

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 of *P. pratensis* based on Next-generation sequencing technology and compared it with other genome sequences of Trib. Poaceae (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/analyzer/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

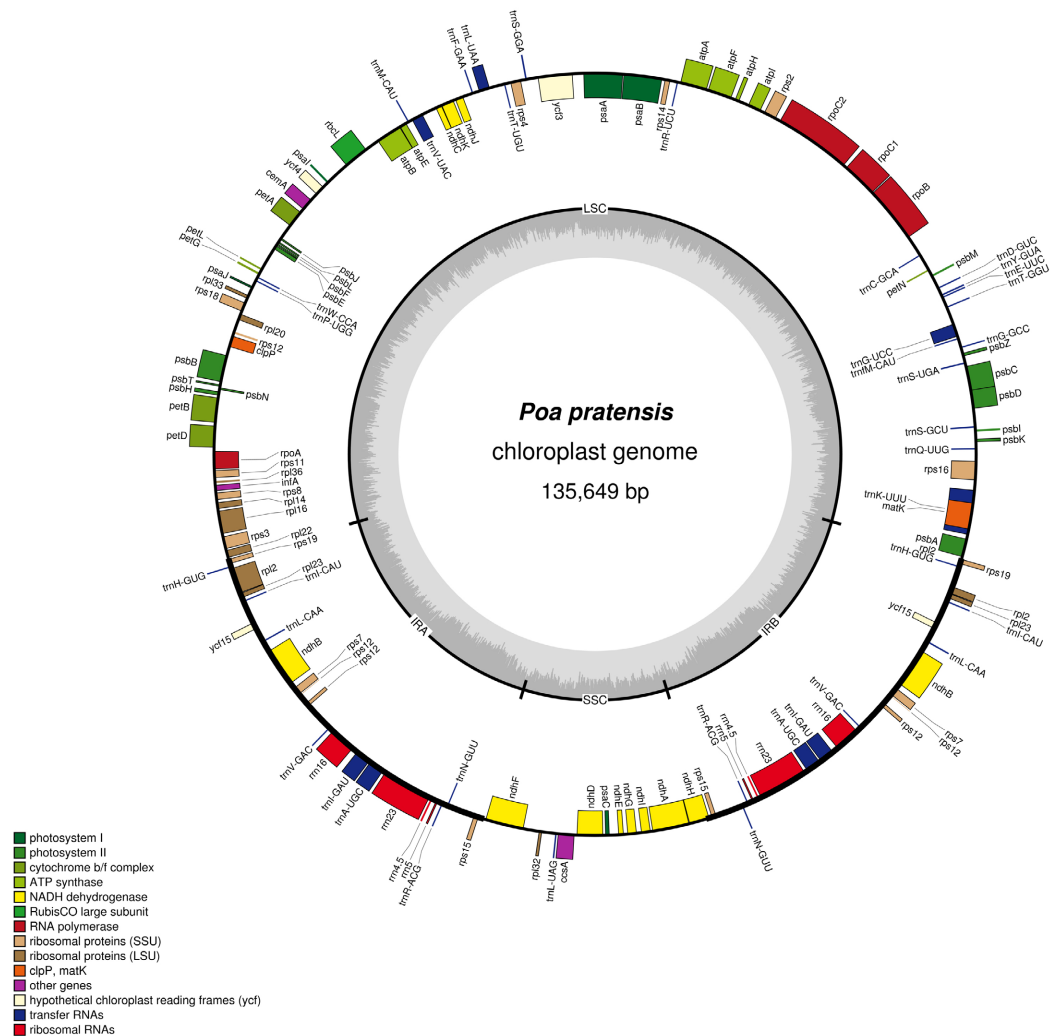


Figure 1. Gene map of the *Poa pratensis* chloroplast genome.

Table 1. Genes identified in the chloroplast genome of *Poa pratensis*.

Category	Gene group	Gene name
	Subunits of photosystem I	psaA, psaB, psaC, psaI, psaJ
	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
	Subunits of cytochrome b/f complex	petA, petB*, petD*, petG, petL, petN
	Subunits of ATP synthase	atpA, atpB, atpE, atpF*, atpH, atpI
	Large subunit of rubisco	rbcL
	Proteins of large ribosomal subunit	rpl14, rpl16*, rpl2* (2), rpl20, rpl22, rpl23 (2), rpl32, rpl33, rpl36
	Proteins of small ribosomal subunit	rps11, rps12** (2), rps14, rps15 (2), rps16*, rps18, rps19 (2), rps2, rps3, rps4, rps7 (2), rps8
	Subunits of RNA polymerase	rpoA, rpoB, rpoC1, rpoC2
	Ribosomal RNAs	rrn16 (2), rrn23 (2), rrn4.5 (2), rrn5 (2)
Self-replication		trnA-UGC* (2), trnC-GCA, trnD-GUC, trnE-UUC, trnF-GAA, trnG-GCC, trnG-UCC*, trnH-GUG (2), trnI-CAU (2), trnI-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
	Maturase	matK
	Protease	clpP
Other genes	Envelope membrane protein	cemA
	c-type cytochrome synthesis gene	ccsA
	Translation initiation factor	infA

Continued

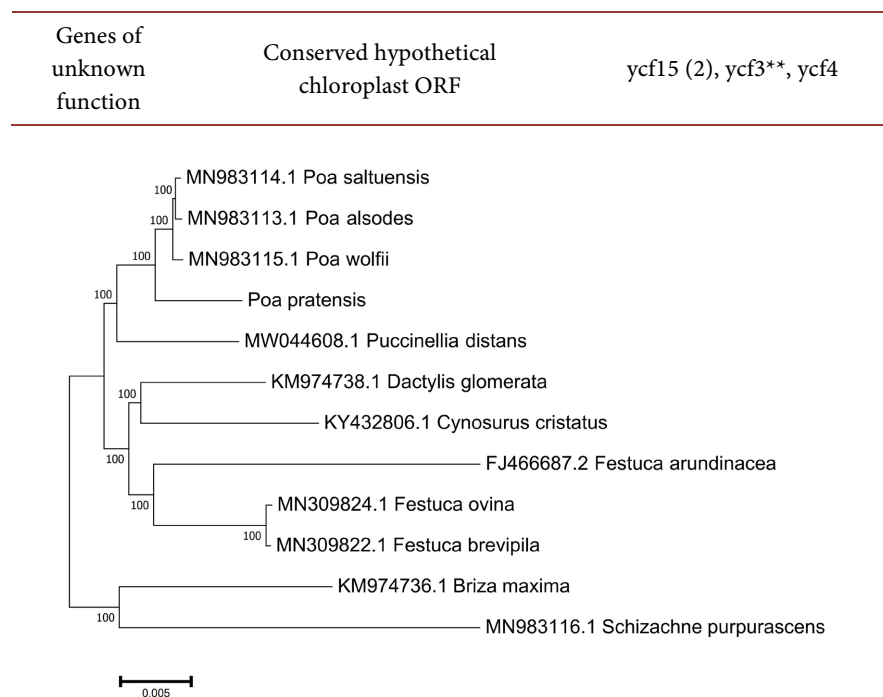


Figure 2. The maximum-likelihood (ML) phylogenetic tree based on complete chloroplast genome sequences.

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/> 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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