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GENE ACTION IN THE INHERITANCE OF AGRONOMIC TRAITS ININTER VARIETAL DIALLEL CROSSES OF *GOSSYPIUM HIRSUTUM* L.

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ABSTRACT

A 5 × 5 complete diallel cross experiment was accomplished having cotton varieties CIM-556, CIM-557, NIBGE-2, Bt-Aone and CIM-786 to estimate gene action, general and specific combining ability for numerous plant traits involving yield and lint characters. The analysis of variance displayed highly significant differences amongst genotypes for all the traits under examination. The outcomes of joint regression analysis discovered that the data for all the traits were adequate for simple additive dominance model. The graphical representation of variance (Vr) and co-variance (Wr) proposed additive gene action with partial dominanceaction. The variety CIM-556 carried maximum dominant genes for seed index and fiber length although variety CIM-786 possessed supreme dominant genes for number of bolls and fiber fineness. The varieties NIBGE-2 and CIM-557 have dominant genes for fiber strength and lint percentage respectively. The variety CIM-786 was bringing into being best general combiner for seed cotton yield and seed index. The variety Bt-Aone appeared to be good general combiner for seed cotton yield. The variety CIM-556 inspected to be most promising general combiner for lint percentage and fiber length. Bt-Aoneexecuted very well in specific crosses with NIBGE-2 and CIM-786 for fineness. It was proposed that the plant traits involving additive type of gene action in their inheritance pattern, simple selection procedure would be convenient for their improvement while characters involving over dominance type of gene action might be considered when heterosis is to be exploited in cotton variety development program.

Key words: *Gossypiumhirsuitum* L, gene action, specific combining ability, general combiningability, agronomic traits

INTRODUCTION

The two vital avenues for cotton production in Pakistan are to increase overall production and to improve lint quality as to ensure meeting demand for domestic as well as foreign buyers. Genetic make-up of variety is the principal factor determining improvement in fibre quality and yield of cotton crop that permit most of the breeders to follow genetic improvement programs. An experiment was conducted involving 8 varieties of upland cotton in full diallel for gene action and yielded straight effects regarding ginning out turn, staple length and seed cotton yield in interspecific crosses of *Gossypiumhirsutum* L. (Anisa*et al.*2004) Moreover, In another experiment trial comprising 8 varieties of upland cotton the presence of non-additive over dominance type of gene action in number of bolls per plant and boll weight of cotton, whereas additive with partial dominance was found in seed index interaction (Murtaza, 2005).Scientific study on gene action concludes that fibre length and fibre strength were influenced by additive type of gene action with partial dominance and the estimates of narrow-sense heritability suggest that both pedigree and recurrent selection method may be useful to effect improvement in both the characters (Nadeem and Azhar, 2005). Another study was performed using diallel crosses involving 5 cotton genotypes and found both additive and non-additive effects for seed cotton yield and other characters like number of bolls per plant, GOT, fiber strength and length and micronaire using varieties CIM-473, NIAB-999 and ACALA-1517/C having high general combing ability (Rauf *et al.* 2006). In an experiment it is concluded that assessed genetic parameters of seed cotton and its components amongst 6 local cotton varieties by applying a half-diallel set of crosses and revealed that the additive and non-additive gene effects were involved in the control of the traits under investigation (Gamal *et al.* 2009)

To obtain such type of genetic information an investigation was carried out involving five American cotton cultivars to study gene action and combining ability for economic traits by using diallel technique

MATERIALS AND METHODS

The experimental material comprising five parental genotypes namely Allah Din-one (Bt-Aone), CIM-556, CIM-557, NIBGE-2 and CIM-786 representing a range of yield and fibre quality traits, were sown in the field at Warble Research Farm Bahauddin Zakariya University, Multan during March 2009. At flowering, the parental lines were crossed in a complete diallel fashion

(5 × 5) to generate 20 F_1 crosses (direct as well as indirect).

