Role of improving combining ability in increasing performance of cotton hybrids

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ABSTRACT

Improvement in performance of this hybrid combination can be achieved by improving ability of the line for combining with the concerned tester. By introducing suitable genetic changes in this line through recombination it is possible to develop new lines which accumulate more diverse favorable alleles fixed in them so as to increase their genetic distance from the tester. This amounts to increasing the ability of these new lines to combine (combining ability) with the tester. Recurrent selection schemes of improving combining ability are an integral part of hybrid breeding programs in cross-pollinated crops and they have contributed to success of hybrid maize. The procedures of improving combing ability cannot be followed in crops like cotton with suitable modification in schemes to suit mating system. Hence there is a need for defining procedures of improving combining ability to serve as a prerequisite in hybrid breeding in cotton. It is possible to recombine two, four or more lines/plants (selected for combining ability) by single, double or multiple crossing respectively. The step of recombination should be followed by selfing and selection for combining ability (with the tester) in segregating generations. If required, additional cycles of such selection for combining ability can occur. In one scheme, crosses can be sorted based on the performance and two most potential crosses involving a common parent can be identified. The segregating lines in F_3/F_4 generations can be tested for their ability to combine with the tester. Assessing recombination variability for combining ability can be done by comparing derived F_1s involving the recombinant F_3/F_4 lines and the tester with the straight crosses and the commercial checks. Developing heterotic gene pool can be done when more lines are found to be giving superior crosses with a tester and such heterotic gene pool can be exploited for developing superior hybrid combinations with the tester. Based on elaborate study of a large set of crosses a quadrangular set of crosses can be identified and utilized for initiating reciprocal selection for combing ability. The data generated from assessing genetic variability in F_4 generation of a cross against two testers is presented here. Two lines RAH-100 and RAH-101 were found to give two of the most productive crosses with RAH-221 and RAH-120 in a diallele. The F_4 lines derived from RAH-100 and RAH-101 were assessed for their ability to combine with the two testers RAH-221 and RAH-120. The derived F_1s were compared with the four straight crosses. The nature and magnitude of variability in ability to combine with the two testers was assessed. The differences in the magnitude of variability released for ability of combine with the two testers are highlighted. The mean seed cotton yield derived F_1s was 30% higher than that of the sunlight crosses while 22% of the F_4 lines showed significantly superior hybrid performance over the straight crosses. The practical implications of these observations in hybrid cotton breeding are discussed.

Introduction

The magnitude of heterosis and the superiority of an F_1 depend upon the degree of dominance revealed by yield influencing loci (d) and the genotypic (allelic frequency differences) differences existing between parents for these loci (y). Hence hybrid breeding basically aims at identifying a combination accumulating dominant favorable allele (heterozygosity) at as many as yield influencing loci as possible. It is not possible to visualize accumulation of all the favorable alleles in a single parent instead the process of hybrid breeding involves identifying two parental lines that represent balanced distribution of favorable alleles between. The identity of the favorable alleles present in the two parents would be different and thus, they complement each other perfectly and ensure the accumulation of maximum number of favorable alleles in the F_1. When a varietal line is crossed to another (say a tester) the genotypic differences with respect to favorable alleles determine "combining ability status" of the variety with reference to the tester.

Improving combining ability

Improvement in performance of a hybrid combination can be achieved by improving ability of the line for combining with the tester. By introducing suitable genetic changes in this line either through recombination or mutation, it is possible to develop new lines which accumulate more diverse favorable alleles fixed in them so as to increase their genetic distance from the tester. This amounts to increasing the ability of these new lines to combine (combining ability) with the tester.

Hybrid breeding programs in cross pollinated crops like maize, are supported by population improvement schemes aimed at improving combining ability, due to which the approach to hybrid development becomes more scientific and purposeful than that based on random crossing of available lines or varieties.

Schemes of improving combining ability

As an integral part of hybrid breeding, the recurrent selection schemes are followed in cross-pollinated crops. (Comstock *et al.*, 1949, Hallaur, 1981) This system involves evaluation of combining ability of random individual plants of the population with the selected tester and evaluation of the F_1 progeny. Based on this, the elite high combiner plants are selected to serve as a source of diverse favorable alleles.

These plants are intermated (randomly mated) to recombine the favorable alleles. The resulting population is now a newer version of the base population with an improvement in ability to combine better with the tester as compared to the base population. With every successive cycle of recurrent selection (for combining ability) there is a continuous improvement in combining ability and the inbreds derived from these improved populations give superior hybrid combinations with the tester concerned.

