

Genetic Retrospect of Seedcotton Yield and its Components from a 6-Parent *Gossypium hirsutum* Diallel Cross Under Water Stress Conditions

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Abstract: A six-by-six complete F₁ *Gossypium hirsutum*, L. diallel cross of three pre-screened drought tolerant and three drought susceptible varieties (CRIS-134, CRIS-342, SINDH-1, NIAB-78, SADORI and BH-160) was evaluated for genetic parameters during 2009 at Sindh Agriculture University farm, Tandojam. The characters studied were number of bolls per plant, sympodial branches per plant, seedcotton yield per plant and lintcotton yield per plant. The objective of such study was to assess the effect of irrigation stress on the genetic inheritance pattern of above quantitative traits as to how far the genetic parameters are affected due to irrigation stress in the F₁ diallel generation. Irrigation treatments were four; normal seven irrigations schedule, five irrigations, four irrigations (medium stress) and three irrigations up to 150 days of crop maturity (stress conditions). CRIS-134 in seven, Sadori in five and CRIS-342 in four and three irrigations treatments were the most recessive parents contributing increasing boll number into their progenies while BH-160 in seven, CRIS-342 in five and Sindh-1 in four and three irrigations treatments proved to be the most dominant parents responsible for contributing decreased boll number per plant into their progenies. Seedcotton per plant was partial dominant in seven irrigations treatment while it inherited as an overdominant trait in five, four and three irrigations respectively. BH-160 was the most recessive of all with increased sympodia contributing attributes in seven and four irrigations whereas Niab-78 in five and CRIS-342 in stress were the most recessive parents. Sindh-1 was the most dominant parent in seven, five and three irrigation treatments while CRIS-342 in four irrigations yielded decreased sympodia contributing attributes into their progenies. Sindh-1 in seven, BH-160 in five and three and CRIS-342 in four irrigations treatments proved to be the most recessive parents with increasing seedcotton yield attributes while CRIS-342 in seven and five and Sindh-1 in four and three irrigations were the most dominant parents contributing decreased seedcotton yield into their progenies. Inheritance trend of lintcotton per plant was similar to that of seedcotton yield per plant.

Keywords: Genetic retrospect, *Gossypium hirsutum*, diallel cross, irrigation stress.

INTRODUCTION

Economically, quite a number of species experience variable soil-water contents depending on irrigation, rainfall, leaf area, transpiration, and evaporation index. Thus, during their life cycle, all crops experience drought of various intensities at one time or the other, causing yield reduction. Drought induces a wide range of plant responses, including stomatal closure, changes in gene expression, accumulation of abscisic acid (ABA), production of osmotically active compounds and the synthesis of protective proteins that scavenge oxygen radicals or act as molecular chaperones [1]. According to Quisenberry [2], drought resistance is the ability of a genotype within a species, to be relatively more productive than others under moisture deficit. Levitt [3] divided drought resistance into drought avoidance and drought tolerance. Short duration growth constitutes an important attribute of drought escape with respect to relative yield advantage of early genotypes under prevailing/available water conditions

[4]. Dehydration avoidance is also synonymously used for drought tolerance enabling higher 'hydration' level under soil or atmospheric water stress. The basic concept of dehydration avoidance is in fact retaining a high level of tissue 'hydration' inspite of stress environment. In that case, plant's various physiological, biological and metabolic processes, involved in growth and yield, are not internally expressed to stress, or are protected from stress.

Crop improvement for drought tolerance through integration of adaptive traits is a promising option. Significant progress in recent years has led to the identification of several traits that have relevance in improving drought tolerance as well as development of suitable high throughout phenotyping strategies. For a comprehensive improvement in drought tolerance, several traits need to be introgressed into a single elite genetic background. The emphasis here is to identify relevant traits and adopt conventional and /or molecular approaches to introgress them into an elite background with higher yield potential. Plant breeders and plant physiologists are of the opinion that genotypes well adapted and higher yielding in drought areas can be bred and managed more effectively and

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efficiently, if their attributes that confer drought resistance, could properly be identified and used as selection criteria in objectively defined breeding programs [5-8]. Numerous studies have consensus that physiological and metabolic changes in plants are caused by water stress [9-10]. Important of these changes are suppression of photosynthesis and deregulated accumulation of growth hormones consequently affecting final crop yield [9]. Thus varietal selection plays an important role in water use efficiency for higher cotton production. Improved production package technologies and scheduling methodology have promoted productivity and water use efficiency. The genetic yield potential of today's cotton plant in our country is at least 5 to 10 times the average yields that we attain each year. The primary cause of potential yield reductions is unfavorable environment, haphazard and irregular application of package of production technology and ill-management of irrigation resources.

The diallel cross among selected parents can provide information on the genetic variances in a population derived by random mating of these parents. Since last three decades, the diallel cross analysis has received considerable rapidity in most of the plant breeding programs because it fulfills specific needs of the plant breeders. The analysis provides a systemic approach for detecting parents and crosses superior for the traits under investigation. In addition, it helps plant breeders to choose most efficient method of selection on the basis of estimates of various genetic parameters. Therefore, systematic and successful hybridization program for yield improvement demands an understanding of the genetic architecture of yield and yield components to be bred [11] and requires information on, (a) inheritance of yield and its morpho-physiological components, (b) the nature of relationship between yield and these components and (c) the efficacy of such genetic inheritance patterns in the selection process. The purpose of the present research endeavors was, firstly, to identify the available cotton germplasm for drought tolerance in different irrigation regimes as against normal/recommended irrigation dose; and secondly, to obtain information regarding the extent of variation of genetic parameters of these identified drought tolerant and susceptible varieties. In addition, the present investigations were extended to identify the hybrids and parents possessing superior dominant gene combinations for drought tolerance for further utilization by cotton breeders while embarking upon any defined cotton breeding strategy.

MATERIALS AND METHODS

Six pre-screened cotton (*Gossypium hirsutum*, L.) varieties for drought resistance [12]; CRIS-134, CRIS-342, Sindh-1 as drought tolerant and NIAB-78, SADORI and BH-160 as drought susceptible were intercrossed and complete F_1 diallel cross created. All 36 entries (15 one-way crosses + 15 reciprocals + 6 parents) were sown as F_1 diallel cross during 2009 in four-replicated Randomized Complete Block Design. All other cultural and agronomic practices were performed as per the need of the crop and experimental design. Three seeds were dibbled per hill spaced at one foot and the rows were distanced at 2.5 feet apart. Later, one healthy plant was left per dibble. Three rows, each 15 feet long, were provided to each entry, per irrigation treatment per replication. Irrigation treatments were four, that is three irrigations (i.e., 55, 95 and 125 days after planting); four irrigations (i.e., 50, 70, 90 and 110 days after planting); five irrigations (i.e., 40, 60, 80, 100 and 120 days after planting) and seven irrigations (normal or control) at 35, 50, 65, 80, 95, 110 and 125 days after planting. At maturity, ten consecutive plants were randomly selected, per entry per replication per irrigation treatment, and treated as index plants for recording observations on number of bolls per plant, number of sympodia per plant, seedcotton yield per plant and lintcotton yield per plant. Quantitative genetic analysis of this diallel experiment followed the procedures of Hayman, Jinks and Aksel and Johnson [11, 13-14]. Before conducting the diallel analysis, the pre-requisite conditions of meeting five assumptions of diallel cross must be satisfied [11]. Here we would explain how our experimental material of 6x6 *Gossypium hirsutum* complete F_1 diallel cross of selected drought susceptible and tolerant varieties satisfied these assumptions.

