

Genetic Analysis of Some Metric Plant Traits in Upland Cotton (*Gossypium hirsutum* L.) through Hybridization

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Abstract Five cotton cultivars (NIAB-884, Bt-101, CRIS-310, MS-39 and UCD-581) were crossed in a complete diallel design to investigate the inheritance pattern of some metric plant traits. Genetic differences were found significant ($b > 0.01$) for all traits under study. Adequacy test showed that all the characters were fully adequate for genetic analysis. Additive component of genotypic variance (D) was significant and predominant for Plant height, number of sympodial branches, boll weight, seed cotton yield, lint percentage, staple length, fibre strength and fibre fineness, while over dominance effects (H1 and H2) mainly contributed for no. bolls per plant. Partial dominance was involved for plant height, no. of sympodial branches, boll weight, and yield of seed cotton, lint percentage, staple length and fibre strength. The value of $H2/4H1$ demonstrated asymmetrical and unequal distribution of dominant genes in the parents for all the traits.

Keywords *Gossypium hirsutum*, Upland Cotton, Genetic Analysis, Dominance, Heritability, Gene Action, Diallel

1. Introduction

Due to immense importance of cotton crop, the breeders had made tremendous efforts for exploiting the potential of the plant for greater yield of seed cotton and improved fibre characteristics. Although total production of cotton in Pakistan has increased significantly the national average yield is still lower than that harvested in other cotton growing countries of the world. For the development of an efficient cotton improvement program, availability of variation in different plant characters is one of the prerequisites of plant breeder. This variation may be more advantageous if it is controlled by significant genetic components. This information about the plant material facilitates the researchers to develop an efficient selection protocol aimed to enhance plant performance.

Several researchers (Khan *et al.*, [1]; Iqbal and Khan, [2]; Esmail *et al.*, [3]; Ahmad and Azhar, [4]; Iqbal and Nadeem, [5] and Nadeem and Azhar, [6]) had advocated the importance of genetic studies of the material before selecting the desirable plants. Mukhtar *et al.* [7] reported additive type of gene action with partial dominance for plant height, number of bolls per plant, boll weight and yield of seed cotton per plant. In order to collect such knowledge, there are several biometric techniques that are used for analyzing the data by breeders these days, and Hayman-Jinks model used in this research is one of them. Purpose of this experiment was to unwind genetic information about some metric traits in upland cotton.

2. Material and Method

2.1. Genetic Material & Glass House Experiment

For the present studies, five parent varieties namely NIAB-884, BT-101, CRIS-310, MS-39 and UCD-581 were grown in earthen pots, in the glasshouse of the department of plant breeding and genetics, in the University of Agriculture, Faisalabad. During germination and growth optimum conditions (Light & temperature) were possibly provided and required agronomic practices were followed. At the time of flowering, all parental lines were crossed in complete diallel fashion (5x5) to develop 20 F1 crosses (direct & reciprocal) along with selfed seed of parents. All necessary precautionary measures were adopted to avoid contamination of the genetic material at the time of crossing and selfing. Plants were properly managed up to maturity. At maturity, crossed and selfed bolls were picked and seed cotton of each cross ginned separately using single roller electric ginner.

2.2. Field Experiment and Laboratory Experiment

The F_0 seed from all the crosses along with their selfed parents were sown in the field following a Randomized

Complete Block Design with three replications. In a replication each of the 25 entries was planted in a single row comprising of 15 plants with plant to plant and row to row distance of 30 cm and 75 cm respectively. All the recommended agronomic practices and plant protection measures were followed from sowing till harvest of the crop. At maturity the data were recorded for plant height (cm), number of sympodial branches, number of bolls per plant, boll weight (g), yield of seed cotton (g) and lint percentage from 10 guarded plants in each entry, both in field as well as laboratory on individual plant basis. For fibre analysis of staple length (mm), fibre strength (g/tex) and fibre fineness (ug/inch), the seed cotton of all the plants in each entry was subjected to ginning by a single roller electric gin in laboratory on individual plant basis. Lint so obtained was placed at 65% humidity and 18-20 C temperature in an air conditioned room using humidifier before fibre testing (Ali et al. [8]. High Volume Instrument (HVI-900- SA; Zelwiger, Uster, UK) was used for fibre analysis.

