

The complete chloroplast genome sequence of *Oryza sativa* *Temperate japonica*

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ABSTRACT

In this study, the complete chloroplast genome of *O. sativa* *Temperate Japonica* *YunJing-24* was assembled using Illumina sequencing data. The complete chloroplast (cp) genome is 134,556 bp in length, including a pair of invert repeats (IRA and IRB) regions of 20,797 bp, large single-copy (LSC) region of 80,615 bp, and small single-copy (SSC) region of 12,347 bp. A total of 129 genes were predicted in the genome, including 87 protein-coding genes, 37 tRNA genes, and 8 rRNA genes. Phylogenetic analysis confirmed the phylogenetic relationship between *O. sativa* *Temperate Japonica* and other representative species.

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Oryza sativa; *Temperate japonica*; chloroplast genome; Poaceae

Rice is one of the important plants of Poaceae and is the main food for human beings. Rice varieties are divided into two major subspecies, *Indica* and *Japonica*, which are different from each other in geographical distribution, morphological, and physiological aspects (Londo et al. 2006). *Indica* is suitable for high temperature, strong light, and wet tropical and subtropical regions. It has the characteristics of weak resistance to fertilizer, light green leaves, slender grains, and easy threshing. However, *Japonica* is suitable for Temperate and subtropical high-altitude areas, with strong cold resistance and fertilizer resistance, dark green leaves, short round grains, not easy to threshing. The *O. sativa* *Temperate Japonica* is one of the five kinds of *O. sativa* *subsp. Japonica* (Xiong et al. 2011; Cheng et al. 2019). The complete chloroplast genome of *O. sativa* *Temperate Japonica* provides significant information for further studies on its taxonomy and population genetics.

Fresh leaves of *O. sativa* *Temperate Japonica* *YunJing-24* was collected from Kunming city, Yunnan province of China (24°23'N, 102°10'E), and the voucher specimen and DNA were deposited at Qingdao University of Science and Technology (specimen code HY0811). The total genomic DNA was extracted from fresh leaves of the sample using a modified CTAB method (Doyle and Doyle 1987). A genomic library with an insert size of 300 bp was constructed and the library was sequenced using the Illumina HiSeq platform in Novogene (Nanjing, China). A total of 945 Mb of 150 bp paired-end reads were generated.

The complete chloroplast genome sequence of *O. sativa* *Temperate Japonica* was assembled using the program NOVOPlasty4.2 software (Dierckxsens et al. 2017), with the

chloroplast genome of *O. sativa* *Tropical Japonica* (GenBank Accession No. KT289404) as the reference sequences and ribulose-1,5-bisphosphate carboxylase/oxygenase (*rbcl*) gene from *O. sativa* *cultivar Vettuver* (GenBank Accession No. MK932669) as the seed sequence. The final complete chloroplast genome annotation was performed using the GeSeq (Michael et al. 2017) and tRNAs were identified using the tRNAscan-SE v2.0.7 (Schattner et al. 2005).

The complete chloroplast genome of *O. sativa* *Temperate Japonica* (GenBank Accession No. MW001303) was 134,556 bp in length, with a GC content of 39.0%. The complete chloroplast genome shows a typical quadripartite structure with a pair of inverted repeats (IRs) of 20,797 bp, separated by a large single-copy region (LSC) of 50,615 bp and a small single-copy region (SSC) of 12,347 bp. A total of 129 genes were identified from *O. sativa* *Temperate Japonica* chloroplast genome, including 87 protein-coding genes, 37 tRNA genes, and 8 rRNA genes, 8 classes of genes (*rps16*, *atpF*, *petB*, *petD*, *rpl16*, *ndhB*, *ndhA*, *rpl2*) were found to contain two exons.

The complete chloroplast genome sequence of *O. sativa* *Temperate Japonica* and other species selected from the Genus *Oryza* were used to construct phylogenetic tree (Figure 1). The sequences were downloaded from the GenBank database and were aligned using MAFFT version 7 (Kato and Standley 2013) and then visualized and manually adjusted using BioEdit (Hall 1999). Mosel selected process in Mega version X (Kumar et al. 2018). GTR + G + I were selected by the Akaike Information Criterion. The maximum-likelihood method was used to infer the phylogenetic relationship, and the phylogenetic tree was constructed with Mega version X using 1000 bootstrap (Minh et al. 2013). The result shows

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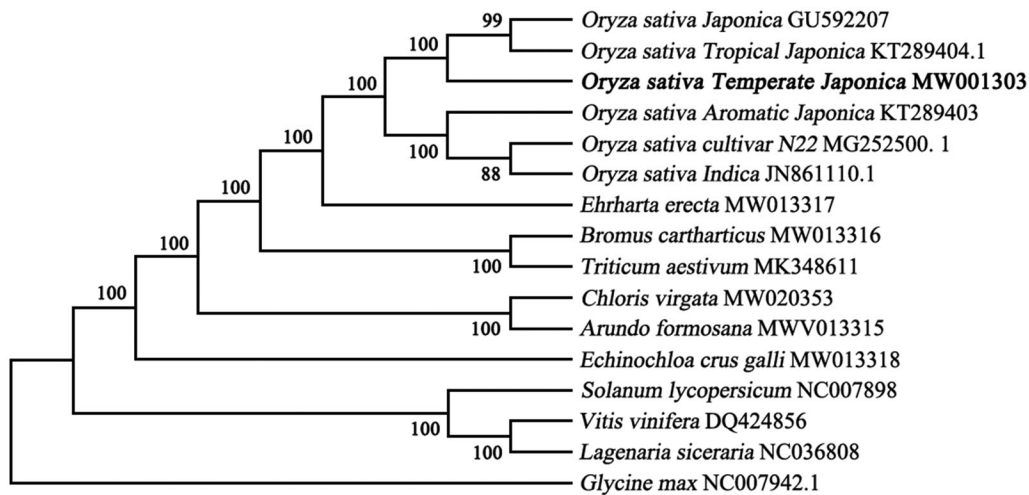


Figure 1. A maximum-likelihood tree illustrates the phylogenetic position of *O. sativa Temperate Japonica* among other species. The number on each node indicates bootstrap support value. After species is the chloroplast genome sequence accession numbers used by GenBank.

that *O. sativa Temperate Japonica* was clustered with other species from genus *Oryza* (Figure 1).

Disclosure statement

No potential conflict of interest was reported by the author(s).

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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/nucleotide/1929697386>) under the accession no. MW001303. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA692344, SRR13447968, and SAMN17320349, respectively.

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