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Genetic Studies for Yield and Yield Related Traits in Wheat under Leaf Rust Attack

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ABSTRACT

Present study was conducted to find gene action under artificial leaf rust attack among 56 F_1 diallel crosses in all possible combinations along with eight parental wheat varieties. Data were recorded for grain yield per plant, tillers per plant, number of grains per spike, 100-grain weight, number of spikelets per spike, spike length, and peduncle length. Highly significant additive and dominance effects with directional dominance effects, asymmetrical gene distribution and important role of specific genes were found for all the traits. Maternal and reciprocal effects were non-significant for all traits except for grains per spike. Analysis for genetic components indicated that additive (d) and dominant (h) were significant for all the traits. However, un-equal distribution of dominant alleles was present in the traits except spikelets per spike. The genetic information obtained would be utilized in wheat breeding program for the development of leaf rust resistant wheat varieties with higher yield potential.

Key Words: Wheat crosses; Gene action; Yield; Leaf rust

INTRODUCTION

Yield of wheat is a complex of traits and is influenced by many biotic and abiotic factors. Among the diseases, leaf rust is a major cause of yield loss in wheat. Grain yield losses vary with the season and cultivated wheat variety as reported 10% yield losses due to leaf rust during 1978 in Pakistan (Hasan, 1979). It may also cause complete loss of the crop, although such extreme damage is rare (Reitz, 1954). The use of disease resistant varieties is the only way to control leaf rust. To undertake such a breeding program, it is imperative to get the information on genetic mechanism for yield and other traits under leaf rust conditions. On this aspect findings were made from 6 × 6 diallel set of wheat that leaf rust resistance appeared to be predominantly controlled by non-additive effects (Khan *et al*., 1994). Polygenic inheritance for leaf rust reaction (Khan *et al*., 1984) and over-dominance and additive types of gene action for grain yield per plant and for yield components Whitehouse *et al.* (1958) for wheat is also advocated. On the other hand, different types of gene action were reported by several researchers that tillers and grain yield were controlled by over-dominance types of gene action and partial dominance for plant height, complete dominance for 100-grain weight and over dominance for tiller number and number of grains (Alam *et al.*, 1990).

Breeding for yield and components is a continuous process and genetic studies were made that dominant genes act in the direction of increasing tiller number and grain weight per plant, plant height conditioned by additive gene action and productive tillering, grain number by dominant gene action and number of grains per ear increased by dominant genes (Lonc & Zalewski, 1991 & 1993). Over-dominance was emphasized for yield and other traits (Prodanovic, 1993; Chowdhry *et al.*, 2002). An important type of gene action, i.e., additive, was found (Petrovic & Cermin, 1994), while Shekhawat *et al.* (2000) studied non-additive type of gene action for grain yield and yield related traits. Partial dominance with additive gene action was also reported (Khan *et al*., 2000). However, genetic control was ascertained for different traits in wheat under leaf rust conditions using complete analysis (Hussain *et al*., 2004).

The objectives of the present investigations were to elucidate the nature of gene action involved for the manifestation of the different traits in wheat under leaf rust conditions. The diallel analysis (Hayman, 1954a & b; Jinks, 1954) provides a handy technique to study the nature of gene action involved in complex genetic characters of economic value. Diallel analysis was thus applied to find out the pattern of gene action for yield and other related traits. The genetic information obtained would be utilized in wheat breeding program for the evolution of new wheat varieties of high yield potential with leaf rust resistance.

