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METHODS AND RESOURCES ARTICLE

The complete chloroplast genome sequence of *Leersia perrieri* of the rice tribe Oryzeae, Poaceae

Ge-Ran Hutang[1,2] · **Li-Zhi Gao**[1]

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Abstract *Leersia perrieri* (A. Camus) Launert is most closely related to the genus *Oryza* in the rice tribe Oryzeae, Poaceae. In this study, we first report the complete chloroplast genome sequence of *L. perrieri*. The circular genome is 136,196 bp in size, and comprises a pair of inverted repeat regions of 21,321 bp each, a large single-copy region of 81,587 bp and a small single-copy region of 11,968 bp. It harbors 130 genes, including 85 protein-coding genes, 37 transfer RNA genes and 8 ribosomal RNA genes. Maximum likelihood phylogenomic analysis shows that *L. perrier* and *L. tisserantii* are grouped into a single phylogenetic cluster and forms the most close outgroup of the genus *Oryza*.

Keywords *Leersia perrieri* · Chloroplast genome · Phylogenomic analyses

Leersia perrieri (A. Camus) Launert belongs to the genus *Leersia* of the tribe Oryzeae in the grass family, which is closely related to the genus *Oryza* with an estimated divergence time of nearly 14 million years ago (Guo and Ge 2005; Tang et al. 2010). In recent years, human activities have seriously destroyed wetland habitats, making the loss and quick decline of natural populations of *L. perrieri*, which usually occur in the wetlands, ditches and marshlands of Africa and Madagascar (Raimondo et al. 2009). As chloroplast sequences in plants can offer useful information for the reconstruction of complex evolutionary relationships, they have been extensively applied to species identification and phylogenetic analysis over the last years (Jansen et al. 2007; Moore et al. 2007; Parks et al. 2009; Ruhsam et al. 2015). The information of chloroplast genomes has been extensively applied in understanding plant genetic diversity and evolution that are of great importance in the conservation genetics (Ye et al. 2014; Zhang et al. 2016). The availability of chloroplast genome of *L. perrieri* will greatly enhance the conservation efforts of this endangered plant species that harbors valuable gene resources for rice breeding programs in the future.

In this study, we sequenced, assembled and annotated the chloroplast genome of *L. perrieri* using high-throughput genome sequencing technology. Live plants of *L. perrieri* were provided by the Genetic Resources Center of the International Rice Research Institute (IRRI) at Los Banos, Philippines. Total genomic DNA was extracted from fresh young leaves with a modified CTAB method (Li et al. 2013). According to the Illumina's protocol, the pair-end libraries were constructed and then sequenced using Hiseq2000 platform, obtaining a total of about 12.94 million high-quality clean reads (~1.09 Gb). We assembled and annotated the cp genome using CLC Genomic Workbench v6.5 (CLC bio, Denmark) and Dogma (https://dogma.ccbb.utexas.edu/), respectively. The annotated genomic sequence had been deposited into the GenBank database under the Accession No. of KY347906.

The circular genome of *L. perrieri* is 136,196 bp in size, and comprises a pair of inverted repeat (IR) regions of 21,321 bp each, a large single-copy region of 81,587 bp and a small single-copy region of 11,968 bp (Fig. 1). The chloroplast genome harbors 130 genes, including 85

✉ Li-Zhi Gao
lgao@mail.kib.ac.cn

[1] Plant Germplasm and Genomics Center, Germplasm Bank of Wild Species in Southwest China, Kunming Institute of Botany, The Chinese Academy of Sciences, Kunming 650201, China

