

COMBINING ABILITY ESTIMATES FOR SOME QUANTITATIVE TRAITS IN UPLAND COTTON

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ABSTRACT

The present research was carried out so as to estimate general combining ability (GCA) which is due to additive genes action, whereas specific combining ability (SCA) is due to dominant and epistatic gene effects of five inbred parents and heterotic effects of 10 F₁ hybrids, developed from half-diallel crosses. Mean squares due to GCA and SCA variance was highly significant for all the characters studied; number of bolls per plant, boll weight, seed cotton yield per plant, seed index and ginning outturn. The variance due to GCA and SCA for mean squares was highly significant, which suggested that additive and non-additive gene action is involved for controlling all the characters. The SCA variance were higher than GCA which indicated the preponderance of dominance of genes for number of bolls per plant, boll weight and seed cotton yield per plant, whilst GCA variance were higher than SCA which manifested the predominance of additive gene for seed index and GOT. Among the parents MNH-886, CIM-506 and CRIS-134 proven best general combiner for all the traits except seed index. It further suggested that these parents can be exploited in crop improvement to maintain the traits studied. As per hybrid combinations MNH-886 X CIM-506, CRIS-134 X MNH-886 and BH-36 X MNH-886 were specific combiners for all the traits studied except GOT. Consequently these can be used for exploitation in hybrid crop development program.

Keywords: combining ability, quantitative traits, GCA, SCA and upland cotton.

INTRODUCTION

Cotton is most important cash and fiber crop of Pakistan. It is being used in textile as well as oil industries and earns foreign exchange through export in the shape of raw cotton, cotton yarn, grey clothes, garments and other cotton made products. Cotton seed is also being used for edible oil which makes about 80% of the national oil production (Agha, 1994). The crop is more economical for poor people and is main source of Labor employment; cotton and its by-products are also source of employment in the developing countries.

Diallel analysis is one of the mating designs where selected parents are crossed in certain order and is used in predicting general combining ability (GCA) and specific combining ability (SCA) of inbred parents. The GCA therefore designates additive genes and is used to determine the performance of parents in general terms whereas, SCA effect is determined by dominant genes and is used to designate the hybrid performance in specific terms. The objectives of this study therefore were to identify potential parents for hybridization and selection programmes. Knowing the types of gene actions through GCA and SCA will also help cotton breeders to formulate an effective breeding strategy to improve various characters in cotton. According to Sprague and Tatum (1942), GCA is due to genes which are largely additive in nature, while SCA is due to the genes with dominance or epistatic in effects. Several other researchers also suggested i.e. Soomro (2007) found the significance of GCA and SCA variances, suggesting the importance of additive as well as dominant genes, nevertheless in their studies, ratio of GCA/SCA was greater than unity further indicating the preponderance of additive genes in the inheritance of seed cotton yield, bolls per plant, boll weight and seed index. Desphande and Baig (2003), Khan *et al.* (2005) and Panhwar (2007) noted that GCA and SCA variances were important yet the magnitude of SCA was higher than GCA implying the preponderance of dominant genes controlling number of bolls, seed cotton yield, ginning outturn% and seed index.

Cotton breeders are trying to develop cotton varieties; those well adapt to our environmental conditions and also produce higher yields, higher ginning outturn percentage, better fiber quality and higher fertilizer response along with increased tolerance to complexes of diseases and insect pests. For breeding programmers, parents be

genetically superior, physiologically efficient, possessing better general and specific combining ability so that they could be utilized for varietal development.

MATERIALS AND METHODS

The experiment was conducted at Halani, district Naushehro Feroze during kharif season 2013. The experimental material was consisted of five parents (CRIS-134, BH-36, MNH-886, CIM-506 & CIM-511) and 10 F₁ hybrids to study combining ability estimates for some quantitative traits in upland cotton (*Gossypium hirsutum* L.). The F₁ seed of 10 hybrids was produced by crossing 5 cultivars, in half diallel crossing fashion.

The 5x5 diallel crosses which included the parents and one set of the hybrids, thus formed a total of 15 genotypes (10 F₁ hybrids and 5 parents) were studied. The F₁ hybrids seed of 10 crosses and 5 parents were planted in a Randomized Complete Block Design. Plant to plant distance was kept at 9 inches and row to row at 2.5 feet. Normal inputs were used whenever required. For recording the data, 15 plants of each genotype from each replication were randomly tagged. The estimates of general combining ability (GCA) and specific combining ability (SCA) and their variances (mean squares) were determined by adopting Griffing's (1956) method-2, model-I as described by Singh and Choudhry (1979). The traits were studied viz. number of bolls per plant, boll weight, seed cotton yield per plant, seed index and ginning outturn percentage.

