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Study of Genetic Architecture of Some Important Agronomic Traits in Durum Wheat (*Triticum durum* Desf.)

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Abstract: Gene action and components of variance analysis were made in a 6X6 diallel cross in durum wheat (*Triticum durum* Desf.). Additive gene effects were more important for all the traits. Complete dominance for yield plant⁻¹ and spike length and over dominance for tillers plant⁻¹ was observed. While plant height, spikelets spike⁻¹, grains spike⁻¹ and 1000-grain weight exhibited partial dominance. Dominant alleles were more frequent in parents for all characters except plant height and 1000-grain weight. Durum wheat genotypes, Altar 84 and Bittern "s" showed relatively higher combining ability

Key words: Wheat, genetic architecture

Introduction

A lot of genetic diversity present in durum wheat can be exploited to obtain new genotypes adaptable to different agroclimatic conditions. But, before such a, economic traits is the prime requisite of the plant breeders.

The diallel analysis technique developed by Hayman (1954) and Jinks (1954) and Jinks (1954) provides a fairly reliable mechanism to properly understand genetic system and gene action involved in the expression of important plant traits.

Chaudhry *et al.* (1975) and Khan *et al.* (1992) reported additive type of gene action with partial dominance for plant height and grains spike⁻¹. Similar results have also been reported by Khan *et al.* (1982) and Hussain *et al.* (1986) for spikelets spike⁻¹ while Alam *et al.* (1990) and Chowdhry *et al.* (1992) for 1000 grain weight.

Over dominance type of gene action was observed by Alam *et al.* (1990) and Chowdhry *et al.* (1992) for number of tillers plant⁻¹. Malik *et al.* (1986) and Wegrzyn *et al.* (1979) reported complete dominance for spike length. Regarding grain yield plant⁻¹ similar findings were reported by Khaliq *et al.* (1991) and Hussain (1978).

The prime objective of the present study was to gather information about the nature of gene action involved in the inheritance of various agronomic characters and estimation of general and specific combining ability effects. The information so derived may be effectively exploited to further streamline the durum wheat improvement programme.

Materials and Methods

A complete diallel set was made by crossing following six genetically divergent true breeding homozygous durum wheat genotypes during 2000-01.

Code No.	Percentage	Code No.	Percentage
V1	Bittern "s"	V4	USAIII/Gs"s"/Cr"s"/Cit"s"
V2	Ru "s"		/3/D-67.2
V3	Gdovz385/Gs "s"	V5	Krf
		V6	Altar 84

F₁'s including reciprocals and parents were planted in the experimental field of the Department of Plant Breeding and Genetics, University of Agriculture Faisalabad, in a triplicated randomized complete block design during crop season 2001-02. Each experimental plot consisted of a single row 205 m long with enter plant and enter row distance of 15 and 30 cm, respectively. Agronomic and plant protection treatments were kept normal for the entire experiment. At maturity, ten randomly selected guarded plants were marked from each plot and data for plant height (cm), number of fertile tillers plant⁻¹, spike length (cm), number of spikelets spike⁻¹, number of grains spike⁻¹, 1000-grain weight (g) and grain yield plant⁻¹ (g) were recorded. The plot means were used for analysis of variance (Steel and Torrie, 1980). Significant differences among genotypes were further analyzed using diallel analysis outlined by Hayman (1954) and Jinks (1954).

Results and Discussion

The results of analyses of variance (Table 1) revealed highly significant (P<0.01) genotypic differences for all the traits studied. The significance of the genotypic differences validate the genetic analysis of the data following the diallel technique.

The results presented in Table 2 exhibited the array means as well as the mean performance of crosses. The parental line V5 with maximum array means appeared to be the best combiner for number of tillers plant⁻¹ (10.5), number of

