Original Research Article

Biometrical approach for the selection of elite crosses combination in wheat (*Triticum aestivum*.L.)

Abstract

This experiment has been conducted based on the biometrical technique (half diallel) suitable for making possible combination with different genotypes based on their sowing pattern like timely sown, late sown, timely sown with irrigated and late sown with rainfed condition with genotypes for present investigation comprised of forty five F_1s developed by crossing 10 lines *viz.,* DBW187, K1601, HD2967, HD3249, DBW321, K1317 K0307, HI 1563, DBW107 and HD3059 following half diallel mating design. The cross combination HD2967X K0307 and K0307X K1601 with positive and significant values were in the order of merit for grain yield per plant and heterosis over economic parent cross HD2967X K0307 with positive and significant values was in the order of merit for grain yield per plant.

***Keywords*: Biometrical technique, wheat, genotypes, heterosis and sowing time with condition**

Introduction

Wheat (Triticum aestivum L., 2n=42) is the most important cereal in the world and was one of the first crops to be domesticated some 10000 years ago **(Harlan and Zohary, 1966).** It is the most important staple food of about two billions people (36% of the world population). Worldwide, wheat provides nearly 55% of the carbohydrates and 20% of food calories consumed globally. Wheat belongs to the family Poaceae (Gramineae) and tribe Triticeae containing more than 15 genera and 300 species including wheat and barley. In 1918, Sakamura reported the chromosome number sets (genomes) for each commonly recognized type, he divided wheat into three groups viz. diploids (2n=14), tetraploids (2n=28) and hexaploids (2n=42) chromosomes.

T. aestivum is a segmental allohexaploid (2n = 6x = 42, AABBDD) originated in the Fertile Crescent area of South-Western Asia **(Lupton 1987),** Polyploidy and massive duplications have resulted in a huge genome in bread wheat, with repetitive DNA sequences accounting for approximately 80% of the genome **(Smith and Flavell, 1974).** The bulk of cultivated wheat varieties belong to the genus Triticum, which includes ordinary bread wheat (T. aestivum) and durum wheat (T. durum, 2n = 4x = 28, AABB), which account for 90% of global wheat production. **(Anonymous, 2007).**

Wheat is grown on around 221.24 million hectares worldwide, with a record yield of 771.64 million tonnes of grain and productivity is 3.49 metric tons per hectare (USDA 2023). India has the most wheat-growing land (14 percent), followed by Russia (12.43 percent), China (11.14 percent), and the United States (6.90 percent), accounting for around 45 percent of the global total. Global wheat production in 2022 is predicted to decline from the 2021 record level by 0.8 per cent, reaching 771.64 million tonnes and marking the first drop in four years. Year-on-year falls in production in Australia, India, Morocco and Ukraine will likely outweigh expected increases in Canada, Iran and Russia Further; it said that in Asia, wheat production in India is forecast at 105.5 million tonnes, down nearly 4 per cent from the record crop gathered in 2021. **(Business Standard 2022-23).** Wheat production in 2022-23 is expected to be between 98 million and 106 million tonnes, down from 107.9 million tonnes in 2020-21 **(USDA report, 2022).** Wheat demand is anticipated to rise by 50% by 2050 compared to current levels.

The success of our wheat varieties is up to a considerable extent due to incorporation of the **Norin 10 genes i.e. Rhtl and Rht2 in** wheat. These dwarfing genes changed the wheat plants type and it becomes more responsive to higher application of fertilizer and better crop management under practices. In 1966, Dr. N.E. Borlaug, a noble laureate introduced the Mexican dwarf wheat genotypes and provides the way for green revolution in India.

Materials and Methods

The present investigation entitled **"Genetic studies for yield and its contributing characters in bread wheat (Triticum aestivum L.)** was conducted at Oil Seed Farm, Kalyanpur, C.S. Azad University of Agriculture and Technology, Kanpur-208002 (U.P.) during *Rabi*, 2021-22. The experimental material for present investigation comprised of forty five F_1s developed by crossing 10 lines *viz.*, DBW187, K1601, HD2967, HD3249, DBW321, K1317 K0307, HI 1563, DBW107 and HD3059 following half diallel mating design. A total of 100 treatments with 10 parents (45 F_1s and 45 F_2s) were evaluated for the study of twelve quantitative characters in wheat.

SATISTICAL AND BIOMETRICAL TECHNIQUES

DIALLEL ANALYSIS:

Testing the validity of the hypothesis:

To test the validity of the hypothesis, i.e., the assumptions regarding diallel analysis as proposed by **Hayman (1954**), such as (i) diploid segregation (ii) no maternal effect, (iii) no linkage (iv) no multiple allelism, (v) independent action of non-allelic genes and (vi) hemozygosity of parents, the t^2 test was applied as suggested by **Hayman (1954a**):

$$\mathbf{t^2 = (n-2)/4\ [(Var\ Vr - Var\ Wr)^2 / Var\ Vr \times Var\ Wr) - Cov^2\ (Vr, Wr)]}$$

which is an F test with 4 and (n-2) degree of freedom.

A significant value of t^2 would indicate the non-uniformity of Wr, Vr and thus, invalidates the hypothesis postulated. The failure of hypothesis is also indicated by non-significant regression coefficient.

$$b = \frac{\text{Cov (Wr,Vr)}}{\text{Var (Vr)}}$$

Where,

$$\text{Cov. (Wr, Vr)} = [\textstyle\sum \text{VrWr} - \frac{\sum \text{Vr} \sum \text{Wr}}{n}] / (n-1) \text{ and}$$

$$\text{Var (Vr)} = [\Sigma\ \text{Vr}^2 - \frac{(\Sigma\ \text{Vr})2}{n}] / (n-1)$$

The standard error of regression coefficient (b) was calculated as:

$$\text{SE (b)} = [(\text{Var Wr} - b\ \text{Cov. Wr} - \text{Vr}) / \text{Var Vr}\ (n-2)]^{0.5}$$

Where,

N = number of parents

Now the significance of differences ‘b’ from zero and unity was tested by using ‘t’ value of (b-0)/SE (b) and (1-b)/SE (b) with (n-2) degree of freedom.

(i) Variance component analysis:

The components of variance in diallel cross were computed in F_1 by the use of equation given by **Hayman (1954a).**

Expectation for F_1 diallel crosses is as follows:

$$Vp = \hat{D} + \hat{E}$$

$$Vr = (^1/_4)\hat{D} + (^1/_4)\hat{H}_1 - (^1/_4)\hat{F} + [(n+1)/2n]\hat{E}$$

$$Wr = (^1/_2)\hat{D} - (^1/_4)\hat{F} + (1/n)\hat{E}$$

$$Vm = (^1/_4)\hat{D} + (^1/_4)\hat{H}_1 - (^1/_4)\hat{H}_2 - (^1/_4)\hat{F} + (1/2\ n)\hat{E}$$

Jinks (1956) and Hayman (1958) gave expectations for F_2 diallel crosses. The expected statistics for F_2 generation are the same of that of F_1 except the contribution of h which is halved by one generation of inbreeding. Hence, the coefficient of H_1 and H_2 are (1/4) of those F_1 statistics while the coefficient of F is halved being second and first degree statistics h^2, respectively (**Jinks, 1956; Hayman 1958; Mather and Jinks, 1971**). These expectations are as follows:

$$Vp = \hat{D} + \hat{E}$$

$$Vr = (1/4)\hat{D} + (1/16)\hat{H}_1 - (1/8)\hat{F} + [(n+1)/2n]\hat{E}$$

$$Wr = (1/2)\hat{D} - (1/8)\hat{F} + (1/n)\hat{E}$$

$$Vm = (1/4)\hat{D} + (1/16)\hat{H}_1 - (1/16)\hat{H}_2 - (1/8)\hat{F} + (1/2\,n)\hat{E}$$

Where,

$\hat{D}$ = Components of variation due to additive effects of genes.

