



Genetic diversity in wild *Dipsacus chinensis* populations from China based on ISSR markers

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ABSTRACT. Wild *Dipsacus chinensis* plants in China have become endangered owing to over-harvesting and habitat fragmentation. We examined the genetic diversity and genetic structure of 90 individuals from three populations using inter-simple sequence repeat markers and found that 106 of 173 bands amplified by 22 informative and reliable primers were polymorphic. These findings correspond to a medium level of genetic diversity. At the species level, the estimates of parameters of genetic diversity were as follows: polymorphic loci (61.27%); effective number of alleles (1.3873); Nei's genetic diversity (0.2202); Shannon's information index (0.3235). At the population level, the estimates were polymorphic loci (9.53%); effective number of alleles (1.0419); Nei's genetic diversity (0.0258); Shannon's information index (0.0402). Nei's coefficient of genetic differentiation was 0.8829, which is consistent with Shannon's coefficient of genetic differentiation (0.8757). Most of the genetic variation existed among populations, and some differentiation may

have resulted from habitat fragmentation and barriers to gene flow (gene flow = 0.0663). Combining our results with those of on-site field investigation, we conclude that the present genetic diversity and genetic structure of natural populations of *D. chinensis* have been strongly affected by harvesting and habitat fragmentation. We also propose strategies for the conservation of this plant.

Key words: *Dipsacus chinensis*; Inter-simple sequence repeat; Genetic diversity