DIALLEL GRAPHIC ANALYSIS OF SEEDCOTTON YIELD AND ITS COMPONENTS FOR DROUGHT TOLERANCE IN UPLAND COTTON

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ABSTRACT

A six-by-six complete *hirsutum* F_1 diallel cross of prescreened three drought tolerant (CRIS-134, CRIS-342 and SINDH-1) and three drought susceptible (NIAB-78, SADORI and BH-160) varieties was evaluated for diallel analysis for genetic parameters and graphic representation under four irrigation regimes for number of bolls per plant, sympodia per plant, lintcotton yield and seedcotton yield per plant during 2009. Irrigation treatments were seven, five four and three up to 150 days after planting.

In the analysis for genetic parameters, bolls per plant were completely dominant in seven while over dominant in five, four and three irrigations. CRIS-134 in seven, Sadori in five and CRIS-342 in four and three irrigation 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 proved to be the most dominant parents responsible for contributing decreased boll number per plant into their progenies. Number of sympodia per plant under all the four irrigation treatments was inherited as partially dominant trait. 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 irrigation condition 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 with decreased sympodia contributing attributes into their progenies. Seedcotton and lintcotton yields were partially dominant in seven while over dominant in five, four and three irrigations. Sindh-1 in seven, BH-160 in five and three and CRIS-342 in four irrigations 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: Diallel graphs, drought tolerance, upland cotton, genetic retrospect.

INTRODUCTION

Drought is one of the most important abiotic stresses affecting plant growth in the world. It often impacts physiological and metabolic processes of plants, while plants have also naturally developed some mechanisms to cope with it. These mechanisms have been classified into drought escape, drought avoidance and drought tolerance (Turner, *et al.* 2001). Drought escape allows plants to finish their life cycles during the period of sufficient water supply. Drought avoidance helps plants to maintain high water status during periods of stress by enhancing water absorption or/and reducing evapotranspiration while drought tolerance means plants maintain turgor and continue metabolism in cells even at low water potential. Both drought avoidance and drought tolerance can be used in the improvement of crops. Drought stress causes severe shedding of small squares resulting in decreased flowering. Water stress during first 14 days after anthesis leads to boll abscission, but large squares/bolls do not shed readily and flowers seldom shed. Therefore, even under severe stress, young plants can

often continue to flower. Water stress from 20 to 30 days after anthesis results in smaller sized bolls and reduced seed weights (Guinn, 1998). Moisture deficit reduces plant growth resulting in stunted plants with reduced leaf area expansion (Turner *et al*., 1986; Ball *et al*., 1994; Gerik *et al*., 1996; Pettigrew, 2004). Varietal selection plays an important role in the 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 recommended package of production technology and ill-management of irrigation resources. Though the ultimate objective of most plant breeding projects is high yield yet its selection has come rather incidental, as a delayed-action step, taken in the final stages of work when perhaps 99% of the lines have been discarded on other grounds as there has been very sporadic genetic guidance. Thus without genetic guidance cotton breeder has no definite rules to systematize the selection of parents, regulate the manipulation of progenies and predict isolation of superior lines/genotypes.

Fortunately the classic research papers of Jinks and Hayman (1953), Hayman (1954a, 1954b, 1958), Jinks (1954), Johnson and Aksel (1959), Crumpacker and Allard (1962) and Aksel and Johnson (1963) revolutionized the plans of cotton breeders in following the systemic approach of diallel analysis and thereby analytically evaluating the over-all genetic retrospect of a particular character. This also enabled the cotton breeders to eliminate the low yielding diallel parental arrays, on a reasonably sound basis and genetic guidance, while evaluating the selection potential of individual crosses. The procedure of quantitative genetic analysis to estimate/compute genetic parameters from the components of genetic variation, essentially involves calculating variances and covariances of arrays of diallel table (whether partial or complete) and regression of variances of parents upon covariances of hybrids to ascertain dominance, additive and non-additive gene action and finally inheritance pattern of a particular character leading to the targeted selection of entries for further utilization/ developing commercial cultivars. This genetic analysis through estimation

of genetic parameters is further supplemented by graphical analysis of regression of W_r on V_r (Hayman, 1954b) by plotting the regression line and the limiting parabola constructed by calculating its points ($W_r^2 = V_r \times V_{0L0}$) and plotting the V_r, $(W_r \times V_{0L0})^{1/2}$ points. The W_r, V_r points lay on the straight line of unit slope within the limits of $W_r^2 = V_r \times V_{0L0}$ and therefore constancy of $Wr - V_r$ entities ensures validity of last three assumptions underlying the genetic analysis. The regression line of unit slope (b = 1.0) through the origin of V_r, W_r gives the line complete dominance ($H_1 = D$ and $V_r = W_r$). Relative to this regression of complete dominance of unit slope, the movement of regression line upwards (that is $H_1<D$ and $V_r < W_r$) would result in decreasing/partial dominance while if it moves downwards (that is, $H_1>D$ or $Vr>Wr$) reveals increasing or over-dominance. Of course, if $H_1 = D = 0$, there will be no dominance and the regression line will represent the average response of all the arrays and would be tangent to the limiting parabola where all the V_r, W_r points would coincide at the point of contact. The effects of failure of some of the assumptions on the diallel graph have been discussed by (Hayman, 1957; Hill, 1964; Nassar, 1965; Mather, 1967 and Coughtrey and Mather, 1970). It appears that the condition of no non-allelic interaction (epistasis) is particularly difficult to satisfy in quite a number of situations where diallel analysis is called for. Certain types of epistasis distort the W_r, V_r graph in characteristic ways and thus permit their detection (Hayman, 1957; Mather, 1967; Coughtrey and Mather, 1970). Under favorable conditions, the departure from rectilinearity of the graph can be corrected by omitting the arrays corresponding to the disturbing and presumably epistatic parents. A useful genetic interpretation of the W_r, V_r graph calculated from the remaining arrays can then be made on the basis of additive-dominance model. To further explore the applicability and usefulness of the above technique in understanding the genetic nature of parental variation, a diallel cross experiment involving six non-randomly chosen (three drought tolerant and three drought susceptible) homozygous genotypes of upland cotton (*Gossypium hirsutum,* L.) was undertaken. The ultimate object was to supplement the genetic parameters interpretations with diallel graphs and to pinpoint which parents contain preponderance of dominant/recessive genes with increasing/decreasing character

attributes for utilizing them judiciously further in drought tolerant cultivar development programme.

MATERIALS AND METHODS

Six pre-screened upland cotton (*Gossypium hirsutum,* L.) varieties for drought resistance (Baloch, 2012); viz., 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 reciprocal hybrids + 6 parents) were sown as F_1 complete diallel cross during 2009 in four-replicated Randomized Complete Block Design. All cultural and agronomic practices were performed as per the need of the crop and experimental design. Three seeds per hill were dibbled one foot apart and the rows were distanced 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 (excluding soaking doze or *rauni*), that is three irrigations (at 55, 95 and 125 days after planting); four irrigations (at 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 from middle row, 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, lintcotton yield per plant and seedcotton yield per plant. Quantitative genetic analysis of this diallel experiment followed the procedures of Hayman (1954b), Jinks (1954) and Aksel and Johnson (1963). Before conducting the diallel analysis, the pre-requisite conditions of meeting five assumptions of diallel cross must be satisfied (Hayman, 1954b). How our experimental material of 6x6 *Gossypium hirsutum* complete F_1 diallel cross of selected drought susceptible and

tolerant varieties satisfied the assumptions underlying the diallel analysis has been reported elsewhere (Baloch *et al.,* 2014).