= $V_0L_0 - \hat{E}$

$\hat{H}_1$ = Components of variation due to dominance effects of genes.

= $V_0L_0 - 4W_0L_{01} + 4V_1L_1 - (3n-2)\hat{E}/n$

$\hat{H}_2$ = $\hat{H}_1[1-(u-v)^2] = 4V_1L_1 - 4V_0\hat{L}_1 - 2E$

Where

U = Proportion of positive genes in the parents.

v = Proportion of negative genes in the parents

$\hat{F}$ = The mean of F_r over the arrays

F_r = $2(V_0L_0 - 4W_0L_{01} + V_1L_1 - Wr - Vr) - 2(n-2)\hat{E}/n$

$\hat{h}^2$ = Dominance effects (as the algebraic sum over all loci in heterozygous phase in all crosses)

$4(M_{L1} - M_{L0})^2 - 4(n-1)\hat{E}/n^2$

$\hat{E}$ = the expected environmental component of variation

(Error SS + Replication SS/d.f.)/number of replication

In order to estimate of the accuracy of the components ($\hat{D}$,$\hat{F}$,$\hat{H}_1$, $\hat{H}_2$, h^2 and $\hat{E}$) of variance, the term of main diagonal of matrix given **Hayman (1954)** with common multipliers S^2/n^5, was used.

Where,

S^2 = ½ var. (Wr-Vr). The formula being:

$SE(\hat{D}) = \pm [S^2 (n^5 + n^4)/n^5]^{0.5}$

$SE(\hat{F}) = \pm [S^2 (4n^5 + 20n^4 - 16n^3 + 16n^2)/n^5]^{0.5}$

$SE(\hat{H}_1) = \pm [S^2 (n^5 + 41n^4 - 12n^3 + 4n^2)/n^5]^{0.5}$

$SE(\hat{H}_{2)} = \pm [S^2 (36n^4)/n^5]^{0.5}$

$SE(\hat{h}^2) = \pm [S^2 (16n^2 + 16n^2 - 32n + 16n)/n^5]^{0.5}$

$SE(\hat{E}) = \pm [S^2 (n^4/n^5)]^{0.5}$

After testing the significance of the components of variation, the mean degree of dominance was calculated as $(\hat{H}_1/\hat{D})^{0.5}$ in F_1 and $[0.25 (\hat{H}_1/\hat{D})]^{0.5}$ in F_2 generation. The proportion of genes with positive and negative effects was calculated as $H_2/4\hat{H}_1$, the proportion of dominant and recessive genes in parents as the ration of $[(4 \hat{D}\hat{H}_1)^{0.5} + 0.5\hat{F}] / [(4 \hat{D}\hat{H}_1)^{0.5} - 0.5\hat{F}]$ in F_1 and $[0.25 (4\hat{D}\hat{H}_1)^{0.5} + 0.5\hat{F}] / [0.25 (4\hat{D}\hat{H}_1)^{0.5} - 0.5\hat{F}]$ in F_2 generation, the number of gene groups which control the character and exhibit dominance as $h^2 / \hat{H}_2$ and the coefficient of correlation between the parental order of dominance (Wr + Vr) and parental measurement (Yr) as r.

(ii). Combining ability analysis:

The combining ability analysis was worked out by the procedure suggested by **Griffings (1956b**) Method 2. Model II. The mathematical model for the combining ability analysis is assumed to be:

$$X_{ijkl} = \mu + g_i + g_j + S_{ij} + e/bc \sum_k \sum_l e_{ijkl}$$

ij = 1,2, 3 …..,n;

k = 1,2,3 …., b;

1 = 1,2, 3….,c.

Where,

X_{ijkl} = The mean of ij^th genotype over k and l.

μ = The population mean

gi = The general combining ability (gca) of the i^th patent

gj = The gca of j^th parent

S_{ij} = The specific combining ability (sca) for the cross betweenith and Jthparents such that $S_{ij}= S_{ji}$

e_{ijkl} = The environmental effect (mean error effect) with the ijklth observation on ith individual in kth block with ith as femal parent and jthas male parent.

The usual restrictions, as $\sum_i gi = 0$, and $\sum_j S_{ij}= S_{ij}= 0$ (for each i) are imposed.

The analysis of variance table for combining ability is as follows:

Chart 1 : ANOVA table for combining ability

Source variation	d.f.	S.S.	M.S.	'F' test
Gca	(n-1)	Sg	Mg	Mg/Me for (n-1), m d.f.
Sca	n(n-1)/2	Ss	Ms	Ms/Me for (n-1)/2, m. d.f.
Error	M	Se	Me	

Where,

Sg = $1/n+2\ [\sum(x_i + x_{ii})^2 – (4/n)\ x.....^2]$

Ss = $\sum_i\sum_j x_{ij}^2 - 1/(n+2)\sum (x_1 + x_{ii})^2 + [2/(n+1)\ (n+2)\ ]x....^2$

M_{e1} = M_e/r

Where,

r = Number of replications

Me = The error M.S. obtained from parents + F_1s and Parents + F_2s

S_g = The sum of squares (S.S) due to gca

S_s = The sum of squares due to sca

n = Number of parents

x.. = The grand total

x_i = Total of the array involving ith as a female parent

x_{ii} = Value of the ith parent of the array

x_{ij} = The value of the cross, with ith as a female parent and jth as a male parent

The components of variance were estimated according to (**Singh, 1990**) as under:

gca expected m.s. = $\sigma^2 + (n+2)/(n-1)\sum g_i^2$

sca expected m.s. = $\sigma^2 + 2/n(n-1) \sum_i \sum_j s^2_{ij}$

The general predictability ration (GPR) was computed as

GPR = $2\sigma^2 gca / 2\sigma^2 gca + \sigma^2 sca$

Average degree of dominance = $(\sigma^2 s/\sigma^2 g)^{0.5}$

Estimates of various effects:

The Various effects were estimated as follows:

gca effect of i^{th} parent (g_i) = $1/(n+2) [(x_i+x_{ii}) - (2/n)\ x..)$

sca effect of ij^{th} cross (S_{ij}) = $x_{ij} - 1/(n+2) [x_i+x_{ii}+x_j+x_{jj}) + 2x./(n+1)(n+2)]$

Where,

gi and S_{ij} = the estimates of the general and specific combining ability effect, respectively,

x_i, x_{ii}, x...x_{ij} = the same as explained earlier,

$x._j$ = total of the arrays involving j^{th} parents as a male and

x_{ij} = the value of the j^{th} parent of the array.