2.3. Statistical Analysis

The data collected was subjected to analysis of variance (Steel et al. [9]) to test significance of genotypic differences for the plant traits under study. The characters showing significant genotypic differences were further analyzed genetically following additive-dominance model of Hayman [10] and Jinks [11]. The suitability of the data sets to additive-dominance model was carried out by one of the scaling test i.e. the joint regression analysis. For genetic analysis the crosses were arranged into arrays. Two statistics i.e. the variance (V_r) of family means within an array and co-variance (W_r) of these means with non-recurrent parent values were calculated. Four genetic components of variation, D (additive effects of genes), H1 and H2 (dominance effects of genes), F value (an estimate of the relative frequency of dominant to recessive alleles in the parental lines and the variation in the dominance over the loci), E (the role of environmental effects) and $h^2_{n.s}$ (the heritability in narrow sense) for each character were estimated. The information on gene action was obtained by plotting the co-variance W_r of each array against its variance V_r .

3. Results and Discussion

Preliminary analysis of variance revealed significant differences ($P \leq 0.01$) for all the characters i.e. Plant height, number of sympodial branches, no. of bolls per plant, boll weight, seed cotton yield, Lint %, staple length, fibre strength and fibre fineness among genotypes. The joint regression analysis revealed that regression coefficient (b) for all the characters deviated significantly from zero but not from unity showing that the data were fit for simple additive-dominance model (Table 1).

Genetic components of variation (Table 1) for all the

characters except no. of bolls per plant indicated that there were additive type of gene action controlling these traits as the value of D was greater than H1 and H2. This also confirmed that assumptions for diallel analysis are met and interpretations made on basis of this analysis had logical statistical basis. It was also cleared from the graph between W_r and V_r that showed that the regression lines intercepted the W_r axis above point of origin (Fig 1 to 8). Similar findings had also been reported by Nadeem & Azhar [12], Basal & Turgut [13] and Ali & Khan [14]. On the other hand the character no. of bolls per plant showed the over dominance type of gene action proved by the graph in which regression line intercepted the W_r axis below the point of origin (fig 9). The value of H1 and H2 for plant height, no. bolls per plant, seed cotton yield, lint percentage, staple length, fibre strength and fibre fineness was unequal, suggesting that there was unequal distribution genes for these traits (Table 1). There was equal distribution of genes in case of no. of sympodial branches and boll weight because H1 was equal to H2.

The positive value of F for plant height, number of sympodial branches, lint percentage, fibre fineness and staple strength indicated more dominant genes for these traits in genetic material, whereas negative value of F for number of bolls per plant, boll weight, seed cotton yield and fibre length confirmed predominance of additive genes in parents. The overall degree of dominance was measured by ratio $(H_1/D)^{0.5}$. It was in range of partial dominance for all traits except for number of bolls per plant which showed over dominance. Estimate of ratio of dominant to recessive genes $(4DH_1)^{0.5} + F / (4DH_1)^{0.5} - F$ (greater than 1) for plant height, no. of sympodial branches, lint percentage, fibre fineness and fibre strength revealed that there were more dominant genes in the parents for these characters and value of $(4DH_1)^{0.5} + F / (4DH_1)^{0.5} - F$ (less than 1) for no. of bolls per plant, boll weight, seed cotton yield and staple length revealed that there were more recessive genes in the parents for these characters. Estimate of the frequency of negative versus positive alleles at loci showing dominance $(H_2/4H_1)$, was less than 0.25 showed that not all the additive components contain dominance effects in all the traits.

