The complete chloroplast genome sequence of desert poplar (Populus euphratica)

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Li-Zhi Gao
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MITOGENOME ANNOUNCEMENT

The complete chloroplast genome sequence of desert poplar (*Populus euphratica*)

Qun-jie Zhang[1,2] and Li-zhi Gao[1]

[1]*Plant Germplasm and Genomics Center, Germplasm Bank of Wild Species in Southwest China, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming, China and* [2]*University of the Chinese Academy of Sciences, Beijing, China*

Abstract

The complete chloroplast sequence of the desert poplar (*Populus euphratica*), a plant well-adapted to salt stress, was determined in this study. The genome consists of 156,766 bp containing a pair of inverted repeats (IRs) of 16,591 bp separated by a large single-copy region and a small single-copy region of 84,888 bp and 27,646 bp, respectively. The chloroplast genome contains 130 known genes, including 89 protein-coding genes, 8 ribosomal RNA genes, and 37 tRNA genes; 18 of these are located in the inverted repeat region.

Keywords

Chloroplast genome, plastid, *Populus euphratica*

History

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Chloroplasts (plastids), originated from free-living cyanobacteria in eukaryotic cells via endosymbiosis, contain their own genome DNA (cpDNA), which is circular and about 150 kb in length (Rodríguez-Ezpeleta et al., 2005; Sato et al., 1999). They are the photosynthetic organelles of plants with great phylogenetic values due to relatively conserved structure and comparatively high substitution rate (Ravi et al., 2008). Up to date, there has been more than 500 eukaryote plastid genomes deposited in the NCBI database (http://www.ncbi.nlm.nih.gov). With the development of high-throughput genome sequencing technology, it becomes much more convenient to acquire the complete cp genome sequences now than ever. They can be obtained by a modified high salt chloroplast isolation method owing to the smaller size compared with the nucleic genome (Shi et al., 2012), or even directly filtered and assembled from total DNA sequence reads (Nock et al., 2011).

Populus euphratica, ranging from western China to northern Africa, is native to desert regions and can be grown under extremely hot and dry climates (Brosche et al., 2005; Gries et al., 2003; Wang et al., 2008). They are distinguished from other congeners by extraordinary adaptabilities to salt-stress (Brinker et al., 2010; Ottow et al., 2005) and thus play a crucial role in maintaining local arid ecosystems (Ma et al., 1997). Notably, it maintains greater growth as well as photosynthetic rates on high salinity earth than other poplar species (Janz et al., 2012; Wang et al., 2008) and can survive concentrations of NaCl in nutrient solution up to 450 mM (Gu et al., 2004).

Until now two chloroplast genomes have been reported in this genus, *P. trichocarpa* (NC_009143; Tuskan et al., 2006) and *P. alba* (NC_008235; Okumura et al., 2006). In this study, we reported and analyzed the complete cp genome of the desert poplar (*P. euphratica*). We obtained the whole genome sequence reads of *P. euphratica* (Ma et al., 2013) and then filtered and assembled the complete cp genome using SOAPdenovo software (Li et al., 2009). The annotation of the assembled genome was performed with Dual Organellar GenoMe Annotator (DOGMA) (http://dogma.ccbb.utexas.edu/). Default parameters were employed to predict protein-coding genes, transfer RNA (tRNA) genes, and ribosome RNA (rRNA) genes (Wyman et al., 2004). BLASTX and BLASTN searches against a custom database of previously published cp genomes identified locations of these putative genes. For genes with low sequence identities, manual annotation was performed to determine the position of start and stop codons depending on the translated amino acid sequence by using the chloroplast/bacterial genetic codes. Plastome map of the species was drawn by OGDraw v 1.2 (Lohse et al., 2007; Figure 1). The complete cp genome sequence together with gene annotations were submitted to the GenBank with the accession number of KJ624919.

The estimated size of the *P. euphratica* plastome is 156,766 bp. The quadripartite structure includes 84,888 bp of LSC and 27,646 bp of SSC separated by a pair of IR copies with the length of 16,591 bp (Figure 1). The GC content is 36.7%, and this AT-rich feature is similar to other plant plastomes (Li et al., 2014; Sato et al., 1999). Coding sequences constitute 57.8% of the *P. euphratica* plastome DNA. There are 113 unique genes, 20 of which are duplicated in IR regions. A total of 79 protein-coding genes (6 duplicated) encode photosynthesis-related proteins, genetic system related proteins, proteins with unique functions and proteins with unknown functions (*ycf*). In addition, 30 unique genes (7 duplicated) and 4 uniquely duplicated genes encode for tRNAs and rRNAs, respectively. It is our hope that this newly characterized *P. euphratica* chloroplast genome will provide useful resources for better understanding the physiology and evolution of the genus *Populus*.

