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MITOGENOME ANNOUNCEMENT

The complete chloroplast genome sequence of American bird pepper (*Capsicum annuum* var. *glabriusculum*)

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Abstract

The complete chloroplast genome sequence of American bird pepper (*Capsicum annuum* var. *glabriusculum*) is reported and characterized in this study. The genome size is 156,612 bp, containing a pair of inverted repeats (IRs) of 25,776 bp separated by a large single-copy region of 87,213 bp and a small single-copy region of 17,851 bp. The chloroplast genome harbors 130 known genes, including 89 protein-coding genes, 8 ribosomal RNA genes, and 37 tRNA genes. A total of 18 of these genes are duplicated in the inverted repeat regions, 16 genes contain 1 intron, and 2 genes and one *ycf* have 2 introns.

Keywords

Capsicum annuum var. *glabriusculum*, chloroplast genome, plastid

History

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Plastids, originated from the free-living cyanobacteria in eukaryotic cells via endosymbiosis, play a crucial role in plant photosynthesis and other metabolic pathways (Rodríguez-Ezpeleta et al., 2005). The majority of angiosperm plants contain about 110 unique genes spread over 150 kb of DNA in their chloroplast genomes. Compared with mitogenomes, the plastomes are of great phylogenetic value owing to relatively conserved structure along with high evolutionary rate (Ravi et al., 2008). To date, over 500 complete plastomes of protists, thallophytes, bryophytes and vascular plants have been sequenced and deposited in NCBI Organelle Genome Resources (<http://www.ncbi.nlm.nih.gov>).

Pepper is an economically important member in the Solanaceae family. The genus *Capsicum* includes about 32 species native to tropical America with a large diversity of fruit shape, size and color (Moscone et al., 2007). Owing to superior adaptability to different agro-climates, peppers are widely cultivated around the world and extensively adopted as food, medicine, and ornamentals in variable cultures. They are rich in essential vitamins, minerals and nutrients that provide great benefit for human health (Marín et al., 2004; Matsufuji et al., 2007).

The cultivated pepper (*Capsicum annuum* L.) chloroplast genome was previously reported (NC_018552; Jo et al., 2011). In this study, we reported and characterized the complete chloroplast genome of its wild progenitor, American bird pepper (*C. annuum* var. *glabriusculum*). The whole genome

sequence reads of American bird pepper were generated by Qin et al. (2014). Using these sequence data, we then filtered and assembled the complete cp genome with SOAPdenovo software (Li et al., 2009). Annotation of the assembled genome was performed with Dual Organellar GenoMe Annotator (DOGMA) using default parameters 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 formerly published cp genomes identified locations of these putative genes. For genes with low sequence identity, manual annotation was executed to determinate the position of start and stop codons subject to the translated amino acid sequence using the chloroplast/bacterial genetic code. Plastome map 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 under the accession number of KJ619462.

The complete plastome of American bird pepper has a total length of 156,612 bp (Figure 1), which harbors a typical genome structure same as other higher plants (Li et al. 2014; Ravi et al., 2008; Sato et al., 1999). In detail, it has a pair of inverted repeats (IRa and IRb) of 17,851 bp that separate a large single copy (LSC) region of 87,213 bp and a small single copy (SSC) region of 25,776 bp (Figure 1). The GC content of the whole plastome was 37.7%, with the IRs had a higher GC content (43.4%) than LSC (34.6%) and SSC (30.2%) region due to the presence of GC-rich rRNA genes. The genic regions account for 58.6% of the genome and include 130 genes (86 protein-coding, eight rRNA, and 37 tRNA genes). Among these genes, 19 contained one or two introns. The chloroplast genome contains 30 different tRNA genes, and seven were present in the IR (Figure 1). This newly determined chloroplast genome sequence will provide valuable data for the future utilization of wild pepper germplasm in the Solanaceae family.