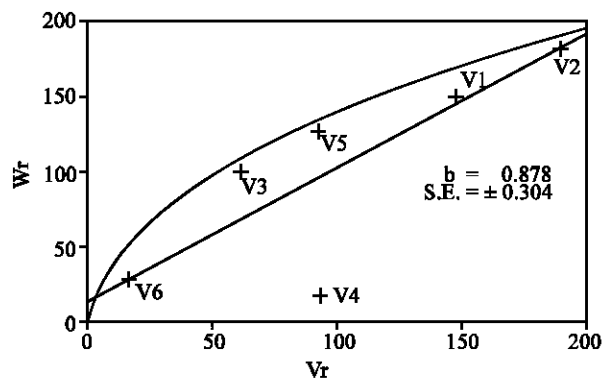


Fig. 1: Vr/Wr graph for plant height

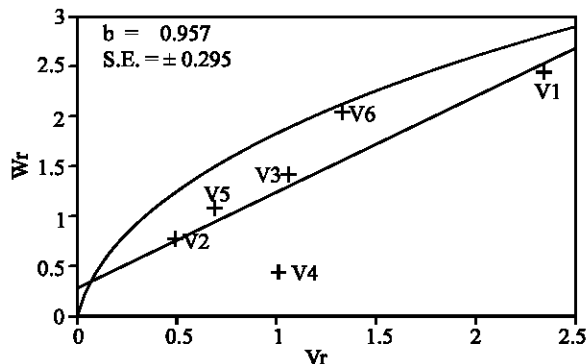


Fig. 4: Vr/Wr graph for spikelets spike⁻¹

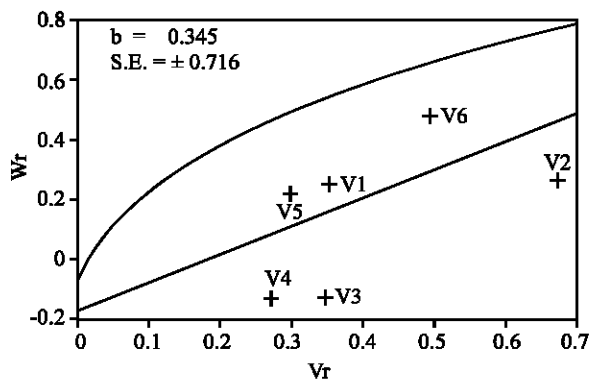


Fig. 2: Vr/Wr graph for tillers plant⁻¹

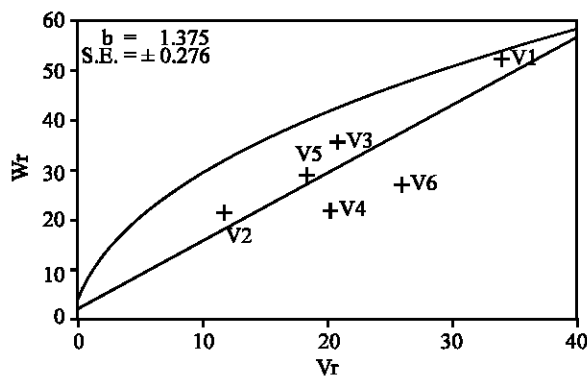


Fig. 5: Vr/Wr graph for grains spike⁻¹

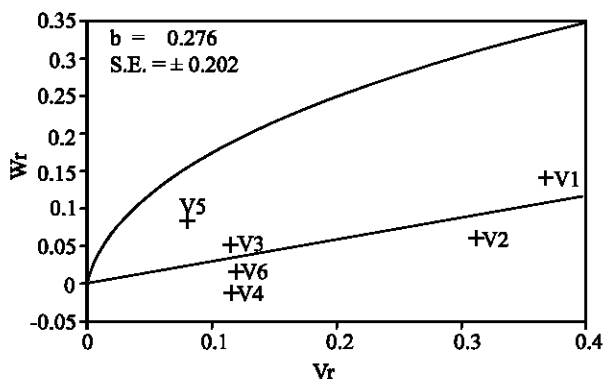


Fig. 3: Vr/Wr graph for spike length

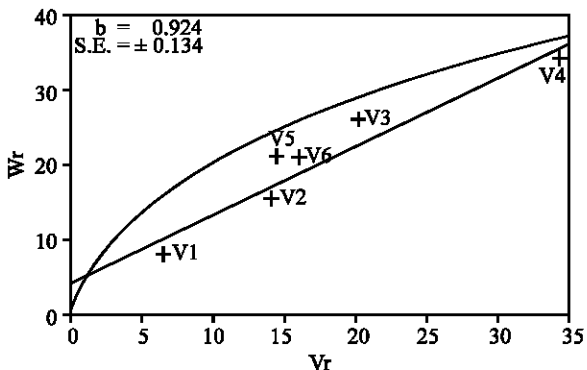


Fig. 6: Vr/Wr graph for 1000-grain weight

spikelets spike⁻¹ (22.99) and grain yield plant⁻¹ (33.22 g). Within array the cross of V3 X V4 indicated higher specific combining ability for number of tillers plant⁻¹, V4XV5 for number of spikelets spike⁻¹ and V1 X V4 for grain yield. Similarly, V1 showed better general combining ability for spike length (8.92 cm) and 1000-grain weight (56.29 g) and the cross V1XV4 and V1XV2 revealed maximum specific combining ability for spike length and 1000-grain weight, respectively.

