Full Length Article

Genetic Effects for Grain Yield and its Related Traits in Doubled Haploid Lines of Wheat

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ABSTRACT

The inheritance of grain yield and its components (number of spikelets per spike, number of tillers, number of grains per spike, plant height) has been studied through a full diallel cross of eight doubled haploids in bread wheat from CIMMYT, Mexico. Regression analysis, average degree of dominance and estimates of narrow sense heritability revealed additive type of gene action for number of grains per spike and plant height and over dominant type of gene effects for number of spikelets per spike, number of tillers. Correlation analysis of dominant genes with the phenotype of the parents revealed recessive gene control for number of tillers, while dominant gene control appeared to account for rest of the traits studied. © 2010 Friends Science Publishers

Key Words: Doubled haploid wheat; Gene effects; Yield components; Diallel

INTRODUCTION

The development of improved varieties of wheat (*Triticum aestivum* L.) has always remained a focal point for wheat breeders all over the world (Edwards, 2001). Yield is a polygenic trait and is greatly influenced by the environmental changes.

Any increment in yield and its related characteristics like plant height, number of spikelets per spike, number of grain per spike and number of tillers through selection and breeding helps to improve unit area production. Several studies in the recent past have identified QTLs for yield and its components in wheat. Gupta *et al.* (2007) reported three QTLs on chromosomes 3A, 7A and 7B for number of tillers in cross PH132 × WL711 (bread wheat). They also reported four QTLs on chromosomes 2A, 4B and 7A for number of grain per spike and three QTLs on chromosomes 2B, 4A and 6A for number of spikelets per spike. Maccaferri *et al.* (2008) have identified 3 QTLs on chromosomes 1B, 3A and 7A for plant height. Also Kuchel *et al.* (2007) reported several QTLs on chromosomes 1B, 4D and 7D for grain yield in bread wheat. But bread wheat genome is very large and consists of three set of chromosomes. Thus in most cases QTLs analysis especially for complex traits such as yield and its components would be not efficient. These analyses are mostly useful for the study of resistance to pathogens for this crop.

The choice of selection and breeding procedures for genetic improvement of wheat or any other crop largely depends on the knowledge of type and relative amount of genetic component and the presence of non-allelic interaction for different characters in the plant materials under experimentation. Diallel crossing has been used most commonly to estimate inheritance and behavior of quantitative characters. Application of Hayman (1954) and Jinks (1954) models in F_1 generation provides information regarding nature and magnitude of the gene-action involved in the inheritance of a character. This information is useful to plant breeders for two reasons viz. types of genetic variation in the traits for which selection is intended and rapid evaluation of yielding capacity by identifying crosses, which will produce superior genotypes.

In the present study, the inheritance of yield and its components has been studied through diallel cross to choose an efficient breeding method for the improvement of grain yield and its components.

MATERIALS AND METHODS

The parental material was composed of eight doubled haploid lines of wheat from CIMMYT (Table I). The crosses were attempted in a diallel fashion including direct crosses and their reciprocals during crop season 2006-2007. The parents and F_{1s} were sown in November, 2007 in a randomized complete block design with three replications in Moghan region, Iran. At maturity, 10 competitive plants were randomly selected to record data for number of spikelets per spike, number of tillers, number of grains per spike, plant height and grain yield per plant. The data were subjected to graphical and component analyses (analysis of

genetic variance component such as D, H_1, H^2, that results showed in Table II) according to Jinks and Hayman (1953) and Hayman (1954 & 1957). Analysis of parental measurement (Yr) and Wr+Vr values (the standard deviation graph) was done following Johnson and Askel (1959).

The t^2 test and the analysis of regression co-efficient test, which tests to overall assumption of diallel was performed according of the model with respect to non-allelic interaction.

RESULTS AND DISCUSSION

The analysis of variance of means (parents & F_1 families) revealed highly significant differences for all of the traits under study (data not shown). The estimates of genetics of variation in grain yield and its component are given in Table II. Although D, H_1 and H_2 items were positive and signification for number of spikelets per spike,

number of tillers and grain yield per plant, the greater magnitude of H_1 and H_2 than that of D revealed that genes with non-additive effects were more important. The Wr/Vr graphs showed that regression line intercepts the Wr-axis below the point of origin for these traits (Fig. 1, 2 & 3) and the ratio of $(H_1/D)^{1/2}$ was greater than unity. These results indicated that number of spikelets per spike, number of tillers and grain yield per plant were affected by over dominance.