Correspondence: Li-zhi Gao, Plant Germplasm and Genomics Center, Germplasm Bank of Wild Species in Southwest China, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming 650204, China. Tel/Fax: +86 8715223277. E-mail: Lgao@mail.kib.ac.cn.

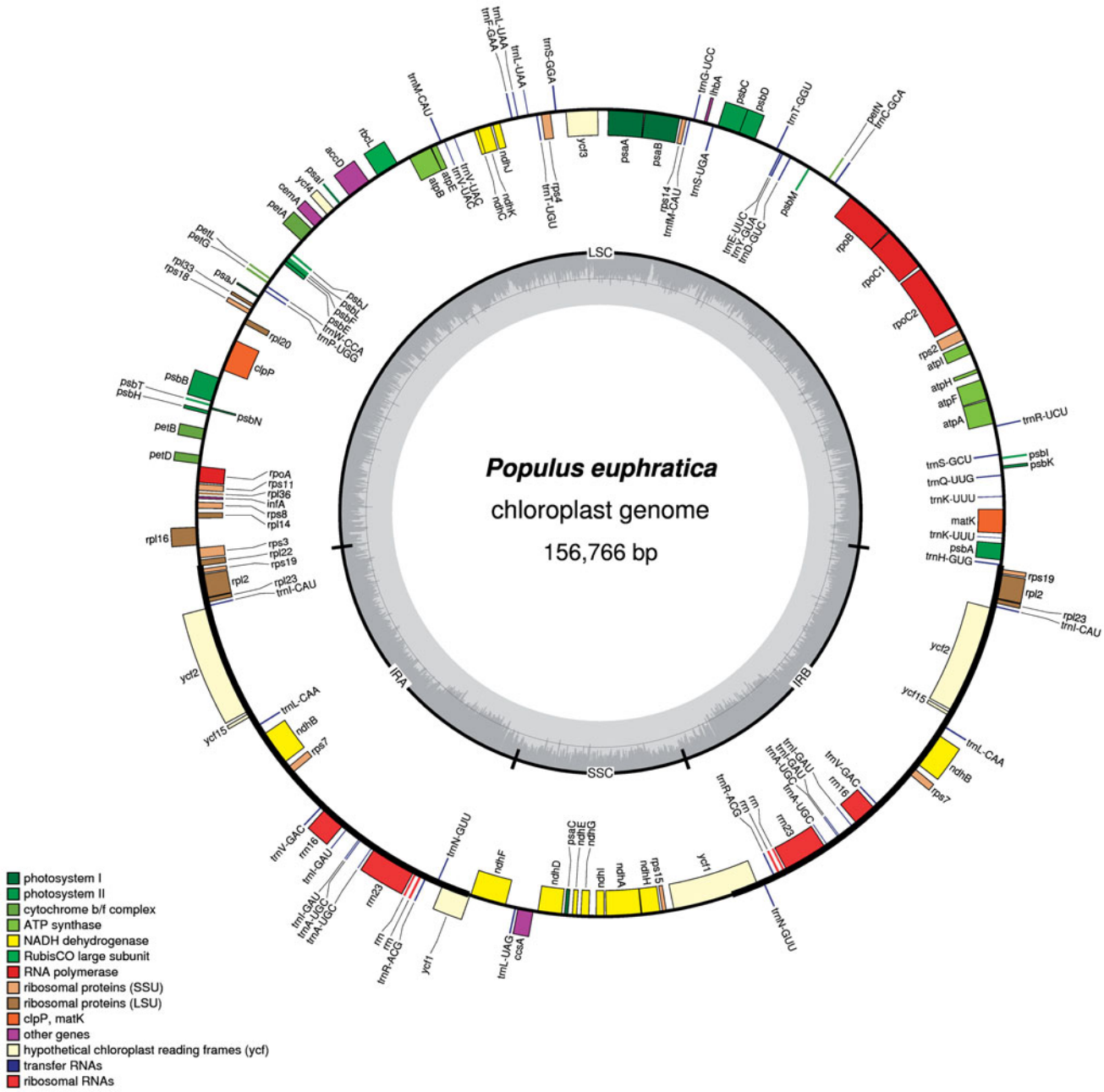

Figure 1. Circular gene map of the *Populus euphratica* chloroplast genome. Genes lying outside of the outer circle are transcribed in the clockwise direction whereas genes inside are transcribed in the counterclockwise direction. Genes belonging to different functional groups are color coded. Area dashed darker gray in the inner circle indicates GC content while the lighter gray corresponds to AT content of the genome.