Parental line V4 proved to be the best general combiner for plant height (118.62 cm) and V6 for number of grains spike⁻¹ (67.91). Cross of V1 with V4 appeared to be the best specific combiner for plant height and with V6 for number of grain spike⁻¹.

Plant height: The graphic representation of plant height revealed that regression line cuts the Wr-axis above the origin (Fig. 1) which is an indication of additive type of

Table 1: Analysis of variance for 6 x 6 Diallel cross

Source of Variation	df	Plant height (cm)	Tillers/plant	Spikelets/spike	Grains/spike	100-grain weight (g)	Grain yield (G)
Replications	2	3.86	0.30	0.04	0.58	1.07	5.42
Genotypes	35	441.13**	4.40**	0.71**	4.79**	79.63**	59.26**
Error	70	4.02	0.99	0.07	0.87	2.07	8.16

Table 2: Array mean performance of F1 hybrids for various characterist

Genotype/Cross	Plant height (Cm)	Tillers/Plant	Spike length (cm)	Spikelets/spikes	Grains spike	1000-grain weight (g)	Yield/Plant (g)
Array means							
V1	103.799	9.583	8.922	20.928	62.635	56.287	32.094
V2	98.985	9.757	8.345	21.617	57.015	52.693	28.343
V3	100.381	10.075	8.489	21.222	61.296	50.088	29.950
V4	118.621	10.227	8.908	22.554	62.957	48.897	30.558
V5	104.050	10.503	8.738	22.986	60.931	50.661	33.217
V6	97.905	10.085	8.654	21.645	67.912	46.496	31.979
Mean performance							
V1 X V2	98.67	8.77	9.16	21.33	58.44	59.36	28.92
V1 X V3	102.60	9.33	8.88	20.57	65.44	57.78	32.99
V1 X V4	125.54	9.77	9.51	22.20	66.96	56.35	35.68
V1 X V5	103.11	9.71	9.04	22.22	58.96	56.85	33.85
V1 X V6	102.66	9.45	9.20	21.20	68.23	51.78	31.51
V2 X V3	94.44	10.21	8.29	21.40	57.60	51.48	29.55
V2 X V4	125.19	10.69	8.53	22.47	58.12	53.79	30.72
V2 X V5	96.17	10.49	8.22	22.30	53.30	52.52	28.90
V2 X V6	93.99	9.42	8.40	21.50	61.56	49.04	29.48
V3 X V4	113.22	10.93	8.88	22.05	63.05	47.84	32.67
V3 X V5	103.22	10.46	8.60	22.77	61.97	51.43	31.39
V3 X V6	96.99	9.79	8.28	20.32	64.60	46.49	31.46
V4 X V5	122.50	10.38	8.97	24.19	62.27	49.27	33.17
V4 X V6	101.62	10.03	9.01	23.02	67.87	46.56	32.37
V5 X V6	99.11	10.72	8.64	22.78	66.52	45.48	31.94

