



GENETIC ANALYSIS FOR SOME GINNING AND FIBER CHARACTERISTICS IN UPLAND COTTON

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Four varieties viz., Chandi-95, CIM-448, NIAB-Karishma and NIAB-78 were crossed in complete diallel fashion (4 x 4) to determine gene action for ginning out turn percentage (GOT), staple length, micronaire value and lint index. Results demonstrated that GOT % was controlled by complete dominance whereas, staple length, micronaire value and lint index were conditioned by partial dominance type of gene action. Chandi-95 had maximum dominant genes for staple length, micronaire value and lint index, while NIAB-78 had maximum dominant genes for GOT % and lint index. The variety NIAB-Karishma recorded the highest array means for GOT % and micronaire values followed by Chandi-95 and NIAB-78 for staple length and lint index, respectively. Whereas, cross combination NIAB-Karishma x NIAB-78 manifested highest values within array means for GOT%, micronaire value and lint index indicating good potential for the improvement of these characters.

Keywords: *Gossypium hirsutum* L., Diallel, Gene action, Array mean, General Combining Ability (GCA), Specific Combining Ability (SCA)

1. Introduction

Cotton (*Gossypium hirsutum* L.) is an important cash crop of Pakistan. It plays a great role in strengthening the national economy. The production per unit area in Pakistan is low as compared to other advanced cotton growing countries. One of the most conspicuous reasons of this low production is inferior genotype of our cotton plants. Therefore, there is a dire need for further genetic improvement of cotton. For the development of improved varieties with desirable quantitative and qualitative traits, the breeder must have a working knowledge of mechanism of inheritance of the economics traits [1, 2]. The diallel analysis technique as outlined by [3, 4, 5] has proved very useful in determining progeny performance in early generations. This will help the breeder to properly utilize the existing scarce genetic sources in fixing the desirable genes in such a manner that lead to the development of improved cotton genotypes [6].

Therefore, the research work was designed to determine the gene action and relative performance with respect to general and specific combining ability of cotton genotypes.

2. Material and Methods

The research work pertaining to the genetic studies in cotton was conducted at experimental field of Nuclear Institute of Agriculture (NIA), Tando Jam during the Kharif season of 2001-02. Four cotton varieties viz., Chandi-95, CIM-448, NIAB-Karishma and NIAB-78 were crossed in all possible combinations and the parents alongwith 12 F₁ hybrids were sown in randomized complete block design (RCBD) with three replications. Four rows (5 m long) each of parents and F₁ were sown per replication. Three seeds per hill were dibbled and plants thinned to ensure uniform stand of only one plant per hill. The inter plant and inter row distance was 30 and 75 cm, respectively. At maturity, 10 plants were randomly selected to record the data on GOT %, staple length, micronaire value and lint index. Nitrogen and phosphorous fertilizers were applied at the rates 120 and 80 kg ha⁻¹. Six irrigations (including soaking dose) were applied as and when needed.

The data were analysed according to [7] standard technique for the analysis of variance. For further genetic analysis, diallel cross technique [3, 4, 5] was used. Variances and co-variances were calculated from each diallel table. Information

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on gene interactions was obtained by plotting the co-variance (W_r) of each array against its variance (V_r). The slope and position of regression plot fitted to the array point lying within a limiting parabola ($W_r^2 = V_r \times V_r$) indicated degree of dominance and presence or absence of gene interactions.

Combining ability of the parents involved in the hybridization was indicated and explained by the array means in the diallel tables for individual characters [8].

3. Results and Discussion

3.1. Ginning outturn percentage (GOT %)

The analysis of variance for GOT % (Table 1) indicated that differences among genotypes were highly significant ($p \leq 0.001$). The value of variance and covariance (Fig.1) revealed that the regression plot cuts the W_r axis slightly above the origin signifying almost complete dominance type of gene action for this trait. As the regression plot deviates significantly from a unit slope some sort of interaction is controlling the phenotypic manifestation for this character. From the position of array points on the regression plot, it was shown that the variety NIAB-78 being the most proximate to the origin had most dominant genes, while CIM-448 being farthest from the point of origin, possessed maximum recessive genes for this character. Previously, it was reported to be controlled by over dominance [2] and additive type of gene action with partial dominance [9, 10]. The varieties NIAB-78 and NIAB-Karishma displayed 34.54 % and 34.43 % ginning out turn, respectively, but showed the highest array mean value (34.48 % each) suggesting that both the varieties proved to be better for general combining ability (GCA) (Table 2) and within the array, the cross NIAB-Karishma and NIAB-78 showed highest value (34.89 %) which exhibited that this cross could be the best for specific combining ability (SCA) for this trait.