Declaration of interest

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References

Brinker M, Brosché M, Vinocur B, Abo-Ogiala A, Fayyaz P, Janz D, Ottow EA, et al. (2010). Linking the salt transcriptome with physiological responses of a salt-resistant *Populus* species as a strategy to identify genes important for stress acclimation. Plant Physiol 154: 697–1709.

Brosche M, Vinocur B, Alatalo ER, Lamminmäki A, Teichmann T, Ottow EA, Djilianov D, et al. (2005). Gene expression and metabolite profiling of *Populus euphratica* growing in the Negev desert. Genome Biol 6:R101.

Gries D, Zeng F, Foetzki A, Arndt SK, Bruelheide H, Thomas FM, Zhang X, Runge M. (2003). Growth and water relations of *Tamarix ramosissima* and *Populus euphratica* on Taklamakan desert dunes in relation to depth to a permanent water table. Plant Cell Environ 26: 725–36.

Gu R, Fonseca S, Puskás LG, Hackler Jr L, Zvara A, Dudits D, Pais MS. (2004). Transcript identification and profiling during salt stress and recovery of *Populus euphratica*. Tree Physiol 24: 265–76.

Janz D, Lautner S, Wildhagen H, Behnke K, Schnitzler JP, Rennenberg H, Fromm J, Polle A. (2012). Salt stress induces the formation of a novel type of 'pressure wood' in two *Populus* species. New Phytol 194: 129–41.

Li H, Cao H, Cai YF, Wang JH, Qu SP, Huang XQ. (2014). The complete chloroplast genome sequence of sugar beet (*Beta vulgaris* ssp. vulgaris). Mitochondrial DNA 25:1–3.

Li R, Yu C, Li Y, Lam TW, Yiu SM, Kristiansen K, Wang J. (2009). SOAP2: An improved ultrafast tool for short read alignment. Bioinformatics 25:1966–7.

Lohse M, Drechsel O, Bock R. (2007). Organellar Genome DRAW (OGDRAW): A tool for the easy generation of high-quality custom graphical maps of plastid and mitochondrial genomes. Curr Genet 52: 267–74.

Ma C, Fung L, Wang S, Huttermann A. (1997). Photosynthetic response of *Populus euphratica* to salt stress. For Ecol Manage 93:56–61.

Ma T, Wang J, Zhou G, Yue Z, Hu Q, Chen Y, Liu B, et al. (2013). Genomic insights into salt adaptation in a desert poplar. Nature Commun 4:2797. doi: 10.1038/ncomms3797.

Nock CJ, Waters DL, Edwards MA, Bowen SG, Rice N, Cordeiro GM, Henry RJ. (2011). Chloroplast genome sequences from total DNA for plant identification. Plant Biotechnol 9:328–33.

Okumura S, Sawada M, Park YW, Hayashi T, Shimamura M, Takase H, Tomizawa KI. (2006). Transformation of poplar (*Populus alba*) plastids and expression of foreign proteins in tree chloroplasts. Transgenic Res 15:637–46.

Ottow EA, Brinker M, Teichmann T, Fritz E, Kaiser W, Brosché M, Kangasjärvi J, et al. (2005). *Populus euphratica* displays apoplastic sodium accumulation, osmotic adjustment by decreases in calcium and soluble carbohydrates, and develops leaf succulence under salt stress. Plant Physiol 139:1762–72.

Ravi V, Khurana JP, Tyagi AK, Khurana P. (2008). An update on chloroplast genomes. Plant Syst Evol 271:101–22.

Rodríguez-Ezpeleta N, Brinkmann H, Burey SC, Roure B, Burger G, Löffelhardt W, Bohnert HJ, et al. (2005). Monophyly of primary photosynthetic eukaryotes: Green plants, red algae, and glaucophytes. Curr Biol 15:1325–30.

Sato S, Nakamura Y, Kaneko T, Asamizu E, Tabata S. (1999). Complete structure of the chloroplast genome of *Arabidopsis thaliana*. DNA Res 6:283–90.

Shi C, Hu N, Huang H, Gao J, Zhao YJ, Gao LZ. (2012). An improved chloroplast DNA extraction procedure for whole plastid genome sequencing. PLoS One 7:e31468.

Tuskan GA, Difazio S, Jansson S, Bohlmann J, Grigoriev I, Hellsten U, Putnam N, et al. (2006). The genome of black cottonwood, *Populus trichocarpa* (Torr. & Gray). Science 313:1596–604.

Wang RG, Chen S, Zhou X, Shen X, Deng L, Zhu H, Shao J, et al. (2008). Ionic homeostasis and reactive oxygen species control in leaves and xylem sap of two poplars subjected to NaCl stress. Tree Physiol 28: 947–57.

Wyman SK, Jansen RK, Boore JL. (2004). Automatic annotation of organellar genomes with DOGMA. Bioinformatics 20:3252–5.