Table 3: Estimation of genetic components of variance for different characters

Components	Plant height	Tillers plant ⁻¹	Spike length	Spikelets spikes ⁻¹	Grains spike ⁻¹	1000-grain weight	Grain yield plant ⁻¹
D	186.72±28.04**	0.51±0.19	0.28±0.07*	3.01±0.31**	78.25±4.31**	38.27±2.00**	65.30±4.97**
H	175.90±71.81	1.02±0.48	0.78±0.18*	1.66±0.79	29.72±10.95	28.60±5.08	71.06±12.61**
H	150.50±63.59	0.47±0.43	0.52±0.16*	1.27±0.70	13.91±9.78	24.80±4.54	39.68±11.26*
F	-18.80±68.50	0.74±0.46	0.34±0.18	0.97±0.76	46.49±10.54*	-2.78±4.89	85.50±12.13**
h	173.48±42.80**	-0.10±0.29	0.95±0.11	3.69±0.47**	-0.78±6.58	77.02±3.06**	40.30±7.58**
(H ₁ /D) ^{1/2}	0.971	1.407	1.676	0.741	0.616	0.865	1.043
(H ₂ /4H ₁)	0.214	0.114	0.166	0.191	0.117	0.217	0.140
((4DH ₁) ^{1/2} +F)/((4DH ₁) ^{1/2} -f)	0.901	3.097	2.148	0.552	2.861	0.919	4.369
h ² /H ₂	1.153	-0.216	1.821	2.911	-0.056	3.105	1.015
H ₁ -H ₂	25.407	0.551	0.264	0.389	15.811	3.801	2.113
Heritability	0.748	0.270	0.397	0.668	0.0680	0.765	0.307

gene action with partial dominance. Almost similar findings have earlier been reported by Chaudhry *et al.* (1975), Hussain *et al.* (1986), Khaliq *et al.* (1991), Chowdhry *et al.* (1992) and Khan *et al.* (1992). Linear regression coefficient (b) did not deviate significantly from unity depicting the absence of interaction of complementary genes.

V6 appeared to contain the most dominant genes for plant height due to its close proximity to the point of origin, where as, maximum number of recessive genes were found in V2. The gene action observed in this study obviously points the possibility of obtaining transgression in segregating population. Suitable height levels can, therefore, be easily fixed.

Number of fertile tillers plant⁻¹: The study revealed that regression line intercepts the Wr-axis on the negative side of the origin and thus indicated over dominance type of gene action (Fig. 2). These result are in confirmation with the earlier findings of Alam *et al.* (1990) and Chowdhry *et al.* (1992). Regression line is of unit slope which signify the absence of genetic interaction in the manifestation of the trait. Array Points distribution of the regression line pointed out that V5 genotype owing to its closeness to origin possessed maximum dominant genes while V2 being away from origin had lowest number of dominant genes. Due to over dominance, the character seems difficult to fix and the progress in selection will be inherently slow.

Spike length: The genetic control of spike length appeared to be conditioned by complete dominance as the regression line passed through the origin (Fig. 3). Whereas, the regression line departs significantly from a unit slope and thus revealed that a component of epistasis was involved in the inheritance of this trait. These results are in agreement with those reported by Wegrzyn *et al.* (1979) and Malik *et al.* (1986). Genotype V5 being closest to the point of origin had excess number of dominant genes and in contrast V1 carried the maximum number of recessive genes for spike length. Fixation of this character would be difficult due to the presence of non-allelic interactions.

Number of spikelets spike⁻¹: The regression line pointed additive gene action with partial dominance and no non-allelic interaction as intercepting the W_r -axis above the origin having unit slope (Fig. 4) has also reported by Hussain *et al.* (1986) and Khan *et al.* (1982). The distribution of varietal points on the regression line demonstrated that V2 possessed mostly dominant genes while V1 had preponderance of recessive alleles. The type of gene action obviously indicated that this trait could be easily improved as there was possibility of getting transgressive segregates allowing selection of genotypes with more number of spikelets spike⁻¹.

Number of grains spike⁻¹: The regression line V_r cut the W_r -axis above the origin and did not deviate significantly from unit (Fig. 5) suggesting additive type of gene action with partial dominance and no other genic interaction. These results are in accordance with those of Chaudhry *et al.* (1975), Khan *et al.* (1982) and Khan *et al.* (1992). V2 depicted higher number of dominant genes as it was closest to the origin while V1 and relatively lesser dominant genes. It is evident from gene action that fairly good progress is selection for higher number of grains spike⁻¹ can be expected.

1000-grain weight: From V_r/W_r graph (Fig. 6), it is evident that regression line intercepted W_r -axis above the origin which suggested additive type of gene action with partial dominance as earlier reported by Chaudhry *et al.* (1975), Khan *et al.* (1982), Alam *et al.* (1990); Khaliq *et al.* (1991) and Chowdhry *et al.* (1992). The regression line in this case was of unit slope indicating the absence of non-allelic interactions. Genotypes V1 was near the origin so it has most of the dominant genes while recessive alleles determined grain weight for V4. In view of the results, selections for higher grain weight can be made effectively by the use of parental line V1.