MATERIALS AND METHODS

Eight genetically diverse bread wheat cultivars were crossed in all possible combinations (including reciprocals)

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during February-March 2003 at the Wheat Research Institute Faisalabad. The brief description of wheat varieties is given in Table I. F_0 crosses along with the parents were planted in the field during the year 2003-04 using a randomized complete block design with three replications. Seed from each of the crosses/genotypes was planted in a single row (3 m long) in each replication. The row to row and plant to plant spacing were kept 30 and 15 cm, respectively. Leaf rust susceptible variety, Morocco, was planted on borders as leaf rust spreader. The experiment was inoculated with mixture of leaf rust strains on the appearance of culm elongation. Plants received recommended inputs and normal agronomic practices. The data were recorded from ten randomly selected plants from each plot for fertile tillers per plant, grains per spike, spikelets per spike, spike length, peduncle length, 100-grain weight and grain yield. The data were subjected to analysis of variance according to (Steel & Torrie, 1980). Where the means were significant, the data were further subjected to diallel analysis technique (Hayman, 1954a & b; Jinks, 1954) and used by Whitehouse *et al.* (1958) for complete analysis and genetic components of gene action. The genetic components of variation were calculated using the procedures given by Hayman (1954b) and Mather and Jinks (1982).

RESULTS

Analysis of variance showed highly significant differences among genotypes for all plant traits indicating presence of adequate genetic variability (Table II). The number of fertile tillers per plant revealed highly significant differences for all components showing greater amount of additive (a) variation with dominant effect (b). Presence of directional dominance effects (b_1), asymmetrical distribution of genes (b_2) and important role of specific genes were observed for producing fertile tillers per plant. Retesting of a and b was not required due to non-significant maternal and reciprocal effects. Genetic variation, additive (D) and dominance (H) were significant (Table IV). Different values of H_1 and H_2 and ratio of $H_2/4H_1$ (0.19) exhibited un-equal distribution of dominant and recessive genes among parents.

Negative and significant value of component F showed that more recessive genes were predominated, which was supported from more recessive genes among the parents, obtained from the value of ratio of dominant and recessive genes (0.44). However, over all predominance of dominant genes effects of heterozygous was observed for this trait. Environmental variance was non-significant. Degree of dominance (2.45) showed the over-dominant type of gene action. Higher value of broad sense heritability (99%) compared to narrow sense heritability (64%) revealed a role of dominant and additive genes for producing more productive tillers.

The analysis of variance for number of grains per spike indicated that both additive (a) and dominant (b) effects were highly significant (Table III). Directional dominance deviations of the genes (b_1) were also significant. Gene distribution among parents was asymmetrical. Highly significant effects of specific genes (b_3) revealed for grains number. Highly significant maternal effects (c) and reciprocal effects (d) were present. The items a and b were retested against c and d mean squares. After retesting, significance of a remained unchanged suggesting that additive effects were not influenced due to any maternal effects. Similarly significance of item b remained un-changed, which indicated that reciprocal differences did not affect the directional dominance, dominant gene distribution and effects of specific genes.

Genetic components, both additive and dominance significantly predominated for grain number indicated un-equal values of H_1 and H_2 with confirmation of $H_2/4H_1$ value (0.21), which suggested dissimilar genes distribution among parents (Table IV). Similarly, F was significantly positive representing greater frequency of dominant genes. More frequent dominant genes were also obtained from ratio of dominant to recessive genes (1.94). Significant dominance effect due to heterozygous loci (h^2) was also measured for this trait. Environmental variance influence was not significant. Greater than one value of degree of dominance revealed over dominance type of gene action. Highest broad sense heritability (99%) and lowest narrow sense heritability (0.29) suggested that greater portion of dominance gene action in the total variation of genetic inheritance.