At maturity, crossed bolls were picked and seed cotton was ginned with single roller ginning machine. The seed from all crosses along with their parents was sown in the field during June-2009 in RCBD with three replications. Each entry was a single row of plants having 30 cm distance apart. Twenty five entries (rows) were planted at a distance of 75cm in each replication. All required agronomic practices and crop protection measures were carried out from sowing to harvesting of the crop. At maturity, data were recorded from five guardedplants on individual plant basis for yield and lint traits viz., seed cotton yield, seed index, lint percentage, fiber length, fiber strength, fiber fineness.Fiber characteristics for different varieties were tested by using High Volume Instrument (HVI-900 SA) at CCRI, Multan. The significant characters were further analyzed genetically by using additive dominance model (Hayman, 1954 and Jinks, 1954). The data were subjected to analysis of variance following Steel et al. (1997)

RESULTS AND DISCUSSION

In the parameters of yield characters analysis of variance for yield of seed cotton, seed index and lint percentage showed significant differences amongst cotton varieties for these traits. Joint regression analysis (Tables 1) showed that the data were adequate for the genetic analysis. The graphic representation (Fig-1-3) showed that regression line intercepted the Wr-axis above the origin revealing additive type of gene action. Epistasis was found to be absent as the regression line did not deviate significantly from unit slope. From the distribution of array points on the regression line in (Fig-1-3) it became evident that for cotton seed yield, variety CIM-557 scored the maximum dominant genes while the variety Bt-Aone had the maximum recessive genes due to their nearest and distal position from the origin, respectively. The variety CIM-786 scoring the maximum array means (299.70) proved to the best general combiner, whereas crosses within the array, cross CIM-557 x CIM-786 possessed the highest value (319.83) showing the best specific combining ability for this character. For seed index, variety CIM-556, being closest to the origin possessed the most dominant genes while variety CIM-557 carried the most recessive genes being farthest from the origin (Fig-2). Table-2 showed that CIM-786 was best general combiner as it scored the maximum mean value (7.44) and CIM-557 x CIM-786 was the best specific combination for these traits with maximum mean value of 7.76. Regarding lint percentage, CIM-557 being closest to the origin had maximum dominant genes while CIM-556 got the most recessive genes due to its farthest position from the origin (Fig-3). For Lint %, best general combiner was CIM-556 with maximum mean value (42.03) and the cross CIM-556 x CIM-786 showed best specific combining ability as it scored the maximum value of (43.02) in the array.

In the traits for lint characters analysis of variance for fibre length, fibre strength and fiber fineness indicated highly significant differences among the genotypes. Mean values for these traits are given in Table-2. Results of joint regression analysis (Table 1) indicated that data for lint characters were valid for additive-dominance model. The Vr/Wr graph (Fig 4-6) indicated that these characters are governed by additive type of gene action as the regression line intercepted Wr axis above the origin. Regarding fiber length, variety CIM-556 has maximum dominant genes as it is nearest to the origin whereas CIM-786 has maximum recessive genes as it is the farthest. CIM-557 has maximum specific combining ability as they scored maximum array mean (30.09) and within array values respectively (Table-2)Concerning fiber strength, from the position of array points on the regression line that NIBGE-2 being closest to the origin had maximum dominant genes while CIM-557 got most of the recessive genes due to its farthest position from the origin (Fig-5). For fibre strength, best general combiner was CIM-557 with maximum mean value (28.25) and the cross CIM-557 x CIM-786 showed best specific combining ability as it scored the maximum value of (28.77) in the array (Table-2). Regarding fiber fineness, variety CIM-557 showed maximum dominant genes being closest to the origin while the variety Bt-Aone contained minimum dominant genes being farthest from the origin (Fig 6). For fiber fineness, we have to be careful while selecting any parent or line because the line showing lower micronaire will be of good quality. Therefore, the best general combining ability in the present studies were shown by the variety CIM-786 is that it scored the minimum (4.67) array mean value. The cross CIM-786 x Bt-Aone showed best specific combining ability (4.57) for this character (Table 2).

