

## The complete chloroplast genome of eggplant (*Solanum melongena* L.)

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### ABSTRACT

Eggplant *Solanum melongena* L. is one of the most economically important vegetable crops. Here, we report the complete chloroplast (cp) genome of eggplant. The cp genome size was 154,289 bp that contained a pair of IR regions of 25,566 bp, one large single-copy (LSC) of 84,749 bp and a small single-copy (SSC) of 18,408 bp, respectively. It encoded 125 predicted unique functional genes, including 84 tRNA genes, 85 protein-coding genes and 8 rRNA genes. The GC content was 37.86%. Phylogenetic analysis clearly showed a close evolutionary relationship between *S. melongena* and other species in the genus *Solanum*. The complete chloroplast genome of *S. melongena* provides valuable data for genetic improvement and allele mining of eggplant germplasm.

### ARTICLE HISTORY

Received 13 April 2016  
Revised 2 May 2016  
Accepted 3 May 2016

### KEYWORDS

Chloroplast genome; eggplant; phylogenetic analysis; *Solanum melongena*

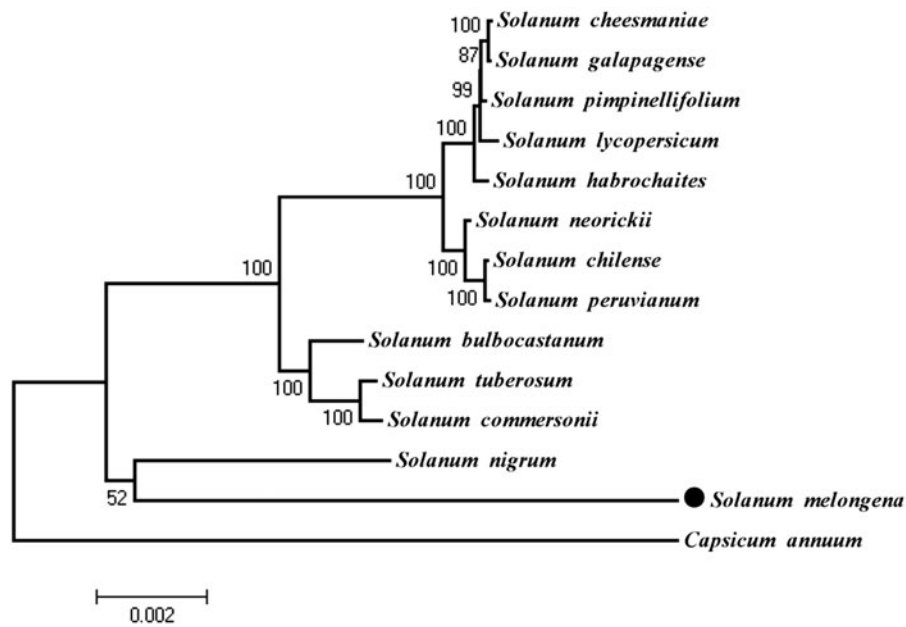
Eggplant (*Solanum melongena* L.) is one of the most economically valuable vegetable species belongs to Solanaceae. It is an important member of the largest genera *Solanum* that consists of more than 1000 plant species. Compared with the other two *Solanum* model species, tomato and potato, eggplant possesses several agronomically unique traits including extra-large fruit size, high tolerance to biotic and abiotic stresses and parthenocarpy without any negative pleiotropic effects (Sakata et al. 1996; Saito et al. 2009). Fruits of eggplant are rich in nutrition contents such as vitamins that have recently been reconsidered as a good source of free radical scavengers, such as anthocyanins and phenolics (Stommel & Whitaker 2003; Azuma et al. 2008). The increase of genetic information in eggplant will not only enhances comparative studies of genetics, physiology, development, and evolution of solanaceous plants, but also accelerates novel allele mining in abundant eggplant germplasm (Daunay and Lester 1988).

Here, we assembled and characterized the complete chloroplast (cp) genome of *S. melongena* from the whole genome sequencing project of eggplant (Hirakawa et al. 2014). The sequenced *S. melongena* was a purebred cultivar ('Nakate-Shinkuro'), one of the founders of modern commercial cultivars and a typical Asian cultivars as well. The cp genome readings of eggplant were filtered by Blastn (Altschul et al. 1990) using the *S. nigrum* cp genome sequence as a reference (Khan et al. 2015). About 813.5 Mb chloroplast readings were obtained and subjected to SOAPdenovo (Li et al. 2009) to assemble into the complete cp genome. Annotation was performed with Dual Organellar Geno Me Annotator (DOGMA, UT Austin, <http://dogma.cccb.utexas.edu>). Ribosome RNA

(rRNA), protein-coding and transfer RNA (tRNA) genes were predicted using default parameters (Wyman et al. 2004). The complete cp genome sequence with all annotated genes was deposited into GenBank under the accession number of KU682719. Thirteen complete cp genomes in Solanaceae were sampled for phylogenetic analysis. MAFFT (version 7.294, <http://mafft.cbrc.jp/alignment/software/>) was used for whole-genome alignments. Maximum-likelihood (ML) analysis was performed by using 'fast bootstrap' algorithm under GTRGAMMAX model, replicated 100 times.

The complete cp genome of *S. melongena* exhibited a circular DNA molecule of 154,289 bp with a typical quadripartite structure. It consisted of a pair of IR regions of 25,566 bp, one large single-copy (LSC) of 84,749 bp and a small single-copy (SSC) of 18,408 bp. The cp genome encoded 125 unique functional genes, including 84 tRNA genes, 85 protein-coding genes and 8 rRNA genes. In addition, the GC content of the cp genome was 37.86%.

The phylogenetic analysis in this study included the 12 cp genomes of *Solanum* species (Chung et al. 2006; Daniell et al. 2006; Wu 2015) and the newly determined cp genome of *S. melongena*, using *Capsicum annuum* (Raveendar et al. 2015) as outgroup. ML analysis yielded in a phylogenetic tree with most of the nodes (8/11) supported by a bootstrap value of 100, and *S. melongena* clustered with *S. nigrum* supported by a bootstrap value of 52 (Figure 1), which was concordant with the previous studies in the genus *Solanum* (Wu 2015). The availability of cp genome of *S. melongena* provides valuable data for the future genetic improvement of this important vegetable species.



**Figure 1.** Maximum-likelihood (ML) phylogenetic tree of *Solanum melongena* and the other 12 *Solanum* species using whole chloroplast genome sequences. *Capsicum annuum* was served as outgroup. The numbers on each node show the ML bootstrap support values. The accession numbers are as below: *Solanum bulbocastanum* (NC\_007943), *Solanum cheesmaniae* (NC\_026876), *Solanum chilense* (NC\_026877), *Solanum commersonii* (NC\_028069), *Solanum galapagense* (NC\_026878), *Solanum habrochaites* (NC\_026879), *Solanum lycopersicum* (NC\_007898), *Solanum neorickii* (NC\_026880), *Solanum nigrum* (NC\_028070), *Solanum peruvianum* (NC\_026881), *Solanum pimpinellifolium* (NC\_026882), *Solanum tuberosum* (NC\_008096), *Capsicum annuum* (NC\_018552).

## Disclosure statement

The authors declare that there are no conflicts of interest and are responsible for the content.

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