The Complete Chloroplast Genome of *Poa pratensis* (Poaceae), a High-Quality Forage

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**Abstract**

*Poa pratensis* L. (Poaceae) is a hardy, persistent, attractive forage and turf grass adapted to a wide range of soils and climate. In this study, we release and detail the complete chloroplast genome sequences of *P. pratensis*. The whole chloroplast genome was 135,649 bp in length and comprised 131 genes, including 85 protein-coding genes, 38 tRNA genes, 8 rRNA genes. The *P. pratensis* chloroplast genome had a GC content of 38.3%. The result of phylogenetic analysis showed that *P. pratensis* was closely related to *P. pratensis* cv. Qinghai and *P. poophagorum*. This study would provide useful genetic information for the protection of *P. pratensis* and other related species.

**Keywords**

*Poa pratensis*, Chloroplast Genome, Phylogenetic Analysis, Poaceae

**1. Introduction**

*Poa pratensis* L., also known as Kentucky bluegrass, belongs to the Poaceae family. It is a hardy, persistent, attractive forage and turf grass adapted to a wide range of soils and climate [1]. *P. pratensis* is widely used in lawns, golf courses, landscapes, and sports fields as a prominent cool-season grass [2], and is the longest-established non-native vascular plant in the Antarctic [3]. The chloroplast genome can provide valuable genomic information for the systematic study and the conservation of rare species [4] [5]. Here, we sequenced and analyzed the complete chloroplast genome genome of *P. pratensis* based on Next-generation sequencing technology and compared it with other genome sequences of Trib. Poeae (Poaceae).
2. Materials and Methods

The samples of *P. pratensis* were collected in Ledu County, China (102.3E, 36.4N) and the voucher specimens (JingML2019002) are deposited in the Herbarium of College of Pharmacy, Qinghai Nationalities University, Xining, China. The whole-genome sequencing was conducted by Nanjing GenePioneer Biotechnologies Inc. (Nanjing, China) with the Illumina NovaSeq Sequencing System. Approximately 6.12 GB of clean data were yielded. The high-quality reads were applied to a *de novo* assembly performed using the program SPAdes assembler v3.10.1 [6]. The trimmed reads were mainly annotated by CpGAVAS2 (http://47.96.249.172.16019/analzer/home; [7]).

3. Results

The complete chloroplast genome (GenBank accession number: MT295102) of *P. pratensis* was 135,649 bp in length having 38.3% of total GC content. This chloroplast genome has a typical quadripartite structure (Figure 1), containing a
Table 1. Genes identified in the chloroplast genome of *Poa pratensis*.

| Category | Gene group | Gene name |
|----------|------------|-----------|
| Photosynthesis | Subunits of photosystem I | psaA, psaB, psaC, psaI, psaJ |
| Photosynthesis | Subunits of photosystem II | psbA, psbB, psbC, psbD, psbE, psbF, psbH, psbI, psbJ, psbK, psbL, psbM, psbN, psbT, psbZ |
| Photosynthesis | Subunits of NADH dehydrogenase | ndhA*, ndhB* (2), ndhC, ndhD, ndhE, ndhF, ndhG, ndhH, ndhI, ndhJ, ndhK |
| Photosynthesis | Subunits of cytochrome b/f complex | petA, petB*, petD*, petG, petL, petN |
| Photosynthesis | Subunits of ATP synthase | atpA, atpB, atpE, atpF*, atpH, atpI |
| Photosynthesis | Large subunit of rubisco | rbcL |
| Proteins of large ribosomal subunit | Proteins of large ribosomal subunit | rpl14, rpl16*, rpl2* (2), rpl20, rpl22, rpl23 (2), rpl32, rpl33, rpl36 |
| Proteins of small ribosomal subunit | Proteins of small ribosomal subunit | rps11, rps12** (2), rps14, rps15 (2), rps16*, rps18, rps19 (2), rps2, rps3, rps4, rps7 (2), rps8 |
| Ribosomal RNAs | Ribosomal RNAs | rrn16 (2), rrn23 (2), rrn4.5 (2), rrn5 (2) |
| Self-replication | Self-replication | trnA-UGC* (2), trnC-GCA, trnD-GUC, trnE-UUC, trnF-GAA, trnG-GCC, trnG-UCC*, trnH-GUG (2), trnL-CAU (2), trnL-GAU* (2), trnK-UUU*, trnL-CAA (2), trnL-UAA*, trnL-UAG, trnM-CAU, trnN-GUU (2), trnP-UGG, trnQ-UUG, trnR-ACG (2), trnR-UCU, trnS-GCU, trnS-GGA, trnS-UGA, trnT-GGU, trnT-UGU, trnV-GAC (2), trnV-UAC*, trnW-CCA, trnY-GUA, trnM-CAU |
| Transfer RNAs | Transfer RNAs | matK |
| Transfer RNAs | Transfer RNAs | clpP |
| Maturase | Maturase | |
| Protease | Protease | |
| Other genes | Other genes | cemA |
| Other genes | Other genes | ccsA |
| Other genes | Other genes | infA |
Genes of unknown function
Conserved hypothetical chloroplast ORF
ycf15 (2), ycf3**, ycf4

Figure 2. The maximum-likelihood (ML) phylogenetic tree based on complete chloroplast genome sequences.

large single-copy region of 79,774 bp, a small single-copy region of 12,771 bp, and two inverted repeat regions of 21,552 bp. A total of 131 genes are successfully annotated, including 85 protein-codon genes, 38 tRNA genes and 8 rRNA genes (Table 1). The rRNA genes, tRNA genes, and protein-coding genes account for about 6.11%, 29.01%, and 64.89% of all annotated genes, respectively.

4. Discussion

In order to reveal the phylogenetic position of P. pratensis with its close allies, a phylogenetic analysis was performed based on twelve complete chloroplast genomes sequence of of Trib. Poeae (Poaceae). The sequences were aligned by MAFFT v7.307 [8] and the maximum-likelihood tree (Figure 2) was built using MEGA7 [9]. Using the Tamura-Nei model model the ML phylogenetic analysis were conducted with MEGA v7.0.26 generating 200 bootstrap replicates to determine measures of nodal support with each run initiating from a random starting tree.

5. Conclusions

According to the result of phylogenetic analysis (Figure 1), the phylogenetic tree showed that P. pratensis was closely related to P. pratensis cv. Qinghai and P. poophagorum. P. pratensis cv. Qinghai is a common cultivated variety of P. pratensis, and its chloroplast genome has been reported by Wei et al. [10]. The P. pratensis cv. Qinghai chloroplast genome reported in paper of Wei et al. [10] is
43 bp shorter, and 6 fewer genes than the chloroplast genome we obtained. Such genomic differences may be the result of artificial domestication. This study would provide useful genetic information for the protection of *P. pratensis* and other related species.

6. Data Availability

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 number MT295102. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA699977, SRR13647703, and SAMN17817424 respectively.

Conflicts of Interest

No potential conflict of interest was reported by the authors.

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