The main outcome of the diallel cross analysis is the estimation of genetic components of variation thereby genetic parameters from second degree statistics estimates of diallel arrays to explain the genetic retrospect and inheritance pattern of a particular character as to whether the character is inherited as dominant or recessive trait. If it is inherited as dominant trait, whether it is completely or partial or over-dominant and whether the increasing nature of that character is dominant over decreasing performance and *vice versa*. On the other hand, there are certain queries which these genetic parameters could not answer. For example, parameter $[(4DH1)^{1/2}+F] \div [(4DH1)^{1/2} - F]$ concludes proportion of dominant and recessive genes in the parents for that corresponding character. If its value is less than unity, recessive genes are in excess and if greater than one, dominant genes are preponderant. But this parameter would not pin point which parent contains the excess of dominant genes and which parent is preponderantly recessive. This can be accomplished through W_r, V_r graphical analysis commonly known as variance – covariance or diallel graphs. In these graphs, mainly the dominance relationship in terms of variance of arrays and covariance between the offspring and their non-recurring parents is shown (environmental variance is neglected/ignored). In this diallel graph, with $[H_1 \div D] = 0$, there is no dominance and the variances and covariances of array estimate (W_r, V_r) = (½D, ¼D) and there will be of course no regression. With dominance, the regression line has unit slope and intersects the W_r axis at its origin with complete dominance $[H_1=D]$, on the positive side with the partial dominance $[H_1<D]$ and on the negative side with over-dominance $[H_1>D]$. Most types of non-allelic interactions affect the regression line in a characteristic way permitting their direction regardless of the degree of dominance. For example complementary type of gene action will increase V_r in relation to W_r particularly for more recessive arrays leading regression line to slope less than unity. The position of (V_r, W_r) on the line reveals the relative proportion of dominant and recessive genes in the parents corresponding to the point at the upper end of the sloping line on the limiting parabola (away from the origin) while the completely

dominant parents will converge at the lower end of the parabola near the origin of the regression line. In case of complete dominance, the regression line itself passes through the origin, that is, W_r, V_r is (0.0) while with partial dominance, it lies above and with over-dominance, below the origin. In the latter case, W_r will be negative.

With such gist about diallel graphs, we have tried to supplement our results of the estimates of genetic parameters (reported by Baloch *et al.*, 2014) with W_r, V_r graphs and have characterized the parents as recessive and dominant ones pinpointing which particular parents are responsible for directional dominance in all the four irrigation regimes. For direction of dominance, Johnson and Aksel's (1959) standardized deviations of parental measurements (Y_r) and parental order of dominance (W_r+V_r), where the deviations of Y_r's and W_r+V_r's from their respective means, were standardized by dividing them with their respective standard deviations. These statistics were considered where abscissa (Y_r) and an ordinate (W_r+V_r) intersecting each other produce four quadrants of the graph classified as (+, +), (-, +), (-, -) and (+, -). The plus and minus signs for W_r+V_r denote 'recessive' and 'dominant' while for Y_r, they refer to 'high' and 'low' performance of the parents respectively. Though these standardized deviation graphs are not separately drawn, yet considering their superimposition upon the W_r, V_r graphs (given in Figures-1 to 4), it is easy to interpret which particular parent is having increasingly dominant genes and which with increasingly recessive genes and *vice versa*.

RESULTS AND DISCUSSION

Before performing diallel graphic analysis as described by Hayman (1954b), the analysis of variance of complete diallel table, to test the validity of no reciprocal differences, was performed (as described by Hayman, 1954a) for all the four quantitative characters under study. Such analysis of variance of diallel tables is presented in Table-1. In this analysis of variance, significant mean

squares for component 'a' imply significant additive gene effects and suggest selection on the basis of significant general combining ability effects which are also of additive nature. Component 'b' indicates that the dominance gene effects are important for selecting the hybrid combinations on the basis of specific combining ability. Component 'b' has further been partitioned into 'b_1', 'b_2' and 'b_3' where 'b_1' tests the mean deviations of hybrids from their mid-parent values in one direction, that is directional dominance, 'b_2' indicates the extent to which mean dominance deviations in a given array differ from other arrays, that means the parental arrays contain more dominant genes from the other and 'b_3' tests the portion of dominance deviations attributable to a particular hybrid. Component 'c' tests the reciprocal differences and its significance invalidates the assumption of no reciprocal differences but could be nullified by replacing the off-diagonal cells of the diallel matrix with the common mean of that cross. In the present case, component 'a' 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 'b_1', 'b_2' and 'b_3', dominance effects also got partitioned into direction of dominance, dominance deviations attributed to the parental arrays and dominance deviations ascribable to the individual hybrids. Accordingly, 'b_1' 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 'b_2' was highly significant ($P<0.01$) indicating that these dominance deviations are attributed to parental arrays and 'b_3' 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

Source of variation	D.F.	Number of bolls per plant	Sympodial branches per plant	Lintcotton yield per plant	Seedcotton yield per plant	Number of bolls per plant	Sympodial branches per plant	Lintcotton yield per plant	Seedcotton yield per plant
Blocks	3	1.55	1.76	0.34	3.52	7.05	0.50	0.26	2.81
a	5	128.41**	141.08**	259.04**	2672.10**	253.13**	130.40**	369.55**	3807.90**
b	15	31.01**	8.42**	24.00**	247.18**	40.18**	7.41**	57.99**	599.16**
b_1	1	22.40**	3.32**	93.51**	964.43**	1.18 ns	0.36 ns	181.84**	1874.37**
b_2	5	13.83**	8.42**	11.29**	116.54**	18.77**	5.68**	36.90**	378.35**
b_3	9	41.51**	8.98**	23.34**	240.07**	54.41**	9.16**	55.95**	580.15**
c	5	1.19 ns	0.22 ns	0.36 ns	3.73 ns	1.89**	7.26**	0.32 **ns**	3.14 ns
d	10	4.60**	0.35 ns	0.58**	6.01**	2.61**	3.32**	0.68**	7.09**
Error	105	0.69	0.35	0.18	1.82	0.38	0.48	0.17	1.74

component 'c' would not be considered in the diallel analysis

Table-1. Mean squares from the analysis of variance of diallel table, for validity test of 6x6 F_1 complete cotton diallel cross, under four irrigation regimes during

Source of variation	D.F.	Number of bolls per plant	Sympodial branches per plant	Lintcotton yield per plant	Seedcotton yield per plant	Number of bolls per plant	Sympodial branches per plant	Lintcotton yield per plant	Seedcotton yield per plant
Blocks	3	5.60	1.46	9.30	95.06	1.39	20.40	1.93	24.12
a	5	510.31**	129.34**	667.53**	6887.30**	446.05**	102.94**	486.17**	5043.05**
b	15	233.81**	8.06**	281.74**	2909.16**	182.08**	7.81**	230.44**	2403.87**
b_1	1	1003.05**	3.84*	1859.65**	19223.71**	1195.45**	12.35**	1939.27**	20527.07**
b_2	5	426.72**	12.29**	403.14**	4160.08**	249.20**	8.27**	247.58**	2528.54**
b_3	9	41.17**	6.18**	38.98**	401.48**	32.19**	7.00**	31.058**	320.91**
c	5	10.32 ns	0.36 ns	2.69 ns	28.27 ns	6.93**	1.36**	8.03**	82.34**
d	10	3.01 ns	0.61 ns	3.29 ns	34.07 ns	1.97 ns	0.41**	1.44 ns	14.95 ns

2009, for four quantitative characters, at Sindh Agriculture University farm, Tandojam.