Table-1. Results of join regression analysis of six characters of cotton

Character	Regression Coefficient*
Seed cotton yield	0.98± 0.70 b value deviate significantly from zero but not from unity
Seed Index	1.07 ± 0.79 b value deviate significantly from zero but not from unity
Lint %age	0.93 ± 0.15 b value deviate significantly from zero but not from unity
Fiber length	1.01 ± 0.14 b value deviate significantly from zero but not from unity
Fiber strength	1.15 ± 0.20 b value deviate significantly from zero but not from unity
Fiber fineness	0.83 ± 0.24 b value deviate significantly from zero but not from unity

*The data fit for genetic analysis

Table-1.2. ANOVA table indicating means square of six characters of cotton

SOV	d.f	Mean Squares (MS)					
		SCY	**SI**	**LP**	**FL**	**FS**	**FF**
Replication	2	54.64 (0.2879)^{NS}	9.31 (6.947761)*	0.14 (0.1176)^{NS}	0.14 (0.4827)^{NS}	0.10 (0.4827)^{NS}	1.39 (0.2768)^{NS}
Genotypes	24	10641.2 (56.0830)**	1.08 (0.8059)^{NS}	13.51 (11.3529)**	2.09 (7.2068)*	4.13 (15.8846)**	0.15 (0.0298)^{NS}
Error	48	189.74	1.34	1.19	0.29	0.26	5.02
CV%		43.26	7.36	12.48	3.42	5.22	7.01

TABLE 2. 5×5 diallel Table for Yield and Lint Traits

S.C.Y = Seed cotton yield S.I = Seed Index
L.P = Lint (%age) F.L = Fiber Length
F.S = Fiber Strength F.F = Fiber Fineness

Trait	Genotype	BT-AONE	CIM-556	CIM-557	NIBGE-2	CIM-786
SCY	BT-AONE	129.5	186.58	276.45	212.48	287.12
	CIM-556	186.58	194.87	263.92	229.28	260.42
	CIM-557	276.45	263.92	317.17	288	319.83
	NIBGE-2	212.48	229.28	288	240.37	292.52
	CIM-786	287.12	260.42	319.83	292.52	338.63
	TOTAL	1092.13	1135.07	1465.37	1262.65	1498.52
	MEAN	218.42C	227.01C	293.07A	252.53B	299.7A
SI	BT-AONE	6.56	6.92	6.85	6.43	7.33
	CIM-556	6.92	7.13	7.2	6.95	7.39
	CIM-557	6.85	7.2	7.57	6.61	7.76
	NIBGE-2	6.43	6.95	6.61	6.24	6.88
	CIM-786	7.33	7.39	7.76	6.88	7.85
	TOTAL	34.09	35.59	35.99	33.11	37.21
	MEAN	6.82B	7.12A	7.2A	6.62B	7.44A
L.P	BT-AONE	41.68	42.21	39.6	41.15	41.05
	CIM-556	42.21	44.28	39.59	41.08	43.02
	CIM-557	39.6	39.59	39.23	40.26	40.19
	NIBGE-2	41.15	41.08	40.26	41.05	41.68
	CIM-786	41.05	43.05	40.19	41.68	42.24
	TOTAL	205.69	210.21	198.87	205.22	208.18
	MEAN	41.14A	42.03A	39.78B	41.04A	41.64B
F.L	BT-AONE	29.57	28.53	30.09	29.5	29.25
	CIM-556	28.53	28.83	28.5	29.05	27.21
	CIM-557	30.09	28.5	30	29.32	28.53
	NIBGE-2	29.5	29.05	29.32	28.7	28.38
	CIM-786	29.25	27.15	28.53	28.85	30.27
	TOTAL	146.94	142.06	146.44	145.42	143.64
	MEAN	29.39A	28.41B	29.29A	29.08AB	28.73B
F.S	BT-AONE	27.9	26.47	28.08	27.68	28
	CIM-556	26.47	26.07	26.93	27.32	27.5
	CIM-557	28.08	26.93	29.77	27.68	28.77
	NIBGE-2	27.68	27.32	27.68	27.03	27.28
	CIM-786	28	27.5	28.77	27.28	28.37
	TOTAL	138.13	134.29	141.23	136.99	139.92
	MEAN	27.63B	26.86C	28.25A	27.4B	27.98B
F.F	BT-AONE	5.27	4.93	4.83	5.17	4.57
	CIM-556	4.93	4.87	4.85	4.88	4.78
	CIM-557	4.83	4.85	4.67	4.68	4.73
	NIBGE-2	5.17	4.88	4.68	4.77	4.82
	CIM-786	4.57	4.78	4.73	4.82	4.43
	TOTAL	24.77	24.31	23.76	24.32	23.33
	MEAN	4.95A	4.86B	4.75C	4.86B	4.67C