RESULTS AND DISCUSSIONS

The analysis of variance for general combining ability (GCA) and specific combining ability (SCA) presented in table 1. The mean squares values due to GCA were highly significant for all the characters viz. number of bolls per plant, boll weight, seed cotton yield per plant, seed index and ginning outturn percentage. The mean squares due to SCA were also highly significant for all the traits studied. The mean squares due to genotypes (hybrid & parents) as well as parents and hybrids individually were also significant for all the traits. The significance of GCA and SCA variances further suggested that both additive and dominant genes control the characters in cotton. These results hence suggested that data is worth for further processing and interpretations.

The results of GCA & SCA effects are presented trait wise as under;

Number of bolls per plant

The number of bolls per plant is yield character in cotton, if number of bolls will increase, simultaneously seed cotton yield will increase. The GCA and SCA effects presented in table 2 & 3. Among the parents MNH-886 was good general combiner for number of bolls per plant, followed by CIM-506 and CRIS-134 was also best combiner for same trait. Among the hybrids MNH-886 X CIM-506 were produced maximum positive SCA effects, followed by CRIS-134 X MNH-886 given positive SCA effects for the same trait. The variance due to GCA and SCA were highly significant, which suggested that additive and non-additive gene action involve for controlling the number of bolls per plant. The SCA variance was greater than GCA which further indicated that preponderance of dominance gene. Similar results have also been reported by Baloch *et al.* (1997), Baloch and Bhutto (2003), Laxman and Ganesh (2003), Solangi *et al.* (2004) and Rauf *et al.* (2005) who also illustrated that the character number of bolls per plant is controlled by both additive and non-additive genes. The magnitude of SCA nevertheless was greater than the GCA indicating predominance of non-additive gene action in the control for this trait. Gul Hassan *et al.* (1999), Kowsalya *et al.* (2000), Banumathy and Patel (2001), Deshpande and Baig (2003), Zhang *et al.* (2003), Neelima *et al.* (2004) and Soomro (2007) have also observed predominant role of non-additive gene action for this trait.

Boll weight

The boll weight is also an important trait of cotton, if maximum boll weight increase ultimately yield will increase as number of bolls per plant will be constant. The GCA and SCA effects depicted in table 2 & 3 respectively. The parent MNH-886 was good general combiner for boll weight, followed by CIM-506 was also best combiner for the same trait. Among the hybrids combination MNH-886 X CIM-506 were observed maximum positive SCA effects, followed by BH-36 X MNH-886 also give positive SCA effects for boll weight. The magnitude of SCA variance was higher than GCA which proposed that predominance of non-additive gene action controlling the trait boll weight. Same results also obtained by Bhutto *et al.* (2001), Banumathy *et al.* (2001), Baloch and Bhutto (2003), Laxman and Ganesh (2003) Solangi *et al.* (2004) and Soomro (2007) who also observed the importance of additive as well as non-additive gene actions in the control of boll weight.

Seed cotton yield per plant

Seed cotton yield per plant is engage exclusive values against all traits in cotton crop, because it plays a vital role in the economy of farmers. The GCA & SCA effect for seed cotton yield per plant is illustrated in Table 2 and 3. Among parents MNH-886 produced highest GCA effects for this trait and proved good general combiner. Whereas CIM-506 was also shown best combiner for the same trait. As discussed hybrids combinations the effects of SCA was greater produced by cross MNH-886 X CIM-506 for seed cotton yield, meanwhile hybrid CRIS-134 X MNH-886 also given positive SCA effects for same trait. The significance of GCA and SCA variances implied the importance of additive as well as dominant genes controlling seed cotton yield in cotton. Nonetheless, the SCA variances were higher than the GCA variances further suggested the preponderance of dominant gene action in the control of seed cotton yield per plant. The present findings are in accordance with those of Baloch and Bhutto (2003), Laxman and Ganesh (2003), Baloch (2004) and Solangi *et al.* (2004) who also reported significant GCA and SCA estimates for this trait. The higher magnitude of SCA variance against the GCA, in present studies, are in consonance with those of Gul Hassan *et al.* (1999), Banumathy *et al.* (2001), Deshpande and Baig (2003), Deshpande *et al.* (2003), Laxman and Ganesh (2003), Zhang *et al.* (2003) and Neelima *et al.* (2004) who also reported higher magnitude of non-additive genes in the control of seed cotton yield.

Table 1. Aanalysis of variance (mean squares) values of GCA and SCA for some quantitative traits.