Estimation of standard errors:

SE (gi) = $[(n-1)\ \sigma^2 e/n\ (n+2)]^{0.5}$

SE (gi-gj) = $[2\ \sigma^2 e/\ (n+2)]^{0.5}$

SE (S_{ij}) = $[(n^2 + n + 2)\ \sigma^2 e/\ (n+1)\ (n+2)]^{0.5}$

SE ($S_{ij} - S_{ik}$) = $[2(n+1)\ \sigma^2 e/\ (n+2)]^{0.5}$

Where,

$\sigma^2 e$ = Me/r, taken as error MS from the combining ability analysis.

Estimation of Heterosis:

Heterosis:

The nature and magnitude of heterosis was computed as per cent increase or decrease of the mean value of F_1 over mid parent (MP), better parent (BP) and economic parents/standard variety/check (check), was estimated with the help of following formula:

Heterosis (%) over MP = $(\bar{F}_1 - \overline{MP}/\overline{MP})$ x 100

Where,

$\bar{F}_1$ = mean of the F_1

$\overline{MP}$ = Mean of the mid parent

Heterosis (%) over BP = $(\bar{F}_1\text{-}\overline{BP}/\overline{BP})$ x 100

Where,

$\bar{F}_1$ = mean of the F_1

$\overline{BP}$ = Mean of the better parent

Heterosis (%) over Check = $(\bar{F}_1\text{-}\overline{Check}/\overline{BCheck})$ x 100

Where,

$\bar{F}_1$ = mean of the F_1

$\overline{check}$ = Mean of the check/economic parent

Test of significance: Significance of heterosis over better parents was tested as;

SE = $(2Me_1/r)^{0.5}$

CD = SE x ‘t’ (‘t’ value at 5% and 1%)

Where,

Me_2 = Error variation obtained from parents + F_{1s} ANNOVA

r = Number of replications

Results & Discussion

Combining Ability In Relation To Yield and Quality Attributes

The combining ability analysis provides useful information in the screening of desirable strains and their cross combinations for their utilization. Such knowledge is a pre-requisite in order to frame a systematic breeding programme leading to rapid and sustained improvement.

Highly significant variances due to gca and sca in both the generations of present study for all the traits revealed that additive as well as non-additive genetic effects were involved in determining the traits. Genetic components analysis also indicated predominance of non- additive genetic estimate for all the characters. similar results were also been reported by **Tiwari and Chakraborty (1989), Ahmad *et al.* (1990), Sharma *et al.* (1991), Singh and Rai (1991), Kulsherestha *et al.* (1991), Zalewski (2001), Kumar *et al.* (2002), Srivastava (2005), Rabbani *et al.*, (2011), Singh *et al.* (2012), Samier (2015) and Kumar (2017).**

Considering simultaneously the *per se* performance and gca effects, good general combiners common in the F_1 and F_2 generations were K 0307, K 1601, K 1317 and HD 3059 for grain yield per plant (g). The consistency of aforesaid combiners for yield and quality contributing traits in both the generations indicated that good general combiners were stable in their performance over generation**.**

On the basis of overall performance, parents HD 2967, K 0307, K 1601, K 1317 and HD 3059 were observed best general combiners for grain yield and other important yield contributing characters as well as quality characters. These parents may be used for simultaneous improvement in grain yield and quality attributes through an inter-mating population involving all possible combinations among themselves.

The sca effects representing dominance and epistatic component of genetic variability would not contribute much for improvement of self-pollinated crops except where commercial exploitation of heterosis in feasible. The crosses involving good general combiners and showing high sca effects may be utilized for further breeding purposes. Desirable transgressive segregants are expected to be produced by making a large number of crosses. **Khrostovska, (1975), Jinks and Jones (1958)** also suggested that the superiority of many hybrids may not be indicated by their ability to produce transgressive segregants due to non-fixable gene action would be important for grain yield. In respect of grain yield per plant; the positive and significant values of sca were associated with five combinations with high mean *per se* performance like HD2976X HI1563, HD2967X DBW107, HD2967X DBW321, K 0307X HI 1563 and K 0307X DBW 321 were observed good specific combiner in F_1 and five crosses, namely HD

2967X K 1317, HD 2976X HI 1563, HD 2967X DBW 321, K 0307X HI 1563 and K 0307X DBW 321 were observed good specific combiner in $F_{2.}$

Heterosis

Heterosis is measured as the mean superiority of F_1 over economic parent; better parent is thus, an important parameter in such studies. Heterosis breeding has come to play a pivotal role in crop improvement programme for obtaining higher production. The first important step in the exploitation of heterosis is to know its magnitude and direction.

In better parent heterosis were ranged from -37.33 (HD3249X HD2967) to 4.64 (HD 2967X K 0307) per cent for grain yield per plant. The cross combinations, namely, HD2967X K0307 and K0307X K1601 with positive and significant values were in the order of merit for grain yield per plant, similar finding was observed by **Ved *et al.*(2006) and Sharma and Sain (2005).** Economic heterosis ranged from -45.45 (HI 1563X DBW 321) to 4.64 (HD 2967X K 0307) per cent for grain yield per plant. The cross combination, *viz.*, HD2967X K0307 with positive and significant values were in the order of merit for grain yield per plant. Similar result was observed **by Singh *et al.* (2007).** Considerable heterosis for grain yield over economic parent was reported by **Salgotra (2002), Punia *et al.* (2005), Kumar and Sharma (2005), Singh *et al.* (2008), Bio-Yin Guang *et al.* (2009), Singh *et al.* (2009).**

Conclusion

The relative ranking of the parents on the basis of per se performance and gca effect in both the generations HD 3249 and HI 1563 for days to 75% flowering, HD 3059 and K 030 for plant height, K0307 and K 1601 for number of tillers per plant, HD 2967 for number of spikelets per spike and spike length, K 0307 and HD 2967 for number of grain per spike, HI 1563 and DBW 107 for days to maturity, DBW 107 and HD 3059 for 1000-seed weight, K 0307 for ear density, DBW 107 for duration of reproductive phase , K 0307 and HI 1563 for protein content and HD 2967and K 0307 foe yield per plant. These parents could be exploited further in breeding programme for simultaneously improved in grain yield and quality attributes. The sca effect for grain yield per plant was significant and considerable good specific combiner were four crosses in F1 and four crosses in F2 generations. These crosses had involved all the three possible combination between high and low gca effects. The cross combinations involving parents HD2967, K 0307, K 1601, and HD 3249 were expected to have fixable, additive or additive x additive gene effects.