The condition of "homozygous parents" in the present studies was satisfied by selfing individual parental lines before they were used in hybridization program [12]. The condition of normal diploid segregation, in the present case, may be met by explaining that though cotton is an amphidiploid (allotetraploid) of A and D genomes [15], it has established itself as genetically stable over the years and behaves as normal diploid in subsequent generations [16]. The progenitor A and D genomes, though differ enough in the resulting allotetraploid ($2n=4x$), yet they facilitate appropriate pairing of each set of chromosomes at meiosis as in normal diploid species [17]. Thus it has been made clear that many genes in *Gossypium* are inherited in functionally diploid

manner. According to Kearsley and Pooni [18] quantitative genetic analysis in such organisms can be performed using standard methods considering normally segregating diploids. "No reciprocal differences" were checked after Hayman's [19] procedure of analysis of variance of diallel tables, where significance of the component 'c' indicates failure of this hypothesis. The remaining three assumptions of 'no multiple allelism', 'independent action of non-allelic genes' and 'uncorrelated gene distribution' were checked by analysis of variance of $W_r - V_r$ values for arrays of each diallel table. Heterogeneity of $W_r - V_r$ variances will reveal non validity of these assumptions. In the present case, the 't' value for $W_r - V_r$ mean squares (Tables 2 to 5) were non-significant for all the characters and therefore the assumptions are satisfied.

After satisfying the validity of assumptions, the quantitative genetic analysis yielded components of genetic variation (D , H_1 , H_2 , F , and h^2) and second degree statistics (variances and covariances) parameters [V_{0L_0} , V_{0L_1} , V_{1L_1} , W_{0L_0} and $(ML_1 - ML_0)^2$] from which the following genetic ratios and parameters were determined: (a) Average degree of dominance $(H_1/D)^{1/2}$. If the value of this ratio is zero, there is no dominance; if it is greater than zero but less than 1, there is partial dominance and if it is greater than 1, it denotes over-dominance. (b) The ratio of dominant and recessive genes in the parents estimated as $[(4DH_1)^{1/2} + F] / [(4DH_1)^{1/2} - F]$. If this ratio is 1, the dominant and recessive genes in the parents are in equal proportion; if it is less than 1, it indicates an excess of recessive genes; but if it is greater than 1, an excess of dominant genes is indicated. (c) The number of groups of genes which control the character and exhibit dominance is given by $[h^2/H_2]$ and (d) the proportion of genes with positive and negative effects in the parents is estimated as $[H_2/4H_1]$. If the positive and negative alleles are symmetrically distributed, this ratio equals to 0.25. Ratio <0.25 indicates preponderance of negative effects and >0.25 excess of positive allele effects.

RESULTS AND DISCUSSION

The assumption of 'no reciprocal differences' as satisfied through analysis of variance of diallel table [19] is shown in Table 1. In this analysis of variance, component 'a' tests the significance of additive gene effects and 'b' the dominance gene effects, while 'b₁' explains the mean deviation of hybrids from their mid-parent values. The dominance deviations if predominantly in one direction will result in significant

'b₁' in the analysis of variance. Component 'b₂' indicates the extent to which the mean dominance of deviations, within a given array of diallel table, differs from those of other arrays. Therefore significance of 'b₂' in the analysis of variance will imply that some of the parents contain excess of dominant alleles controlling the particular character. Component 'b₃' tests the portion of dominance deviations attributable to individual particular hybrid. The differences between reciprocal crosses are assessed by the significance of component 'c' and the maternal effects are reflected by component 'd'. In the present case, additive gene effects components in normal seven irrigations treatment was significant for all the characters implying the importance of additive gene effects and general combining ability of the parents. Component 'b' was also significant for all the four characters indicating that the dominance gene effects were important explaining additive x nonadditive and nonadditive x nonadditive gene effects interaction for these characters. Partitioning 'b' component of variation into 'b₁', 'b₂' and 'b₃' components, dominance effects get also partitioned into direction of dominance, dominance deviations attributed to the parental arrays and dominance deviations ascribable to the individual hybrids. Accordingly, 'b₁' was highly significant ($P < 0.01$) for all the four characters implying that the dominance was unidirectional. Component b_1 was nonsignificant for number of bolls per plant and sympodia per plant only in five irrigations treatment signifying that the selection for these characters would not yield fruitful results. Component 'b₂' was highly significant ($P < 0.01$) indicating that these dominance deviations are attributed to parental arrays and 'b₃' was highly significant ($P < 0.01$) also implying that the dominance was caused by the hybrid combinations in other words due to divergent heterozygosity of the hybrids. Component 'c' was non-significant in seven and four irrigations treatments but highly significant in other treatments. Due to significant component 'c', the assumption of 'no differences between the reciprocal crosses' gets non-validated in the diallel analysis. This non-validity is removed by plugging in the common mean of a cross and its reciprocal in the off-diagonal cells of the diallel matrix. Component 'd' was highly significant for bolls per plant, seedcotton yield per plant and lintcotton yield per plant. These maternal effects not ascribed to component 'c' would not be considered in the diallel analysis especially when the common mean of the cross and its reciprocal has been plugged in the diallel matrix. These diallel tables were constructed by putting the common mean of a hybrid

and its reciprocal irrespective of the fact that whether the reciprocal differences were significant or not (Tables 2 to 5) and then analysis carried out. These tables have been supplemented by variances and covariances and other second degree statistics parameters from which the genetic components of variation were calculated. These components of genetic variation are also given in these diallel tables individually for each character. From these components of genetic variation, genetic parameters were calculated which provided the basis for interpreting the genetic retrospect and inheritance pattern of a particular character and thus interpreted accordingly. Genetic parameters are also given in these diallel tables.

Inheritance of Bolls Per Plant

Number of bolls per plant under normal seven irrigation treatment (Table 2) was inherited as an over dominant trait because the average degree of dominance parameter $[H_1 \div D]^{1/2}$ measured 1.033. The proportion of dominant and recessive genes in the parents $[(4DH_1)^{1/2} + F] \div [(4DH_1)^{1/2} - F]$ was 0.509 indicating that parents contained preponderantly recessive genes in them. The proportion of negative and positive allele effects in the parents $[H_2 \div 4H_1]$ was 0.219 indicating that negative allele affects excessively distributed in the parents were responsible for contributing decreased boll number attributes into their progenies through their recessive genes. The number of groups of genes controlling dominance loci in the

Table 1: Mean squares from the analysis of variance of diallel table, for validity test of 6x6 F₁ complete cotton diallel cross, under four irrigation regimes during 2009, for four characters, at Sindh Agriculture University farm, Tandojam