Source of variance	D.F	Number of bolls per plant	Boll weight	Seed cotton yield/plant	Seed Index	GOT %
Replication	3	2.745	1.874	36.824	0.037	0.814
Genotypes	14	112.45**	0.52**	19207.18**	1.43**	7.15**
Hybrids	9	89.87**	0.47**	1322.41**	0.89**	6.12**
Parents	4	21.45**	0.07**	298.51**	4.21**	8.27**
GCA	4	86.47**	0.67**	1526.22**	3.89**	21.64**
SCA	10	126.61**	0.78**	2691.18**	0.82**	2.87**
Error	42	0.978	0.016	9.751	0.098	0.319

** Significant at (5%) and (1%) probability

Table 2. GCA Effects of parents by for some quantitative traits.

Parents	TRAITS				
	Number of bolls per plant	Boll weight	Seed cotton yield/plant	Seed Index	GOT %
CRIS-134	0.98	-0.92	3.45	0.34	1.21
BH-36	-2.37	-0.08	4.31	0.98	-0.92
MNH-886	3.75	0.91	5.23	0.81	3.57
CIM-506	2.28	0.52	4.71	0.72	3.25
CIM-511	-1.81	-0.53	2.21	-0.35	-0.52
SE (gi.)	0.28	0.04	0.97	0.09	0.16

Table 3. SC Effects for some quantitative traits.

Hybrids	Characters				
	No of bolls per plant	Boll weight	Seed cotton yield/plant	Seed Index	GOT %
CRIS-134 X BH-36	+1.78	-0.35	+12.86	+0.57	-3.12
CRIS-134 X MNH-886	+3.45	+0.13	+18.21	+0.12	-2.71
CRIS-134 X CIM-506	+1.91	+0.11	+3.51	-0.81	+0.81
CRIS-134 X CIM-511	-3.21	-0.67	-12.31	-2.21	-3.12
BH-36 X MNH-886	+1.87	+0.57	+15.28	+2.17	-3.41
BH-36 X CIM-506	-5.78	-0.47	+11.81	+0.43	-6.35
BH-36 X CIM-511	-2.47	-0.91	-36.12	+0.11	-2.61
MNH-886 X CIM-506	+9.78	+0.81	+41.89	+1.91	+0.27
MNH-886 X CIM-511	+0.93	-0.34	+10.51	-1.24	+0.91
CIM-506 X CIM-511	-3.71	-1.07	-2.31	-2.14	-5.41
SE (Si.)	0.78	0.11	2.35	0.23	0.41

Seed index

Seed index and seed cotton yield have very closely link, because seed index will increase than its affects at the same time increase the seed cotton yield. The GCA & SCA effects are presented in Table 2 & 3. The parent BH-36 given highest positive GCA effects and proved to be best general combiner for seed index. Whilst parent MNH-886 also best general combiner for the same trait. Within hybrids performance the cross BH-36 X MNH-886 produced maximum SCA effects for seed index, followed by cross MNH-886 X CIM-506 given positive SCA effects for the trait seed index. The significance of GCA and SCA variances further suggested that both additive and dominant types of genes control the trait seed index. However, GCA variances were greater than the SCA variances implied predominance of additive as compared to dominant genes action. Similar results have also been reported by Liu and Han (1998), Gul Hassan *et al.* (1999), Meena *et al.* (2001), Luxman and Ganesh (2003) and Neelima *et al.* (2004) who also found the significance of GCA and SCA variances for seed index. The higher magnitude of GCA over the SCA for seed index in present study is in agreement with those reported by Gul Hassan *et al.* (1999), Banumathy *et al.* (2001), Deshpande and Baig (2003), Luxman and Ganesh (2003).

Ginning outturn %

The GCA & SCA effects for the character ginning outturn percentage are depicted in Table 2 & 3. Among the parent MNH-886 obtained maximum positive GCA effects and demonstrated best general combiner for GOT. Whereas CIM-506 also proved good combiner for this trait. As per hybrids combinations the cross MNH-886 X CIM-511 manifested highest positive values of SCA effects for GOT, followed by CRIS-134 X CIM-506 with positive SCA effects for same trait. The significance of GCA and SCA variances hence suggested the importance of both additive and dominant genes controlling ginning outturn percent in cotton. Yet, GCA variances are greater than the SCA implied preponderance of additive against the dominant genes. Present results are in consonance with those of Zia-ul-Islam *et al.* (2001), Laxman and Ganesh (2003) and Solangi *et al.* (2004).

Conclusion

The variance due to GCA and SCA for mean squares was highly significant, which suggested that additive and non-additive gene action involved are for controlling all the characters. Among the parents MNH-886, CIM-506 and CRIS-134 proven best general combiner for all the traits except seed index. It further suggested that these parents can be exploited in crop improvement for maintain the traits studied. As per hybrid combinations MNH-886 X CIM-506, CRIS-134 X MNH-886 and BH-36 X MNH-886 were specific combiners for all the traits studied except GOT. Consequently these can be used for exploitation in hybrid crop development program.

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