ABSTRACT

Prunus campanulata ‘Fugui’ is newly bred cultivar. Here, we report its complete chloroplast genome. The length of the P. campanulata ‘Fugui’ chloroplast genome is 157,948 bp, with a large single-copy region of 85,948 bp, a small single-copy region of 19,128 bp and a pair of inverted repeat regions of 26,436 bp each. The genome contains 90 protein-coding genes, 65 transfer RNA genes and 9 ribosomal RNA genes. In addition, the genome contains 67 simple sequence repeats. Phylogenetic analysis revealed that P. campanulata ‘Fugui’ is genetically related to previously reported P. campanulata.

KEYWORDS

Chloroplast; genome assembly; next generation sequencing; Prunus campanulata

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polymorphisms (SNPs) and 42 insertion and deletions (indels) were identified among P. campanulata 'Fugui' chloroplast genome. Furthermore, a total of 67 simple sequence repeats (SSR) were discovered in P. campanulata 'Fugui' genome. These SSRs included 63 mononucleotides (A/T/G/C), 4 dinucleotides (TA/AT). Compared to the other two P. campanulata chloroplast genomes, that both displayed 66 mononucleotides and 4 dinucleotide type SSRs, P. campanulata 'Fugui' genome contained less mononucleotide SSRs than them, but the same dinucleotide SSRs to them. Pi values ranged from 0.0000 to 0.0120, among them three regions showed high value great than 0.005 within the sites of 42755–43259 bp, 78780–79563 bp and 109602–110351 bp, representing as hot-spots in the genome. These regions contained rps2, ropC2, ndhK, ndhC and rpl14 genes.

Ethical approval
Experiments were performed in accordance with the recommendations of the Ethics Committee of South China Agricultural University. These policies were enacted according to the Chinese National Forestry and Grassland Administration for the plant collection protocols. The study species is not ethically sensitive and endangered.

Authors’ contributions
Q.Z. designed the study and funded the genome sequencing; X.C.Y. and M.X.Z. collected the samples and molecular materials; Z.F.W., X.C.Y., M.X.Z. and Q.Z. performed the analyses; Z.F.W. drafted the manuscript; X.C.Y., M.X.Z. and Q.Z. revised the manuscript. All authors provided comments and final approval.

Disclosure statement
No potential conflict of interest was reported by the author(s).

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