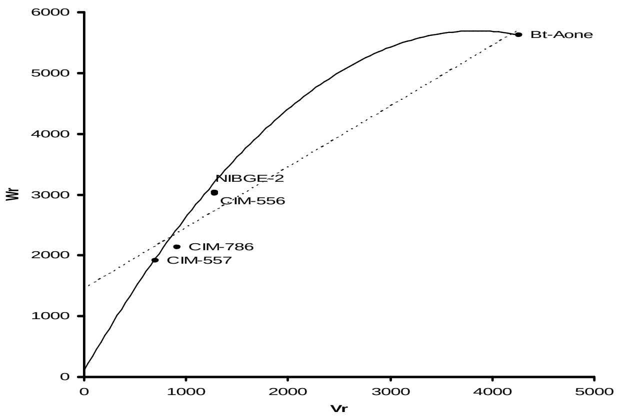

Fig.1: Seed cotton yield

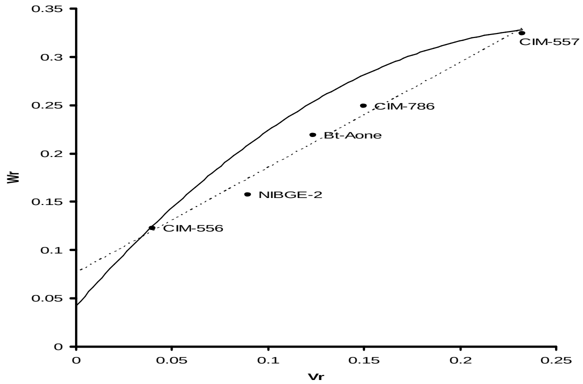

Fig.2: Seed index

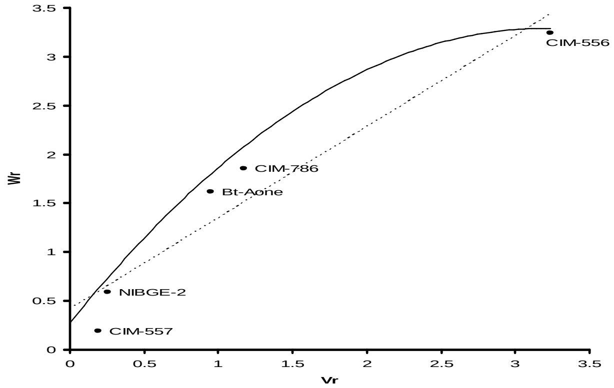

Fig.3: Lint (%age)