SEVEN IRRIGATIONS FIVE IRRIGATIONS

FOUR IRRIGATIONS THREE IRRIGATIONS

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

Error	105	4.83	0.63	4.24	43.78	1.05	0.41	0.96	9.44

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 it's reciprocal irrespective of the fact whether the reciprocal differences were significant or not and then analysis carried out (Baloch *et al*., 2014).

Graphic analysis of number of bolls/plant:

In the seven irrigations treatment, boll number was inherited as completely dominant trait as the regression line of unit slope cut the limiting parabola tangent and W_r, V_r axis through its origin (Figure-1). Parent CRIS-134 was regarded as the most recessives of all as it contained preponderantly recessive genes and lied farthest from the origin on the regression line. Because of its position in the (+, +) quadrant of high recessive in the diallel graph, CRIS-134 was responsible for contributing increased attributes of bolls/plant. The next second most recessive parent was CRIS-342 as it lied farthest but next to Niab-78 in the (+,+) quadrant but on far left side bordering (-, +) quadrant indicating that its contribution to increased boll number attributes, though positive, yet was quite weaker than CRIS-134. The most preponderantly dominant parents were Niab-78 and BH-160 as both of them lied nearest to the regression line origin and parabola W_r, V_r intercept. Also, since both of these parents occupied (-,-) quadrant of low dominants in the diallel graph, they were responsible for contributing decreased

attributes of bolls per plant into their progenies through their dominant genes. The remaining two parents Sindh-1 and Sadori were preponderantly recessive and contributed decreased attributes of boll number per plant into their progenies through their recessive genes because of their position in the (-,+) quadrant of low recessives.

In case of five irrigations treatment, the average degree of dominance was greater than unity and therefore over-dominance was interpreted for inheritance of boll number because the regression line of unit slope cut the limiting the parabola tangent and W_r, V_r axis intercept below its origin. Here parent-5 (Sadori) was the recessive of all the parents as its lied farthest from the origin of regression line on the unit slope and contributed increased attributes of boll number/plant due to its occupancy in the (+,+) quadrant of high recessives. The second most recessive parent was Niab-78 followed by CRIS-134 and Sindh-1, which were also preponderantly recessive as all the three lied next to Sadori along the regression line farthest from the origin of W_r, V_r and parabola intercept. All these three parents were responsible for contributing decreased attributes of boll number/plant into their progenies through their recessive genes because of their occupancy in (-, +) quadrant of low recessives. The most preponderantly dominant parent was CRIS-342 as it lied nearest to the regression origin and contributed decreased attributes of bolls/plant into its progeny due to its occupancy in (-,-) quadrant of low dominants. Remaining parent-6 (BH-160) was preponderantly recessive and was responsible for contributing increased attributes of number of bolls/plant into its progeny through its recessive genes because of its position in the (+, +) quadrant of high recessives but its contribution was weaker than Sadori.

With respect to four irrigations treatment, the average degree of dominance was greater than one, that is $[H1 \div D]^{1/2} > 1.0$, and therefore boll number/plant also inherited as over dominant trait in this treatment. This was also supported by the diallel graph where the regression line cut the limiting parabola and W_r, V_r axis intercept below its origin. Deviations of parental arrays from the regression line were also minimum which suggested complimentary type

of dominance gene action in the inheritance pattern of boll number/plant. The most preponderantly recessive parents were CRIS-134 and CRIS-342 which lied away from the regression origin and W_r, V_r intercept and since they were positioned in (+,+) quadrant of high recessives they were responsible for producing increased boll number attributes into their progenies. Parent-3 (Sindh-1) could be regarded as the most preponderantly dominant parent as it lied nearest to the origin of W_r, V_r and parabola intercept. Since this parent occupied (-,-) quadrant of low dominants, it was mostly responsible for producing decreased attributes of number of bolls per plant into its progenies. Remaining three parents Niab-78, Sadori and BH-160 grouped themselves together little bit away from regression origin and Sindh-1; but not away in the sense that they could be regarded as excessively recessives. Therefore it can safely be concluded that these parents, more or less, contained proportionately equal distribution of dominant and recessive genes and were responsible for contributing sometimes increased boll number attributes (depending upon favorable conditions) and sometimes decreased boll number (when unfavorable environment prevails).

In case of stress irrigation condition of three irrigations, the inheritance pattern of boll number also remained as over-dominant because the regression line cut the limiting parabola and W_r, V_r axis below their origin. The position of parental arrays along the regression line of unit slope got quite altered under stress conditions. Parent CRIS-342 became the mostly preponderantly recessive one as it lied farthest from the origin of regression line followed by three others in the line, i.e., CRIS-134, BH-160 and Sadori in the (+, +) quadrant of high recessives and therefore all these four preponderantly recessive parents were responsible for contributing increased boll number attributes into their progenies. Sindh-1 was the most excessively dominant parent as it lied nearest to the origin of W_r, V_r intercept and parabola tangent on the regression slope. Also, since it occupied (-,-) quadrant of low dominants, it was responsible for producing decreased boll number per plant attributes into its progenies though it dominant genes. Parent-4 (Niab-78) contained more or less equal distribution of dominant and recessive genes but some times more of dominant genes (under favorable

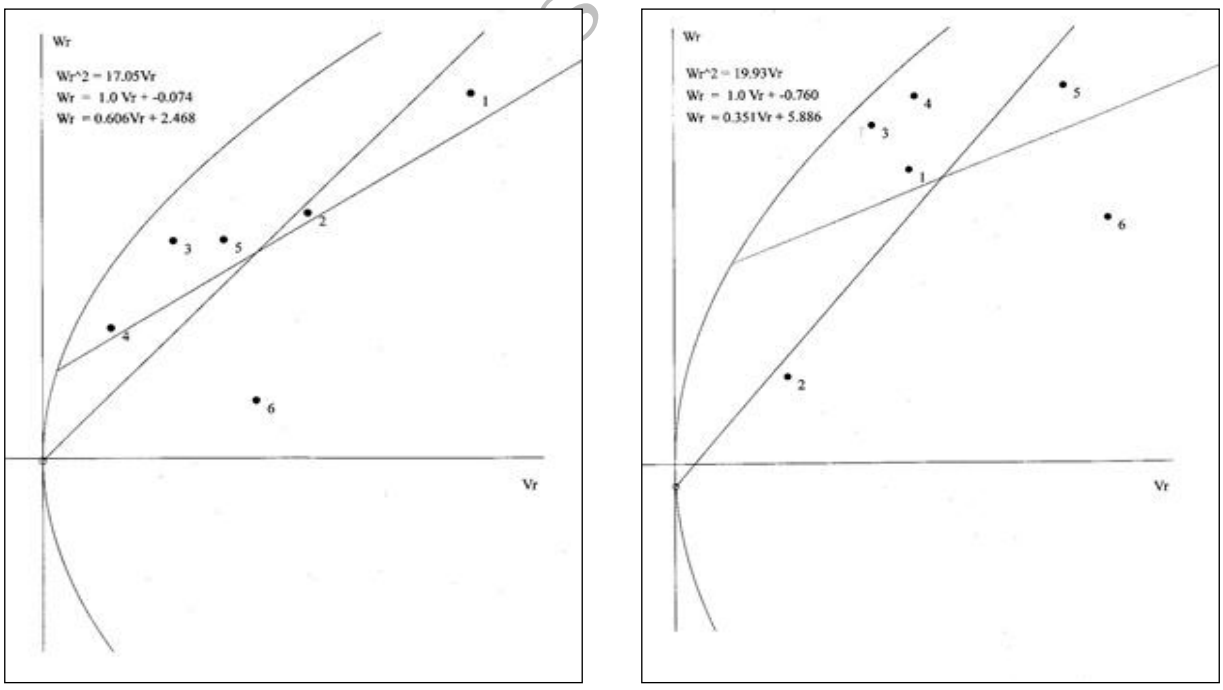
conditions) and was more of less responsible for increased boll number attributes into its progeny.