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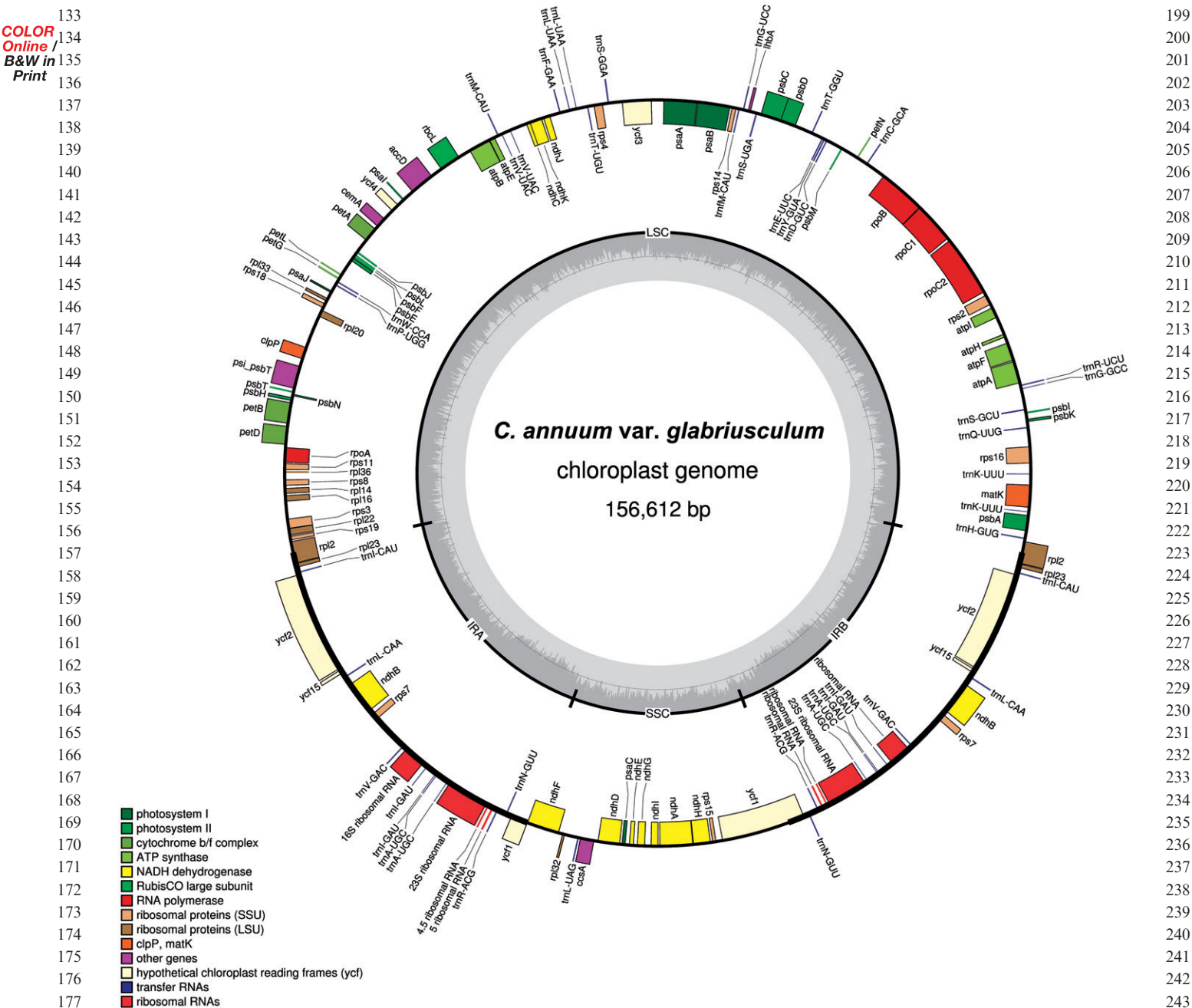


Figure 1. Genome map of American bird pepper. Genes lying outside of the outer circle are transcribed in the clockwise direction whereas genes inside are transcribed in the counterclockwise direction. Genes belonging to different functional groups are color coded. Area dashed darker gray in the inner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

Declaration of Interest

This work was supported by National Science Foundation of China (U0936603), Key Project of Natural Science Foundation of Yunnan Province (2008CC016), the Hundreds Talents Program of the Chinese Academy of Sciences (CAS), Talent Program of Yunnan Province (20080A009), a grant from the Chinese Academy of Science (KSCX2-YW-N-029), a grant from Chinese Department of Science and Technology (973 Program 2007CB815703), Frontier Grant of Kunming Institute of Botany, CAS (672705232515), and a start-up grant from Kunming Institute of Botany, CAS. The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

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