Narrow sense heritability for number of tillers (0.154) and grain yield per plant (0.084) was very low, while for number of spikelets per spike almost was medium enough (Table II). Straight forward selection from the segregation population of the characters does not seem possible and the genetic variation existed in these characters may be improved successfully following reciprocal recurrent selection. Furthermore, the characteristics in which over dominance was involved may advantageously to be utilized by the breeders to develop hybrids, as suggested by

Table I: Pedigree of parents

1-TEG/GANFRENCH/6/CMH79A.955/4/AGA/3/4*SN64/CN067//INIA66/5/NAC
2-CMH80.638/CMH75A.411//CMH80.638/3/ELVIRA/6/CMH79A.955/4/AGA/3/4*SN64/CN067
3-CMH76.1084/2*CMH72A.429//ELVIRA/6/CMH79A.955/4/AGA/3/4*SN64/CN067
4-CMH81.794/4/CHEN/AEGILOPS SQUARROSA (TAUS)//FCT/3/STAR/6/CMH79A.955/4
5-VEE/CMH77A.917//VEE/3/ELVIRA/6/CMH79A.955/4/AGA/3/4*SN64/CN067//INIA66/5/NAC
6-CMH79A.955/CMH74A.487//CMH81A.744/3/ELVIRA/6/CMH79A.955/4/AGA/3/4*SN64
7-STDS10/CIRCUS/6/CMH79A.955/4/AGA/3/4*SN64/CN067//INIA66/5/NAC
8-CMH83.2578/GANFRENCH/6/CMH79A955/4/AGA/3/4*SN64/CN067//INIA66/5/NAC

### Table II: Components of diallel variance and their estimates for different traits in doubled haploid wheat

Components	N.S.S	N.T	N.G.S	P.H	G.Y.P
$\hat{D}$	0.437** ± 0.116	0.929** ± 0.053	75.37** ± 6.73	25.04** ± 1.66	5.39** ± 1.94
$\hat{F}$	0.0315$^{n.s}$ ± 0.27	1.48** ± 0.125	38.05* ± 15.91	2.62$^{n.s}$ ± 3.93	8.1$^{n.s}$ ± 4.6
$\hat{H}_1$	0.799** ± 0.26	2.117** ± 0.122	28.4$^{n.s}$ ± 15.48	13.88** ± 3.82	21.97** ± 4.48
$\hat{H}_2$	0.634** ± 0.23	1.351** ± 0.106	22.3$^{n.s}$ ± 13.47	5.15$^{n.s}$ ± 3.32	17.73** ± 3.89
$\hat{h}^2$	0.92** ± 0.15	0.192** ± 0.071	8.31$^{n.s}$ ± 9.03	20.75** ± 2.23	- 1.56$^{n.s}$ ± 2.61
$\hat{E}$	0.41** ± 0.035	1.13** ± 0.018	15.03** ± 2.24	5.05** ± 0.55	3.88** ± 0.649
Proportion of components of variance					
$(H_1/D)^{1/2}$	1.352	2.278	0.614	0.744	2.02
$H_2/4H_1$	0.189	0.159	0.196	0.093	0.202
$[(4DH_1)^{1/2} + F/(4DH_1)^{1/2} - F]$	1.07	3.23	2.39	1.15	2.185
R $(W_r + V_r, Y_r)$	- 0.265	0.602	- 0.335	-0.691	- 0.651
h_b^2	0.519	0.647	0.645	0.769	0.572
h_n^2	0.334	0.154	0.513	0.711	0.084

