBank (accession number of MN176145).

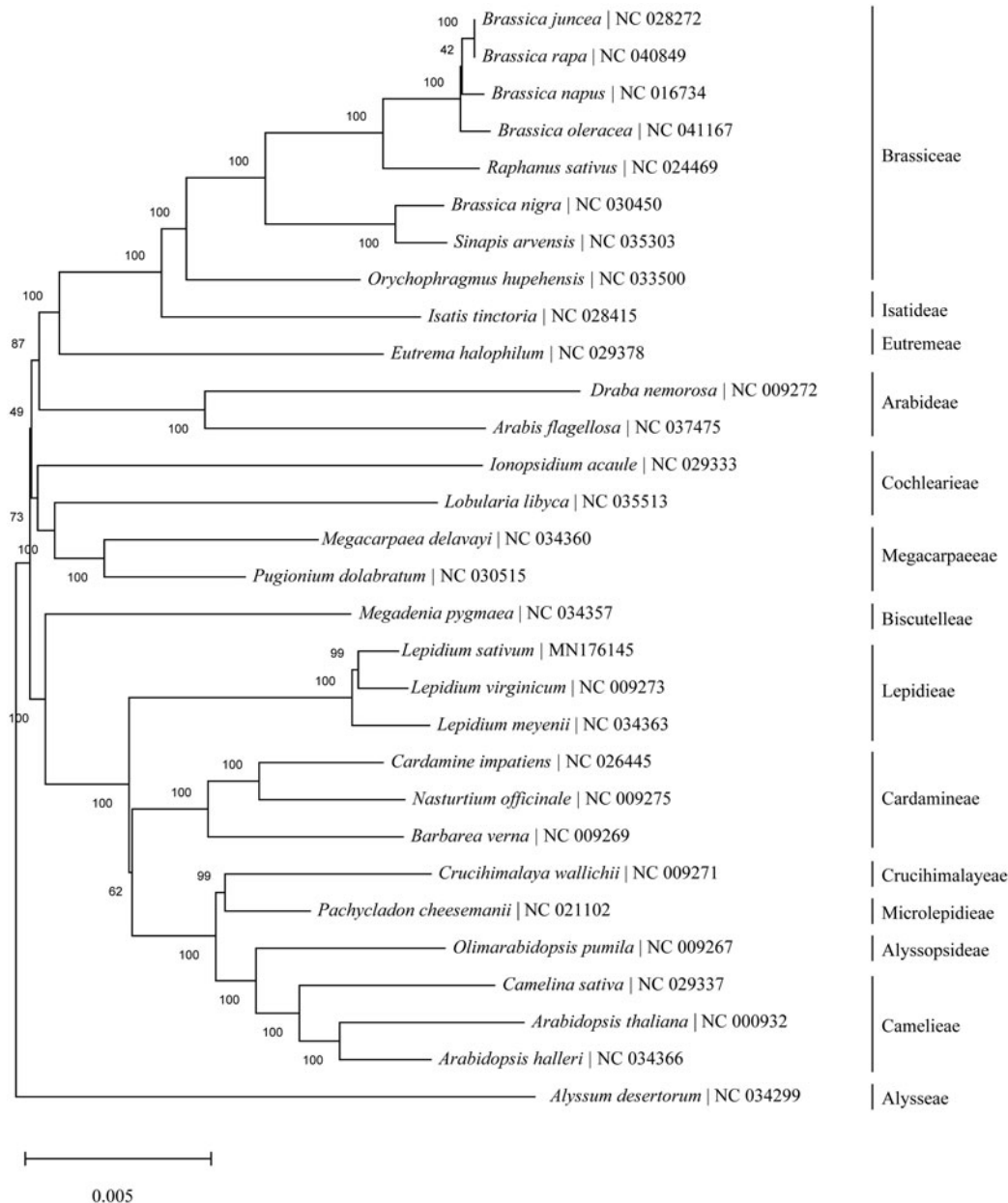
The complete cp genome sequence of garden cress is 154,997 bp in length, comprising of a large single-copy (LSC) region of 84,007 bp and a small single-copy (SSC) region of 18,008 bp, which is separated by a pair of inverted repeat (IRA and IRB) regions of 26,491 bp. Totally, 128 genes were assembled, including 83 protein coding genes (four genes with two copys), 37 tRNA genes and 8 rRNA genes. Among these genes, 83, 13 and 16 genes were distributed in LSC, SSC, IRa and IRb regions, respectively. Overall GC content of the whole genome is 36.31%. And 73 simple sequence repeats loci with a length of at least 10 bp were identified in the whole cp genome.

To decipher the phylogenetic relationships, 29 cp genome sequences of Brassicaceae family were downloaded from GenBank to construct phylogenetic trees by maximum likelihood analysis of protein coding genes using MEGA7 (Kumar et al. 2016). The bootstrap analysis with 1000 replicates was used to confirm the stability of each tree node. Compared to *L. meyenii*, another member of *Lepidium* genus, garden cress is more related with *L. virginicum*. The decipherment of chloroplast genome sequence of garden cress will be helpful for further study on its phylogenetic study, population genetics and molecular breeding (Figure 1).

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**Figure 1.** Phylogenetic tree of 30 Brassicaceae species, based on protein-coding genes in the cp genome. The tree was generated by maximum likelihood analysis of the conserved region. The bootstrap values were based on 1000 replicates.

## Disclosure statement

No potential conflict of interest was reported by the authors.

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