PLASTOME ANNOUNCEMENT

Characterization of the complete chloroplast genome sequence of Cardamine lyrata Bunge (Brassicaceae)

Xinhan Xu, a,b, Xuan Yao, a Caijuan Zhang, a and Pengguo Xia a

a Key Laboratory of Plant Secondary Metabolism and Regulation of Zhejiang Province, College of Life Sciences and Medicine, Zhejiang Sci-Tech University, Hangzhou, China; b Hangzhou Sanyeqing Agricultural Science and Technology Co. Ltd., Hangzhou, China

ABSTRACT

Cardamine lyrata Bunge 1833 grows near paddy fields, streams and shallow water. Its young stems and leaves can be eaten. It can also be used as medicine and has the effect of clearing away heat and dampness. The complete chloroplast genome sequence of the C. lyrata was determined and assembled. The complete genome is 155,170 bp in length, including a large single-copy region (LSC) of 84,270 bp, a small single-copy region (SSC) of 17,918 bp and two copies of inverted repeat (IR) regions of 26,491 bp. The overall GC content of C. lyrata is 36.2%. The genome of C. lyrata contains 131 genes, including 85 protein-coding genes (PCGs), 37 tRNAs, and 8 rRNAs. Phylogenetic analysis suggested that the ten species in Cardamine were clustered together into a single branch within the Brassicaceae family and C. amariniformis is at the base of the tree and C. lyrata and C. fallax are sister groups of the inner clade.

In this study, the materials of C. lyrata were from Zhenping County, Ankang City, Shaanxi Province (31°51'52.63"N, 109°34'11.4"E, and altitude 1206 m). A specimen was deposited in the Herbarium of Xi’an Botanical Garden (voucher number: Xun Lulu et al. LB19895, Lulu Xun, xunlulu20032006@126.com). The total genomic DNA of leaves was extracted by CTAB method (Doyle 1987) and sent to Majorbio (http://www.majorbio.com, China) for library construction and sequencing. Illumina NovaSeq 6000 platform was used for paired-end (PE) reads generation preparation with 2 × 150 bp PE reads. Libraries were size selected for 400 bp inserts. The raw sequencing data were Trimmed and filtered by Fastp software (Chen et al. 2018). The extracted DNA was deposited at Key Laboratory of Plant Secondary Metabolism and Regulation of Zhejiang Province, Zhejiang Sci-Tech University (http://sky.zstu.edu.cn) under the voucher number ZSTUX0102 (collected by Pengguo Xia and xpg_xpg@zstu.edu.cn). Using GetOrganelle v1.7.0 (Jin et al. 2020) assembled the entire chloroplast genome. Geneous Prime was used for gene annotation with reference to C. fallax (MZ043778). Genomic data were submitted to Genbank with serial number MZ846206.

The results showed that the complete chloroplast genome of was 155,170 bp, and the average GC content was 36.2%. The chloroplast genome consists of two reverse repeat regions (IR repeat) of 26,491 bp, a large single copy region (LSC) of 84,270 bp and a small single copy region (SSC) of 17,918 bp. We found that the complete chloroplast genome encoded 131 genes, including 85 protein coding genes, 37 tRNA genes and 8 rRNA genes.

In order to determine the phylogenetic position of C. lyrata in Brassicaceae, 17 Brassicaceae chloroplast genomes were downloaded from GenBank, and all protein coding gene sequences were compared with MAFFT (Nakamura et al. 2018). Carica papaya was used as the outgroup. The phylogeny was constructed by maximum likelihood (ML) method with IQTREE (Minh et al. 2020) software under the optimal model of TVM + F + R (Figure 1). The bootstrap value was 1000. The result of analysis showed that the Cardamine species formed a monophyletic clade within the Brassicaceae family and C. lyrata was the closest to C. fallax. Our results provide valuable data and shed light on the phylogenomic study of Brassicaceae.
Ethical approval

Research and collection of plant material was conducted according to the guidelines provided by Herbarium of Xi’an Botanical Garden. Permission was granted by Herbarium of Xi’an Botanical Garden to carry out research on the species.

Author contributions

P.X. conceived and designed this study. X. X. and C. Z. conducted analysis. X. X. and C. Z. contributed the analytical methods. X. Y. and C. Z wrote the manuscript. P.X. edited the manuscript. All authors have read and agreed to the published version of the manuscript.

Disclosure statement

No conflict of interest exists in the submission of this manuscript, and manuscript is approved by all authors for publication. And we declared comply with the International Union for Conservation of Nature (IUCN) policies research involving species at risk of extinction, the Convention on Biological Diversity and the Convention on the Trade in Endangered Species of Wild Fauna and Flora. No potential conflict of interest was reported by the author(s).

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