3.2. Staple length

The analysis of variance for staple length (Table 1) indicates that the differences among the genotypes were highly significant. The variance and covariance plot (Fig.2) for this character indicated that the regression line passed above the origin of W_r axis, indicating the additive type of gene action with partial dominance. The results are in concurrence to [10, 11, 12] where also reported partial dominance type of gene action for this trait. The regression line deviated significantly from a

unit slope showing some non-allelic interaction in this trait. Chandi-95 being nearer to the origin had maximum dominant genes and NIAB-78 being farther from the origin had maximum recessive genes for this trait. Among the parents, Chandi-95 harbored maximum array mean (29.57 mm) which indicated that Chandi-95 was good general combiner (Table 3), whereas, NIAB-78 x Chandi-95 had highest value (29.90 mm) indicating the best specific combiner as compared to other crosses.

3.3. Micronaire value

The analysis of variance for micronaire value (Table 1) showed that differences among the genotype were highly significant. The regression line intercepted the W_r axis above the origin showing additive type of gene action with partial dominance (Fig 3). These results are in conformity with the results of [13] who reported partial dominance type of gene action for this trait. The regression line deviated significantly from a unit slope showing some non-allelic interaction in this trait. Further, it showed that variety Chandi-95 possessed maximum dominant genes being closer to the origin and variety NIAB-78 had maximum recessive genes for this trait. The variety NIAB-Karishma harbored highest array mean ($4.30 \mu\text{g inch}^{-1}$) which showed that it was good general combiner for this trait (Table 4). Within the array, the cross of NIAB-Karishma x NIAB-78 had the highest value ($4.40 \mu\text{g inch}^{-1}$) suggesting that this cross was the best specific combiner for this trait.

Contrary to other traits, the parents and the crosses having least mean values would be preferred for the improvement of the trait. The lesser the value the finer would be the fiber.

3.4. Lint index

The analysis of variance for lint index (Table 1) revealed that the differences among the genotypes were highly significant. The W_r/V_r graph (Fig. 4) showed that the regression line passes W_r axis above the origin, which indicated the additive type of gene action with partial dominance. The earlier studies [11, 14, 15, 16] reported the similar results. However, the studies [17] deviated by ascribing over dominance type of gene action for lint index. As the regression line deviates significantly from a unit slope, there appears some interaction of non-allelic genes in this respect. The variety NIAB-78, being nearer to the origin, had maximum dominant genes whereas, variety NIAB-Karishma being

Table 1. Mean squares for different qualitative characters of *Gossypium hirsutum* L.

Source of variation	D.F.	G.O.T %	Staple length (mm)	Micronaire value ($\mu\text{g inch}^{-1}$)	Lint index (g)
Genotypes	15	0.544**	3.730**	0.100**	0.055**
Replications	2	0.025	0.005	0.004	0.009
Error	30	0.06	0.033	0.0007	0.004

Table 2. Diallel averages for ginning out turn percentage, variance (Vr) and covariance (Wr) for F₁ generation.

Varieties	Chandi-95	CIM-448	NIAB-Karishma	NIAB-78	Vr	Wr
Chandi-95	34.52	34.46	34.34	34.39	0.0062	0.1360
CIM-448	33.27	33.92	34.34	34.09	0.2089	0.0452
NIAB-Karishma	34.31	33.56	34.43	34.89	0.3042	0.0329
NIAB-78	33.90	34.31	34.83	34.54	0.1541	0.0655
Array Means	34.00	34.06	34.48	34.48	0.1683	0.0699

Table 3. Diallel averages for staple length, variance (Vr) and covariance (Wr) for F₁ generation.

Varieties	Chandi-95	CIM-448	NIAB-Karishma	NIAB-78	Vr	Wr
Chandi-95	30.00	28.70	28.30	28.40	0.620	0.294
CIM-448	29.10	27.70	27.90	27.40	0.560	0.709
NIAB-Karishma	29.30	28.23	26.87	27.10	1.260	1.212
NIAB-78	29.90	27.30	26.30	26.70	2.623	1.083
Array Means	29.57	27.98	27.34	27.47	1.265	0.824

Table 4. Diallel averages for micronaire value, variance (Vr) and covariance (Wr) for F₁ generation.