Highly significant both additive (d) and dominance (b) effects indicated that directional dominant effect played no evident role, while symmetrical gene distribution (b2) and

Table I. Parentage of wheat varieties used in the experiments

Variety	Parentage
SA 42	(C271/LR64//SON64)
LU 26	(BLS/KHUSHAL69)
MH 97	(Attila) =ND/VG9144/KAL/BB/3/ YACO/4/VEE#5
Nacozari F 76	(BLUE JAY'S')
Chenab70	(C271-WT(E) XSON64)
Crow	(FR1316/3/MCM/KT//Y50/4/ ZA75/5/BJY'S')
Parula	(FRN/3/2*FR//KAD/GB/4/BB/CHA)
Inqilab91	(WL711/CROW'S')

Table II. Analysis of variance for the characters studied in 8x8 diallel cross of wheat

	MEANS SQUARES		
Traits	**Replications (df=2)**	**Genotypes (df=63)**	**Error (df=126)**
Tillers per plant	0.06	12.11**	0.04
Grains per spike	0.01	54.95**	0.04
Spikelets per spike	1.14	1.38**	0.34
Spike length	0.63	4.29**	0.17
Peduncle length	0.89	16.35**	0.49
100-grain weight	0.001	1.24**	0.03
Grain yield per plant	0.41	62.23**	0.47

** $P \geq 0.01$

Table III. Means squares values for complete analysis of variance of 8 x 8 diallel cross for various traits

Item	DF	Tillers plant^{-1}	Grains spike^{-1}	Spikelets spike^{-1}	Spike length (cm)	Peduncle length (cm)	100-grain weight (g)	Grain yield (g plant^{-1})
a	7	70.32**	139.28**	7.78**	12.56**	109.7**	4.61**	259.13**
b	28	9.61**	83.03**	1.12**	6.51**	8.37**	1.63**	75.19**
b1	1	49.95**	849.31**	0.01**	36.54**	9.84**	10.87**	907.27**
b2	7	7.41**	39.79**	0.17**	2.55**	3.62**	0.63**	27.76**
b3	20	8.37**	59.85**	1.50**	6.39**	9.96**	1.51**	50.19**
c	7	0.05	5.32**	0.02	0.02	1.07	0.003	0.05
d	21	0.06	2.93**	0.04	0.01	0.96	0.002	0.04
Blocks	2	0.06	0.01	1.14	0.63	0.89	0.001	0.41
b x a	14	0.09	0.04	0.35	0.30	0.32	0.02	0.28
b x b	56	0.05	0.03	0.36	0.28	0.59	0.03	0.31
bxb1	2	0.02	0.02	0.18	0.24	0.04	0.01	0.82
bx b2	14	0.07	0.03	0.45	0.53	0.86	0.03	0.19
bx b3	40	0.04	0.03	0.34	0.20	0.52	0.03	0.32
b x c	14	0.301	0.06	0.32	0.03	0.33	0.03	0.76
bx d	42	0.03	0.05	0.30	0.03	0.47	0.02	0.66
Block interaction	126	0.04	0.04	0.34	0.17	0.49	0.03	0.47
Retesting against	c	-	26.19**	-	-	-	-	-
	d b	-	290.86**	-	-	-	-	-
	b1		13.63**	-	-	-	-	-
	b2		20.50**	-	-	-	-	-
	b3		28.36**	-	-	-	-	-

**= P>0.01

a=Additive effects, b= General dominance effects, b1= Directional dominance effects, b2 = Effects due to unequal distribution of dominance, b3 = Effects due to dominance deviation unique to F_1's, c = Maternal effects, d = Non-maternal reciprocal effects

