RESEARCH PAPER

Productivity and fiber quality improvement through transgressive breeding in *desi* cotton

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ABSTRACT

The identification of transgressive segregants for economically important trait such as seed cotton yield along with quality is an important aspect of any practical breeding programme. The F_2 of five diverse cotton (*Gossypium* spp.) crosses were evaluated as well as the number of transgressive segregants. The experimental material consisted of seven diverse parents involving five crosses. Female parent's *viz.*, RDC-88, DD-8NLE, Blach-1 and 9749 were crossed with male parents *viz.*, MDL 2582, DLSA-17 and MDL 2601. The F_2 of cross DD-8NLE x MDL 2582 exhibited the highest number transgressive segregants (105) than earlier reports, followed by RDC 88 x MDL 2601 (98) for all the characters in total. The F_2 of the cross DD-8NLE x MDL 2582 exhibited the highest number transgressive segregants for number of bolls per plant, boll eight, seed index, GOT and seed cotton yield per plant. Highest number of transgressive segregants for halo length by the cross RDC-88 x MDL-2601 and for lint yield and lint index were by the cross RDC-88 x MDL-2582. This indicates importance of DD-8NLE and RDC-88 as a female parent in the breeding programme to get high yield along with good quality.

Key words : Diverse cross, F₂ population, Parents, Segregants and traits

INTRODUCTION

Transgressive breeding aims at improving yield or its contributing characters through transgressive segregation. Such plants are produced by an accumulation of the plus or favorable genes from both the parents as a consequence of recombination. Obviously, the parents involved in hybridization must combine well with each other and preferably be genetically diverse that is quiet different. In such a situation, each parent is expected to contribute different plus genes, which when brought together by recombination gives rise to transgressive segregation. As a result, the intensity of character in the transgressive segregants that is in the new variety is greater than that in either of the parents. Genetic studies indicates that transgressive segregation mostly results from the appearance, in individual genotypes, of combination of alleles from both the parents that have effects in the same direction (complementary gene action); (De Vicente and Tanksley, 1993; Ricseberg et al., 1999.) That is, hybrid individuals those combine 'plus' alleles from both parents or 'minus' alleles from both the parents are likely to have the extreme phenotypes. Other mechanisms have been have been proposed for transgressive segregation such as an increased mutation rate, the exposure of recessive allele in segregation hybrid populations, epistasis and over dominance, but alternative mechanisms have received little support (Ricseberg et *al.*, 1999). Considering this principle the experiment was conducted to get the lines with high yield and good quality of fiber through transgressive breeding.

MATERIALS AND METHODS

The experimental material formed part of the material under staff research project in the Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad. The material for the present investigation was generated by involving four genotypes viz., DD-8NLE, Blach-1, RDC-88 and 9749 belonging to Gossypium herbaceum which were used as female parents and three genotypes of G. arboreum viz., MDL 2582, DLSA-17 and MDL-2601 were used as male parents (Table1). The five crosses were made for the present investigation to generate breeding material. The following F₂ progenies of different cross combinations were used for the study viz., DD-8NLE x MDL 2582, Blach-1 x DLSA-17, RDC 88 x MDL 2601, 9749 x MDL 2601 and RDC 88 x MDL 2582. All the five single crosses (F_1s) were advanced to F_2 generation during *Kharif* 2005.

The experiment was conducted without replications as it was segregating material. The sowing was done on 12^{th} July 2006 with a spacing of 30 cm between plants and 90 cm between rows with row length of 5.1 meters. Each F₂ was raised with minimum of 500 plant population and all standard agronomic practices were followed to

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