GENETIC ANALYSIS OF SOME IMPORTANT ECONOMIC TRAITS IN BREAD WHEAT *(Triticum aestivum L.)*

Muhammad Shafique Tahir, Khurshid Alam*
Muhammad Aslam Chowdhry* and Javed Ahmad
Wheat Research Institute, Faisalabad.
**Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad.*

Graphic and component analysis of five different genotypes of bread wheat *(Triticum aestivum L)* namely LU-26, Pak.81, Pb. 85, S-131 and S-1080, indicated the presence of additive genetic variance with partial dominance for peduncle length, spike length. spike lets per spike and number of grains per spike while complete dominance was reported for grain yield per plant. Wheat genotypes Pak. 81 and S-131 showed relatively higher combining ability. From the preponderance of additive genetic control and absence of epistasis, it may be suggested that careful selection of desirable traits in early segregating generations would provide fruitful results.

INTRODUCTION

The diallel analysis developed by Hayman (1954) and Jinks (1954) provide a fairly reliable mechanism to properly understand the nature of gene action involved in the development of complex genetic characters having economic value. The type of gene action, allelic and non-allelic interactions involved in the inheritance of quantitative traits is indicated through graphical and component analysis showing distribution and proportion of dominant and recessive alleles among parents. In various diallel crosses, both additive and non-additive types of gene actions were reported to be involved in quantitative characters in wheat (Hsu and Walton, 1970; Verma et al., 1984; Shafiq, 1987; Bebyakin and Korobova, 1990; Chowdhry et al., 1992; Waldia et al., 1994). Thus the information obtained from the present study not only confirms the earlier findings but may also be effectively exploited to keep up the breeding tempo of wheat improvement efforts.

MATERIALS AND METHODS

Five genetically diverse varieties/lines of bread wheat *(Triticum aestivum L.)* namely LU-26, Pak. 81, Pb. 85, S-131, S-1018 and their fifteen possible F_1 crosses including reciprocals were planted in the field in November 1987. The experiment was arranged in a randomized complete block design with three replications having Sm long rows. Inter-plant and inter-row distances were kept as 15 and 30 cm, respectively. Normal agronomic care was provided to the crop and ten plants from each entry were randomly selected for recording data on peduncle length, spike length, spike lets per spike, number of grains per spike and grain yield per plant.

The data were analyzed statistically using analysis of variance technique (Steel and Torrie, 1980). Significant differences among genotypes were further analyzed using diallel analysis technique developed by Hayman (1954) and links (1954).

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among genotypes. The results of diallel analysis for various traits are discussed as below;

A review of Table I indicates that the parental line Pak. 81 with maximum array m~a'I\':',a\I\I~a,,~~ \1::\ \;)\;, \\'1.1:. \:)\:,':'\ ~I::\mb\'I\extQ\: number of grains per spike and grain yield per plant. Within the array the cross of Pak.81 xS-131 showed highest specific combining ability for grain yield per plant. Similarly, S-131 showed better general combining ability f~r spike length and spikelet per spike. Cross LU-26xS- 131 showed maximum specific combining ability for spike length while maximum specific combining ability for spikelets per spike was observed in crosses Pb. 85xS-131 and Pb. 85xS- 10 18. Parental line LU-26 proved to be the best general combiner for peduncle length and cross ofLU-26 with S-131 showed maximum specific combining ability for peduncle length.

Peduncle Length:

From the WrNr graph pattern it is obvious that since regression line intercepted the Wr-axis above the origin (Figl.l), additive type of gene action with partial dominance was involved. As line deviated non-significantly from unit slope, absence of epistasis was therefore interpreted for this character. The information derived from the present study confirmed the findings of Hsu and Walton (1970) Nanda *et al.,* (1982) and Khan et al. (1992).

The distribution of varietal array points on the regression line revealed that S-1O18 owing to its proximity to origin contained maximum dominant genes.

Spike Length:

The WrNr graph showed that regression line intercepted the Wr-axis above the origin (Fig. 1.2) and made a tangent with parabola, indicating additive gene action with partial dominance. Since regression line did not deviate significantly from unity, therefore non-allelic interaction was not indicated. Similar results were also reported by Hsu and Walton (1970), Chowdhry et aI., (1982). and Khan et »J., (J992t The relative location of array points on regression line showed that S-131 had most of the dominant genes while Pak.8l carried most recessive alleles.