[2] University of Chinese Academy of Sciences, Beijing 100039, China

Fig. 1 The chloroplast genome of *L. perrieri*

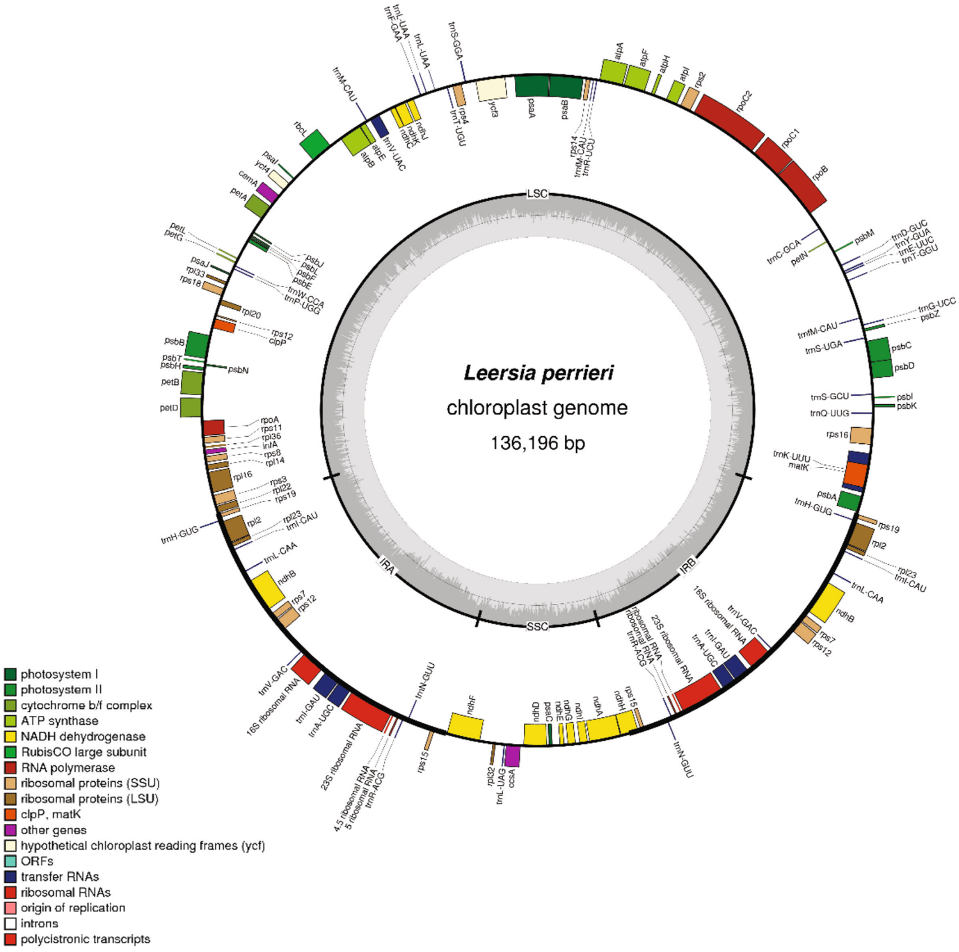
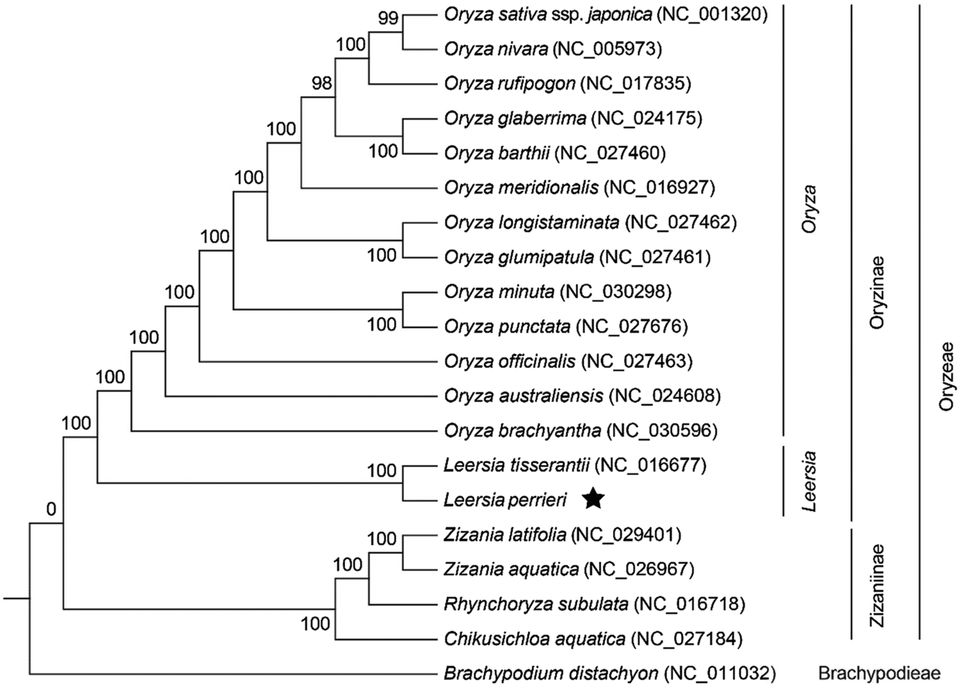


Fig. 2 Maximum likelihood (ML) tree inferred using MEGA (version 5.05) based on whole chloroplast genome sequences from *L. perrieri* and 19 other grass species



protein-coding genes, 37 transfer RNA genes and 8 ribosomal RNA genes. Of them, 70 genes are located on the negative strand and 60 resided on the positive strand. We found 13 genes contain introns, including *rpl2, ndhB, ndhA, rpl16, petD, petB, rps12, ycf3, atpF*, and *rps16*. The base composition is asymmetric (A: 30.70%; T: 30.40%; C: 19.38%; G: 19.52%) with an overall GC content of 38.90%.

To examine the phylogenetic position of *L. perrieri*, we constructed the phylogenetic tree between *L. perrieri* and 18 other closely related grass species, including 13 from Oryzinae, 4 from Zizaniinae and 1 from *Leersia*, using MEGA software (version 5.05) (Tamura et al. 2011) based on whole chloroplast genome sequences with maximum likelihood method (Fig. 2). *Brachypodium distachyon* from the subfamily Brachypodieae was selected as outgroup. Our results show that the topology of the phylogenetic tree agrees with the traditional tribe-level taxonomy of the genus *Oryza. L. perrieri* together with *L. Tisserantii* were clustered into a single phylogenetic cluster and formed the most close outgroup of the genus *Oryza*. The complete chloroplast genome of *L. perrieri* will build a strong foundation for its efficient conservation that greatly help to protect the precious rice gene pool from loss.

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Compliance with ethical standards

Conflict of interest The authors declare no competing financial interests.

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