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VARIABILITY AND GENETIC DIVERSITY OF DIFFERENT CHINESE BROOMRAPE POPULATIONS

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Broomrape (*Orobanche cumana* Wallr.) is a parasitic seeds plant of sunflower, it has become one of the most destructive diseases of sunflower, thus limiting the sunflower production worldly. The main purpose of this research is to evaluate the genetic variation of broomrape populations, collected from different China regions, based on the morphological characteristics of broomrape seeds, the physiological race identification and genetic structure analysis. This research will provide useful genetic information for sunflower broomrape breeding.

First, analyze the seeds morphology of broomrape collected from different location of China, then identification the physiological races of the broomrape population using differential hosts; then constructing the genetic structure by using the selected SSR and ISSR primers.

Via morphological description of the broomrape seeds, all the seeds samples in this study were identified as *O. cumana.* The variation of seeds size level within and between different population is at a medium level; the physiological races are classified into two categories G and H; highly polymorphic was identified with SSR and ISSR primers, and genetic cluster analysis also divides based on the geographical and physiological race of tested population.

There is no significant and statistical difference in the morphological of testa seeds of different Chinese population of broomrape. G and H are the main race type among different tested population, especially race H is the new discovery in Chinese broomrape population. The genetic cluster indicated that the Chinese populations of broomrape have relevant correlation to race type H. Compared with race G, H showed more stronger polymorphism genetically. The combined usage of genotyping technology with dominant (ISSR) and co-dominant (SSR) markers in *O. cumana* populations studies shows that the genetic difference is variable between physiological races. Therefore, this study provides new data on the phenotypic diversity and genetic structure of *O. cumana* populations collected from China. This will be the useful information for understanding the complex biology of sunflower broomrape and for developing effective strategies for sunflower broomrape control.

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