Spike\ets Per Spike~

As evident from the regression pattern (Fig. 1.3), the genetic control for this trait appeared to be additive with partial dominance ana a\so ausence 0\ e1"\"3,\as"" a." \\\e reg,re.",,\Qn line deviated non-significantly from unit slope. This information confirm the findings of Chapman and McNeal (1971), Shafiq (1987) and Waldia *et al., (1994).*

The relative position of array points on the regression line showed that Pb. 85 possess most dominant genes while opposite was true of S-1O18 which carried most recessive gencs.

Number of grains per spike:

The WrNr graph showed that regression line intercepted the WrNr above origin (Fig 1.4), indicating additive expression with partial dominance for this trait. The information derived from study confirmed the findings of Verma *et al.,* (1984), Shafiq (1987), Bebyakin and Korobova (1990) and Khan *et al. (1992).* The genotype LU-26 being close to the point of origin had most of the dominant genes while Pak.8l possessed most of the recessive genes as it was away from origin.

Grain Yield:

The inheritance pattern for grain yield appeared to be complete dominance type as regression line passed through the origin (Fig. 1.5) These findings are in agreement with the results of Bhullar et aI., (1982), Verma et al., (1984) and Chowdhry et al., (1992). The array points distribution on regression line revealed that S-1018 was proximate to origin hence depicted maximum number of dominant genes

Table 1: General and specific combining ability effects calculated from the array means for various plant traits of 5x5 diallel cross.

Genotypes	Peducnle length	Spike length	Spikelets per spike	Grain per spike	Grain Yield / Plant
LU-26	17.502	12.3	19.002	60.452	28.489
Pak.81	15.438	11.9	20.266	64.396	31.962
Pb. 85	15.434	12.0	20.468	62.532	29.128
S-131	17.468	13.1	20.568	63.286	30.324
S-1018	16.634	11.7	19.100	62.632	30.799
MEAN OVER REPLICATIONS AND RECIPROCALS					
LU-26 X Pak. 81	16.67	12.00	19.67	60.33	28.04
LU-26 X Pb. 85	16.00	12.17	19.00	59.33	25.47
LU-26 X S-131	19.17	13.17	19.67	62.27	30.01
LU-26XS-1018	17.67	11.83	18.00	60.00	32.85
Pak. 81 X Pb. 85	14.67	12.00	20.33	64.83	33.33
Pak.81XS-131	16.17	13.00	21.00	65.33	34.49
Pak. 81 X S-lO18	16.67	11.50	19.33	63.16	33.07
Pb. 85 X S-131	17.00	12.00	21.17	62.00	27.28
Pb. 85 X S-1018	16.83	11.50	21.17	66.17	31.09
S-131 X S-1018	17.67	12.50	19.67	64.50	29.46

Table 2: Component of variation (± SE) for various characters of Wheat *(Triticum aestivum* L.)

Parameters	Peducnle length	Spike length	Spikelets per spike	Grain per spike	Grain Yield / Plant
D	5.74 ± 0.46**	1.19 ± 0.27*	2.81 ± 0.44**	7.27 ± 2.45	2.22 ± 1.42
F	1.96 ± 1.20	0.04 ± 0.07	0.81±1.15	4.13 ± 3.59	-2.23 ± 3.67
HI	3.71 ± 1.25	0.06 ± 0.07	1.45 ± 1.20	5.97 ± 3.68	21.53 ± 3.83*
H2	3.40 ± 1.13	-0.04 ± 0.06	1.17 ± 1.08	3.20 ± 3.47	19.15±3.47*
h2	1.10 ± 0.77	0.33 ± 0.04*	-0.08 ± 0.73	19.89 ± 2.85**	7.78 ± 2.34*
E	0.33 ± 0.19	0.12 ± 0.01 **	O.17±0.18	5.92 ± 2.24	1.74 ± 0.58

Derived Values	Peducnle length	Spike length	Spikelets per spike	Grain per spike	Grain Yield/ Plant
(H,/D)o.5	0.80	-0.23	0.72	0.91	3.11
Hi4H1	0.23	0.16	0.20	0.13	0.22
(4DH I fS +F)/(4DH I)os-F;	1.54	0.76	1.50	1.91	0.72
h2/H2	0.68	-8.30	-0.07	6.23	0.41

* = P<0.05, ** = P<O.Ol

Fig. 1.1 The regression of Wr on Vr for peduncle length.