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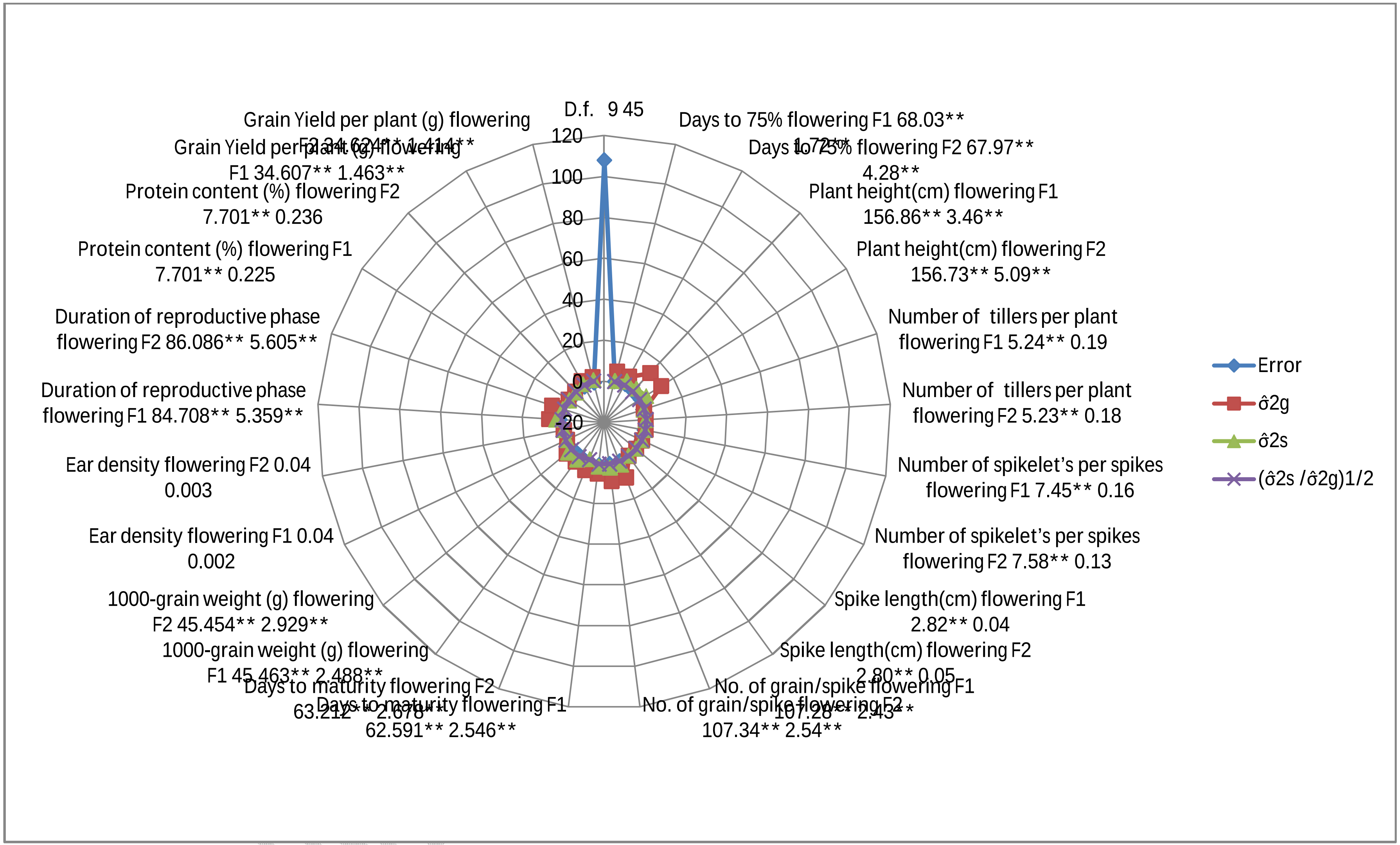

Figure 1: ANOVA for combining ability and related statistics of 12 characters in a 10 parent of diallel cross in F_1 and F_2 generations of wheat.

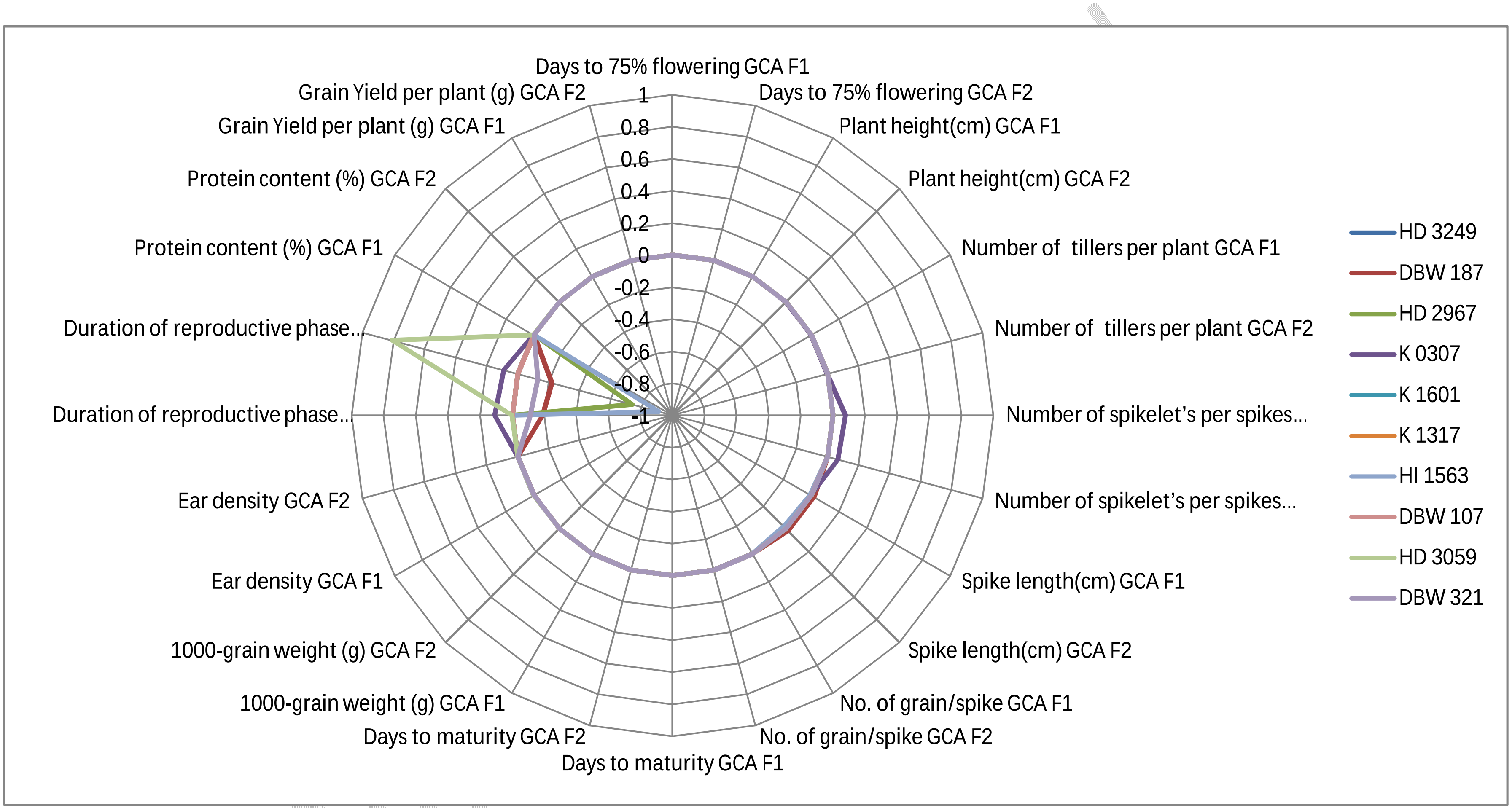

Figure 2: Estimates of GCA effects and corresponding mean performance of the parents for 12 characters in a 10 parent's diallel cross in F_1 and F_2 generations of wheat

