Characterization of the complete chloroplast genome of *Hordeum vulgare* L. var. *trifurcatum* with phylogenetic analysis

Yuanhang Ren, Hu Xia, Lidan Lu and Gang Zhao

Key Laboratory of Coarse Cereal Processing, Ministry of Agriculture and Rural Affairs, Sichuan Engineering and Technology Research Center of Coarse Cereal Industrialization, School of Food and Biological Engineering, Chengdu University, Chengdu, P. R. China

**ABSTRACT**

In the present study, the complete chloroplast genome of *Hordeum vulgare* L. var. *trifurcatum* was sequenced, assembled and compared with closely related species. The chloroplast genome of *Hordeum vulgare* L. var. *trifurcatum* was composed of 84 protein-coding genes (PCG), 8 ribosomal RNA (rRNA) genes, and 38 transfer RNA (tRNA) genes. The *Hordeum vulgare* L. var. *trifurcatum* chloroplast genome is 136,485 bp in size, with the GC content of 38.32%. Phylogenetic analysis based on the combined chloroplast gene dataset indicated that the *Hordeum vulgare* L. var. *trifurcatum* exhibited a close relationship with *Hordeum vulgare* subsp. *spontaneum* and *Hordeum vulgare* subsp. *vulgare*.

**KEYWORDS**

Tibetan hulless barley; chloroplast genome; phylogenetic analysis; molecular marker

**CONTACT** Lidan Lu (ulletdan@cdu.edu.cn) Key Laboratory of Coarse Cereal Processing, Ministry of Agriculture and Rural Affairs, School of Food and Biological Engineering, Chengdu University, Chengdu, Sichuan, 610106, China

© 2021 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group.

This is an Open Access article distributed under the terms of the Creative Commons Attribution License (http://creativecommons.org/licenses/by/4.0/), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.
38.32%, which is larger than that of *Hordeum vulgare* subsp. *spontaneum* (38.30%). The base compositions of the *Hordeum vulgare* L. var. *trifurcatum* chloroplast genome were as follows: A (30.93%), T (30.76%), G (19.22%) and C (19.10%). The complete chloroplast genome of *Hordeum vulgare* L. var. *trifurcatum* contains 84 protein-coding genes, 8 ribosomal RNA genes, and 38 transfer RNA (tRNA) genes. The number of protein-coding genes in *Hordeum vulgare* L. var. *trifurcatum* chloroplast genome was more than that in two subspecies (*Hordeum vulgare* L. var. *trifurcatum* and *Hordeum vulgare* subsp. *vulgare*), while the number of tRNA was less than that in the two subspecies. To investigate the phylogenetic status of *Hordeum vulgare* L. var. *trifurcatum*, we constructed a phylogenetic tree for 15 species. The protein-coding region of 13 genes conserved in the 15 species was used to construct combined a chloroplast gene set according to previous methods (Li, Xiang, et al. 2019; Wu et al. 2021). Bayesian (BI) analysis method (Li, Wu, et al. 2021) was used to construct the phylogenetic tree based on combined protein-coding genes of chloroplast genome as described by previous methods (Li, Yang, et al. 2020; Cheng et al. 2021; Li, Li, et al. 2021). MrBayes v3.2.6 (Ronquist et al. 2012) was used to construct the phylogenetic tree using Bayesian inference (BI) method. Two independent runs with four chains (three heated and one cold) each were conducted simultaneously for $2 \times 10^6$ generations. Each run was sampled every 100 generations. We assumed that stationarity had been reached when estimated sample size (ESS) was greater than 100, and the potential scale reduction factor (PSRF) approached 1.0. The first 25% samples were discarded as burn-in, and the remaining trees were used to calculate Bayesian posterior probabilities (BPP) in a 50% majority-rule consensus tree (Li, Ren, et al. 2019). According to the phylogenetic tree (Figure 1), the *Hordeum vulgare* L. var. *trifurcatum* exhibited a close relationship with *Hordeum vulgare* subsp. *spontaneum* (Bdolach et al. 2019) and *Hordeum vulgare* subsp. *vulgare* (Zeng et al. 2017).

**Disclosure statement**

The authors have declared that no competing interests exist.

**Funding**

This work was funded by Sichuan Science and Technology Program [2021YJ0477].

**Data availability statement**

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at [https://www.ncbi.nlm.nih.gov/](https://www.ncbi.nlm.nih.gov/) under the accession no. MW017635. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA717119, SRR14082750, and SAMN18478699, respectively.