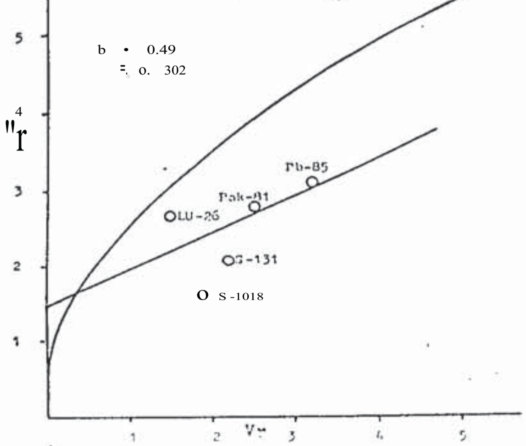


Fig. 1.2 The regression of Wr on Vr for spike length.

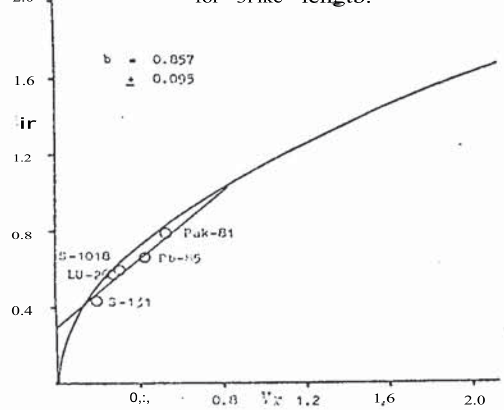


Fig. 1.3 The regression of Wr on Vr for spikelets per spike.

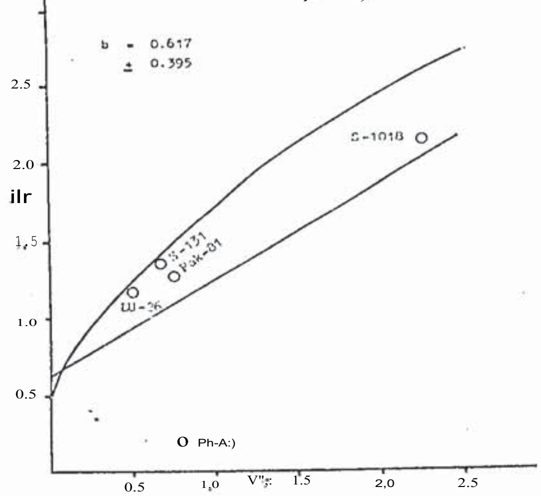


Fig. 1.4 The regression of Wr on Vr for ...

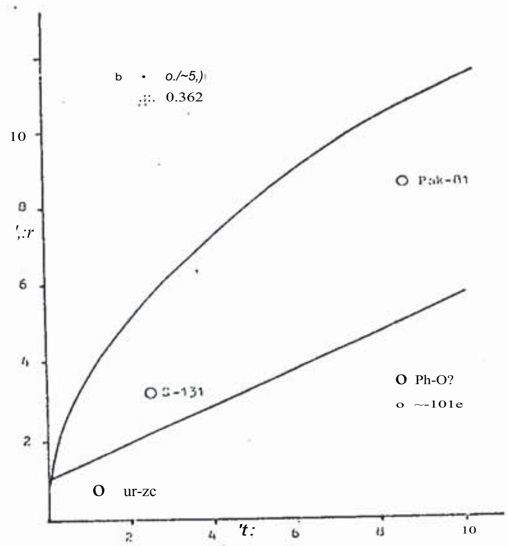
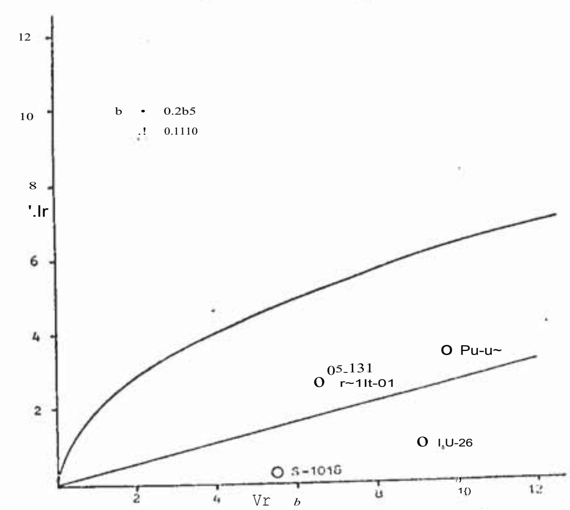


Fig. 1.5 The regression of Wr on Vr for ...