Source of variation	D.F.	Number of bolls per plant	Sympodial branches per plant	Seedcotton yield per plant	Lintcotton yield per plant	Number of bolls per plant	Sympodial branches per plant	Seedcotton yield per plant	Lintcotton yield per plant
Reps.	3	1.55	1.76	3.52	0.34	7.05	0.50	2.81	0.26
a	5	128.41**	141.08**	2672.10**	259.04**	253.13**	130.40**	3807.90**	369.55**
b	15	31.01**	8.42**	247.18**	24.00**	40.18**	7.41**	599.16**	57.99**
b ₁	1	22.40**	3.32**	964.43**	93.51**	1.18 ns	0.36 ns	1874.37**	181.84**
b ₂	5	13.83**	8.42**	116.54**	11.29**	18.77**	5.68**	378.35**	36.90**
b ₃	9	41.51**	8.98**	240.07**	23.34**	54.41**	9.16**	580.15**	55.95**
c	5	1.19 ns	0.22 ns	3.73 ns	0.36 ns	1.89**	7.26**	3.14 ns	0.32 ns
d	10	4.60**	0.35 ns	6.01**	0.58**	2.61**	3.32**	7.09**	0.68**
Error	105	0.69	0.35	1.82	0.18	0.38	0.48	1.74	0.17
SEVEN IRRIGATIONS						FIVE IRRIGATIONS			

Source of variation	D.F.	Number of bolls per plant	Sympodial branches per plant	Seedcotton yield per plant	Lintcotton yield per plant	Number of bolls per plant	Sympodial branches per plant	Seedcotton yield per plant	Lintcotton yield per plant
Reps.	3	5.60	1.46	95.06	9.30	1.39	20.40	24.12	1.93
a	5	510.31**	129.34**	6887.30**	667.53**	446.05**	102.94**	5043.05**	486.17**
b	15	233.81**	8.06**	2909.16**	281.74**	182.08**	7.81**	2403.87**	230.44**
b ₁	1	1003.05**	3.84*	19223.71**	1859.65**	1195.45**	12.35**	20527.07**	1939.27**
b ₂	5	426.72**	12.29**	4160.08**	403.14**	249.20**	8.27**	2528.54**	247.58**
b ₃	9	41.17**	6.18**	401.48**	38.98**	32.19**	7.00**	320.91**	31.058**
c	5	10.32ns	0.36ns	28.27ns	2.69ns	6.93**	1.36**	82.34**	8.03**
d	10	3.01ns	0.61ns	34.07ns	3.29ns	1.97ns	0.41**	14.95ns	1.44ns
Error	105	4.83	0.63	43.78	4.24	1.05	0.41	9.44	0.96
FOUR IRRIGATIONS						THREE IRRIGATIONS			

Note: *Significant at 5% probability level. **Significant at 1% probability level. ns = non-significant.

parents $[h^2+H_2]$ was 0.20 implying that at least one group of genes is operative in governing/conditioning the inheritance pattern of number of bolls/plant. The broad sense heritability was 99.9% and the narrow sense heritability was 57.3% indicating that number of bolls/plant is highly heritable and further significant amount of improvement up to the tune of 57% could be realized if progenies are selected under defined high selection pressure following pedigree progeny selection procedure.

In case of five irrigations, the average degree of dominance measured $[H_1+D]^{1/2}=1.320$ indicating that boll number was inherited as an over dominant trait. The number of dominant and recessive genes in the parents $[(4DH_1)^{1/2} + F] \div [(4DH_1)^{1/2} - F]$ was 0.433 implying that parents contained preponderance of recessive genes in them. The proportion of negative and positive allele effects in the parents $[H_2+4H_1]$ was 0.026 implying that negative allele effects are in excess in the parents that are responsible for contributing decreased boll number attributes into their progenies. The number of group of genes controlling dominance loci in the parents $[h^2+H_2]$ was equal to 0.032 indicating that at least one group of genes was responsible/operative in governing/conditioning the inheritance pattern of boll number in this irrigation treatment. The broad sense heritability was 99.6% and narrow sense heritability was 97% indicating that boll number in five irrigations treatment is also highly heritable and quite responsive under intensive selection pressure to yield significant improvement through pedigree selection pressure.

Under four irrigations treatment, boll number was also inherited as an overdominant trait as the average degree of dominance $[H_1+D]^{1/2}$ was equal to 1.207. The proportion of dominant and recessive genes in the parents $[(4DH_1)^{1/2} + F] \div [(4DH_1)^{1/2} - F]$ was equal to 0.310 meaning that recessive genes are in preponderance in the parents. The distribution of negative and positive allele effects in the parents as determined by $[H_2+4H_1]$ was 0.149 meaning that the negative allele effects were more pronounced in the parents in this asymmetrical distribution and were responsible for contributing decreased boll number attributes into their progenies through their recessive genes. Parameter $[h^2+H_2]$ measuring number of group of genes that controlled dominance at the parents' loci was equal to 2.03 indicating that at least two groups of genes are operative and govern the inheritance pattern of boll number. The broad sense heritability was 99.4% and the narrow sense heritability was 71.6% depicting that boll number in this irrigation treatment is also highly

heritable and significant amount of improvement could be realized if progeny rows are screened under defined selection pressure.

In case three irrigations, the average degree of dominance $[H_1+D]^{1/2}$ was equal to 1.216 meaning that the boll number was also over-dominantly inherited. The proportion of dominant to recessive genes in the parents as given by $[(4DH_1)^{1/2} + F] \div [(4DH_1)^{1/2} - F]$ was 0.343 implying that recessive genes were in preponderance in the parents. The distribution of positive and negative allele effects in the parents $[H_2+4H_1]$ was 0.075 meaning that negative allele effects were excessively distributed in the parents and were responsible for contributing decreased boll number attributes into their progenies through their recessive genes. The number of groups of genes controlling dominance loci in the parents $[h^2+H_2]$ was 1.832 implying that at least two groups of genes are governing the inheritance pattern of bolls/plant in this stress irrigation treatment. The broad sense heritability was 99.8% and the narrow sense heritability was 67% showing that bolls/plant is highly heritable character and quite a substantial improvement could be realized while selecting the desired progenies from single progeny rows under high selection pressure from this stress irrigation treatment.

Inheritance of Sympodial Branches

In seven irrigations treatment, $[H_1+D]^{1/2}$ was 0.941 depicting nearly complete dominance inheritance pattern of sympodial branches per plant (Table 3). The proportion of dominant to recessive genes in the parents $[(4DH_1)^{1/2} + F] \div [(4DH_1)^{1/2} - F]$ was 0.343 implying that the recessive genes are in preponderance in the parents. The proportion of positive and negative allele effects $[H_2+4H_1]$ was equal to 0.188, and since this estimate was <0.25 , excess of negative allele effects in the parents contributing decreased sympodial branches/plant attributes into their progenies.

The number of effective factors as given by $[h^2+H_2]$ was 0.103 implied that at least one group of genes controls the dominance at parents' loci and governs the inheritance pattern of sympodial branches in this treatment. The broad sense heritability was 98.9% and the narrow sense heritability was 84.2% suggesting that the character is highly heritable and significant improvement, up to the tune of 84%, can be brought about if desired combinations are selected under defined intensive selection pressure from progeny rows.