Table 1: Estimates of specific combining ability effect and corresponding mean performance for 12 attribute in the 45 crosses of F_1 and F_2 generation

Characters / Crosses	Days to 75% flowering		Plant height (cm)		. of productive tillers/pl		No. of spikelets/spike		Spike length (cm)		No. of grain/spike		Days to maturity		Grain weight (g)		Ear density		Duration of reproductive phase		Protein content (%)		Grain yield/plant (g)	
	SCA		SCA		SCA		SCA		SCA		SCA		SCA		SCA		SCA		SCA		SCA		SCA	
	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
HD3249X DBW187	-1.03 **	-1.64 **	1.19 **	0.80 *	-0.17 **	-0.24 **	-0.22 **	-0.34 **	0.03	-0.03	-2.09 **	-2.27 **	0.90 *	0.81	-0.84 **	-1.05 **	-0.03 *	-0.03	1.93 **	1.84 *	0.46 **	0.42 **	1.03 **	0.98 **
HD3249X HD2967	-2.31 **	-2.92 **	0.73 *	0.34	0.1	0.04	-0.1	-0.22 **	0.18 **	0.11	-1.80 **	-1.98 **	1.90 **	2.72 **	-0.27 *	-0.47 **	-0.04 **	-0.05 **	4.21 **	5.03 **	-0.37 **	-0.42 **	-2.57 **	-2.61 **
HD3249X K0307	-1.06 **	-1.67 **	1.04 **	0.64	-0.83 **	-0.88 **	-0.08	-0.19 *	-0.28 **	-0.33 **	-1.40 **	-1.58 **	0.56	0.47	0.13	-0.09	0.05 **	0.05 **	1.62 **	1.53 *	-0.75 **	-0.80 **	-1.27 **	-1.32 **
HD3249X K1601	0.27	-0.34	-0.07	-0.47	-0.88 **	-0.94 **	-0.13	-0.25 **	0.16 **	0.11	0.52 *	0.33	-1.10 **	-1.19	2.28 **	2.08 **	-0.04 **	-0.05 **	-1.38 **	-1.47	0.05	0	-0.93 **	-0.98 **
HD3249X K1317	0.47	-0.12	-4.21 **	-4.61 **	0.09	0.03	-0.11	-0.26 **	-0.26 **	-0.32 **	-1.04 **	-1.22 **	-1.08 **	-1.17	0.30 **	0.11	0.04 **	0.04 **	-1.54 **	-1.63 *	-0.24 **	-0.29 **	0.24 **	0.20 **
HD3249X HI1563	-0.76 *	-1.37 **	-0.98 **	-1.39 **	0.14 **	0.08	0.27 **	0.17 *	0.03	-0.02	1.86 **	1.68 **	1.90 **	2.11 **	0.43 **	0.23	0.02	0.02	2.65 **	2.87 **	-0.58 **	-0.63 **	0.35 **	0.31 **
HD3249X DBW107	-0.37	-0.98 *	0.27	-0.13	0.13 *	0.06	0.19 *	0.06	-0.1	-0.16 **	1.50 **	1.34 **	3.09 **	3.00 **	-1.88 **	-2.08 **	0.04 **	0.04 **	3.46 **	3.37 **	-0.19 **	-0.23 **	-0.27 **	-0.30 **
HD3249X HD3059	2.16 **	1.58 **	0.3	-0.1	0.19 **	0.13 *	0.59 **	0.48 **	0.34 **	0.27 **	-0.01	-0.19	-1.94 **	-2.03 **	-1.12 **	-1.32 **	-0.02	-0.01	-4.10 **	-4.19 **	-0.69 **	-0.73 **	-0.28 **	-0.32 **
HD3249X DBW321	1.52 **	0.91 *	1.82 **	1.41 **	0.30 **	0.23 **	0.43 **	0.34 **	0.16 **	0.1	-0.04	-0.21	-3.30 **	-3.39 **	0.19	0.02	0.01	0.01	-4.82 **	-4.91 **	-0.07 *	-0.12 **	-0.02	-0.06
DBW187X HD2967	-1.23 **	-1.84 **	1.89 **	1.41 **	0.42 **	0.36 **	-0.07	-0.19 *	-0.29 **	-0.36 **	-0.37	-0.55 *	1.59 **	1.53 *	0.26 *	0.06	0.04 **	0.05 **	2.82 **	2.76 **	-0.27 **	-0.32 **	-1.78 **	-1.83 **
DBW187X K0307	0.02	-0.59	1.00 **	0.61	-0.58 **	-0.64 **	-0.12	-0.24 **	-0.18 **	-0.23 **	-0.70 **	-0.88 **	2.26 **	2.28 **	0.36 **	0.31 **	0.02	0.02	2.23 **	2.26 **	-0.67 **	-0.72 **	-1.42 **	-1.47 **
DBW187X K1601	-1.64 **	-2.26 **	-0.44	-0.84 *	-0.62 **	-0.68 **	-0.17 *	-0.29 **	-0.05	-0.1	0.91 **	0.73 **	-1.08 **	-1.06	2.48 **	2.28 **	-0.01	-0.01	0.57	0.59	-0.02	-0.07 *	-0.91 **	-0.96 **
DBW187X K1317	0.22	-0.37	-4.25 **	-4.64 **	-0.02	-0.08	-0.18 *	-0.30 **	-0.03	-0.09	-0.95 **	-1.13 **	-2.05 **	-2.03 **	0.44 **	0.14	-0.01	-0.01	-2.27 **	-2.24 **	-0.20 **	-0.24 **	0.03	-0.02