All the traits exhibited higher estimates of narrow sense heritability except for number of bolls per plant which confirmed involvement of fixable and heritable additive gene effect for these traits (Basal & Turgut [13], Ali & Khan, [14]). These characters can be improved through single plant selection. Among parents UCD-581 has maximum number of dominant genes for number of bolls per plant, staple length and fibre strength while maximum recessive genes for seed cotton yield, MS-39 has maximum dominant genes for boll weight, seed cotton yield and lint percentage and maximum recessive genes for plant height, staple length and fibre fineness. NIAB-884 has high frequency of dominant genes for plant height and recessive genes for sympodial branches, number of bolls per plant, boll weight and lint percentage (Fig 1-9).

Table 1. Components of variations for quantitative traits in cotton

Components	Plant Height	No. of Sympodial branches	No. of Bolls/Plant	Boll Weight	Seed Cotton Yield	Lint %	Staple Length	Fibre fineness	Staple Strength
MS _G	21.47**	20.29**	153.27**	29.46**	3.06**	35.15**	5.26**	8.59**	32.53**
B	1.00 ± 0.08	1.07 ± 0.16	0.86 ± 0.07	0.87 ± 0.15	0.86 ± 0.24	0.85 ± 0.20	0.86 ± 0.09	1.00 ± 0.16	0.90 ± 0.20
V _o L _o	50.23	13.82	4.17	0.13	434.91	430.65	0.95	0.14	3.24
V ₁ L ₁	20.86	5.92	3.78	0.07	233.68	161.79	0.52	5.46	1.53
W _o L _o	12.83	3.29	13.52	6.58	178.21	132.77	0.40	4.37	1.18
D	49.20	13.53	4.05	13.23	301.72	422.83	10.12	9.31	3.19
H ₁	15.42	2.56	42.83	7.75	-133.3	294.25	9.65	7.29	1.72
H ₂	12.64	2.13	31.95	7.02	-76.71	236.14	0.12	4.38	1.30
F	15.77	3.61	-6.92	-4.99	-224.7	204.76	-0.34	0.05	0.30
h ²	6.10	-0.12	41.14	0.10	-84.87	-3.07	0.19	3.21	9.96
E	1.03	0.29	0.12	3.75	133.19	7.82	0.14	8.90	5.91
(H ₁ /D) ^{0.5}	0.55	0.44	3.25	0.78	0/66	0.83	0.34	0.75	0.73
H ₂ /4H ₁	0.20	0.21	0.19	0.23	0.14	0.20	0.30	0.15	0.19
(4DH ₁) ^{0.5} + F/ (4DH ₁) ^{0.5} - F	1.80	1.88	0.58	0.60	0.28	1.82	0.24	1.70	1.14
h ² _{ns}	0.81	0.86	0.57	0.81	0.67	0.67	0.76	0.73	0.83

MS_G= Genotypic mean square, **b**= Regression coefficient, V_oL_o= Variance of parents, V₁L₁= Means of V₁, W_oL_o= Means of W₁, **D**= Additive effect, **H**₁= Component of variation due to dominance effect of genes, **H**₂= Component of variation due to dominance effect of genes correlated with genes distribution, **F**= Relative frequency of dominant and recessive alleles, **h**²= Over all dominance effects of heterozygous loci, **E**= Environmental influence, (H₁/D)^{0.5}= Dominance ratio, H₂/4H₁= Proportion of genes with positive and negative effects in parents, (4DH₁)^{0.5} + F/ (4DH₁)^{0.5} - F= Proportion of dominant and recessive genes in the parents, h²_{ns}= Narrow sense heritability