In cross pollinated crops many procedures have been outlined to develop diverse sources as the base material and systematically exploit them and create maximum diversity (with respect to these favorable alleles) between the lines developed from the two opposite sources reciprocal recurrent selection is the best example of such a procedure ensuring maximum genetic diversity with respect to favorable allelic status and exploiting the same for developing superior hybrids (Schnell, 1961; Sprague and Eberhart, 1977). In this scheme two complimentary populations A and B are selected based on diversity and plants representing the two population are crossed with each other to identify those of A capable of combining well with B and evaluated for combining ability in the above manner. The superior plants (of A) based on this combining ability test (with B) are represented through selfed seed for intermating among themselves to develop a renewed version of A (A^1). The population A^1 and B^1 are thus improved versions capable of combining better between them then the original versions A and B. Few cycles of such recurrent selections are followed to ensure maximum diversity with respect to favorable allelic status between the improved versions of A and B often at this stage inbreds are developed from these improved populations and used to develop new superior hybrid combination between A and B sources.

The procedures of improving combing ability cannot be followed in this exact manner in crops like cotton, Sorghum rice and other predominantly or exclusively self-pollinated crops.

Modification in schemes to suit the mating systems

Hybrid breeding has been instrumental in increasing cotton productivity. However, there are no reports of utilizing schemes of improving combining ability as a base line approach in breeding hybrid cotton. Hence there is a need for defining procedures of improving combining ability to serve as a prerequisite in hybrid breeding. In cotton, intermating large number of plants selected for combining ability is not feasible. Moreover cotton can be subjected to selfing, selecting and developing of lines without any inbreeding depression, Hence the principles of conventional recurrent selection schemes can be applied with suitable changes to suit its mating system.

The first step hence would be selection of plants/lines for ability to combine with the chosen tester(s) in the second step these should be crossed to create recombination variability. Expectedly, the segregants would reveal blends of favorable alleles distributed between these parents.

A suitable base population must first be identified for initiating the scheme of improving combining ability. If set of two or more parents (A, B, C etc.) are found to combine well with tester (Say T) the segregating population derived from intermating these lines A, B, C etc can serve as base population for improving combining ability. It is possible to recombine two, four or more lines/plants (selected for combining ability) by single, double or multiple crossing respectively. The step of recombination done in this manner should be followed by third step of selfing and selection for combining ability (with the tester) in segregating generations. This defines one cycle of improving combining ability. If required, additional cycles of such selection for combining ability can be taken.

Identification of diverse base material

The choice of base material for initiating the program is very crucial. It is very important to determine the base material of varietal lines to be used for initiating the program on improving combining ability and the testers in view of the involved efforts aimed at increasing hybrid performance. In the next phase selected plants/lines can be involved in suitable manner to create variability for combining ability

Some methods are explained here which are aimed at generating genetic variability for combining ability and exploiting the same for developing lines improved in ability to combine with the tester(s) and enhancing the potential limit of performance of the hybrid combinations.

Simple triangular selection

Cotton genotypes reveal wide diversity in terms of plant type and morpho-physiological traits. Whenever such diverse types are crossed, the F_1s generally tend to be more heterotic. Hence such types can be involved to develop crosses based on line x tester, diallele and other patterns of crossing. These mating designs facilitate more crosses of a common tester or testers. These crosses can be sorted and based on the performance; two most potential crosses involving a common parent can be identified. The step of creating recombination variability for combining ability begins with the identification of this triangular set of superior crosses involving a common parent. To represent numerically, suppose A x B, and A x C are found to be highly potential, and involve a common parent A. It means that both B and C parents have ability to combine well with A. The favorable alleles status of B and C parents can show differences in terms of the identity of the favorable alleles. The segregating population devised form the cross B x C reveals a one-time recombination of these favorable alleles distributed between these parents. The segregating lines in F_3/F_4 generations can be tested for their ability to combine with the tester concerned. The lines, which accumulate the favorable alleles, distributed between the parents B and C can combine better with A.

Nature and magnitude of recombination variability for combining ability

The choice B and C parents determines the magnitude and nature of variability generated for ability to combine with A. The ability of combining with A is revealed by performance of B x A and C x A crosses. However existence of genetic diversity for identity of favorable alleles between B and C is indicated by performance of the cross B x C Parents giving superior cross (B x C) should be preferred because superior performance of B x C confirms existence of genetic diversity between B and C (Figure 1).