Table 2: Estimates of Genetic Components of Variation, Genetic Parameters, Variances and Covariances for Number of Bolls/Plant in 6×6 F₁ Complete Cotton Diallel Cross During 2009 at Sindh Agriculture University Farm, Tandojam**SEVEN IRRIGATIONS:**

Parents	CRIS-134	CRIS342	SINDH1	NIAB-78	SADORI	BH-160	Wr	Vr	Wr- Vr	Wr+ Vr	
CRIS-134	43.595	40.821	38.931	38.300	36.945	32.954	11.313	12.940	-01.628	24.253	
CRIS-342	40.821	41.233	34.994	35.145	40.056	39.838	07.625	08.084	-0.459	15.708	
SINDH-1	38.931	34.994	32.653	35.293	35.273	35.290	06.784	04.045	02.740	10.829	
NIAB-78	38.300	35.145	35.293	36.648	35.040	34.175	04.086	02.173	01.912	06.259	
SADORI	36.945	40.056	35.273	35.040	36.145	33.004	06.811	05.552	01.259	12.363	
BH-160	32.954	39.838	35.290	34.175	33.004	34.500	01.815	06.516	-4.700	08.331	
Genetic components of variation	D =	15.321	Genetic parameters	$[H_1/D]^{1/2} =$			1.033	V_0L_0		15.478	
	H ₁ =	15.599		$[(4DH_1)^{1/2} + F] \div [(4DH_1)^{1/2} - F] =$			0.509	V_0L_1		02.403	
	H ₂ =	13.636		$[h^2/H_2] =$			0.200	V_1L_1		05.888	
	F =	07.732		$[H_2/4H_1] =$			0.219	W_0L_{01}		05.754	
	h ² =	02.723		$[h^2_{(b)}] =$			0.990	$(ML_1-ML_0)^2$		14.378	
	E =	00.156		$[h^2_{(n)}] =$			0.573	t' value Var. of Wr -Vr n.s.			

FIVE IRRIGATIONS:

CRIS-134	40.200	36.368	37.491	35.841	34.208	31.308	09.782	09.040	00.742	18.822	
CRIS-342	36.368	35.110	32.468	33.131	37.463	37.144	02.908	04.395	-1.487	07.303	
SINDH-1	37.491	32.468	29.505	31.636	31.334	30.893	11.277	07.621	03.656	18.898	
NIAB-78	35.841	33.131	31.636	29.850	30.560	26.879	12.243	09.257	02.986	21.500	
SADORI	34.208	37.463	31.334	30.560	32.688	25.935	12.588	14.896	-2.309	27.484	
BH-160	31.308	37.144	30.893	26.879	25.935	28.253	08.186	16.566	-8.380	24.752	
Genetic components of variation	D =	17.866	Genetic parameter	$[H_1/D]^{1/2} =$			01.32	V_0L_0		17.977	
	H ₁ =	19.994		$[(4DH_1)^{1/2} + F] \div [(4DH_1)^{1/2} - F] =$			0.433	V_0L_1		04.737	
	H ₂ =	17.301		$[h^2/H_2] =$			0.0320	V_1L_1		09.249	
	F =	01.814		$[H_2/4H_1] =$			0.026	W_0L_{01}		08.529	
	h ² =	00.058		$[h^2_{(b)}] =$			0.995	$(ML_1-ML_0)^2$		12.971	
	E =	00.110		$[h^2_{(n)}] =$			0.969	t' Var. of Wr - Vr n.s.			

FOUR IRRIGATIONS:

CRIS-134	40.460	47.066	28.519	30.224	28.528	32.230	18.934	57.663	-38.730	76.597	
CRIS-342	47.066	25.390	40.971	43.413	40.375	42.618	21.441	56.592	-35.151	78.033	
SINDH-1	28.519	40.971	27.665	31.441	32.546	31.993	-13.214	22.358	-35.572	09.144	
NIAB-78	30.224	43.413	31.441	24.455	32.679	30.909	-05.310	38.416	-43.726	33.107	
SADORI	28.528	40.375	32.546	32.679	22.620	29.911	-02.933	34.110	-37.043	31.177	
BH-160	32.230	42.618	31.993	30.909	29.911	26.280	00.093	30.086	-29.993	30.179	
Genetic components of variation	D =	36.02	Genetic parameters	$[H_1/D]^{1/2} =$			1.207	V_0L_0		37.098	
	H ₁ =	165.6		$[(4DH_1)^{1/2} + F] \div [(4DH_1)^{1/2} - F] =$			0.310	V_0L_1		09.554	
	H ₂ =	102.7		$[h^2/H_2] =$			2.029	V_1L_1		35.825	
	F =	61.29		$[H_2/4H_1] =$			0.149	W_0L_{01}		02.850	
	h ² =	124.4		$[h^2_{(b)}] =$			0.994	$(ML_1-ML_0)^2$		13.782	
	E =	01.08		$[h^2_{(n)}] =$			0.716	t' of var. of Wr-Vr n.s.			

(Table 2). continued

THREE IRRIGATIONS:

CRIS-134	26.820	36.416	21.660	21.573	21.233	22.551	08.360	35.345	-26.986	43.705	
CRIS-342	36.416	18.278	31.215	32.465	29.795	31.813	09.301	37.893	-28.591	47.194	
SINDH-1	21.660	31.215	18.893	21.538	23.358	24.591	-3.859	17.838	-21.696	13.979	
NIAB-78	21.573	32.465	21.538	16.930	23.196	21.604	-0.124	26.503	-26.627	26.379	
SADORI	21.233	29.795	23.358	23.196	14.333	21.739	04.757	24.606	-19.848	29.363	
BH-160	22.551	31.813	24.591	21.604	21.739	14.670	06.819	30.629	-23.810	37.448	
Genetic components of variation	D =	20.510	Genetic parameters	$[H_1/D]^{1/2} =$			1.216	V_0L_0		20.747	
	H ₁ =	118.48		$[(4DH_1)^{1/2} + F] + [(4DH_1)^{1/2} - F]=$			0.343	V_0L_1		08.350	
	H ₂ =	81.348		$[h^2/H_2]=$			1.832	V_1L_1		28.802	
	F =	24.342		$[H_2/4H_1] =$			0.075	W_0L_{01}		04.209	
	h ² =	149.09		$[h^2_{(b)}] =$			0.998	$(ML_1-ML_0)^2$		10.687	
	E =	0.236		$[h^2_{(n)}] =$			0.676	't' of Var. of Wr - Vr n.s.			

Table 3: Estimates of Genetic Components of Variation, Genetic Parameters, Variances and Covariances for Symptodia Per Plant in 6x6 F₁ Complete Cotton Diallel Cross During 2009 at Sindh Agriculture University Farm, Tandojam

SEVEN IRRIGATIONS:

Parents	CRIS-134	CRIS342	SINDH1	NIAB-78	SADORI	BH-160	Wr	Vr	Wr- Vr	Wr+ Vr	
CRIS-134	19.375	24.325	20.863	19.525	19.713	19.313	05.266	03.801	01.465	09.067	
CRIS-342	24.325	25.975	21.800	22.838	21.438	24.363	03.529	03.024	00.505	06.553	
SINDH-1	20.863	21.800	20.725	19.388	18.350	17.000	03.200	03.204	-0.004	06.404	
NIAB-78	19.525	22.838	19.388	19.175	16.563	18.150	05.371	04.280	01.091	09.651	
SADORI	19.713	21.438	18.350	16.563	18.025	18.013	03.748	02.827	00.920	06.575	
BH-160	19.313	24.363	17.000	18.150	18.013	19.825	06.305	06.810	-0.505	13.116	
Genetic components of variation	D =	7.837	Genetic parameters	$[H_1/D]^{1/2} =$			0.941	V_0L_0		7.925	
	H ₁ =	5.376		$[(4DH_1)^{1/2} + F] + [(4DH_1)^{1/2} - F]=$			0.343	V_0L_1		2.939	
	H ₂ =	4.036		$[h^2/H_2]=$			0.103	V_1L_1		3.991	
	F =	-2.545		$[H_2/4H_1] =$			0.188	W_0L_{01}		4.570	
	h ² =	0.416		$[h^2_{(b)}] =$			0.989	$(ML_1-ML_0)^2$		8.379	
	E =	0.088		$[h^2_{(n)}] =$			0.842	't' of Var. of Wr -Vr n.s.			

