



Genetic diversity and relationship of chicory (*Cichorium intybus* L.) using sequence-related amplified polymorphism markers

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ABSTRACT Chicory is a crop with economically important roles and is cultivated worldwide. The genetic diversity and relationship of 80 accessions of chicories and endives were evaluated by sequence-related amplified polymorphism (SRAP) markers to provide a theoretical basis for future breeding programs in China. The polymorphic rate was 96.83%, and the average polymorphic information content was 0.323, suggesting the rich genetic diversity of chicory. The genetic diversity degree of chicory was higher ($G_s = 0.677$) than that of endive ($G_s = 0.701$). The accessions with the highest genetic diversity (effective number of alleles, $N_E = 1.609$; Nei's genetic diversity, $H = 0.372$; Shannon information index, $I = 0.556$) were from Italy. The richest genetic diversity was revealed in a chicory line ($N_E = 1.478$, $H = 0.289$, $I = 0.443$) among the

3 types (line, wild, and cultivar). The chicory genetic structure of 8 geographical groups showed that the genetic differentiation coefficient (G_{ST}) was 14.20% and the number of immigrants per generation (N_m) was 3.020. A G_{ST} of 6.80% and an N_m of 6.853 were obtained from different types. This observation suggests that these chicory lines, especially those from the Mediterranean region, have potential for providing rich genetic resources for further breeding programs, that the chicory genetic structure among different countries obviously differs with a certain amount of gene flow, and that SRAP markers could be applied to analyze genetic relationships and classifications of *Cichorium intybus* and *C. endivia*.

Key words: Chicory; Cluster analysis; Genetic diversity; Genetic relationship; Sequence-related amplified polymorphism