Genetic studies of a male-sterile, female-fertile soybean mutant

Adilson Luiz Seifert*1; Leones Alves de Almeida2 and Romeu Afonso de Souza Kiihl3
1Departamento de Agronomia, Centro de Ciências Agrárias, Universidade Estadual de Londrina (UEL), Caixa Postal 6001, CEP 86051-990, Londrina, PR, Brasil; 2Empresa Brasileira de Pesquisa Agropecuária (EMBRAPA Soja), Caixa Postal 231, CEP 86001-970, Londrina, PR, Brasil. (*Corresponding Author. E-mail: seifert@uel.br)

ABSTRACT

Studies on a new spontaneous male-sterile / female-fertile soybean mutant identified by the Embrapa Soybean breeding program were carried out in Londrina, PR. The mutant showing segregation for male-sterility (BR93-12879) was selected within F₂ progeny lines derived from the IAS-5 (3) X OCEPAR 9-SS1 cross performed in 1993. The F₁, F₂ and F₃ generations of cross among heterozygous plants of the BR93-12879 line and recessive homozygous plants (male-sterile) of the T 266H (ms₃,ms₄), T 259H (ms₄,ms₅), T 273H (ms₅,ms₆), T 274H (ms₆,ms₇), T 277H (ms₇,ms₈) and T 295H (ms₈,ms₉) lines were studied to identify whether the new mutation is conditioned by a new allele or by a mutation in one of the six loci already described in the literature. The F₁, F₂ and F₃ plants from the crosses were visually classified as male-sterile or male-fertile. Results from the allele test and inheritance study among the mutant genotype and the recessive homozygous male-sterile lines (ms₃, ms₄, ms₅, ms₆, ms₇ and ms₈) showed that a single recessive gene controls the male-sterile trait of BR93-12879. This gene is allele to the already described ms₁-gene and resulted from a genetic mutation in the ms₁-loci.

KEY WORDS: Glycine max, genetics.

INTRODUCTION

Male-sterile / female-fertile mutations are found in many cultivated plant species, but their detection in soybean (Glycine max (L.) Merrill) is relatively recent. Since the description of the first completely male-sterile mutant in soybean (Brim and Young, 1971), genetic and cytogenetic studies have identified six independent loci with pairs of recessive alleles conditioning male-sterility. The following alleles have been identified in these studies: ms₁ ms₂, in genotype T 260H (Brim and Young, 1971), the ms₃ ms₄ in T 259H (Bernard and Creemens, 1975), the ms₅ ms₆ in T 273H (Palmer et al., 1980), ms₇ ms₈ in T 274H (Delannay and Palmer, 1982), ms₉ ms₀ in T 277H (Buss, 1983) and ms₉ ms₁ in T 295H (Skorupska and Palmer, 1989).

The male-sterile / female-fertile trait may contribute to genetic studies and facilitate the production of many hybrid seeds necessary for breeding programs where recurrent selection is used.

Several male-sterile genotypes were selected within segregant soybean populations from the Embrapa Soybean breeding program at Londrina PR. BR93-12879 is a spontaneous mutation detected during the population development process and was selected due to its excellent agronomic performance.

This study was planned to investigate the inheritance of the BR93-12879 male-sterile trait. Allele tests between this line and the known sources of male sterility genes were carried out to check whether this mutation defines a new locus controlling the character or represents an independent mutation in the already described loci.

MATERIALS AND METHODS

Allele tests were performed to investigate the inheritance of the male-sterile spontaneous mutation of BR93-12879. The male-sterile mutants ms₁, ms₂, ms₃, ms₄, ms₅, ms₆, ms₇ and ms₈ already identified, respectively, in T 266H (Boerma and Cooper, 1978), T 259H, T 273H, T 274H e T 295H lines were used. T 266H was used instead of T 260H due to its greater female fertility. Line BR93-12879 was identified in 1993 in a F₃ progeny test selected from the segregant population of the IAS-5(3) X OCEPAR 9-SS1 cross. BR93-12879 seeds segregated for the male-sterile trait and six lines were obtained from the Soybean Germplasm Bank of Embrapa Soybean at Londrina PR.

The F₁, F₂ and F₃ generations derived from crosses involving BR93-12879 plants heterozygous for male sterility and the six lines were studied in
experiments carried out at Embrapa Soybean in 1998, 1999 and 2000. The heterozygous BR93-12879 plants were used as male parent in the crosses.

The parents used in the crosses and the F₁ plants were cultivated in a greenhouse. The F₁ and F₂ generations were conducted in the field with progeny identification. At maturity, the F₁, F₂ and F₃ plants of each progeny were visually classified as normal male-fertile phenotype or male-sterile. The frequencies of plants in each class was recorded.

A chi-square test ($\chi^2$) (LeClerg et al., 1939) was used to analyze the frequency distribution of plants in the two classes and test the hypotheses of monogenic or digenic inheritance.

RESULTS AND DISCUSSION

Results obtained from the F₁, F₂ and F₃ generations of crosses involving the BR93-12879 mutant and the known male-sterile lines showed that male sterility in the BR93-12879 is monogenic inherited controlled by a pair of recessive alleles that condition male-sterility.