DBW187X HI1563	-0.34	-0.95 *	-1.29 **	-1.68 **	0.17 **	0.1	0.23 **	0.13	0.46 **	0.41 **	1.59 **	1.41 **	-1.08 **	-1.08	0.87 **	0.66 **	-0.07 **	-0.07 **	-0.74	-0.74	-0.32 **	-0.37 **	0.76 **	0.73 **
DBW187X DBW107	0.38	-0.23	0.64 *	0.24	0.29 **	0.24 **	0.15 *	0.02	0.33 **	0.27 **	-0.2	-0.37	1.12 **	1.14	-1.17 **	-1.38 **	-0.05 **	-0.05 **	0.73	0.76	-0.09 **	-0.14 **	-0.08	-0.12 *
DBW187X HD3059	1.58 **	0.99 *	-0.04	-0.44	0.25 **	0.18 **	0.55 **	0.44 **	0.07	0.01	1.89 **	1.71 **	-0.91 *	-0.89	-0.52 **	-0.72 **	0.04 **	0.05 **	-2.49 **	-2.47 **	0.06 *	0.01	0.10 *	0.06
DBW187X DBW321	0.61	-0.01	-0.72 *	-1.12 **	0.42 **	0.36 **	0.46 **	0.39 **	-0.07	-0.14 *	1.99 **	1.82 **	0.73 *	0.75	-0.14	-0.34 **	0.07 **	0.08 **	0.12	0.14	0.05	0	0.30 **	0.26 **
HD2967X K0307	0.41	-0.2	-1.29 **	-1.68 **	-0.24 **	-0.29 **	-0.13	-0.25 **	0.17 **	0.18 **	0.59 **	0.41	0.59	0.53	0.53 **	0.32 **	-0.04 **	-0.05 **	0.18	0.12	-0.35 **	-0.40 **	-0.15 **	-0.19 **
HD2967X K1601	2.41 **	1.80 **	-2.00 **	-2.39 **	-0.28 **	-0.35 **	-0.18 *	-0.30 **	0.04	-0.02	0.69 **	0.51 *	-2.41 **	-2.47 **	1.38 **	1.19 **	-0.02 *	-0.02	-4.82 **	-4.88 **	0.28 **	0.23 **	0.05	0.01
HD2967X K1317	0.94 **	0.36	-2.07 **	-2.47 **	-0.05	-0.12 *	-0.20 **	-0.34 **	-0.04	-0.11	-1.39 **	-1.57 **	-1.05 **	-1.11	0.11	-0.08	-0.01	-0.01	-1.99 **	-2.05 **	0.07 *	0.02	1.19 **	1.29 **
HD2976X HI1563	1.72 **	1.11 **	1.09 **	0.7	0.07	0	0.22 **	0.12	0.11 *	0.06	0.84 **	0.67 **	-1.74 **	-1.83 **	0.14	-0.06	0	0	-3.46 **	-3.55 **	-0.05	-0.10 **	2.19 **	2.04 **
HD2967X DBW107	-0.23	-0.84 *	-0.22	-0.61	0.06	-0.01	0.14	0.04	-0.09	-0.15 *	-0.65 **	-0.81 **	-1.88 **	-1.94 **	-1.57 **	-1.77 **	0.03 *	0.03 *	-1.65 **	-1.72 *	0.26 **	0.21 **	1.41 **	1.26 **
HD2967X HD3059	0.63 *	0.05	-1.96 **	-2.36 **	-0.08	-0.15 **	0.53 **	0.43 **	0.02	-0.05	0.91 **	0.73 **	-1.24 **	-1.31	-0.72 **	-0.91 **	0.04 **	0.05 **	-1.88 **	-1.94 *	0.11 **	0.06	1.03 **	1.00 **
HD2967X DBW321	-0.01	-0.62	1.16 **	0.76 *	0.06	-0.01	0.45 **	0.35 **	0.35 **	0.28 **	1.21 **	1.04 **	0.4	0.33	-0.2	-0.40 **	-0.03 **	-0.03 *	0.4	0.34	0.50 **	0.45 **	1.73 **	1.70 **
K0307X K1601	0.66 *	0.05	-1.46 **	-1.86 **	-0.31 **	-0.38 **	-0.59 **	-0.71 **	0.04	-0.16 **	1.09 **	0.91 **	0.92 *	0.94	2.11 **	1.90 **	-0.06 **	-0.04 *	0.26	0.28	0.56 **	0.51 **	-0.35 **	-0.40 **
K0307X K1317	-0.81 *	-1.39 **	-0.23	-0.64	0.65 **	0.58 **	-0.08	-0.22 **	0.16 **	0.11	-0.79 **	-0.97 **	-1.05 **	-1.03	0.37 **	0.17	-0.04 **	-0.04 **	-0.24	-0.22	0.19 **	0.14 **	0.79 **	0.75 **
K0307X HI1563	0.97 **	0.36	-2.57 **	-2.97 **	0.40 **	0.33 **	0.34 **	0.24 **	-0.09	-0.22 **	0.31	0.13	-1.08 **	-1.08	-0.60 **	-0.81 **	0.05 **	0.07 **	-2.04 **	-2.05 **	0.07 *	0.02	1.86 **	1.83 **
K0307X DBW107	-1.64 **	-2.26 **	2.62 **	2.22 **	0.63 **	0.55 **	0.13	0	-0.22 **	-0.26 **	-1.18 **	-1.35 **	-1.55 **	-1.53 *	-2.01 **	-2.22 **	0.05 **	0.05 **	0.1	0.12	0.55 **	0.50 **	0.95 **	0.91 **
K0307X HD3059	0.88 **	0.3	-0.33	-0.73 *	0.45 **	0.38 **	0.26 **	0.15	0.19 **	0.14 *	0.51 *	0.33	-0.58	-0.56	-1.75 **	-1.96 **	-0.02 *	-0.02 ns	-1.46 **	-1.44	0.21 **	0.16 **	0.60 **	0.56 **
