

Preliminary research for molecular markers of two invasive toxic weeds, *Cenchrus* L. (Poaceae) species, based on NGS technique

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The genus *Cenchrus* (Poaceae), containing ca. 23 species, is distributed throughout Australia, Africa, Indian sub-continent, and America. In Korea, *Cenchrus longispinus* (Hack.) Fernald, especially introduced to Daecheong Island in 1999, is one of the most hazardous invasive plant which causes serious environmental threats, biodiversity damages and physically negative impact on humans and animals. Based on the next-generation sequencing (NGS) technology, we characterized the chloroplast (cp) genome sequences of *C. longispinus* which contains a large single copy (LSC; 80,223 bp), a small single copy (SSC; 12,449 bp), separated by a pair of inverted repeats (IRs; 22,236 bp). Additionally, we analyzed the cp genome sequences of *Cenchrus echinatus* L. which contains a large single copy (LSC; 80,220 bp), a small single copy (SSC; 12,439 bp), separated by a pair of inverted repeats (IRs; 22,236 bp). These cp genomes consist of 75 unique genes, 4 rRNA coding genes, 33 tRNA coding genes and 21 duplicated in the IR regions, of which the gene content and organization are similar to the other Poaceae cp genomes. We selected 40 potential regions in cp genomes of two *Cenchrus* species and one Korean *Pennisetum* species to develop new single nucleotide polymorphism (SNP) markers for identifying *C. longispinus* based on amplification-refractory mutation system (ARMS) technique. The markers, inferred from SNP in *matK* and *ndhF* genes, show effectiveness to recognize *C. longispinus* from *C. echinatus* and Korean native species *Pennisetum alopecuroides* (L.) Spreng.

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