FIVE IRRIGATIONS:

CRIS-134	17.000	21.800	18.825	17.213	17.600	17.038	04.971	03.493	01.478	08.464	
CRIS-342	21.800	23.700	20.013	20.813	19.650	21.225	03.462	02.115	01.348	05.577	
SINDH-1	18.825	20.013	18.250	18.850	16.313	15.613	02.995	02.812	00.183	05.807	
NIAB-78	17.213	20.813	18.850	16.950	14.313	15.525	05.738	05.389	00.350	11.127	
SADORI	17.600	19.650	16.313	14.313	15.700	15.888	04.237	03.386	00.850	07.623	
BH-160	17.038	21.225	15.613	15.525	15.888	17.475	05.484	04.664	00.820	10.148	
Genetic components of variation	D =	7.88	Genetic parameters	$[H_1/D]^{1/2} =$			0.799	V_0L_0		8.006	
	H ₁ =	4.33		$[(4DH_1)^{1/2} + F] + [(4DH_1)^{1/2} - F]=$			0.401	V_0L_1		2.717	
	H ₂ =	3.47		$[h^2/H_2]=$			0.155	V_1L_1		3.643	
	F =	-0.75		$[H_2/4H_1] =$			0.005	W_0L_{01}		4.481	
	h ² =	-0.01		$[h^2_{(b)}] =$			0.973	$(ML_1-ML_0)^2$		7.519	
	E =	0.12		$[h^2_{(n)}] =$			0.975	't' of Var. of Wr - Vr n.s.			

(Table 3). Continued.

FOUR IRRIGATIONS:

CRIS-134	14.950	19.813	17.263	15.600	15.763	15.725	04.257	03.182	01.075	07.439	
CRIS-342	19.813	21.425	18.100	19.225	17.700	19.950	02.501	01.836	00.665	04.337	
SINDH-1	17.263	18.100	16.825	15.113	14.225	13.775	02.752	03.098	-0.346	05.850	
NIAB-78	15.600	19.225	15.113	15.950	12.325	14.238	05.023	05.172	-0.149	10.196	
SADORI	15.763	17.700	14.225	12.325	14.350	13.800	03.066	03.385	-0.320	06.451	
BH-160	15.725	19.950	13.775	14.238	13.800	16.175	05.012	05.539	-0.527	10.551	
Genetic components of variation	D =	6.186	Genetic parameters	$[H_1/D]^{1/2} =$			0.884	V_0L_0		6.344	
	H ₁ =	5.658		$[(4DH_1)^{1/2} + F] + [(4DH_1)^{1/2} - F]=$			0.329	V_0L_1		2.695	
	H ₂ =	3.724		$[h^2/H_2]=$			-5.726	V_1L_1		3.702	
	F =	0.453		$[H_2/4H_1] =$			0.030	W_0L_{01}		3.769	
	h ² =	-2.596		$[h^2_{(b)}] =$			0.926	$(ML_1-ML_0)^2$		6.739	
	E =	0.453		$[h^2_{(n)}] =$			0.910	t' of var. of Wr-Vr n.s.			

THREE IRRIGATIONS:

CRIS-134	17.600	21.213	19.663	17.700	17.200	17.113	04.237	02.746	01.491	06.983	
CRIS-342	213.21	24.075	18.188	19.425	17.800	19.913	06.108	05.295	00.813	11.403	
SINDH-1	19.663	18.188	17.600	17.400	15.875	14.850	01.907	02.899	-0.992	04.805	
NIAB-78	17.700	19.425	17.400	17.300	14.700	15.913	04.051	02.612	01.439	06.663	
SADORI	17.200	17.800	15.875	14.700	15.625	14.888	02.624	01.553	01.071	04.176	
BH-160	17.113	19.913	14.850	15.913	14.888	17.250	04.920	03.622	01.299	08.542	
Genetic components of variation	D =	8.610	Genetic parameters	$[H_1/D]^{1/2} =$			0.693	V_0L_0		8.714	
	H ₁ =	5.025		$[(4DH_1)^{1/2} + F] + [(4DH_1)^{1/2} - F]=$			0.369	V_0L_1		2.145	
	H ₂ =	3.706		$[h^2/H_2]=$			1.194	V_1L_1		3.121	
	F =	1.392		$[H_2/4H_1] =$			0.094	W_0L_{01}		3.974	
	h ² =	1.663		$[h^2_{(b)}] =$			0.980	$(ML_1-ML_0)^2$		7.273	
	E =	0.103		$[h^2_{(n)}] =$			0.863	t' of Var. of Wr - Vr n.s.			

Table 4: Estimates of Genetic Components of Variation, Genetic Parameters, Variances and Covariances for Seed-Cotton Yield in 6×6 F₁ Complete Cotton Diallel Cross During 2009 at Sindh Agriculture University Farm, Tandojam

SEVEN IRRIGATIONS:

Parents	CRIS-134	CRIS342	SINDH1	NIAB-78	SADORI	BH-160	Wr	Vr	Wr- Vr	Wr+ Vr	
CRIS-134	135.125	145.613	130.413	130.325	126.375	115.788	109.852	96.644	13.208	206.497	
CRIS-342	145.613	139.675	127.975	130.425	134.813	140.638	76.335	44.533	31.803	120.868	
SINDH-1	130.413	127.975	101.200	116.988	118.213	120.750	138.062	106.995	31.067	245.057	
NIAB-78	130.325	130.425	116.988	110.850	116.775	113.913	116.449	71.091	45.358	187.540	
SADORI	126.375	134.813	118.213	116.775	114.625	112.413	112.994	71.677	41.317	184.672	
BH-160	115.788	140.638	120.750	113.913	112.413	109.425	105.162	128.466	-23.304	233.628	
Genetic components of variation	D =	235.54	Genetic parameters	$[H_1/D]^{1/2} =$			0.801	V_0L_0		235.991	
	H ₁ =	141.81		$[(4DH_1)^{1/2} + F] + [(4DH_1)^{1/2} - F]=$			0.301	V_0L_1		55.668	
	H ₂ =	122.72		$[h^2/H_2]=$			1.090	V_1L_1		86.568	
	F =	32.139		$[H_2/4H_1] =$			0.216	W_0L_{01}		109.809	
	h ² =	133.72		$[h^2_{(b)}] =$			0.998	$(ML_1-ML_0)^2$		52.261	
	E =	0.454		$[h^2_{(n)}] =$			0.781	t' of Var. of Wr - Vr n.s.			

(Table 4). Continued.

