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研究论文

一对复等位基因控制的油菜(Brassica napus L.)显性核不育系609AB的遗传验证

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摘要 在确认609AB不育系类型的基础上，采用临保系测验法和测交后代可育株自交与回交等方法，有效区分了甘蓝型油菜显性核不育的一对复等位和两对显性基因互作控制的两种遗传模式。不育系类型鉴定结果表明609AB是纯合型显性核不育系；遗传分析证明所测恢复系的抑制基因均与Ms等位，不育系可育株的抑制基因也与不育基因等位，确认其育性符合一对复等位基因遗传模式，Ms为显性雄性不育基因，Mf为Ms的等位显性抑制位点，ms为正常可育位点，并且Mf>Ms>ms。在这一不育系群体中不育株的基因型为MsMs，可育株的基因型为MsMf，相应的恢复系为MfMf，临保系为msms。探讨了甘蓝型油菜显性核不育遗传的可能模式。

关键词 甘蓝型油菜 显性核不育 等位抑制基因 一对复等位基因遗传

分类号 S565

Genetic Verification of Multiple Allelic Gene for Dominant Genic Male Sterility in 609AB (Brassica napus L.)

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Abstract The interaction mode between double dominant genes presented by Li S L and his colleagues is widely accepted as an inheritance pattern for the dominant genic male sterility (DGMS) in Brassica napus. In the mode, the expression of Ms designated as the dominant male sterile gene can be suppressed by the non-allelic inhibitory gene Mf (or Rf in previous reports). Even though it is supported by some ingenious genetic tests, there are two shortcomings in previous studies. One is that the inference has been drawn from the fertility performance in F2 generation in some experiments. This makes us be in a dilemma because it’s practically difficult to distinguish the segregating ratio 13∶3 for double gene inheritance from the ratio 3∶1 for multiple allele inheritance. Another shortcoming is that only one or two restorers are applied to the elaborate genetic examinations, which can’t exclude the possibility that the allelic inhibitor may exist in the other restorers. Furthermore, multiple allelic dominant genic sterility is identified in Chinese cabbage with the same genome as B. rapa, one of the ancestral species of B. napus, though the two gene pattern has been confirmed in the same species. The present study was an attempt to verify the genetic mechanism for DGMS in a newly bred sterile line 609AB from a spontaneous mutant found in a double-low strain 609. Various types of testcrosses and backcrosses were made between 609AB and the breeding lines involved, and the fertility segregation was recorded in Wuhan and/or in Hezhen county, Gansu in spring and summer season, respectively. The segregation ratios of 1∶1 in the sibmated progenies and 3∶1 in the selfed progenies of the fertile plants revealed that 609AB was a homozygous sterile type (Table 1). The two hereditary patterns for DGMS could not be effectively determined through the F2 segregating generation because observed data might fit well to the both patterns according to the Chi-square test (Table 2). The testcrosses made between restored F1 and the temporary maintainers segregated in a ratio of 1∶1 and the subsequent generation populations from the test families and backcrosses contained only fertile individuals (Table 3). All the restorers tested had the allelism of the Ms. In addition, the inhibition gene in the fertile plants from 609AB was also demonstrated to be allelic to the Ms, because there were only fertile plants in the backcross populations (table 4). These results clearly indicate that 609AB was controlled by multiple alleles of one gene, with Mf dominant over Ms and Ms over ms, the recessive allele for normal fertility. Therefore, the genotypes of the sterile and fertile plants in 609AB are MsMs and MsMf respectively, while the corresponding restorers and the temporary maintainers are of genotypes MfMf and msms, respectively. The sterile material can also be utilized in a Three-line system, but the breeding for a homozygous sterile line homologous to the corresponding maintainer will be entirely different.

Key words Brassica napus Dominant genic male sterility Allelic inhibitor Multiple alleles of one gene

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