Table IV. Estimates of genetic components variations of various traits

Components	Tillers plant^{-1}	Grains spike^{-1}	Spikelets spike^{-1}	Spike length (cm)	Peduncle length (cm)	100-grain weight (g)	Grain yield (g plant^{-1})
D	1.37* ± 0.43	30.11* ± 4.68	0.63* ± 0.12	0.98* ± 0.36	8.19* ± 0.58	0.44* ± 0.08	8.87* ± 3.11
H_1	8.23 ± 0.99	65.28* ± 10.75	0.55* ± 0.28	4.85* ± 0.83	6.14* ± 1.33	1.22* ± 0.18	56.75* ± 7.14
H_2	6.37* ± 0.86	55.33* ± 9.35	0.57* ± 0.24	4.25* ± 0.72	5.33* ± 1.16	1.07* ± 0.16	49.89* ± 6.21
F	-2.64* ± 1.01	28.45* ± 11.05	-0.02* ± 0.0029	0.55 ± 0.85	-0.11* ± 0.014	0.20 ± 0.19	-5.84* ± 0.734
h^2	7.28* ± 0.58	123.85* ± 6.27	-0.04* ± 0.016	5.31* ± 0.48	1.38 ± 0.77	1.58* ± 0.11	132.26* ± 4.17
E	0.01 ± 0.015	0.01 ± 0.015	0.09* ± 0.004	0.04* ±0.012	0.12* ± 0.02	0.01* ± 0.003	0.12* ± 0.0106
$(H1/D)^{1/2}$	2.45	1.47	0.93	2.22	0.87	1.67	2.53
$H_1/4H_1$	0.19	0.21	0.26	0.22	0.22	0.22	0.22
$(4D H_1)^{1/2} + F / (4DH_1)^{1/2} - F$	0.44	1.94	0.96	1.29	0.98	1.33	0.77
Heritability (ns)	0.64	0.29	0.58	0.32	0.76	0.41	0.46
Heritability (bs)	0.99	0.99	0.84	0.97	0.97	0.98	0.99

* = value is significant when it exceed 1.96 after divided by its standard error

D=Additive variation, H_1=Variation due to dominant effect of genes, H_2= Variation due to dominant effect of genes correlated for gene distribution, F=Relative frequency of dominant and recessive alleles, h^2 = over all dominance effect of heterozygous loci, E = Environmental variance, (, $H_1/D)^{1/2}$= Average degree of dominance, , $H_1/4H_1$ =Proportion of genes with positive and negative effects in the parents, $(4D H_1)^{1/2} + F / (4DH_1)^{1/2} - F$ =Proportion

specific gene controlling effects were observed for this trait (Table III). No maternal and reciprocal effects were present. Both additive and dominance components were of significant effects. Equal values of H_1 and H_2 with trend of $H_2/4H_1$ (0.26) indicated similar distribution of positive and negative genes (Table III). Component F was negative but non-significant and ratio of dominance to recessive genes to near to one. Negative and non-significant value of h^2 component but environmental variance was significant, which influenced the manifestation of this trait. Degree of dominance was less than unity showing partial dominance. Higher broad sense heritability (0.84) showed more dominant gene predominated for producing spikelets per spike. Additive (a), dominance (b), directional dominance effects (b_1), un-equal distribution of dominance effects (b_2) and role of specific genes (b_3) were highly significant for spike length, while maternal and reciprocal effects were non-significant (Table III).

It was observed that additive and dominance effects were significant, which indicated both type of additive and dominance gene action for spike length. Similar values of H_1 and H_2 but low ratio of $H_2/4H_1$ (0.22) showed somewhat similar distribution of positive and negative genes among parents. The mean degree of dominance with a higher value of 2.22 indicated over dominant type of gene action. Non-significant positive value of F but high ratio (1.29) of dominance and recessive genes were computed, which showed more frequency of dominant genes among parents for this trait, This was also evident from high broad sense heritability (97%) for the spike length. Significant

directional dominance deviations genes (b_1) and specific genes effects were observed with symmetrical gene distribution for this trait. Maternal and reciprocal effects were absent.

Genetic components analysis indicated that both additive and dominance variation were significant (Table IV). Values of H_1 and H_2 were somewhat different and low value of $H_2/4H_1$ ratio (0.21) was confirmed from generally equal distribution of positive value of F. This showed that positive and negative genes were at par. Similar trend was obtained from the ratio dominance and recessive (0.98). Non-significant h^2 was obtained for this trait. Higher broad sense heritability (97%) and moderate narrow sense heritability (76%) indicated more dominant genes with additive effect for increase of peduncle length which was confirmed by low value (0.84) of degree of dominance. Overall, dominant effect due to heterozygous loci was also minutely.

