The chloroplast genome of *Elytrigia repens* (L.) Nevski (Poaceae: Triticeae), a widespread perennial grass from Qinghai-Tibetan Plateau, China

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**ABSTRACT**

*Elytrigia repens* (L.) Nevski, belonging to Triticeae of Poaceae, is a wild-growing perennial grass, widely distributed in Qinghai-Tibetan Plateau of China. In this study, the complete chloroplast genome of *E. repens* was sequenced and analyzed. The complete chloroplast genome size is 134,749 bp with 38.3% GC content. It includes 136 genes, including 89 protein-coding genes, 39 tRNAs genes, and 8 rRNAs genes. Based on chloroplast genome sequences, further phylogenetic analyses between *E. repens* and other Triticeae species revealed that *E. repens*, *Connorochloa tenuis* and three *Elymus* species formed a distinct clade, showing closer relationships.

*Elytrigia repens* (L.) Nevski belongs to Triticeae of Poaceae. In Qinghai-Tibetan Plateau of China, *E. repens* is a widespread wild-growing perennial grass. Previous cultivation and physiological studies of *E. repens* demonstrated its tolerance to various abiotic stresses, and adaptability for soil and water conservation and rangeland improvement (Mahelka 2006; Gift et al. 2008; Pätsc et al. 2019). Additionally, *E. repens* was proved to be suitable for phytoremediation of soils contaminated with the metal ion. Its roots could accumulate significant amounts of zinc (Laidinen et al. 2018). Furthermore, the intergeneric hybrids between *Triticum aestivum* and *E. repens* could survive and produce seeds (Franke et al. 2008), which would generate well genetic resources for wheat breeding. *E. repens* is an allopolyploid grass. The nuclear genome of *E. repens* is assumed to inherit from *Pseudoroegneria* (St), *Hordeum* (H), and distant genetic sources (Pastova et al. 2019). Whereas, few nuclear and even organelle genomic sequences of *E. repens* are currently available. Compared to its complicated nuclear genome (Mahelka et al. 2005; Meng et al. 2012), the sequencing of *E. repens* chloroplast genome is simple, which could provide sequence resources for comparative genomics and evolutionary studies between *E. repens* and other Triticeae species.

The samples of *E. repens* were collected in Xining at an altitude of 2,324 m (36°73′79″ N, 101°74′86″ E), Qinghai Province, China. The voucher specimen (Accession number: FFK2012631141) was deposited in the National duplicate genebank for crops in Xining (Contact person: Dr. Liling Jiang). Total genomic DNA was extracted from fresh leaves using the improved CTAB method (Yu et al. 2019). According to the manufacturer’s protocol, 350 bp paired-end DNA library was constructed, and subsequently sequenced in Illumina NovaSeq PE150 Platform (Modi et al. 2021). Through filtering of adapter and low-quality bases, 8.8 Gb clean raw reads were generated, with 93% bases’ quality score meeting Q30. Using chloroplast genome sequences of *Triticum aestivum* (NC_002762) (Ogihara et al. 2002) and *Hordeum vulgare* (NC_008590) as references, our high-quality clean reads were assembled into circular scaffolds through SOAPdenovo V2.04 (Luo et al. 2012). The detailed parameters for genome assembling are as follows: avg_ins = 150, reverse_seq = 0, asm_ -flags = 3, pair_num_cutoff = 3, and map_len = 32.

The *E. repens* chloroplast genome is 134,749 bp in length with the overall GC content of 38.3%, which includes a large single-copy region (LSC) of 80,426 bp, a small single-copy region (SSC) of 12,769 bp, and independently inverted repeat region a and b (IRa and IRb) of 20,777 bp. In the chloroplast genome, a total of 136 genes were annotated through PGA software (Qu et al. 2019), including 89 protein-coding genes, 39 tRNAs genes, and 8 rRNAs genes. Twenty-two genes have two copies, including thirteen protein-coding genes and nine tRNAs genes. Additionally, nine protein-coding genes and six tRNAs genes contain an intron, respectively. Ycf3 even comprises two introns. Interestingly, the genomic sequences

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revealed RNA editing occurs in the start codon of rpl2. The chloroplast genome sequence and detailed genome annotation of *E. repens* had been submitted to GenBank under accession number MZ169384.

Furthermore, using *Oryza sativa* (NC_008155) as the outgroup, a Maximum-Likelihood phylogenetic tree was constructed (Figure 1), based on the chloroplast genome sequences of *E. repens* and other 15 Triticeae species by IQ-TREE 1.6.12 (Nguyen et al. 2015). The best suitable model for tree construction was calculated by ModelFinder (Kalyaanamoorthy et al. 2017). Phylogenetic analyses revealed that the 16 Triticeae species clustered into three main groups with 100% bootstrap value support. Furthermore, *E. repens*, *Connorochloa tenuis* and three *Elymus* species, including *Elymus kamoji*, *Elymus trachycaulus* and *Elymus dahuicus*, formed a distinct clade, representing closer relationships (Figure 1). In this study, the chloroplast genome of *E. repens* is completely sequenced and annotated, facilitating the elucidation of phylogenetic relationships between *E. repens* and its closely related species in Triticeae at the chloroplast-genome level.

**Disclosure statement**

All the authors declared no potential conflicts of interest.

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**Data availability statement**

The chloroplast genome sequence of *E. repens* sequenced in this study is deposited in NCBI GenBank database, accession number MZ169384. The associated accession number in SRA, BioSample and BioProject database is SRR14535700, SAMN19184023 and PRJNA729858, respectively (www.ncbi.nlm.nih.gov/bioproject/PRJNA729858).

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