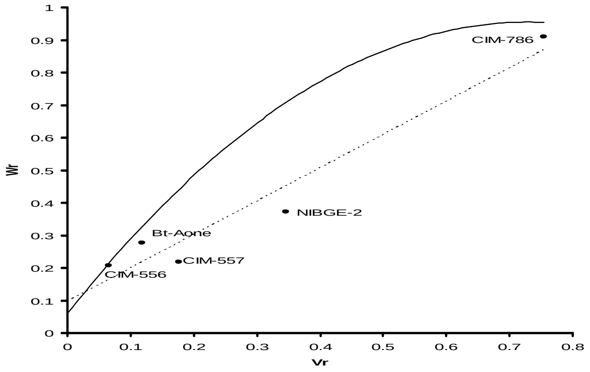

Fig-4: Fibre Length

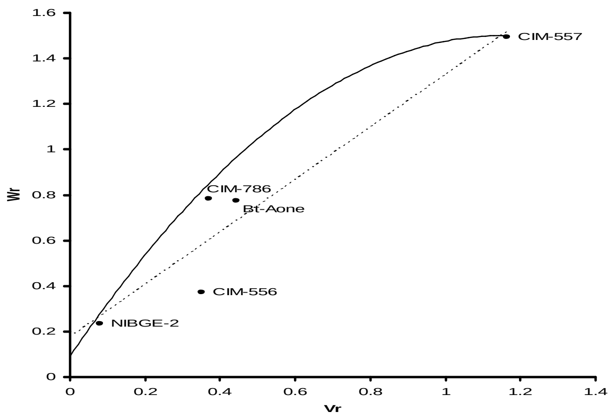

Fig.5: Fibre strength

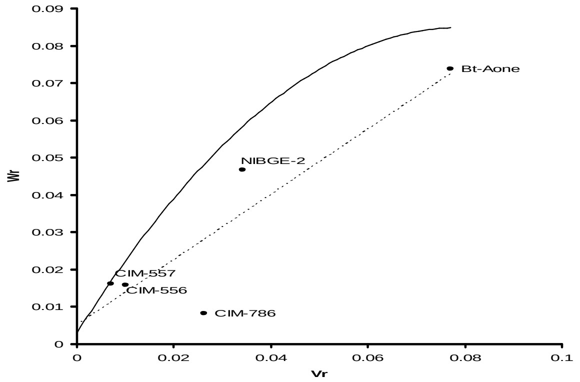

Fig-6: Fibre Fineness

Cinclusions: It is concluded that yield characters: seed cotton yield, seed index and lint percentage fiber length, fiber strength and fiber fineness were controlled by additive type of gene action with partial dominance. Under a situation when there is additive type of gene action without the involvement of any epistatic effects, the breeder can improve such characters through simple selection procedures. While over dominance occurs when most of the progenies perform better than their parents showing heterosis. Therefore, the progenies showing heterotic effects may be considered in a breeding program for developing hybrid cotton as this study make available detailed information concerning specific and general combiner lines. Present study also suggested that breeders can use CIM-786, CIM-556 and CIM-557 for the improvement of yield parameters while NIBGE-2, CIM-557 and Bt-Aone for the enhancement of fiber characters for future breeding programs.

REFERENCES

Anisa, L., G.M. Baloch, M.B. Kumbhar and B. A. Ansari. (2004). Combing ability analysis for yield and yield components in cotton. Indus cotton. 1(2): 54-57.

Azhar, M. T., A. A. Khan. (2005). Combining ability analysis of seed cotton yield and its components in cotton (*Gossypiumhirsutum*). P. J. S. I. R. 48 (5): 358-361.

Farooq, O. (2011). Pakistan Economic Survey (2010-11) Chapter-2. MINFAL, Islamabad.

Hayman, B. I. (1954). The theory and analysis of diallel crosses. Genetics, 39: 789-809.

Gamal I.A. Mohamed, S.H.M. Abd-El-Halem and E.M.A. Ibrahim. (2009). A Genetic Analysis of Yield and its Components of Egyptian Cotton (*Gossypiumbarbadense*L.) Under Divergent Environments. *American-Eurasian* J. Agric. & Environ. Sci., 5 (1): 05-13

Hayman, B. I. (1954). The theory and analysis of diallelcrosses. Genetics, 39: 789-809.

Iqbal, M., R. S .A. Khan, K. Hayat and N. I. Khan. (2005). Genetic variation andcombining ability for yield and fibre traits among cotton F1 hybrid population. J. Biol. Sci., 5(6): 713-716.

Jinks, J. L., (1954). The analysis of continuous variations in diallel crosses of Nicotianarustica L. varieties. Genetics, 39: 767-788.

Murtaza, N., (2005). Study of gene effects for boll number, boll weight and seed index in cotton. J. C. E. Agric., 6(3): 255-262.

Nadeem, K. and F. M. Azhar (2004). Genetic analysis of seed cotton yield and its components in *Gossypiumhirsutum* L. Int. J. Agric. Biol., 6(5): 865-868.

Nadeem, K. and F. M. Azhar (2005). Analysis of fibre length and fibre strength of *Gossypiumhirsutum* L. Int. J. Agric. Biol., 7(2): 263-265.

Rauf S., H. Munir, S.M.A. Basra and E. Abdullojon (2006) Combining ability analysis in upland cotton (*Gossypiumhirsutum* L.) Int. J. Agri. Bio. 8(3): 341-343.

Steel R.G.D, J.H.Torrie and D.A. Dickey, (1997). Principles and Procedures of Statistics: A Biometrical Approach. 3rd Ed. McGraw Hill Book Co. New York, USA.