The analysis for 100-grain weight displayed highly significant additive (a) and dominant effects (b). Directional dominance deviations of the genes (b_1) were also found highly significant (Table III). Unequal genes distribution (b_2) and important role of specific genes (b_3) were observed among parents for grain weight accumulation. No maternal and reciprocal effects were found for this trait. As regards components of genetic variation expressed significant dominance (H) and additive (D) gene effects for 100-grain weight (Table IV). Values of H_1 and H_2 were somewhat similar and ratio of $H_2/4H_1$ (0.22) also showed equal distribution of positive and negative genes. Non-significant positive value of F and higher value of proportion for dominant and recessive genes revealed more dominant genes to be predominated for greater grain weight that was supported by higher value of h^2, which indicated the over all prevalence of dominant genes for this trait. Similarly, higher broad sense heritability exhibited more dominant genes involved for this trait. The high value (1.33) for the ratio of degree of dominance represented over dominance type of gene action.

Analysis of variance for grain yield indicated the presence of both additive and dominant gene effects (Table III). Directional dominance effect (b_1) and asymmetry of genes distribution (b_2) among parents were highly significant. The involvement of specific gene effects and no maternal and reciprocal effects were observed for grain yield. Genetic components of variation for grain yield displayed both additive (D) and dominance (H) components (Table IV). However, values of H_1 and H_2 were different with low value of $H_2/4H_1$ (0.22) indicated the dissimilar distribution of positive and negative gene. Negative but non-significant F with ratio of dominant and recessive genes (0.77) indicated the greater frequency of recessive genes. Overall dominant genes effect due to heterozygous loci was prominent. Higher degree of dominance (2.53) indicated over dominance type of gene action. High broad sense heritability (99%) and moderate narrow sense heritability (46%) showed greater dominant genes with additive genes from total genetic inheritance of variation for higher grain yield.

DISCUSSION

Highly significant additive and dominant affects with directional dominance effects, asymmetrical gene distribution and important role of specific genes were found for all the traits. Maternal and reciprocal effects were non-significant for all traits except for grains per spike. It means that materials were genetically diverging and can be exploited as a source for the purpose.

Significant differences for genetic components; additive and dominant for all the traits indicated efficient creation of genetic variability. However, un-equal distribution of dominant alleles was observed in all traits except spikelets per spike. Partial dominance type of gene action was predominated for the traits; spikelets per spike and peduncle length, while tillers, grains per spike, spike length, grain weight and grain yield controlled by over dominance type of gene action revealed potential of genotypes for the manifestation of these traits.

As ascertained the nature of gene action by Fida (2003) under normal and leaf rust conditions that tillers per plant, 1000-grain weight and grain yield per plant genetically controlled by additive genes with partial dominance. However, number of grains per spike was complicated with complete dominance and additive type of gene action under normal and leaf rust environments, respectively. Higher broad sense heritability and low narrow sense heritability, which showed generally greater dominant genes with additive additive from total genetic inheritance of variation for all traits. Hence, selection criteria would be fruitful in early generation for these traits. Gene action was also reported for yield and yield related traits in wheat (Khan *et al*., 1984; Alam *et al*., 1990; Lonc & Zalewski, 1991; Khan *et al*., 1994; Khan *et al*., 2000; Chowdhry *et al.*, 2002; Hussain *et al.*, 2004). Thus this genetic umbrella of different traits would be proceeded further in order to achieve high yield potential with leaf rust resistant.

CONCLUSION

The genetic information obtained in this study can be utilized for the development of successful wheat breeding program. Results indicated that dominance gene effects were mostly involved for all the traits, while genetic components analysis showed partial dominance with additive and over-dominance types of gene actions. Hence, selection of desirable single plant from segregating generation may be fruitful for the traits under leaf rust conditions in wheat breeding program.

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