Varieties	Chandi-95	CIM-448	NIAB-Karishma	NIAB-78	Vr	Wr
Chandi-95	4.00	4.00	4.16	4.09	0.006	0.027
CIM-448	3.94	4.35	4.20	4.12	0.029	0.024
NIAB-Karishma	4.15	4.22	4.56	4.40	0.034	0.025
NIAB-78	4.30	4.19	4.15	4.53	0.029	0.045
Array Means	4.10	4.18	4.30	4.28	0.024	0.030

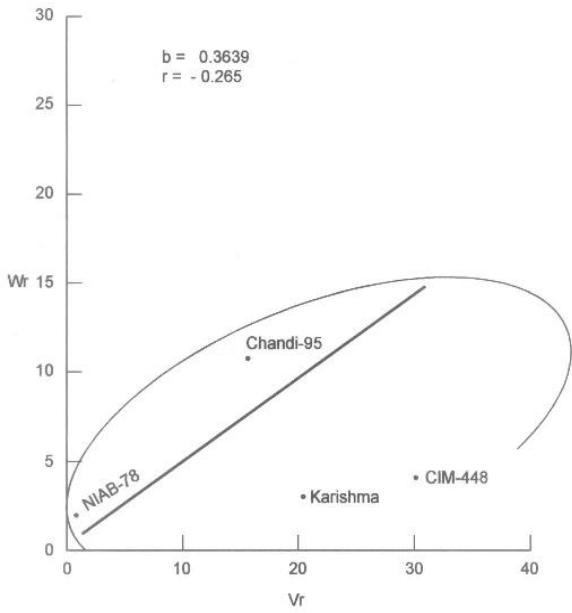


Figure 1. Wr / Vr graph for G.O.T %.

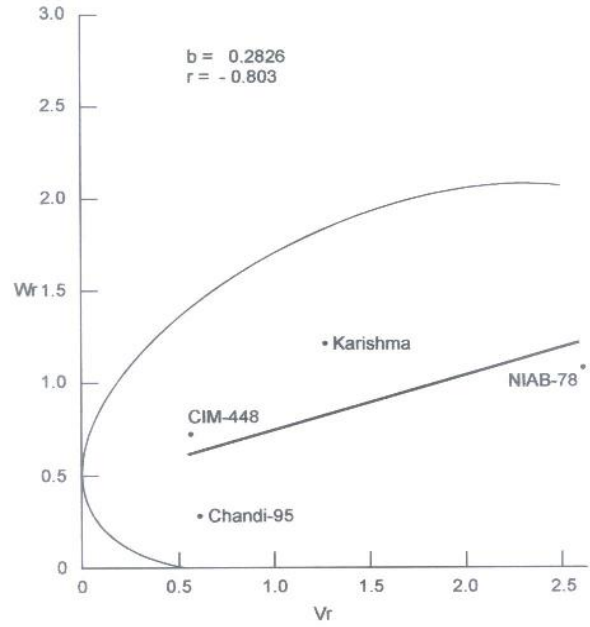


Figure 2. Wr / Vr graph for staple length.

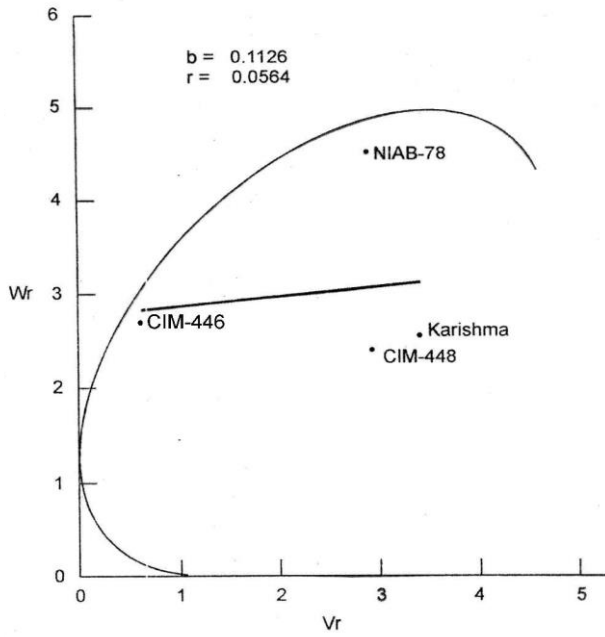


Figure 3. Wr / Vr graph for micronaire value .