Grain yield plant⁻¹: The genetic control of grain yield plant⁻¹ appeared to be conditioned by complete dominance as regression line passed through the origin (Fig. 7). Regression line did not deviate significantly from unit slope, which indicated the absence of epistasis. The results are in conformity with those obtained by Hussain (1978) and Khaliq *et al.* (1991). In the V_r/W_r graph it is appeared that V6 had mostly dominant genes, while V4 being away from origin carried recessive genes. It was concluded that yield was conditioned mostly by genes having complete dominance. Absence of genic interactions would permit the use of simple selection techniques for the improvement of grain yield plant⁻¹.

Component analysis: The additive components of variance (D) were significant for all the character, except number of tillers plant⁻¹ while the dominance

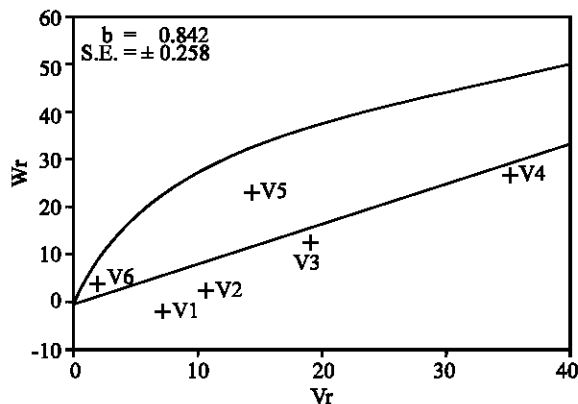


Fig. 7: V_r/W_r graph for Grain yield plant⁻¹

components of variance (H_1) were significant for spike length, 1000-grain weight and grain yield plant⁻¹ (Table 3). The variance due to D was higher than H_1 for plant height, spikelets spike⁻¹, grains spike⁻¹ and 1000-grain weight indicating preponderance of additive gene effects for these traits. Consequently in view of this and higher heritability values, selection could be operated with fair degree of success for these traits. Almost similar results were earlier been reported by Khan *et al.* (1982).

The values for dominance components of variance (H_2) which measures proportion of dominance variance due to positive and negative gene effect were highly significant for spike length, 1000-grain weight and grain yield. The estimates of F were only significant for number of grains spike⁻¹ and grain yield (Table 3). The negative value in case of plant height and 1000-grain weight suggested excess of recessive alleles. While in other traits positive F value revealed excess of dominant alleles.

The mean degree of dominance (H_i/D)^{1/2} was partial for plant height, spikelets spike⁻¹, grain spike⁻¹ and 1000-grain weight and over for number of tillers plant⁻¹ and spike length while complete for grain yield (Table 3).

The degree of dominance revealed by graphic analyses is similar except in case of spike length. This consistency may arise due to the fact that the estimates obtained through the formula (H_i/D)^{1/2} at the best give an approximate value of the degree of dominance in real sense (Sharma and Gupta, 1979).

The ratio H₂/4H₁ was less than 0.25 for all traits indicating unequal frequencies of positive and negative alleles in parental lines (Table 3). H₁-H₂ were far from zero, thus supported the asymmetry of positive and negative genes in parents.

The proportion of dominant and recessive alleles in the parents ($(4DH_1)^{1/2} + F / (4DH_1)^{1/2} - F$) was less than unit for plant height and 1000-grain weight reflecting the presence of excess of recessive alleles in the parents, while for all other traits parents have excess of dominant alleles.

Heritability estimates were high for 1000-grain weight (0.77), plant height (0.75), grains spike⁻¹ (0.68) and spikelets spike⁻¹ (0.67). Grain yield and tillers plant⁻¹ exhibited low heritability. Low to medium heritability for yield and high for yield components had been reported by Fonseca and Patterson (1969) and Khan *et al.* (1982).

In the light of available information from diallel analysis about genetic make up and presence of allelomorphs in different parents, successful hybridization programme may be outlined for the improvement of yield components. Crosses between these parents have shown additive type of gene action for most of the traits, which suggested that useful selection of desirable traits in early segregating generations would provide fruitful results. However, in view of over dominance for tillers plant⁻¹, selection would be difficult in early segregating generations as character is not easily fixable.

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