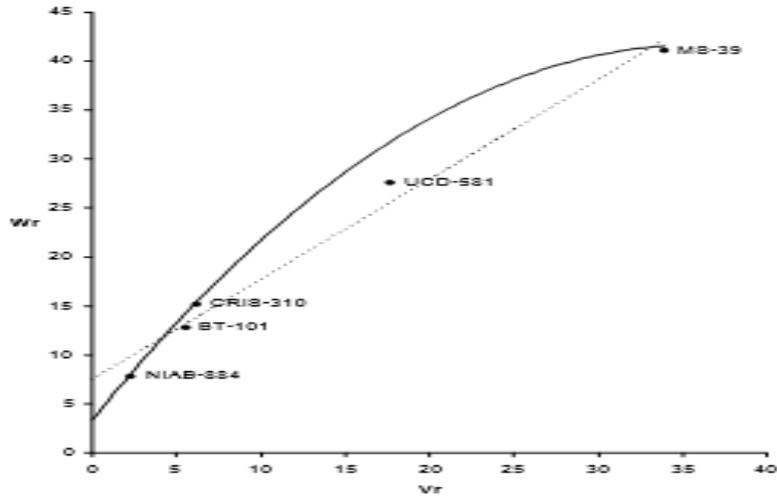


Figure 1. W_r/V_r graph for Plant height

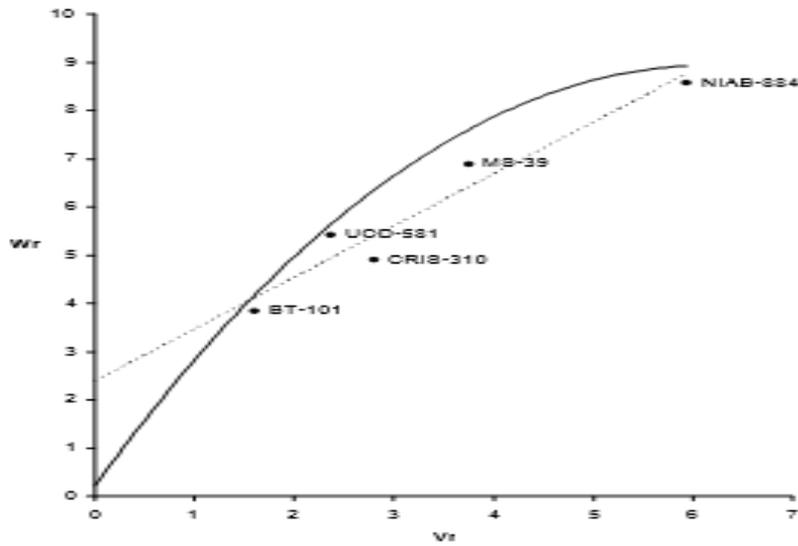


Figure 2. W_r/V_r graph for Sympodial branches

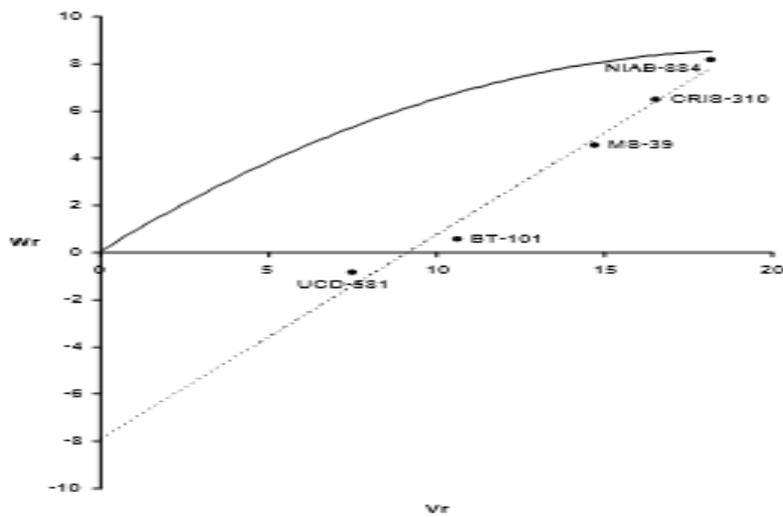


Figure 3. W_r/V_r graph for Bolls/Plant

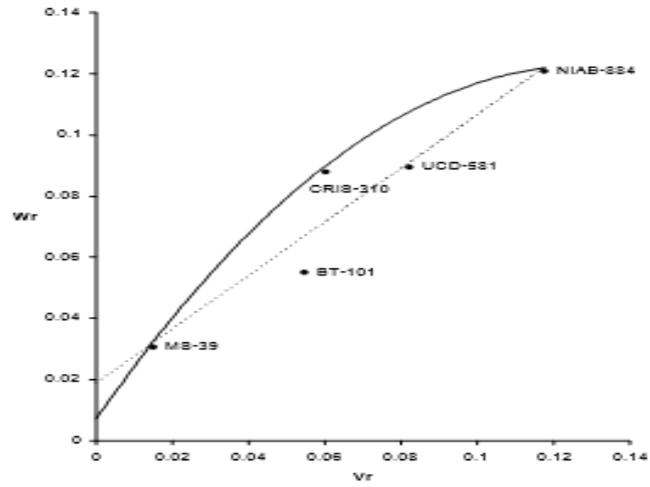


Figure 4. W_r/V_r graph for Boll weight

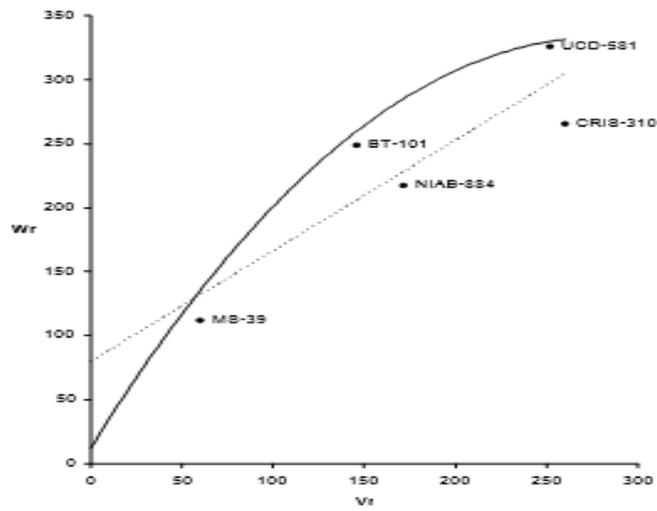


Figure 5. W_r/V_r graph for Seed cotton yield

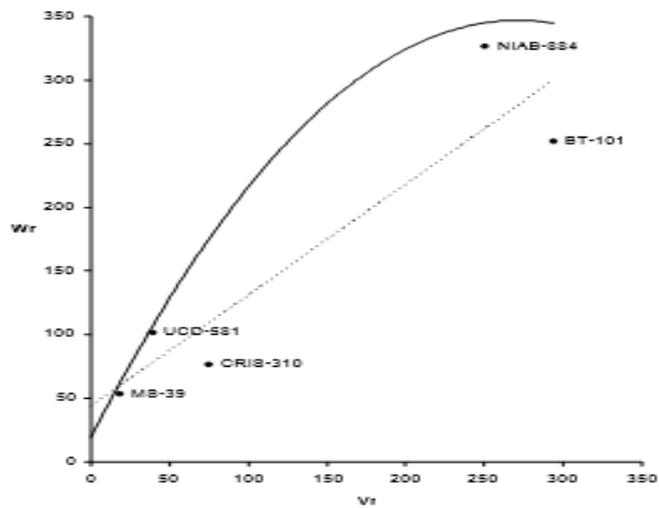