K0307X DBW321	0.58	-0.03	-2.01 **	-2.41 **	0.50 **	0.42 **	0.37 **	0.27 **	0.25 **	0.20 **	2.01 **	1.84 **	0.06	0.08	-0.34 **	-0.55 **	-0.02 *	-0.03	-0.52	-0.49	0.80 **	0.75 **	1.73 **	1.69 **
K1601X K1317	-0.81 *	-1.39 **	4.99 **	4.59 **	0.45 **	0.37 **	-0.09	-0.24 **	-0.04	-0.09	-1.29 **	-1.46 **	0.62	0.64	-0.61 **	-0.80 **	0	-0.01	1.43 **	1.45	-0.50 **	-0.55 **	0.73 **	0.68 **
K1601X HI1563	0.3	-0.31	1.35 **	0.95 **	0.50 **	0.44 **	0.22 **	0.12	-0.05	-0.08	-0.78 **	-0.96 **	0.92 *	0.92	0.09	-0.11	0.03 *	0.03	0.62	0.62	-0.27 **	-0.32 **	1.43 **	1.40 **
K1601X DBW107	-1.98 **	-2.59 **	-0.16	-0.56	0.65 **	0.59 **	0.41 **	0.28 **	0.05	0.01	-2.54 **	-2.70 **	-0.88 *	-0.86	-3.02 **	-3.22 **	0.03 *	0.02	1.10 *	1.12	-0.04	-0.09 **	0.62 **	0.60 **
K1601X HD3059	-0.45	-1.03 *	1.06 **	0.66	0.78 **	0.72 **	0.41 **	0.31 **	-0.17 **	-0.22 **	-0.79 **	-0.96 **	1.09 **	1.11	-2.80 **	-3.00 **	0.07 **	0.07 **	1.54 **	1.56 *	0.28 **	0.23 **	0.11 *	0.05
K1601X DBW321	-1.42 **	-2.03 **	-3.18 **	-3.59 **	0.62 **	0.56 **	0.65 **	0.55 **	-0.21 **	-0.26 **	-0.49 *	-0.65 **	2.06 **	2.08 **	-1.79 **	-1.99 **	0.11 **	0.11 **	3.48 **	3.51 **	-0.15 **	-0.20 **	0.93 **	0.89 **
K1317X HI1563	0.83 **	0.24	2.08 **	1.68 **	-0.07	-0.13 *	0.11	0.01	0.14 *	0.09	1.13 **	0.95 **	0.62	0.61	1.61 **	1.42 **	-0.02	-0.02	-0.21	-0.22	-0.01	-0.06	0.24 **	0.21 **
K1317X DBW107	0.55	-0.03	-0.96 **	-1.37 **	0.15 **	0.09	0.36 **	0.47 **	0.04	-0.02	-1.16 **	-1.32 **	-0.52	-0.5	-0.90 **	-1.09 **	0.03 *	0.05 **	-1.07 *	-1.05	0.17 **	0.12 **	-0.68 **	-0.80 **
K1317X HD3059	-1.59 **	-2.48 **	-1.84 **	-2.24 **	-0.32 **	-0.38 **	0.29 **	0.16	0.21 **	0.15 *	2.60 **	2.42 **	0.45	0.47	-1.34 **	-1.53 **	-0.02	-0.02	2.04 **	2.06 **	-0.11 **	-0.16 **	-0.25 **	-0.29 **
K1317X DBW321	-0.56	-1.14 **	0.41	0.01	-0.11 *	-0.17 **	0.60 **	0.48 **	0.04	-0.03	1.76 **	1.60 **	1.42 **	1.44 *	-0.40 **	-0.59 **	0.06 **	0.06 **	1.98 **	2.01 **	0.37 **	0.32 **	-0.36 **	-0.50 **
HI1563X DBW107	0.66 *	0.05	-0.47	-0.87 *	-0.03	-0.09	-0.26 **	-0.37 **	-0.38 **	-0.52 **	-2.72 **	-2.89 **	-0.88 *	-0.89	-1.34 **	-1.53 **	0.05 **	0.08 **	-1.54 **	-1.55 *	0.68 **	0.63 **	-1.54 **	-1.55 **
HI1563X HD3059	-0.48	-1.06 *	0.32	-0.08	-0.50 **	-0.56 **	-0.59 **	-0.68 **	-0.20 **	-0.25 **	-0.57 **	-0.75 **	-0.91 *	-0.92	-1.65 **	-1.84 **	-0.02	-0.02	-0.43	-0.44	0.32 **	0.27 **	-1.65 **	-1.77 **
HI1563X DBW321	-4.12 **	-4.73 **	-0.26	-0.66	-0.36 **	-0.42 **	-0.05	-0.36 **	-0.41 **	-0.46 **	-1.73 **	-1.90 **	-2.27 **	-2.28 **	-0.70 **	-0.90 **	0.08 **	0.06 **	1.85 **	1.84 *	0.28 **	0.23 **	-1.59 **	-1.61 **
DBW107 X HD3059	-0.42	-1.01 *	1.01 **	0.61	-0.28 **	-0.34 **	-0.41 **	-0.66 **	0.20 **	0.14 *	2.67 **	2.51 **	-1.05 **	-1.03	2.91 **	2.71 **	-0.09 **	-0.10 **	-0.63	-0.61	-0.82 **	-0.87 **	0.23 **	0.21 **
DBW107 X DBW321	1.61 **	0.99 *	-1.24 **	-1.64 **	-0.71 **	-0.77 **	-0.29 **	-0.41 **	0.19 **	0.14 *	1.97 **	1.66 **	-1.41 **	-1.39 *	3.46 **	3.26 **	-0.07 **	-0.07 **	-3.02 **	-2.99 **	-0.15 **	-0.20 **	0.13 *	0.1
DH3069 X DBW321	-0.53	-1.12 **	1.55 **	1.15 **	-0.05	-0.11	-0.53 **	-0.62 **	-0.23 **	-0.29 **	-2.94 **	-3.10 **	1.90 **	1.92 **	2.71 **	2.51 **	0.01	0.02	2.43 **	2.45 **	0.76 **	0.71 **	0.78 **	0.75 **