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H2	3.40 ± 1.13	-0.04 ± 0.06	1.17 ± 1.08	3.20 ± 3.47	19.15 ± 3.47*
h2	1.10 ± 0.77	0.33 ± 0.04*	-0.08 ± 0.73	19.89 ± 2.85**	7.78 ± 2.34*
E	0.33 ± 0.19	0.]2±0.01**	0.17 ± 0.]8	5.92 ± 2.24	1.74 ± 0.58

Derived Values	Peducnle length	Spike length	Spikelets per spike	Grain per spike	Grain Yield/ Plant
(H1/D)o.5	0.80	-0.23	0.72	0.91	3.11
H2/4H,	0.23	0.16	0.20	0.13	0.22
(4DH 1)05+F)/(4DH1 t5_F)	1.54	0.76	1.50	1.91	0.72
h2/H2	0.68	-8.30	-0.07	6.23	0.4]

* = P<0.05, ** = P<O.01

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F	1.96 ± 1.20	0.04 ± 0.07	0.81 ± 1.15	4.13 ± 3.59	-2.23 ± 3.67
HI	3.71 ± 1.25	0.06 ± 0.07	1.45 ± 1.20	5.97 ± 3.68	21.53 ± 3.83*
H2	3.40 ± 1.13	-0.04 ± 0.06	1.17 ± 1.08	3.20 ± 3.47	19.15 ± 3.47*
h2	1.10 ± 0.77	0.33 ± 0.04*	-0.08 ± 0.73	19.89 ± 2.85**	7.78 ± 2.34*
E	0.33 ± 0.19	0.12 ± 0.01 **	0.17 ± 0.18	5.92 ± 2.24	1.74 ± 0.58
Derived Values	**Peducnle length**	**Spike length**	**Spikelets per spike**	**Grain per spike**	**Grain Yield/ Plant**
(H/D)O.5	0.80	-0.23	0.72	0.91	3.11
$H_2/4H_1$	0.23	0.16	0.20	0.13	0.22
(4DHl)o.5 +F)/(4DHl)o5_F)	1.54	0.76	1.50	1.91	0.72
h_2/H_2	0.68	-8.30	-0.07	6.23	0.41

* = P<0.05, ** = P<O.01

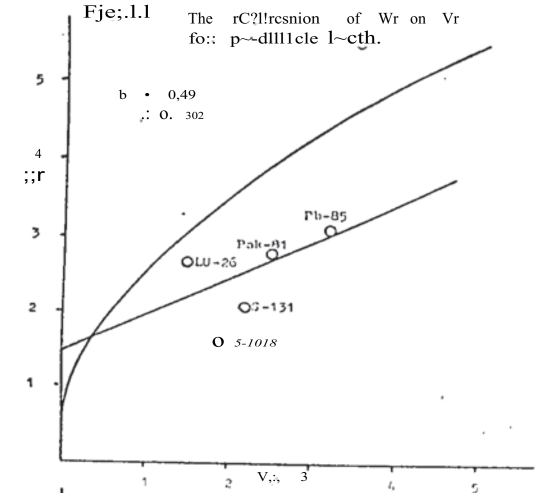

Fig. 1.1 The regression of Wr on Vr for peduncle length.

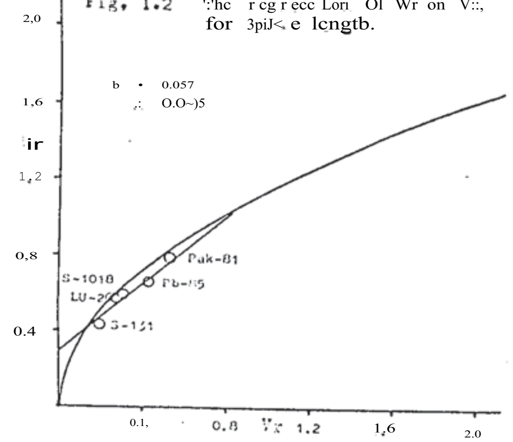

Fig. 1.2 The regression of Wr on Vr for spike length.