Graphic analysis of sympodia/plant:

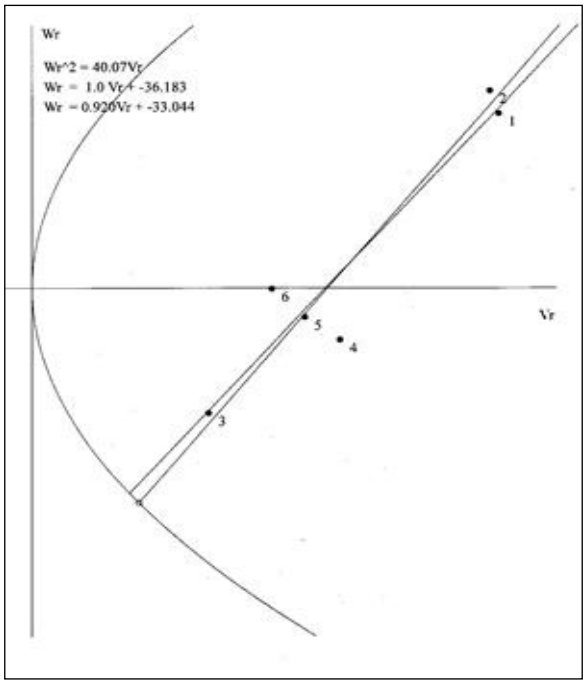
Number of sympodia per plant under normal irrigation conditions was inherited as partially dominant trait as average degree of dominance $[H1 \div D]^{1/2}$ parameter measured < 1.0 (it was 0.94) and therefore the regression line cut the W_r, V_r axis and limiting parabola tangent above its origin (in Figure-2). Parent BH-160 was regarded as the most recessive parents of all as it lied farthest from the point of intercept of W_r, V_r axis and parabola tangent on the regression line and since it occupied (+,+) quadrant of high recessives, it contributed positively for increased sympodia attributes into its progeny. The most dominant parent was Sindh-1 as it

Figure-1: Diallel graph for number of bolls per plant from 6x6 complete cotton F_1 diallel cross planted under four irrigation regimes (seven, five, four and three) during 2009 at Sindh Agriculture University farm, Tandojam.

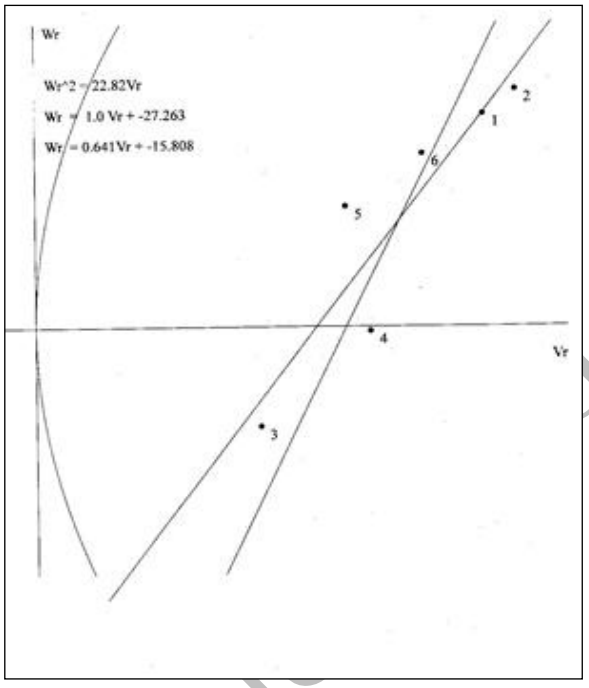
P1=CRIS-134 P2=CRIS-342 P3=Sindh-1 P4=Niab-78 P5=Sadori P6=BH-160



Seven Irrigations **Five Irrigations**



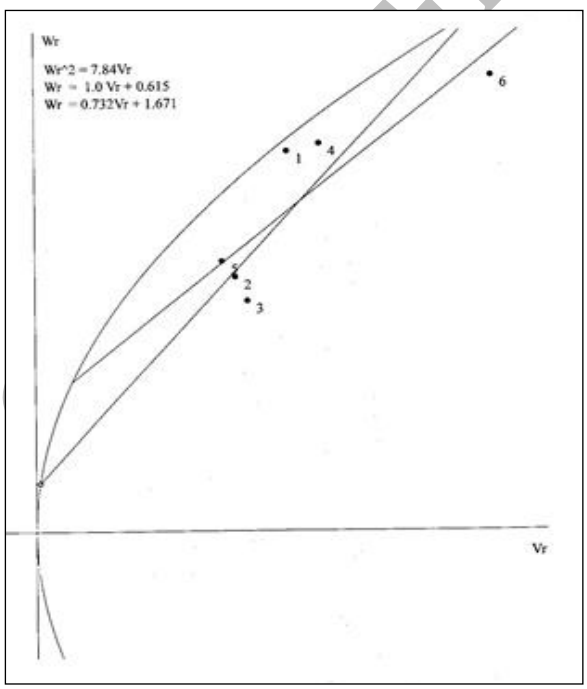
Four Irrigations



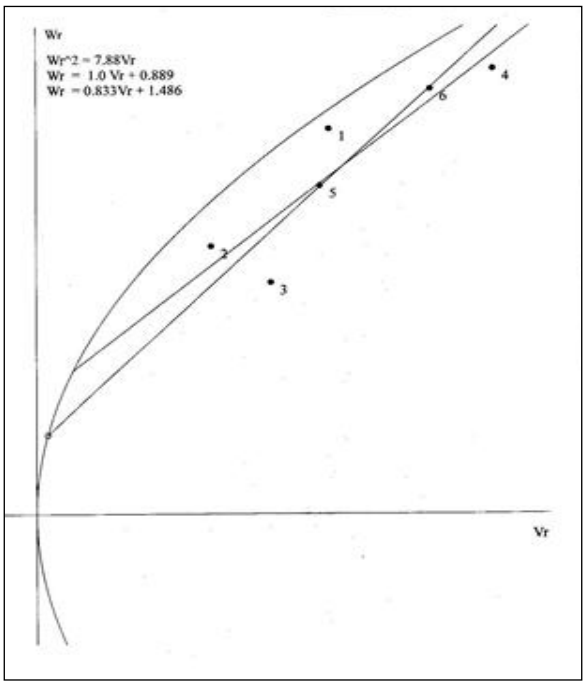
Three Irrigations

Figure-2: Diallel graph for number of sympodia per plant from 6x6 complete cotton F_1 diallel cross planted under four irrigation regimes (seven, five, four and three) during 2009 at Sindh Agriculture University farm, Tandojam.