These results are in agreement with studies that identified six loci with recessive alleles that condition male-sterility in soybean genotypes (Brim and Young, 1971; Bernard and Creemens, 1975; Palmer et al. 1980; Delannay and Palmer, 1982; Buss, 1983; Skorupska and Palmer, 1989).

Several segregation ratios may appear in the F₁ and F₂ generations of the studied crosses. If the mutant gene is allelic to one of the genes already described for male sterility, a 1:1 ratio of fertile and sterile plants is expected in the F₁ and a 3:1 ratio in the in the F₂. If two independent heterozygous loci, each with two completely dominant alleles for fertility, are involved in the control of the trait, no male-sterile plant is expected in the F₁ generation. In the F₂ generation a 1:1 ratio is expected of families presenting 3:1 and 9:7 segregation ratios of fertile and sterile plants.

The occurrence of male-sterile F₁ plants was observed only in the T 266H X BR93-12879 cross at the ratio of seven normal to five sterile plants. The segregation in the F₁ generation at the expected 1:1 ratio was an indication that the mutant is an allele in the ms₁ locus of the T 266H line. In a total of 223 plants from the F₂ population, 169 fertile and 54 male-sterile individuals were observed (Table 1). The high homogeneity and the non-significant deviation from the expected 3:1 segregation ratio proved that the male-sterile trait in BR93-12879 is inherited as a recessive gene segregating in the ms₁ locus. These data were confirmed by the results from the F₃ family segregation, where no significant difference was found between the expected and the observed 3:1 segregation ratio (Table 2). The available data did not allow any inference as to whether the mutation in BR93-12879 and the ms₁ locus of T 266H carry identical alleles. Genetic studies by Brim and Young (1971); Palmer and Winger (1975); Boerma and Cooper (1978); Palmer et al. (1978); Yee and Jian (1983); Skorupska and Palmer (1987, 1988), reported seven independent mutations for the ms₁ locus.

The F₂ generation of the cross between the T 259H, T 273H, T 274H, T 277H and T 295H genotypes with the BR93-12879 tester line showed 3:1 and 9:7 segregation ratios among the progenies (Table 1). Results from the chi-square tests and the absence of male-sterile F₁ plants were good indicators of ms₂, ms₃, ms₄, ms₅ and ms₆ loci independent segregation. Segregation within the F₂ families crosses confirms the hypothesis of no allelism among the referred loci (Table 2).

CONCLUSION

The following conclusions can be drawn from the genetic segregation results obtained from the crosses involving the male-sterile / female-fertile BR93-12879 soybean line:

1. The male-sterile trait in the BR93-12879 line has single locus Mendelian inheritance controlled by recessive homozygote alleles.
2. The male-sterile mutant represents a mutation in the ms₁ locus, allelic to the ms₁ gene.

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Cruzamento IAS-5(3) X OCEPAR 9-SS1 realizado teste de progêneses, plantas-F 
(x BR93-12879), foi selecionado em linhagens de apresentando segregação para macho-esterilidade da Embrapa Soja, em Londrina-PR. O mutante fértil identificado no programa de melhoramento mutante espontâneo de soja macho-estéril / fêmea-

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RESUMO

Estudos genéticos de um mutante macho-estéril, fêmea-fértil em soja

Foram conduzidos estudos genéticos com um novo mutante espontâneo de soja macho-estéril / fêmea-fértil identificado no programa de melhoramento da Embrapa Soja, em Londrina-PR. O mutante apresentando segregação para macho-esterilidade (BR93-12879), foi selecionado em linhagens de teste de progênicas, plantas-F, provenientes do cruzamento IAS-5(3) X OCEPAR 9-SS1 realizado em 1993. As gerações F<sub>1</sub>, F<sub>2</sub> e F<sub>3</sub> de cruzamentos entre plantas heterozigotas da linhagem BR93-12879 e plantas homozigotas recessivas (macho-estéreis) das linhagens T 266H (ms<sub>5</sub>ms<sub>5</sub>), T 259H (ms<sub>5</sub>ms<sub>5</sub>), T 273H (ms<sub>5</sub>ms<sub>5</sub>), T 274H (ms<sub>5</sub>ms<sub>5</sub>), T 277H (ms<sub>5</sub>ms<sub>5</sub>), T 295H (ms<sub>5</sub>ms<sub>5</sub>) e BR93-12879 (ms<sub>5</sub>ms<sub>5</sub>) foram estudadas objetivando identificar se a nova mutação é condicionada por um novo alelo ou por uma mutação ocorrida em um dos seis locos já descritos. As plantas F<sub>1</sub>, F<sub>2</sub> e F<sub>3</sub> dos cruzamentos foram visualmente classificadas como apresentando fenótipo normal de fertilidade masculina ou macho-estéreil. Os resultados obtidos no teste de alelismo e estudo de herança

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entre o genótipo mutante e as linhagens macho-estéreis em homozigose recessiva (ms₁, ms₂, ms₃, ms₄, ms₅ e ms₆) forneceram evidências de que a característica macho-estéril da linhagem BR93-12879 possui herança mendeliana simples recessiva e representa uma mutação gênica ocorrida no loco ms, alélica ao gene ms₁ já descrito.

REFERENCES


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