FIVE IRRIGATIONS:

CRIE-134	118.775	121.138	119.563	117.438	112.175	102.613	53.035	47.925	05.110	100.960	
CRIS-342	121.138	111.275	114.638	120.488	122.225	126.500	-25.425	30.257	-55.682	04.832	
SINDH-1	119.563	114.638	87.175	99.725	100.413	101.300	143.32	135.33	7.990	278.642	
NIAB-78	117.438	120.488	99.725	91.425	96.338	83.288	184.36	215.50	-31.143	399.864	
SADORI	112.175	122.225	100.413	96.338	96.600	81.750	163.19	197.07	-33.879	360.260	
BH-160	102.613	126.500	101.300	83.288	81.750	84.500	148.50	299.27	-150.77	447.781	
Genetic components of variation	D =	189.95	Genetic parameters	$[H_1/D]^{1/2} =$			1.202	V_0L_0		190.387	
	H ₁ =	361.48		$[(4DH_1)^{1/2} + F] + [(4DH_1)^{1/2} - F]=$			0.413	V_0L_1		79.332	
	H ₂ =	298.73		$[h^2/H_2]=$			4.035	V_1L_1		154.226	
	F =	-64.46		$[H_2/4H_1] =$			0.054	W_0L_{01}		111.164	
	h ² =	260.11		$[h^2_{(b)}] =$			0.999	$(ML_1-ML_0)^2$		44.989	
	E =	0.436		$[h^2_{(n)}] =$			1.072	t' of Var. of Wr - Vr n.s.			

FOUR IRRIGATIONS:

CRIS-134	119.633	152.574	92.433	96.830	92.053	99.735	168.330	561.456	-393.126	729.786	
CRIS-342	152.574	76.795	132.758	141.604	125.036	138.235	184.150	709.378	-525.228	893.528	
SINDH-1	92.433	132.758	77.785	95.213	100.303	101.408	-63.134	329.764	-392.898	266.630	
NIAB-78	96.830	141.604	95.213	67.880	99.015	94.075	41.525	565.356	-523.831	606.881	
SADORI	92.053	125.036	100.303	99.015	62.733	93.251	60.228	399.680	-339.452	459.908	
BH-160	99.735	138.238	101.408	94.075	93.251	70.978	62.483	477.205	-414.722	539.688	
Genetic components of variation	D =	410.7	Genetic parameters	$[H_1/D]^{1/2} =$			1.301	V_0L_0		421.889	
	H ₁ =	2118		$[(4DH_1)^{1/2} + F] + [(4DH_1)^{1/2} - F]=$			0.338	V_0L_1		143.488	
	H ₂ =	1433		$[h^2/H_2]=$			5.061	V_1L_1		507.140	
	F =	526.5		$[H_2/4H_1] =$			0.092	W_0L_{01}		75.597	
	h ² =	2664		$[h^2_{(b)}] =$			0.995	$(ML_1-ML_0)^2$		45.959	
	E =	10.94		$[h^2_{(n)}] =$			0.559	t' of var. of Wr-Vr n.s.			

THREE IRRIGATIONS:

CRIS-134	83.628	123.859	74.531	74.256	70.588	76.333	69.353	402.407	-333.05	471.760	
CRIS-342	123.859	55.555	106.231	109.216	101.939	107.629	96.980	545.411	-448.43	642.391	
SINDH-1	74.531	106.231	54.585	72.065	77.169	82.728	-21.17	283.097	-304.26	261.928	
NIAB-78	74.256	109.216	72.065	50.863	78.901	71.879	18.828	355.782	-336.95	374.609	
SADORI	70.588	101.939	77.169	78.901	41.418	70.283	77.953	379.887	-301.93	457.846	
BH-160	76.333	107.629	82.728	71.879	70.283	40.743	123.649	466.334	-342.68	589.983	
Genetic components of variation	D =	242.275	Genetic parameters	$[H_1/D]^{1/2} =$			1.201	V_0L_0		244.635	
	H ₁ =	1617.06		$[(4DH_1)^{1/2} + F] + [(4DH_1)^{1/2} - F]=$			0.370	V_0L_1		105.052	
	H ₂ =	1197.35		$[h^2/H_2]=$			11.744	V_1L_1		405.486	
	F =	242.658		$[H_2/4H_1] =$			0.051	W_0L_{01}		60.933	
	h ² =	2849.78		$[h^2_{(b)}] =$			0.999	$(ML_1-ML_0)^2$		36.045	
	E =	2.3598		$[h^2_{(n)}] =$			1.829	t' of Var. of Wr - Vr n.s.			

Table 5: Estimates of Genetic Components of Variation, Genetic Parameters, Variances and Covariances for Lint-Cotton Yield in 6×6 F₁ Complete Cotton Diallel Cross During 2009 at Sindh Agriculture University Farm, Tandojam**SEVEN IRRIGATIONS:**

Parents	CRIS-134	CRIS342	SINDH1	NIAB-78	SADORI	BH-160	Wr	Vr	Wr- Vr	Wr+ Vr	
CRIS-134	42.058	45.320	40.589	40.561	39.334	36.039	10.643	09.360	01.284	20.003	
CRIS-342	45.320	43.473	39.830	40.593	41.959	43.771	07.397	04.315	03.083	11.712	
SINDH-1	40.589	39.830	31.498	36.411	36.794	37.580	13.374	10.362	03.012	23.736	
NIAB-78	40.561	40.593	36.411	34.500	36.346	35.454	11.280	06.885	04.395	18.162	
SADORI	39.334	41.959	36.794	36.346	35.675	34.985	10.947	06.945	04.001	17.892	
BH-160	36.039	43.771	37.580	35.454	34.985	34.058	10.191	12.443	-2.253	22.634	
Genetic components of variation	D =	22.820	Genetic parameters	$[H_1/D]^{1/2} =$			0.810	V_0L_0		22.864	
	H ₁ =	13.766		$[(4DH_1)^{1/2} + F] \div [(4DH_1)^{1/2} - F]=$			0.302	V_0L_1		05.393	
	H ₂ =	11.916		$[h^2/H_2]=$			1.088	V_1L_1		08.385	
	F =	03.101		$[H_2/4H_1] =$			0.216	W_0L_{01}		10.639	
	h ² =	12.965		$[h^2_{(b)}] =$			0.998	$(ML_1-ML_0)^2$		16.266	
	E =	00.043		$[h^2_{(n)}] =$			0.781	t' of Var. of Wr -Vr n.s.			

FIVE IRRIGATIONS:

CRIS-134	36.968	37.701	37.213	36.551	34.913	31.936	05.136	04.643	00.493	09.779	
CRIS-342	37.701	34.633	35.681	37.499	38.041	39.371	-2.464	02.930	-5.394	00.465	
SINDH-1	37.213	35.681	27.130	31.038	31.253	31.528	13.889	13.116	00.773	27.006	
NIAB-78	36.551	37.499	31.038	28.455	29.984	25.920	17.860	20.878	-3.018	38.737	
SADORI	34.913	38.041	31.253	29.984	30.065	25.441	15.809	19.096	-3.287	34.905	
BH-160	31.936	39.371	31.528	25.920	25.441	26.300	14.385	28.996	-14.611	43.381	
Genetic components of variation	D =	18.40	Genetic parameters	$[H_1/D]^{1/2} =$			1.025	V_0L_0		18.445	
	H ₁ =	35.03		$[(4DH_1)^{1/2} + F] \div [(4DH_1)^{1/2} - F]=$			0.413	V_0L_1		07.686	
	H ₂ =	28.91		$[h^2/H_2]=$			4.033	V_1L_1		14.943	
	F =	-6.25		$[H_2/4H_1] =$			0.054	W_0L_{01}		10.769	
	h ² =	25.23		$[h^2_{(b)}] =$			0.999	$(ML_1-ML_0)^2$		14.002	
	E =	0.041		$[h^2_{(n)}] =$			1.073	t' of Var. of Wr - Vr n.s.			