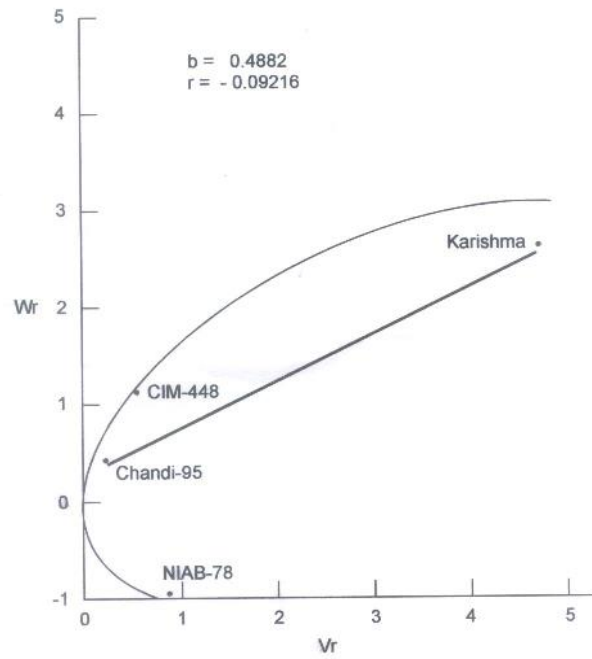


Figure 4. Wr / Vr graph for lint index.

Table 5. Diallel averages for lint index, variance (Vr) and covariance (Wr) for F₁ generation.

Varieties	Chandi-95	CIM-448	NIAB-Karishma	NIAB-78	Vr	Wr
Chandi-95	4.72	4.71	4.61	4.65	0.0026	0.0042
CIM-448	4.45	4.48	4.45	4.61	0.0058	0.0200
NIAB-Karishma	4.69	4.44	4.36	4.82	0.0458	0.0260
NIAB-78	4.59	4.65	4.81	4.65	0.0089	0.0099
Array Means	4.61	4.57	4.55	4.68	0.0157	0.0100

farthest from the origin, demonstrated that this variety had maximum recessive genes for this character. Results (Table 5) showed that variety NIAB-78 had maximum array mean value (4.68 g) showing the better general combining ability for the trait lint index. Among the crosses, the combination of NIAB-Karishma x NIAB-78 proved to be the best specific combiner showing the highest value (4.82 g) as compared to other crosses.

4. Conclusion

The varieties NIAB-Karishma and Chandi-95 being good general combiners for GOT %, micronaire value and staple length, will make good breeding material to be exploited in breeding programmes for the improvement of these characters. However, the cross NIAB-Karishma x NIAB-78 in specific was better performing and could be exploited in producing hybrid cotton.

References

- [1] M.A. Chandio, M.S. Kalwar and G.M. Baloch, Pak. J. Sci. Res., **54** (2002) 31.
- [2] M.A. Khan, A.S. Larik and Z.A. Soomro, Asian J. Plant Sci., **1** (2002) 130.
- [3] B.I., Hayman, Genetics, **39** (1954) 789.
- [4] B.I., Hayman, Genetics, **43** (1954) 63.
- [5] J.L. Jinks, Genetics, **39** (1954) 767.
- [6] M.A. Khan, Z.A. Soomro and N. Leghari, Pak. J. Appl. Sci., **3** (2003) 129.
- [7] R.A. Fisher, Statistical methods for research workers, 13th ed. P. 248-298, Oliver and Boyd, London (1958).
- [8] I.A. Khan, A. Ali, M. Zubair and I. Ahmad Khan, The Pak Cottons, **44** (2000) 25.
- [9] M.D. Keerio, M.S. Kalwar, M.I. Memon and Z.A. Soomro, Pak. J. Bot., **27** (1995) 425.
- [10] A.S. Larik, S.R. Ansari and M.B. Kumbhar, Pak. J. Bot. **29** (1997) 97.
- [11] S. Ahmed, M.D. Khan, M. Hassan, Ali and L.H. Akhtar, Pak. J. Plant Sci., **2** (1996) 101.
- [12] M.S. Kalwar, M.I. Lander and G.M. Baloch, The Pak. Cottons, **42** (1998) 61.
- [13] N. Murtaza, M.A. Khan, I.A. Khan, T.M. Khan and A.M. Khan, Pak. J. Agric. Sci., **29** (1992) 284.
- [14] M. Tarique, M.A. Khan and G. Idris, Sarhad J. Agric., **XI** (1995) 607.
- [15] Q.K. Ahmed, I.A. Khan, M. Zubair and M. Tariq, The Pak. Cottons, **41** (1997) 6.
- [16] B. Hussain, A.M. Amin and M.A. Khan, J. Agric. Res., **36** (1998) 103.
- [17] M. Subhan, H.U. Khan and R. Ahmed, Pak. J. Biol. Sci., **3** (2002) 2087.