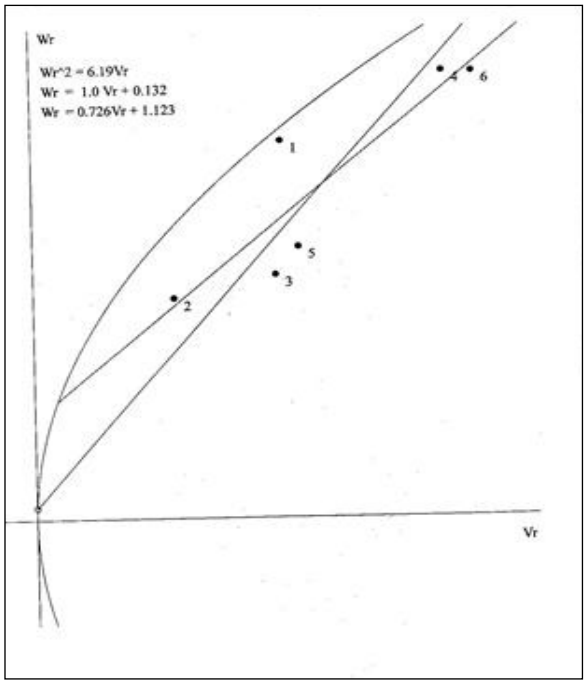
P1=CRIS-134 P2=CRIS-342 P3=Sindh-1 P4=Niab-78 P5=Sadori P6=BH-160



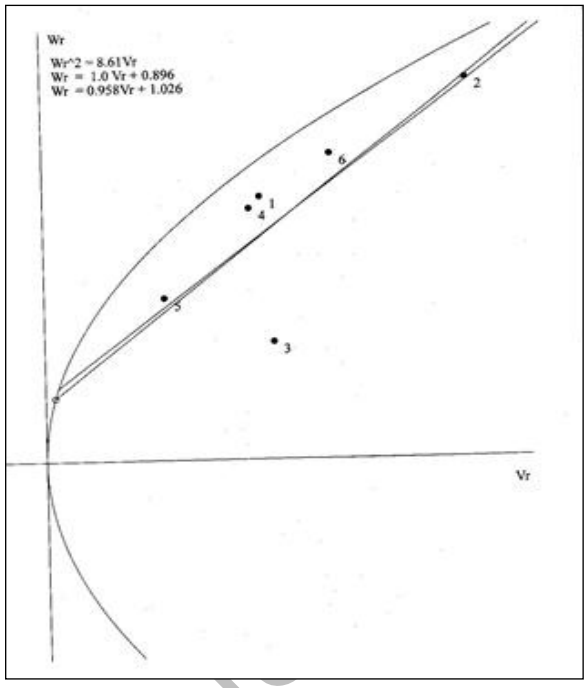
Seven Irrigations



Five Irrigations



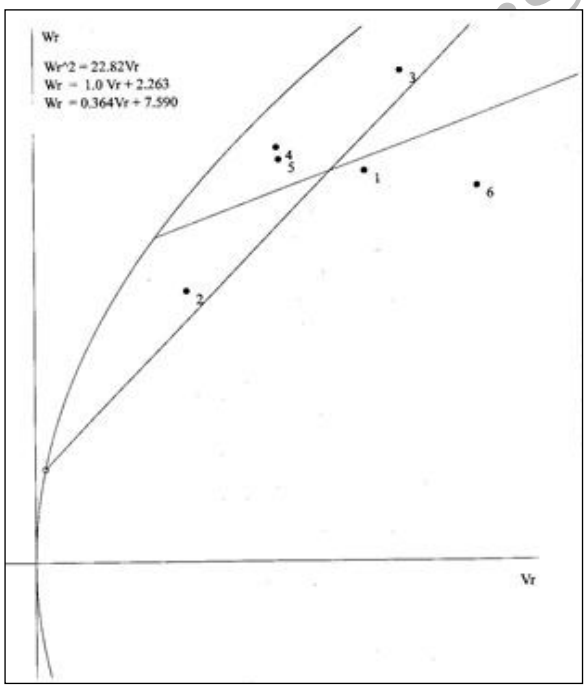
Four Irrigations



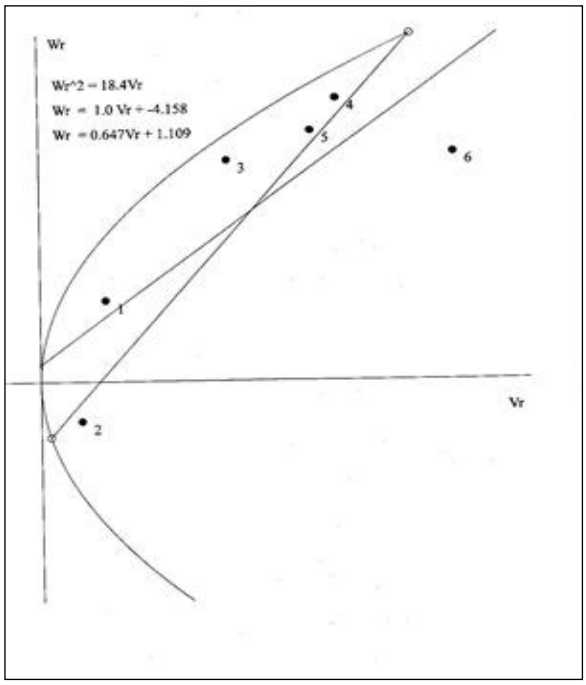
Three Irrigations

Figure-3: Diallel graph for lintcotton yield per plant from 6x6 complete cotton F_1 diallel cross planted under four irrigation regimes (seven, five, four and three) during 2009 at Sindh Agriculture University farm, Tandojam.

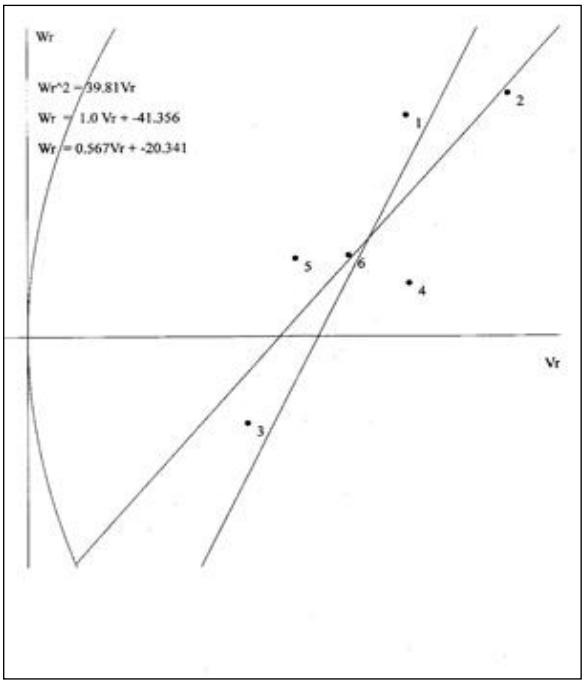
P1=CRIS-134 P2=CRIS-342 P3=Sindh-1 P4=Niab-78 P5=Sadori P6=BH-160