FOUR IRRIGATIONS:

CRIS-134	37.235	47.486	28.768	30.138	28.651	31.041	16.310	54.386	-38.076	70.695	
CRIS-342	47.486	23.903	41.319	44.073	38.916	43.024	17.835	68.708	-50.873	86.544	
SINDH-1	28.768	41.319	24.210	29.633	31.219	31.563	-6.118	31.943	-38.061	25.825	
NIAB-78	30.138	44.073	29.633	21.128	30.816	29.279	04.026	54.764	-50.738	58.790	
SADORI	28.651	38.916	31.219	30.816	19.525	29.024	05.838	38.716	-32.878	44.554	
BH-160	31.041	43.024	31.563	29.279	29.024	22.090	06.057	46.229	-40.172	52.286	
Genetic components of variation	D =	39.81	Genetic parameters	$[H_1/D]^{1/2} =$			1.009	V_0L_0		40.871	
	H ₁ =	205.2		$[(4DH_1)^{1/2} + F] \div [(4DH_1)^{1/2} - F]=$			0.338	V_0L_1		13.900	
	H ₂ =	138.8		$[h^2/H_2]=$			5.052	V_1L_1		49.124	
	F =	51.02		$[H_2/4H_1] =$			0.092	W_0L_{01}		07.325	
	h ² =	257.7		$[h^2_{(b)}] =$			0.995	$(ML_1-ML_0)^2$		14.304	
	E =	1.060		$[h^2_{(n)}] =$			0.561	t' of var. of Wr-Vr n.s.			

(Table 5). Continued.

THREE IRRIGATIONS:

CRIS-134	26.030	38.550	23.196	23.111	21.968	23.756	06.721	38.988	-32.267	45.710
CRIS-342	38.550	17.290	33.064	33.993	31.728	33.498	09.401	52.840	-43.438	62.241
SINDH-1	23.196	33.064	16.993	22.430	24.018	25.746	-2.057	27.414	-29.471	25.356
NIAB-78	23.111	33.993	22.430	15.830	24.558	22.374	01.819	34.465	-32.646	36.284
SADORI	21.968	31.728	24.018	24.558	12.890	21.874	07.550	36.804	-29.255	44.354
BH-160	23.756	33.498	25.746	22.374	21.874	12.680	11.978	45.171	-33.193	57.149
Genetic components of variation	D =	23.571	Genetic parameters	$[H_1/D]^{1/2} =$			1.015	V_0L_0	23.707	
	H ₁ =	155.84		$[(4DH_1)^{1/2} + F] \div [(4DH_1)^{1/2} - F] =$			0.368	V_0L_1	10.177	
	H ₂ =	114.75		$[h^2/H_2] =$			11.105	V_1L_1	39.280	
	F =	24.242		$[H_2/4H_1] =$			0.053	W_0L_{01}	05.902	
	h ² =	269.22		$[h^2_{(b)}] =$			0.998	$(ML_1-ML_0)^2$	11.218	
	E =	00.241		$[h^2_{(n)}] =$			2.228	't' of Var. of Wr - Vr n.s.		

In case of five irrigations, the average degree of dominance $[H_1 \div D]^{1/2}$ was 0.799 depicting partial dominance inheritance pattern of sympodial branches in this treatment. The proportion of dominant and recessive genes in the parents $[(4DH_1)^{1/2} + F] \div [(4DH_1)^{1/2} - F]$ was 0.401 showing that some of the parents contained excess of recessive genes in them. The distribution of positive and negative allele effects in the parents $[H_2 \div 4H_1]$ was equal to 0.005 suggesting that negative allele effect are in preponderance in parents in this asymmetrical distribution and contribute decreased sympodial branches/plant attributes into their progenies. The numbers of group of genes controlling dominance at parents' loci are $[h^2 \div H_2] = 0.155$ meaning that at least one group of genes is controlling/governing the inheritance pattern of sympodial branches in this treatment. The broad and narrow sense heritability was 97.5% depicting that the character is highly heritable in this irrigation treatment and quite a significant amount of improvement is expected to be brought about while selecting the genotypes/hybrid combinations under high selection pressure from the progeny rows.

In case of four irrigations treatment, the mean degree of dominance $[H_1 \div D]^{1/2}$ was 0.884 meaning that sympodial branches are also inherited as partial dominant trait in this medium stress treatment. $[(4DH_1)^{1/2} + F] \div [(4DH_1)^{1/2} - F]$ was equal to 0.329 implying that the parents contained excess of recessive genes in them. The distribution of positive and negative allele effects in the parents $[H_2 \div 4H_1]$ was 0.030 implying that negative allele effects are in preponderance in the parents and are responsible for contributing decreased sympodial branches/plant attributes into their progenies through their recessive

genes. The numbers of effective factors that control the dominance at parents' loci are $[h^2 \div H_2] = 5.726$ implying that at least six groups of genes are controlling the inheritance pattern of this character in this medium stress irrigation treatment. The broad and narrow sense heritability was 92% depicting that sympodial branches are also highly heritable in this treatment and quite a significant amount of improvement is realized if selection is made under intensive selection pressure from the hybrid progenies rows.

Under stress conditions of three irrigations treatment, sympodial branches/plant also inherited as partial dominant trait as the mean degree of dominance $[H_1 \div D]^{1/2}$ was equal to 0.693. The proportion of dominant and recessive genes $[(4DH_1)^{1/2} + F] \div [(4DH_1)^{1/2} - F]$ was equal to 0.369 implying that the recessive genes are in preponderance in the parents and the distribution of positive and negative allele effects $[H_2 \div 4H_1]$ was 0.094 suggesting negative allele effects, contributing decreased attributes, are in preponderance. $[h^2 \div H_2] = 1.194$ implied that at least one group of genes is governing the inheritance pattern of sympodial branches in this stress irrigation treatment. The broad sense heritability was 98% and narrow sense heritability was 86% suggesting that the character is also highly heritable even under stress conditions and quite significant improvement could be brought about while selecting the desired genotypes from progeny rows even under high selection pressure.

Inheritance of Seedcotton Yield

Seedcotton inherited as partial dominant trait in the normal seven irrigations treatment as $[H_1 \div D]^{1/2}$ was equal to 0.801 (Table 4). The proportion of dominant to

recessive genes in the parents $[(4DH_1)^{1/2} + F] \div [(4DH_1)^{1/2} - F]$ was 0.301 indicating that recessive genes were in excess in the parents. The proportion of positive and negative allele effects in the parents $[H_2 \div 4H_1] = 0.216$ and since this was less than 0.25 (equilibrium stage where negative and positive allele effects are equally distributed in the parents), negative effects are quite pronounced and are responsible for contributing somewhat decreased yielding capacity attributes into their progenies. The number of group of factors controlling the dominant loci in the parents $[h^2 \div H_2]$ was 1.09 indicating that at least one group of genes is operative and governs/conditions the inheritance pattern of yield in this treatment. The broad sense heritability was 99.8% and the narrow sense heritability was 78% meaning that seedcotton yield/plant is highly heritable and sufficient improvement, up to the tune of 78%, could be realized if desired genotypes are selected under defined intensive selection pressure from the single progeny rows hybrid combinations.