The nature of variability for combining ability among these F_3/F_4 lines would be determined by commonly fixed favorable allelic status (cfa) and specifically fixed favorable allelic status (sfa) of the lines. The favorable alleles, which are common between the two parents, are inherited enblock by all the segregating lines. If the parents B and C are different for favorable alleles, the segregating lines differ with respect to number and identify of favorable alleles fixed in them. The F_3 or F_4 lines differ with respect to these specifically fixed favorable alleles (sfa) while all of them commonly inherit cfa status. Evaluation of these lines for their ability to combine with A will identify those lines which accumulate maximum number of favorable alleles distributed between B and C.

Assessing recombination variability for combining ability

These derived F_1s involving the recombinant F_3/F_4 lines and the tester should be compared with the straight crosses B x A and C x A and off course the commercial checks. If the two parents B and C show greater differences in the favorable allelic status correspondingly the segregating lines will show greater variability for the ability to combine with the tester In such cases the frequency and magnitude of transgressive segregation for combing ability would be higher.

Developing heterotic gene pool

If more lines are found to be giving superior crosses with a tester then it is possible to initiate multiple crosses among such lines selected for combining ability and this can lead to creation broad gene pool of recombination variability for combining ability as the population developed in this manner based on number of components improved in ability to combine with the tester. This heterotic gene pool can be exploited for developing superior hybrid combinations with the tester concerned.

Reciprocal selection for combining ability

Based on elaborate study of a large set of crosses a quadrangular set of crosses can be identified in which A and B parents combine well with C and D. This combination of four parents can be utilized for initiating reciprocal selection for combing ability.

Though combination of four parents are selected based on high non parental cross combinations performance, it is desirable if the hybrid performance of A x B and C x D yield higher as this reflects higher genetic differences between them for favorable allelic status (Figure 2).

The data generated from assessing recombination variability in F_4 generation of a cross against two testers is presented here. Two lines RAH-100 and RAH-101 were found to give the most productive crosses with RAH-221 and RAH-120 in a detailed study. The F_4 lines derived from RAH-100 and RAH-101 were assessed for their ability to combine with the two testers RAH-221 and RAH-120. The derived F_1s were compared with the four straight crosses. The nature and magnitude of variability in ability to combine with the two testers was assessed. The differences in the magnitude of variability released for ability of combine with the two testers are highlighted. The mean seed cotton yield derived F_1s was 30% higher than that of the straight crosses while 22% of the F_4 lines showed significantly superior hybrid performance over the straight crosses.

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Table 1. *Seed cotton yields of a selection of the quadrangular set of crosses for initiating reciprocal selection for combining ability.*

						Parental combinations		
Combination	A x C	A x D	B x C	B x D	Mean	A x B	C x D	Mean
RAH-100 RAH-221	1958.0	1865.3	1610.8	2135.0	1892.27	1731.2	1462.7	1596.95
RAH-101 RAH-120								

Table 2. *Performance of most potential derived F_1s from.*

	F$_4$ lines (of RAH 100 x RAH-101).	
	F4 line x Tester	Seed cotton yield (kg/ha)
Derived F$_1$s	4 x RAH 221	2480
	7 x RAH-221	2412
	6 x RAH-221	2400
	4 x RAH-120	2364
	10 x RAH-120	2352
	7x RAH-120	23.24
	6x RAH-120	2315
	12x RAH-221	2267
	5 x RAH-221	2212
	14x RAH-221	2145
	18 x RAH-120	2106
	Mean of 52 derived F$_1$s	1889.4
Straight crosses	RAH-100 x RAH-221	1864
	RAH-101 X RAH-221	1612
	RAH-101 X RAH-120	1610
	RAH-101 X RAH-120	1605
	Mean of straight crosses	1672.7
	Percent Improvement	13.20
C. Commercial checks	DHH-11	1602
	NHH-44	1415
CD at 5%		184.0
CV (%)		12.62

Table3. F_4 *lines of RAH-221 x RAH-120.*

F_4 line x tester	Seed cotton yield (kg/ha)
6 x RAH 101	2322
5 X RAH-100	2310
4 X RAH-101	2288
6 X RAH-100	2260
4 X RAH-100	2215
8X RAH-101	2112
5 X RAH-101	2072
9 X RAH-100	2012
9 X RAH-101	2006
4 X RAH-101	1998
Mean of 20 derived F_1s	1762.2
Per cent improvement	5.35

Figure 1. The choice of lines B and C parents representing narrow and wider distance between them.

Figure 2. Two situations representing narrow and wider genetic diversity between lines chosen in rectangular four-parent combination.