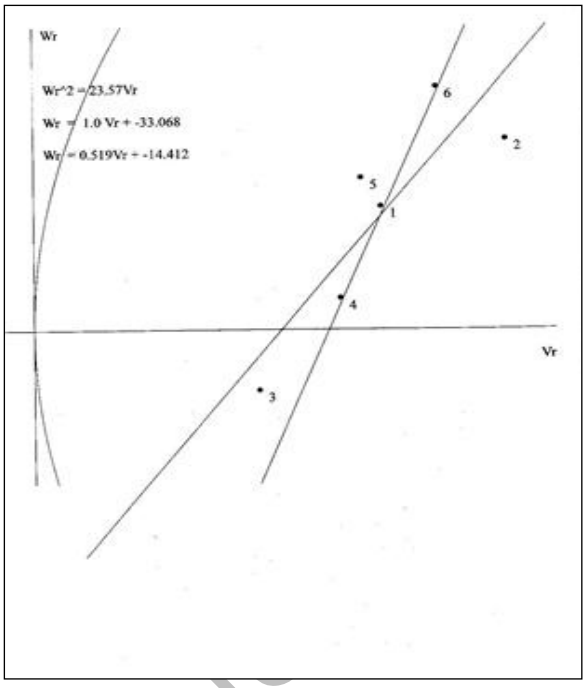
Seven Irrigations



Five Irrigations



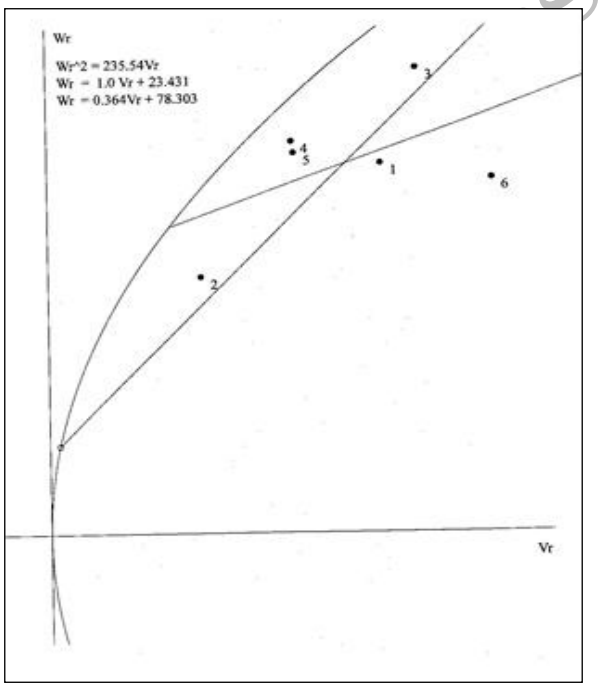
Four Irrigations



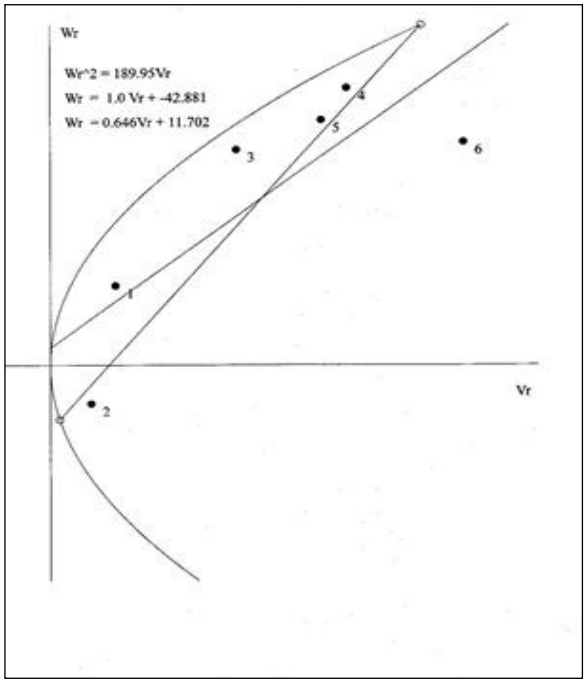
Three Irrigations

Figure-4: Diallel graph for seedcotton yield per plant from 6x6 complete cotton F_1 diallel cross planted under four irrigation regimes (seven, five, four and three) during 2009 at Sindh Agriculture University farm, Tandojam.

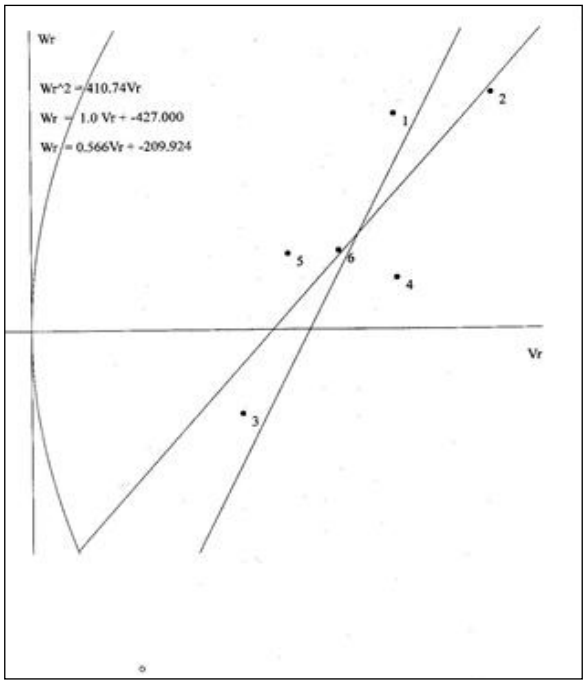
P1= CRIS-134	P2=CRIS-342	P3=Sindh-1	P4=Niab-78	P5=Sadori	P6=BH-160



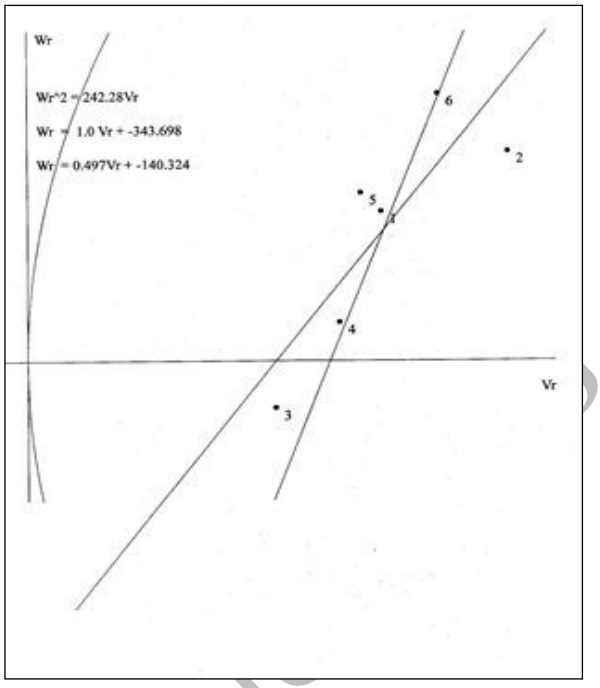
Seven Irrigations



Five Irrigations



Four Irrigations



Three Irrigations

contained preponderantly dominant genes and positioned nearer to the origin of regression line in the (-,-) quadrant of low dominants and therefore was responsible for contributing decreased attributes for sympodia/plant into its progenies. Parents CRIS-342 and Sadori also grouped with Sindh-1 in having excess of dominant genes but their containment was weaker than Sindh-1 and therefore their decreased contribution for sympodial branches was also weaker than Sindh-1. The remaining two parents CRIS-134 and Niab-78, though preponderantly recessive, were weaker than BH-160 and were responsible for decreased contribution of sympodia into their progenies through their recessive genes.