**, *: significant, at P = 0.01 and P = 0.05, respectively D: additive variance, H_1 and H_2: dominance genetic variance and corrected dominance genetic variance, F: product of additive by dominance, h^2: square of difference P vs All, E: environmental variance, whole, $(H_1/D)^{1/2}$: average of degree dominance, $H_2/4H_1$: Proportion of genes with positive and negative effects in parents, $[(4DH_1)^{1/2} + F/(4DH_1)^{1/2} - F]$: Proportion of dominant and recessive genes in parents, R $(W_r + V_r, Y_r)$: correlation between parental measurement (Yr) and Wr+Vr values, h_b^2: Heritability for diallel in a broad sense, h_n^2: Heritability for diallel in a narrow sense, N.S.S: Number of spikelet per spike, N.T: Number of tiller, N.G.S: Number of grains per spike, P.H: Plant height, G.Y.P: Grain yield per plant
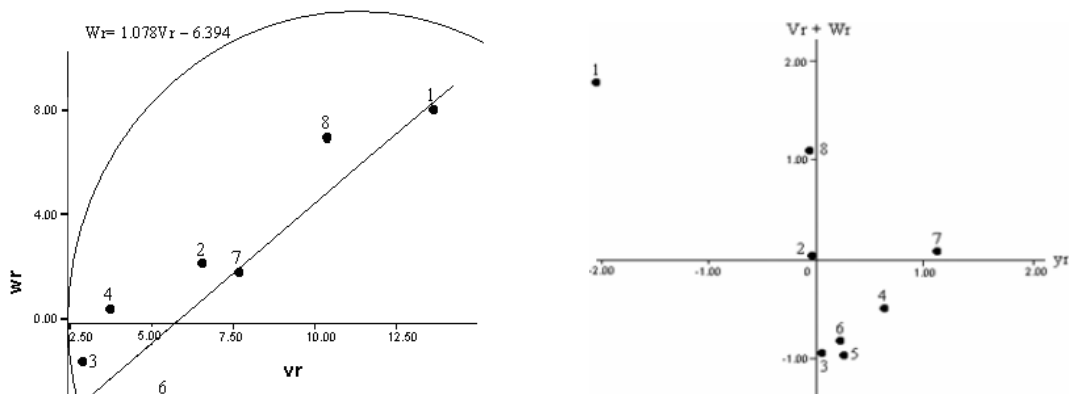
Fig. 1: Wr/Vr and standard deviation graph of number of spikelets per spike
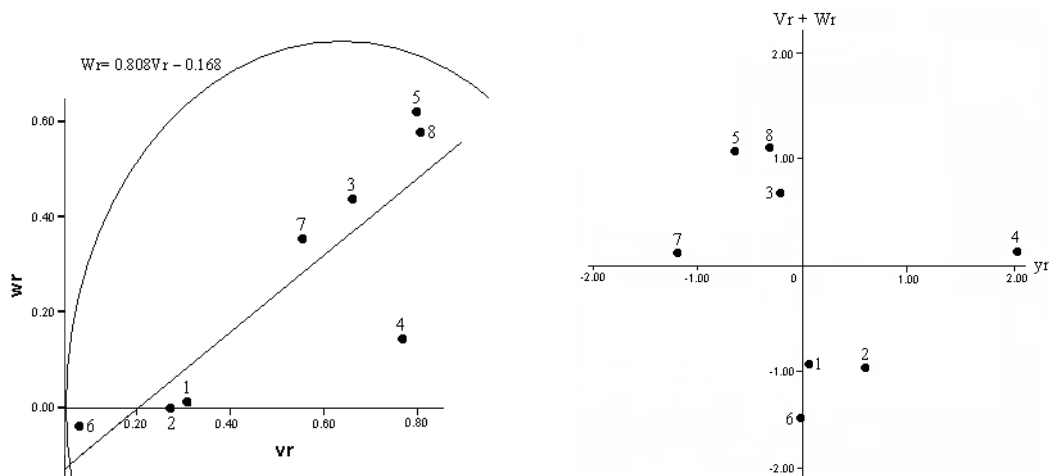
Fig. 2: Wr/Vr and standard deviation graph of number of tillers
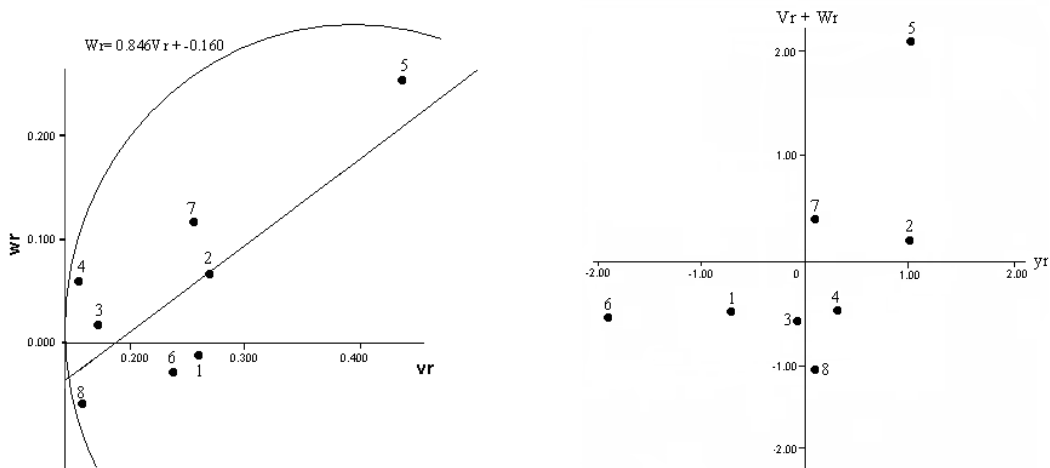
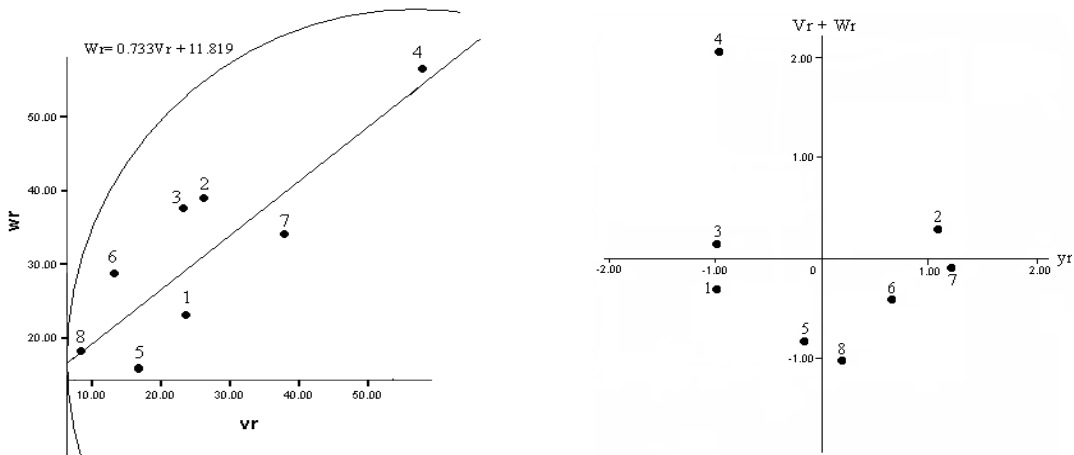**Fig. 3: Wr/Vr and standard deviation graph of grain yield per plant**