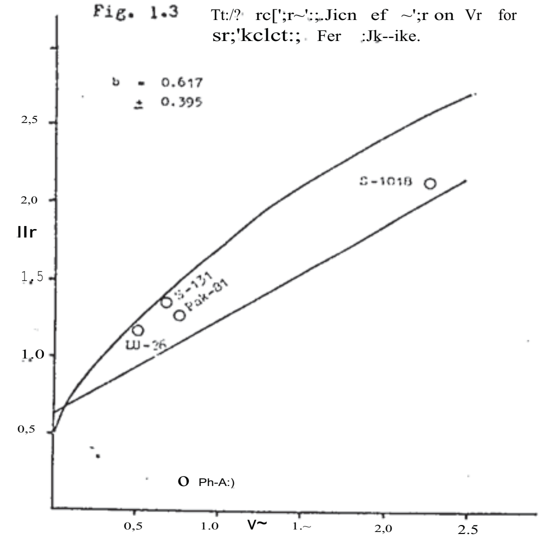

Fig. 1.3 The regression of Wr on Vr for spikelets per spike.

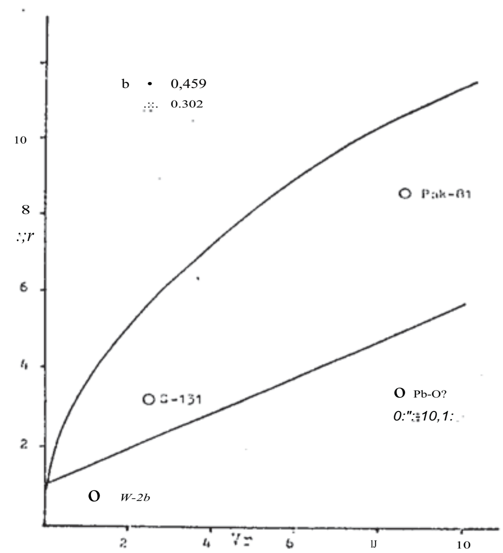

Fig. 1.4 The regression of Wr on Vr for number of grains per spike.

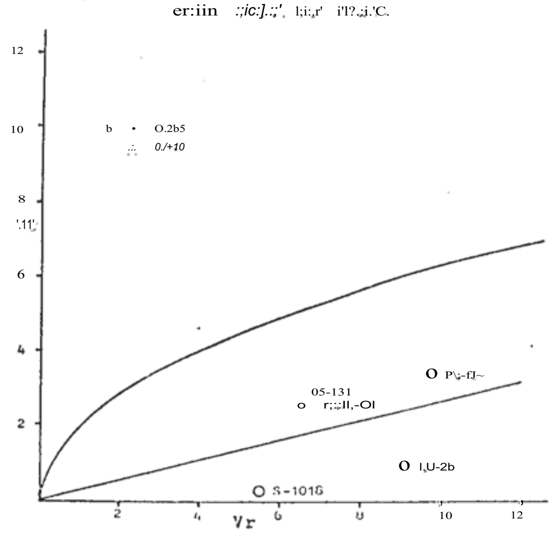

Fig. 1.5 The regression of Wr on Vr for grain yield per plant.

while Pb. 85 possessed relatively few dominant genes as it was away from origin.

Component Analysis:

The variance due to additive component (D) was higher than dominance component (HI and H_2) for all traits except grain yield per plant indicating pre ponderance of additive gene effects for yield components. the value for dominant component of variance (H 1 and H2) which implies proportion of dominance variance due to positive and negative gene effects was significant for grain yield per plant (Table 2).

The positive values of F (mean of variance of additive and dominance effects) for all traits except grain yield per plant indicated that there were more dominant than recessive alleles regardless of positive or negative direction. The mean degree of dominance (HI/D)o.s was partial for peduncle length, spike lets per spike and grains per spike while over-dominant for grain yield per plant. The degree of dominance revealed by graphic analysis is similar in all other traits except grain yield per plant. This situation may arise because the estimates of mean degree of dominance give an approximate value in real sense (Sharma and Ahmad, 1979).

The proportion of genes with positive and negative effects ($H_2/4H_1$) was less than 0.25 for all traits indicating that positive and negative allele frequencies were unequal in parental lines.

The proportion of dominant and recessive genes In the parents ($4DH_1$)o.S+F) / ((4DH\)o.s-F) was less than unity in spike length and grain yield per plant indicating excess of recessive alleles in the parents. These estimates were higher than unity for all other traits, suggesting high proportion of dominant alleles in the population.

In conclusion, diallel analysis hybridization programs can be outlined for improving agronomic traits. Crosses between parents viz; LU-26, Pak.81, Pb. 85 and S-131 have shown additive type of gene action for peduncle length, spikelets per spike and number of grains per spike, which suggested that careful selection of desirable traits in early segregating generations would provide fruitful results.

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