Under five irrigation treatment, sympodial branches were also inherited as partially dominant trait $[H_1/D]^{1/2} = 0.899$ because the regression line cut the W_r, V_r axis and limiting parabola above their origin of intercept. Here parent Niab-78 was the most recessive of all as it lied away from the regression origin in the (+, +) quadrant of high recessives and was responsible for contributing increased attributes for sympodial branches into its offspring. Parent

BH-160 was the second most recessive parent in (+, +) quadrant contributing positively for sympodial branches per plant through its recessive genes. The most dominant parent of all was Sindh-1 due to its nearness to parabola and W_r, V_r intercept in (-,-) quadrant of low dominants and therefore contribute negatively for sympodial branches into its offspring. CRIS-342 was also preponderantly dominant in the (-,-) quadrant but its contribution for sympodial branches attributes was weaker than Sindh-1. The remaining two parents CRIS-134 and Sadori were preponderantly recessives and also contributed positively for sympodial branches but as compared to Niab-78, their contribution was weak.

In case of four irrigations treatment, the average degree of dominance was $[H1 \div D]^{1/2} < 1.0$ and therefore like other two treatments of seven and five irrigations, sympodial branches per plant in this treatment also inherited as partial dominant trait. Here, parents Niab-78 and BH-160 both were preponderantly recessive as they lied farthest from the W_r, V_r intercept origin and since they occupied (+,+) quadrant of high recessive, they were responsible for increased contribution of sympodia attributes into their progeny. CRIS-134 was also recessive but its contribution for giving sympodial branches attributes was negative/decreased due to its position/occupancy in the (-,+) quadrant of low recessives. The most dominant parent of all was CRIS-342 as it lied nearest to the origin of W_r, V_r intercept and parabola tangent and was responsible for decreased contribution of sympodial branches/plant into its progenies for its occupancy in the (-,-) quadrant of low dominants. The remaining two parents Sindh-1 and Sadori through contained excess of dominant genes and lied in the (-,-) quadrant of low dominants, yet their contribution for producing sympodial branches attributes was quite weaker as compared to CRIS-342.

Under stress conditions of three irrigations treatment, though sympodial branches still continued to be inherited as partial dominant trait, as in other irrigation treatments, yet the distribution of parents on the regression line on unit slope and containment of dominant and recessive genes in them was quite different. Here the most dominant parent CRIS-342 in other irrigation treatments

became the most recessive one in this stress irrigation treatment as it lied farthest from the origin of W_r, V_r intercept and parabola tangent. It also continued to contribute positively for sympodial branches/plant through its recessive genes. The most dominant parents of all were Sindh-1 and Sadori as they lied nearest to the W_r, V_r and parabola intercept in the (-,-) quadrant of low dominants and contributed negatively for sympodial branches. Parent 1 and 4 (CRIS-134 and Niab-78) were preponderantly recessive but contributed negatively for sympodial branches/plant due to their position in the (-,+) quadrant of low recessives. Finally parent BH-160 was excessively recessive and contributed positively to the sympodial branches/plant but its contribution quite weaker than CRIS-342.

Graphic analysis of lintcotton yield/plant:

Like seedcotton yield, lintcotton yield also inherited as partial dominant trait in normal seven irrigations treatment as the average degree of dominance $[H_1 \div D]^{1/2}$ was less than unity and therefore the regression line cut the limiting parabola and W_r, V_r axis above its origin (Figure-3). Parent Sindh-1 was categorized as the most preponderantly recessive parent as it lied farthest from the W_r, V_r and parabola intercept. Since it occupied (+,+) quadrant in the diallel graph (Figure-3), it was responsible for contributing increased lint yield attributes into its progenies through its recessive genes. Parent BH-160 was also excessively recessive as it lied next to Sindh-1 on the regression line (but it carried greater deviation from the regression line) and therefore contained weaker recessive genes as compared to Sindh-1. Since BH-160 was placed in the (+, +) quadrant of high recessives, it contributed increased lint yield attributes (but weaker than Sindh-1) into its progenies. CRIS-134 was also categorized at par with BH-160 as preponderantly recessive in the (+, +) quadrant of high recessives. Parents Niab-78 and Sadori were also low performing recessives (weaker than Sindh-1) as they lied away from the W_r, V_r intercept with parabola but since their occupancy was in the (-, +) quadrant of low recessives, they were responsible for contributing decreased lint yield attributes into their progenies through their recessive genes. The most dominant parent was CRIS-342 as it lied nearest to the parabola and regression intercept in the (-,-) quadrant of low

dominants and contributed decreased lint yield attributes to its progeny through its dominant genes.

In case of five irrigations, like seedcotton yield, the lintcotton yield also changed its inheritance pattern from partially dominant to overdominant trait as the average degree of dominance $[H_1 \div D]^{1/2}$ was greater than unity and therefore the regression line cut the limiting parabola and W_r, V_r intercept below its origin. Here, parents 4, 5 and 6 (Niab-78, Sindh-1 and BH-160) were categorized as the most recessive parents of all (Niab-78 was excessively recessive) as they lied away from the origin of W_r, V_r axis and parabola intercept around the regression line. Also, since they occupied (+, +) quadrant of high recessives they were responsible for contributing increased lint yield attributes into their progenies through their recessive genes. Next recessive parent after these three, was Sindh-1 as it also lied away from the W_r, V_r and parabola intercept on the regression line but since it was placed in the (-,+) quadrant of low recessives, it was responsible for contributing decreased lint yield attributes into its progenies. CRIS-342 was the most preponderantly dominant parent of all as it lied nearest to the W_r, V_r and parabola intercept on the regression line and occupied (-,-) quadrant of low dominants contributing decreased lint yield attributes into its progenies. CRIS-134 was also categorized as the second most dominant parent, after CRIS-342, as it lied next to CRIS-342 and since it was also in the (-,-) quadrant of low dominants, it was contributing decreased lint yield attributes (but still weaker than CRIS-342) into its progenies. Since both the parents were dominant and in (-,-) quadrant of low dominants, it is concluded that low lint yielding capacity was dominant over high lint yield capacity in this five irrigations treatment.

