

Complete chloroplast genome sequences of a major invasive species, *Cenchrus longispinus*, in Daechong Island

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The genus *Cenchrus* (Poaceae), containing ca. 97 species, is distributed throughout Australia, Africa and Indian sub-continent and which was introduced to the United States and Mexico for use in improved pasture. In Korea, especially Daechong Island, it is one of the most hazardous invasive plant, which causes serious environmental threats, biodiversity damages and physically negative impact on humans and animals. It can cause serious damage to farms, fields and white sand beaches. However, the chloroplast (cp) genome sequences and information of *Cenchrus longispinus* have been not addressed, so we provide the complete cp genome of *Cenchrus longispinus* using next-generation sequencing technology. The size of cp genomes of this Daechong Island species (*Cenchrus longispinus*) is 137,144 bp, and it shows a typical quadripartite structure. Consisting of the large single copy (LSC; 80,223 bp), small single copy (SSC; 12,449 bp), separated by a pair of inverted repeats (IRs; 22,236 bp). This cp genome contains 75 unique genes, 4 rRNA coding genes, 33 tRNA coding genes and 21 duplicated in the IR regions, with the gene content and organization are similar to other Poaceae cp genomes. Our comparative analysis identified four cpDNA regions (*rpl16*, *rbcl*, *ndhH* and *ndhF*) from three *Cenchrus* species, two *Setaria* species and one *Pennisetum* species which may be useful for molecular identification.

Key words: *Cenchrus longispinus*, invasive plant, chloroplast genome

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