Chowdhry *et al.* (2002); Dere and Yildirim (2006); Akhtar and Chowdhry (2006). However, Khan *et al.* (2000) and Habib and Khan (2003) reported partial dominance for this trait. Chowdhry *et al.* (2001); Rahman *et al.* (2003) and Habib and Khan (2003) also found over-dominant type of inheritance for number of spikelets per spike. Awan *et al.* (2005) found additive effect for number of tillers.

As the magnitude of H_1 is greater than H_2 distribution of negative and positive alleles were un-equally distributed in the parents and further proof of this un-equal distribution

Fig. 4: Wr/Vr and standard deviation graph of number of grains per spike

Fig. 5: Wr/Vr and standard deviation graph of plant height
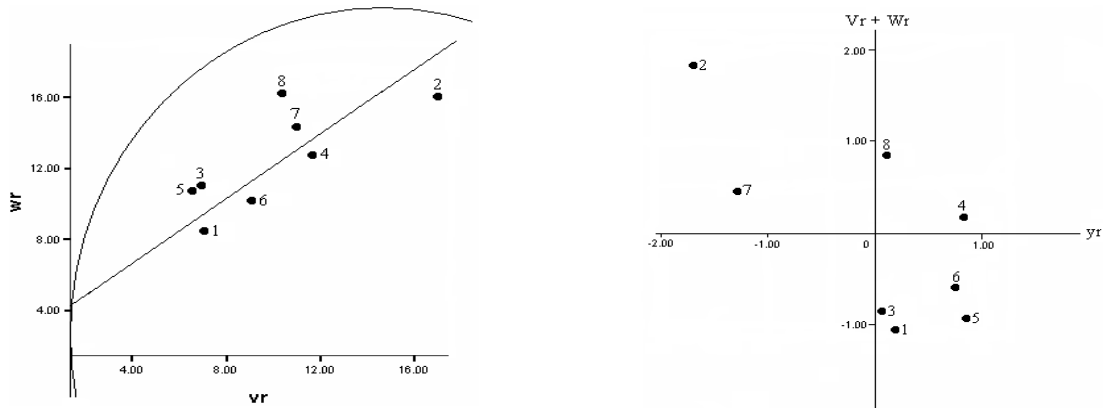
of alleles over loci is provided by the ratio $H_2/4H_1$, which is lesser than its maximum value of 0.25 (Table II). Positive value of F for number of spikelets per spike, number of tillers and grain yield per plant suggested that dominant alleles were more abundant than the recessive alleles in the parents and it was supported by the ratio of $[(4DH_1)^{1/2} + F/(4DH_1)^{1/2} - F]$, which was greater than unity for these traits. The study of Wr/Vr graph showed that parent 6 had maximum number of dominant genes and parents 5 and 8 beings away from origin carried maximum number of recessive genes for number of spikelets per spike (Fig. 1). Parent 8 had maximum number of dominant genes and parent 5 carried maximum number of recessive genes for number of tillers (Fig. 2). Also the regression line and standard deviation graph revealed that parents 5, 3 and 6 had the most dominant genes, while parents 1 and 8 had the most recessive genes for grain yield per plant being located farthest from the origin (Fig. 3). Correlation analysis of the genotypes showed recessive gene control for number of tillers. However, this analysis showed dominant gene control for number of spikelets per spike and grain yield per plant (Table II).

The genetic components of variation for number of grains per spike and plant height revealed that genes with additive properties influenced the inheritance of these characters (Table II). Although in number of grains per spike only value of additive component (D) was significant in plant height both of D and H_1 were significant, but D value was more than H_1. The lesser ratio of $(H_1/D)^{1/2}$ from unity indicated partial dominance occurring in the inheritance of these traits. The estimate of narrow sense heritability is 0.513 and 0.711 for number of grain per spike and plant height, respectively. Dabholkar (1992) stated that when additive effects are larger than the non-additive, it is suggested that selection in early segregation generation would be effective. Chowdhry *et al.* (2001) and Khan and Habib (2003) showed similar results, while studying plant height. Also Rahman *et al.* (2003) and Habib and Khan (2003) reported similar finding for number of grains per spike.

Different studies have shown that reduction in height causes increase of yield in wheat (Singh *et al.,* 2001; Kumar & Sharma, 2003; Zhang *et al.,* 2004). The green revolution i.e., significant increment in wheat yield has primarily been

realized through the introduction of Norin-10 dwarfing genes. Presently most of the wheat cultivars possess the dwarfing genes derived from the Norin-10 source (Rht-1 & Rht-2) either singly or together (Mishra & Kushwaha, 1995; Akhtar & Chowdhry, 2006). The difference H_1-H_2 indicated the un-equal distribution of genes for number of grains per spike and plant height and this claim is strengthened by the ratio of $H_2/4H_1$, which was lesser than 0.25 (Table II). Ratio of $[(4DH_1)^{1/2} + F/(4DH_1)^{1/2} - F]$ more than unity for number of grains per spike indicated that dominant genes were more frequent. But in plant height this ratio was near unity and showed that frequency of dominance and recessive genes was equal. The relative distribution of array points along the regression line indicated that for number of grains per spike, parent 8 and 5 had the most dominant genes, while parent 4 had the most recessive genes being farthest from origin (Fig. 4). The parental order of dominance for plant height was almost similar to Wr/Vr and standard deviation graph. Parental orders of dominance are in order of parents 1, 5, 3, 6, 4, 7, 8 and 2 (Fig. 5). Correlation analysis of the genotypes showed dominant gene control, for number of grains per spike and plant height (Table II).

CONCLUSION

Diallel analysis suggested that both additive and dominance effects were important for all of the traits evaluated (except number of grains per spike). In this study, but dominance had a more pronounced effects for grain yields per plant, number of tillers and number of spikelets per spike. For these traits bi-parental matting or diallel selective matting and heterosis breeding has been suggested. Dominance was partial and the narrow sense heritability estimate for plant height and number of grains per spike was high, including the preponderance of the additive effects. There for, to improve these traits methods based on direct selection such as pedigree can be applied.

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