With respect to four irrigations treatment, lint yield was also over dominantly inherited as the average degree of dominance was greater than unity and the regression line cut the limiting parabola and W_r, V_r intercept below its origin. Here, parents 1 and 2 (CRIS-134 and CRIS-342) were regarded as the most recessive of all the six (CRIS-342 still more recessive than CRIS-

134) parents as they lied farthest/away from the W_r, V_r intercept and parabola tangent and since they were positioned in the (+,+) quadrant in the high recessives, they were responsible for contributing increased lint yield attributes into their progenies. Parent Sindh-1 was considered as the most preponderantly dominant parent as it lied nearest to the origin of W_r, V_r axis and parabola intercept and since it occupied (-,-) quadrant of low dominants, it was mainly responsible for decreased lint yield attributes contribution to its progenies through its dominant genies. Parents Niab-78, Sadori and BH-160 were more or less recessives, Niab-78 in the (+, +) quadrant of high recessives but weaker than CRIS-134 and CRIS-342 contributing weak increased lint yield attributes into its progenies through its recessive genes. Other two parents, though recessive, occupied themselves in the (-, +) quadrant and mainly contributed decreased lint yield attributes to their progenies through their recessive genes.

In case of stress irrigation, lint yield also inherited as overdominant trait as the average degree of dominance $[H_1 \div D]^{1/2}$ was greater than unity and therefore regression line cut the limiting parabola and W_r, V_r axis intercept below its origin. Parents CRIS-342 and BH-160 were regarded as the most recessive parents of all as they lied farthest from W_r, V_r intercept and limiting parabola tangent on the regression line of unit slope. These parents contained preponderantly recessive genes and since they occupied (+, +) quadrant of high recessives, they mainly contributed increased lint yield attributes to their progenies. Parents 1 and 5 (CRIS-134 and Sadori) were also categorized as preponderantly recessives (but weaker than CRIS-342 and BH-160) and occupied also (+, +) quadrant of high recessives but their positive contribution of increased lint yield attributes to their progenies through their recessive genes was weaker than CRIS-342 and BH-160. Parent Sindh-1 was regarded as the most dominant parent of all as it lied nearest to the origin of parabola tangent and W_r, V_r intercept in the (-,-) quadrant of low dominants. Therefore it was mainly responsible for contributing decreased lintcotton yield attributes to its progeny through its dominant genes. Finally, parent Niab-78 was regarded as less dominant parent, as compared to Sindh-1, as it lied next to Sindh-1 in the

(+,-) quadrant of high dominants but its increased contribution of lint yield attributes to its progenies was quite weaker than Sindh-1.

Graphic analysis of seedcotton yield:

Under seven irrigations treatment, seedcotton yield was inherited partially dominant as the average degree of dominance $[H_1 \div D]^{1/2}$ was < 1.0 and the regression line cut the W_r, V_r axis and limiting parabola tangent intercept above its origin (Figure-4). Sindh-1 was the most recessive parent of all as it lied farthest from the point of intercept of W_r, V_r axis and parabola tangent and since it occupied (+, +) quadrant of high recessives it was responsible for contributing increasing yield attributes to its progenies through its recessive genes. Parents CRIS-134 and BH-160 were also preponderantly recessive in the (+, +) quadrant of high recessives but their contribution to increased yield attributes was comparatively weaker than Sindh-1. Also, parents 4 and 5 (Niab-78 and Sadori) were preponderantly recessive as they also lied away from the point of intercept of W_r, V_r axis and limiting parabola and since they occupied (-,+) quadrant of low recessives they were contributing decreased yield attributes to their offspring through their recessive genes. Remaining parent (CRIS-342) was regarded as the most dominant parent of all as it lied nearest to the parabola intercept and W_r, V_r axis and in the (-,-) quadrant of low dominants and therefore was responsible for contributing decreased seedcotton yield attributes to their progeny.

In case of five irrigations treatment, seedcotton yield was inherited as overdominant trait as the average degree of dominance $[H_1 \div D]^{1/2}$ was > 1.0 and the regression line cut the limiting parabola and W_r, V_r axis intercept below its origin. Distribution of parents containing dominant and recessive genes in them got changed rendering Niab-78, Sadori and BH-160 as preponderantly recessive (Niab-78 being the most recessive of all) and since they occupied (+,+) quadrant of high recessives they were responsible for contributing increased seedcotton yield attributes into their progenies though

their recessive genes. Sindh-1 was also recessive (contained proportionately more recessive genes than the dominant ones) but lied in the (-, +) quadrant of low recessives and therefore contributed decreasing seedcotton yield attributes in its progenies. CRIS-342 was preponderantly dominant of all the parents as it lied nearest to the parabola tangent and W_r, V_r intercept origin. And since it occupied (-,-) quadrant it was mostly responsible for contributing decreased seedcotton yield attributes into its progenies though its dominant genes. Remaining parent CRIS-134 was also preponderantly dominant contributing decreased yield attributes to its progeny (but weaker than CRIS-342) as it lied in the (-,-) quadrant of low dominants but next to CRIS-342.

In case of four irrigations treatment, seedcotton yield again inherited as overdominant trait as the average degree of dominance $[H_1 \div D]^{1/2}$ was > 1.0 and the regression line cut the limiting parabola and W_r, V_r axis intercept below its origin. The position of the parents with respect to proportion of dominant and recessive genes also got changed due to more stress conditions. Here the most dominant parent CRIS-342 under five irrigations treatment became the most recessive of all in four irrigations treatment as it lied farthest from the regression line origin intersecting the W_r, V_r, axis and limiting parabola. Since this parent CRIS-342 occupied (+, +) quadrant of high recessives, it mostly contributed increased yield attributes to its progeny through its recessive genes. CRIS-134 also showed same trend of recessiveness in the (+,+) quadrant. Parent Sindh-1 was the most dominant of all as it lied nearest to the origin of parabola and W_r, V_r intercept in the (-,-) quadrant of low dominants and therefore contributed decreased yield attributes into its progeny though its dominant genes. Remaining three parents Niab-78, Sadori and BH-160 more or less occupied center of the regression line mostly having recessive genes with weaker positive contribution of seedcotton yield into their progenies. If given favorable environments, these parents would develop the tendency of obtaining more dominant genes and would be able to contribute increased seedcotton yield attributes.

With respect to stress irrigation condition of three irrigations, seedcotton yield again inherited as overdominant trait as the average degree of dominance $[H_1 \div D]^{1/2}$ was greater than unity and the regression line cut the limiting parabola and W_r, V_r axis intercept below the origin of regression line. BH-160 was the most recessive parent of all as it lied away from the W_r, V_r and parabola intercept origin on the regression line containing preponderantly recessive genes and since it occupied (+,+) quadrant of high recessives it was responsible for contributing increased yielding attributes into its progeny through its recessive genes. BH-160 was followed by second most recessive parent CRIS-342 containing excessive recessive genes as it lied next to BH-160 on the regression line of unit slope in the (+,+) quadrant of high recessives and also contributed increased seedcotton yield attributes to its hybrid progenies through its recessive genes. The most dominant parent of all was Sindh-1 as it lied nearest to the origin of regression line and parabola, W_r, V_r intercept and since it occupied (-,-) quadrant of low dominants it was responsible for contributing decreased yield attributes into its progenies. Niab-78 was the second most dominant parent next to Sindh-1 and lied on the regression line in the (-,-) quadrant of low recessives thus was responsible for contributing decreased yielding attributes (but still weaker than Sindh-1) into its progenies through its dominant genes. Remaining two parents CRIS-134 and Sadori grouped together away from the W_r, V_r and parabola intercept on the regression line and were categorized as preponderantly recessive parents and since they occupied (+,+) quadrant of high recessives they were contributing increased yield attributes into their progenies (but still weaker than CRIS-342 and BH-160) through their recessive genes.

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