

Development of Chloroplast Microsatellite Markers for Invasive *Carduus* (Asteraceae) between East Asia and North America

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The genus *Carduus* (Asteraceae), containing ca. 90 species, is mainly distributed in Eurasia and Africa. *Carduus* species are one of the most hazardous invasive species, which causes serious environmental threats and biodiversity damages in North America. Thus, the member of *Carduus* are targeted for classical biological control in this region. Here, we provide the complete cp genome of *Carduus crispus* using next-generation sequencing technology. The size of cp genomes of *C. crispus* is 152,342 bp. It shows a typical quadripartite structure, consisting of the large single copy (LSC; 83,254 bp), small single copy (SSC; 18,706 bp), separated by a pair of inverted repeats (IRs; 25,191 bp). It contains 115 unique genes of which 21 genes duplicated in the IR regions. The cpSSR regions of *Carduus* species were searched through the complete chloroplast genome sequence using a tandem repeat search tool in Geneious with the parameters set to ≥ 7 mononucleotide repeats, ≥ 4 di- and trinucleotide repeats, and ≥ 3 tetra-, penta-, and hexanucleotide repeats. A total of 22 repeat motifs were identified, which may be useful for molecular identification of Korean *Carduus* species (*C. crispus*), and providing a guideline for its conservation.

Key words: *Carduus crispus*, Invasive plant, Chloroplast microsatellite markers

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