Figure 6. W_r/V_r graph for Lint %

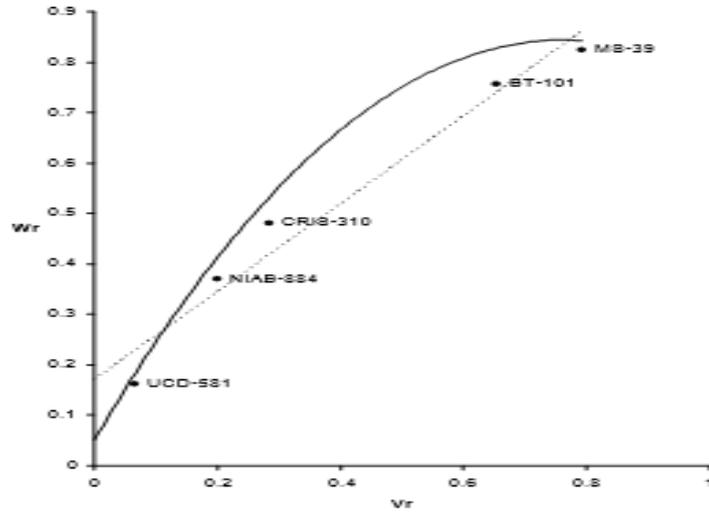


Figure 7. W_r/V_r graph for Staple length

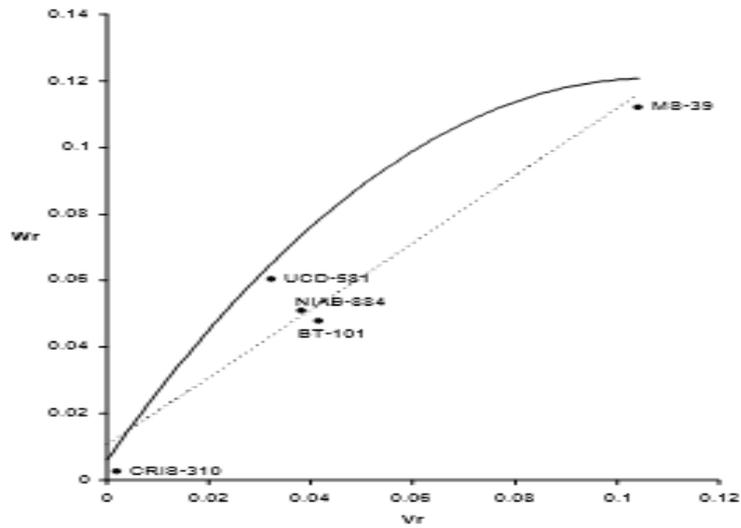


Figure 8. W_r/V_r graph for Fibre fineness

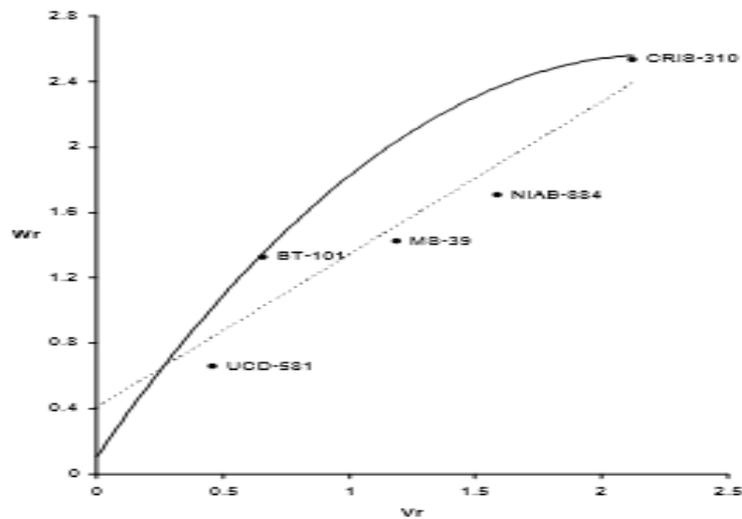


Figure 9. W_r/V_r graph for Fibre strength

4. Conclusion

The inheritance pattern of variation for different quantitative characters in five genotypes of cotton revealed by the diallel data appeared to be complex. Although genetic variation for the characters appeared to be influenced predominantly by genes with additive, or over dominance effects, the presence of additive component is encouraging. It would seem likely that additively based variations in the characters under study should be exploited through selection in early generation while those with over dominance, selection should be delayed to later generations and in that case it is suggested to go for a hybrid development.

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