In case of five irrigations, the average degree of dominance $[H_1 \div D]^{1/2}$ was equal to 1.202 indicating that seedcotton yield is over dominantly inherited. The proportion of dominant and recessive genes in the parents $[(4DH_1)^{1/2} + F] \div [(4DH_1)^{1/2} - F]$ was 0.413 indicating that some of the parents preponderantly contained recessive genes in them as compared to others. The distribution of negative and positive allele effects in the parents $[H_2 \div 4H_1]$ was equal to 0.054 indicating that negative allele effects are in excess in the parents that contribute decreased yielding capacity attributes into their progenies. The number of group of genes controlling dominance in the parents loci $[h^2 \div H_2] = 4.03$ suggested that at least four groups of genes are operative and govern the inheritance pattern of seedcotton yield/plant in this irrigation treatment. The broad sense heritability was 99.9% and the narrow sense heritability was 107% indicating that seedcotton yield is highly heritable in this irrigation treatment and quite significant yield improvement could be realized while selecting desirable hybrid combinations for yield under high/intensive selection pressure from the single progeny rows following pedigree method.

In case of four irrigations, seedcotton yield also inherited as an overdominant trait as the average degree of dominance $[H_1 \div D]^{1/2} = 1.3$ was greater than unity. The proportion of dominant to recessive genes in the parents $[(4DH_1)^{1/2} + F] \div [(4DH_1)^{1/2} - F]$ was equal to 0.338 and since this value was less than one, recessive genes were interpreted in excess in the parents. The distribution of positive and negative allele

effects in the parents as given by $[H_2 \div 4H_1]$ was 0.092 which was less than 0.25 meaning that negative allele effects were in preponderance in the parents and were responsible for contributing decreased yield attributes into their progenies. The number of group of genes controlling dominance loci in the parents $[h^2 \div H_2]$ was equal to 5.06 indicating that at least five groups of genes are operative that condition the inheritance pattern of seedcotton yield/plant in this medium irrigation stress treatment. The broad sense heritability of 99.5% and the narrow sense heritability of 55.9% imply that though the seedcotton yield/plant is highly heritable character under medium irrigation stress, yet not very substantial yield improvement could be realized if desired plants/genotypes are selected under high selection pressure.

In case of three irrigations treatment, average degree of dominance $[H_1 \div D]^{1/2}$ was 1.2 and therefore seedcotton yield was also inherited as over-dominant trait in this stress irrigation treatment. The proportion of dominant to recessive genes in the parents as measured by $[(4DH_1)^{1/2} + F] \div [(4DH_1)^{1/2} - F]$ was 0.370 implying that parents contained excess of recessive genes in them. The proportion of positive and negative allele effects in the parents $[H_2 \div 4H_1]$ was 0.051 indicating negative allele effects are preponderantly distributed in the parents and are responsible for contributing decreased yield attributes into their progenies through their recessive genes. The group of effective factors controlling dominance loci in the parents was $[h^2 \div H_2] = 11.7$ implied that yield is polygenically controlled by at least eleven groups of genes conditioning the inheritance pattern of seedcotton yield in this stress irrigation treatment. The broad sense heritability was 99.9% and the narrow sense heritability was 182% meaning that quite significant amount of improvement in yield could be sought under stress irrigation treatment if progenies with desired yield attributes are selected under intensive selection pressure.

Inheritance of Lint Yield

In seven irrigations treatment (Table 5), lint yield was inherited as partially dominant character as the average degree of dominance measured $[H_1 \div D]^{1/2} = 0.810$. The proportion of dominant and recessive genes in the parents $[(4DH_1)^{1/2} + F] \div [(4DH_1)^{1/2} - F]$ was equal to 0.302 indicating that most of the parents contained preponderance of recessive genes in them. The proportion of positive and negative allele effects in the parents $[H_2 \div 4H_1]$ was 0.216

showing that negative alleles were in excess in the parents and were responsible for contributing decreased lint yield/plant attributes into their progenies through their recessive genes. The number of groups of genes controlling dominance at the parents' loci $[h^2+H_2]$ was equal to 1.088 implying that there were at least one to two groups of genes controlling the inheritance pattern of lint yield in this irrigation treatment. The broad sense heritability was 99.8% and the narrow sense heritability was 78% showing that the character is highly heritable and subsequently significant improvement up to the tune of 75% could be realized in lint yield while selecting the desired genotypes/hybrid combinations under intensive selection pressure.

In case of five irrigations, lint yield again inherited as an overdominant trait because the average degree of dominance $[H_1+D]^{1/2}$ measured 1.025. The proportion of dominant to recessive genes in the parents as estimated by parameter $[(4DH_1)^{1/2} + F] \div [(4DH_1)^{1/2} - F]$ was equal to 0.413 implying that there was preponderance of recessive genes in the parents. The proportion of positive and negative allele effects in the parents $[H_2+4H_1]$ was 0.054 implying that the negative allele effects are in excess in the parents and are responsible for contributing decreased lint yield attributes into their progenies. The number of groups of genes controlling the inheritance pattern $[h^2+H_2]$ was 4.033 indicating that at least four groups of genes were governing of inheritance pattern of lint yield and controlling dominance at the parents' loci. The broad sense heritability was 99.9% and narrow sense heritability as 107% showing that the character is also highly heritable in this irrigation treatment and subsequently significant amount of improvement could be realized while selecting the desired hybrid combinations under intensive selection pressure from the progeny rows keeping in mind the pedigree of those single progeny rows.

In case of four irrigations, the average degree of dominance $[H_1+D]^{1/2}$ was equal to 1.009 and therefore lint yield again inherited as an overdominant trait. The proportion of dominant and recessive genes in the parents $[(4DH_1)^{1/2} + F] \div [(4DH_1)^{1/2} - F]$ was equal to 0.338 meaning that the recessive genes are excessively contained in some of the parents than others. The proportion of positive to negative allele effects in the parents $[H_2+4H_1]=0.092$ meant that negative allele effects were in excess in the parents and were responsible for contributing decreased lint yield attributes into their progenies. The number of

groups of genes controlling dominance loci in the parents was $[h^2+H_2]=5.05$ implying that at least five groups of genes were operative and conditioned the inheritance pattern of this character. The broad sense heritability was 99% implying that lint yield per plant was highly heritable in this medium stress irrigation treatment and if intensive selection pressure is applied/exercised, lint yield would be responsive up to 56% giving improvement for selecting desirable genotypes from the progeny rows.

In case of three irrigations treatment, the average degree of dominance was $[H_1+D]^{1/2}=1.015$ depicting that lint yield was also over dominantly inherited under stress irrigation conditions. The proportion of dominant to recessive genes in the parents $[(4DH_1)^{1/2} + F] \div [(4DH_1)^{1/2} - F]$ was equal to 0.368 implying that recessive genes are in excess in the parents as compared to the dominant ones. The proportion of negative and positive allele effects in the parents $[H_2+4H_1]$ was 0.053 implying that negative allele effects, responsible for contributing decreasing lint yield attributes, were in excess in the parents. The number of group of genes controlling the dominance loci in the parents $[h^2+H_2]$ was equal to 11.105 indicating that lint yield in stress conditions was polygenically controlled. The broad sense heritability was 99.8% and narrow sense heritability was 220% implying that the character under stress conditions is highly heritable and quite significant amount of improvement could be realized in selecting the desired progenies under high selection pressure.

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