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APPLICATION OF SSR MARKERS TO REVEAL THE GENETIC DIVERSITY OF SUNFLOWER BROOMRAPE IN CHINA

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ABSTRACT

Broomrape (Orobanche cumana Wallr.) is a kind of parasitic seed plant seriously affecting the sunflower industry in China. To clarify the genetic relationship of sunflower broomrape in China, SSR markers were used to determine the population genetic diversity of 93 broomrape samples which were collected from different provinces of China. Results showed 14 SSR primers were screened out from 50 SSR primers, based on their highly polymorphism among tested samples. A total of 108 out of 112 bands were identified as polymorphic bands. The percentage of polymorphic bands was 96.43%. Both Shannon index and Nei's diversity index were raised with these ample population size increasing. Among tested samples, broomrape collected form Inner Mongolia and Xinjiang provinces showed most highly polymorphism. Their Shannon indices were 0.4380 and 0.4967 respectively. Genetic clustering results showed that the samples from 6 different provinces could be divided into 2 clades. Inner Mongolia, Yunnan, Xinjiang, Hebei and Gansu samples were clustered into one clade, and Shanxi were clustered into another separated clade. Samples collected from Gansu and Shanxi province showed the closest relationship, while the same samples from Gansu showed the furthest relationship with samples collected from Xinjiang region.

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