Table 2: Estimation of heterosis over economic parent (HD 2967) for 12 characters in a 10 parent diallel cross in wheat.

Characters/ Crosses	Days to 75% flowering	Plant height (cm)	No. of productive tillers/plant	No. of spikelets/spike	Spike length (cm)	No. of grain/spike	Days to maturity	Grain weight (g)	Ear density	Duration of reproductive phase	Protein content (%)	Grain yield/plant (g)
HD3249X DBW187	-6.93 **	3.53 **	8.25 **	-4.86 **	-7.44 **	-16.43 **	-0.53	1.24	2.41	16.67 **	-20.16 **	-39.65 **
HD3249X HD2967	-8.03 **	1.19	1.94	-1.71	-0.3	-15.24 **	0	-1.65	-1.68	21.57 **	-17.67 **	-37.33 **
HD3249X K0307	-8.03 **	-5.41 **	10.19 **	-6.86 **	-6.25 **	-12.62 **	-1.33	-1.49	-0.94	16.67 **	-15.89 **	-33.27 **
HD3249X K1601	-10.95 **	-0.45	13.59 **	-6.86 **	-3.57	-18.43 **	-4.26 **	-2.81 **	-3.74	13.73 *	-18.15 **	-35.01 **
HD3249X K1317	-6.20 **	-9.67 **	7.28 *	-6.00 **	-8.93 **	-16.31 **	-3.72 **	0.41	2.86	2.94	-16.77 **	-36.17 **
HD3249X HI1563	-12.77 **	-4.71 **	6.31 *	-8.57 **	-7.74 **	-17.98 **	-4.79 **	-2.48 *	-1.27	16.67 **	-15.89 **	-43.91 **
HD3249X DBW107	-7.30 **	-0.1	1.94	-8.86 **	-11.31 **	-11.31 **	-3.46 **	3.96 **	2.31	6.86	-19.78 **	-41.20 **
HD3249X HD3059	-6.57 **	-7.71 **	7.28 *	-6.57 **	-10.71 **	-22.62 **	-4.26 **	2.97 **	4.25	1.96	-19.90 **	-38.49 **
HD3249X DBW321	-5.11 **	3.39 **	3.4	-10.57 **	-14.29 **	-23.93 **	-4.52 **	1.24	3.88	-2.94	-21.41 **	-44.29 **
DBW187X HD2967	-0.36	2.44 *	16.99 **	-1.57	-6.25 **	-1.31	0	4.54 **	4.55 *	0.98	-10.13 **	-24.56 **
DBW187X K0307	-0.36	-5.41 **	24.27 **	-7.00 **	-7.14 **	0	0.27	3.96 **	-0.19	1.96	-8.50 **	-25.92 **
DBW187X K1601	-6.57 **	-0.8	27.67 **	-7.00 **	-7.14 **	-6.36 **	-3.99 **	2.56 *	-0.16	2.94	-11.88 **	-26.69 **
DBW187X K1317	0	-9.67 **	16.02 **	-6.29 **	-8.63 **	-4.76 **	-4.26 **	5.61 **	2.22	-15.69 **	-9.63 **	-29.21 **
DBW187X HI1563	-5.84 **	-4.99 **	16.99 **	-8.71 **	-5.65 **	-7.08 **	-6.91 **	3.47 **	-3.65	-9.8	-7.17 **	-33.27 **
DBW187X DBW107	0	0.31	14.56 **	-9.00 **	-9.23 **	-2.98 *	-4.79 **	10.56 **	-0.13	-17.65 **	-12.26 **	-31.91 **
DBW187X HD3059	-0.73	-8.03 **	18.45 **	-6.71 **	-14.88 **	-7.86 **	-3.19 **	9.32 **	9.12 **	-9.8	-7.50 **	-28.05 **
DBW187X DBW321	0.36	0.77	15.53 **	-10.43 **	-18.15 **	-8.93 **	-1.06	5.28 **	9.00 **	-4.9	-13.76 **	-34.24 **
HD2967X K0307	0.36	-9.67 **	18.93 **	-4.43 **	1.79	2.98 *	-1.33	0.08	-6.43 **	-5.88	2.66 **	4.64 **
HD2967X K1601	-1.82	-4.29 **	22.33 **	-4.43 **	-0.6	-6.07 **	-5.32 **	-4.46 **	-4.21	-14.71 **	-0.85	2.13
HD2967X K1317	1.09	-9.25 **	5.34	-3.71 **	-2.98	-4.88 **	-3.72 **	0.5	-1.24	-16.67 **	1.15	0.77
HD2976X HI1563	-3.28 *	-4.36 **	5.34	-6.14 **	-2.98	-7.74 **	-7.71 **	-2.64 *	-3.53	-19.61 **	3.66 **	-1.74
HD2967X DBW107	-0.36	-2.44 *	0.97	-6.43 **	-7.14 **	-3.10 *	-7.45 **	5.28 **	0.45	-26.47 **	-0.85	0
HD2967X HD3059	-1.46	-11.90 **	3.4	-4.14 **	-9.52 **	-8.93 **	-3.72 **	4.54 **	5.53 *	-9.8	1.65	0.58
HD2967X DBW321	0	0.87	0	-7.86 **	-8.63 **	-9.64 **	-1.6	0.83	0.52	-5.88	-1.6	-2.71 *
K0307X K1601	-5.11 **	-10.65 **	43.69 **	-11.43 **	-2.38	-3.45 *	-2.93 **	-3.47 **	-9.60 **	2.94	5.92 **	-3.68 **
K0307X K1317	-2.19	-14.24 **	37.38 **	-8.43 **	-2.98	-1.9	-3.99 **	0.33	-5.97 **	-8.82	6.67 **	-5.03 **
K0307X HI1563	-5.47 **	-15.11 **	32.04 **	-10.86 **	-6.55 **	-6.79 **	-7.45 **	-5.28 **	-4.98 *	-12.75 *	9.18 **	-7.16 **
K0307X DBW107	-3.28 *	-6.39 **	31.07 **	-11.71 **	-10.12 **	-2.14	-7.45 **	3.38 **	-2.17	-18.63 **	5.92 **	-6.19 **
K0307X HD3059	-2.55	-17.10 **	33.01 **	-10.57 **	-9.82 **	-7.74 **	-3.46 **	1.16	-1.17	-5.88	7.04 **	-5.42 **
K0307X DBW321	-0.73	-9.35 **	28.16 **	-13.43 **	-11.31 **	-6.31 **	-2.13	-0.33	-2.75	-5.88 ns	5.29 **	-6.19 **
K1601X K1317	-6.57 **	-2.65 *	38.35 **	-8.29 **	-5.95 **	-12.02 **	-4.26 **	-8.75 **	-2.78	1.96	-6.74 **	-9.09 **
K1601X HI1563	-10.58 **	-4.89 **	37.38 **	-11.14 **	-7.44 **	-17.98 **	-7.45 **	-10.23 **	-4.37	0.98	-1.6	-13.35 **
K1601X DBW107	-8.03 **	-3.18 *	35.44 **	-10.29 **	-8.93 **	-13.81 **	-8.51 **	-5.78 **	-1.81	-9.8	-6.74 **	-11.80 **
K1601X HD3059	-8.39 **	-9.53 **	41.75 **	-9.67 **	-14.29 **	-19.29 **	-3.72 **	-8.09 **	5.04 *	8.82	-0.73	-11.99 **
K1601X DBW321	-7.30 **	-4.47 **	33.98 **	-12.00 **	-16.67 **	-20.00 **	-2.13	-10.56 **	5.20 *	11.76 *	-10.13 **	-14.51 **
K1317X HI1563	-5.47 **	-9.01 **	8.74 **	-10.86 **	-7.44 **	-9.64 **	-7.18 **	1.65	-4.04	-11.76 *	3.91 **	-28.24 **
K1317X DBW107	-0.73	-8.90 **	7.77 **	-9.71 **	-10.71 **	-6.43 **	-7.71 **	7.59 **	0.74	-26.47 **	-1.6	-27.27 **
K1317X HD3059	-5.11 **	-17.45 **	5.34	-9.43 **	-12.50 **	-8.33 **	-3.72 **	3.63 **	3.14	0	-0.1	-22.05 **
K1317X DBW321	-1.82	-5.58 **	2.91	-11.43 **	-16.07 **	-11.07 **	-2.13	0.99	5.18 *	-2.94	-2.61 **	-29.98 **
HI1563X DBW107	-5.84 **	-6.81 **	3.4	-16.57 **	-15.77 **	-16.07 **	-11.44 **	3.30 **	-1.27	-26.47 **	5.67 **	-40.62 **
HI1563X HD3059	-9.12 **	-13.61 **	0.97	-17.43 **	-17.56 **	-20.83 **	-8.24 **	-0.33	-0.16	-5.88	6.54 **	-38.49 **
HI1563X DBW321	-10.95 **	-4.71 **	-2.43	-18.43 **	-21.43 **	-24.17 **	-8.51 **	-2.97 **	3.45	-1.96	0.15	-45.45 **
DBW107 X HD3059	-4.01 **	-9.60 **	0	-16.57 **	-16.37 **	-7.74 **	-7.98 **	23.10 **	-0.67	-18.63 **	-8.87 **	-21.28 **
DBW107 X DBW321	0.36	-2.44 *	-11.65 **	-19.43 **	-18.45 **	-10.24 **	-7.45 **	19.47 **	-1.6	-28.43 **	-10.00 **	-29.21 **
DH3069 X DBW321	-4.01 **	-7.16 **	2.43	-19.86 **	-25.60 **	-27.62 **	-1.6	14.77 **	7.39 **	4.9	0.53	-22.63 **