Gene Action Analysis for Yield and Yield Contributing Traits in Bread Wheat

*Ankita Singh, Anil Kumar

**Deptt. of Genetics and Plant Breeding R.No.152, Golden Jubilee Hostel GBPUA&T,
Pantnagar-263145 Uttarakhand
Deptt. of Genetics and Plant Breeding, GBPUA&T,
Pantnagar-263145, Uttarakhand*

Abstract The present investigation was undertaken for analysis of gene action involved in grain yield and yield contributing traits in 15 parental genotypes (12 lines and 3 testers) and 36 F_1 hybrids in a line x tester scheme. The F_1s along parents and two commercial check varieties viz. UP 2338 and PBW 343 were evaluated using Randomized Block Design. Highly significant differences were observed among genotypes for all the characters studied. Days to 75% heading, flag leaf area plant height and spike length were governed by partial dominance, whereas all other characters were governed by overdominance. Estimates of variance due to general combining ability (gca) and specific combining ability (sca) and their ratio revealed that both additive and non-additive gene effects were important for different characters studied.

Key Words: Gene action, gene effects, line x tester, bread wheat

1. INTRODUCTION

Wheat is the most important and strategic cereal crop for the majority of world's population. India is one of the major producers of wheat and occupies second position after China. Much of the emphasis on wheat breeding has been placed on increasing productivity of the crop. This has been in response to the pressure for an adequate food supply caused by constantly increasing population in India and the world as a whole. Global demand for wheat is growing at approximately 2% per year, twice the current rate of gain in genetic yield potential [6]. Therefore, development of new improved wheat cultivars with high genetic potential for yield and its related traits has become a permanent goal in the breeding programmes.   It is a general agreement that germplasm diversity and genetic relatedness among elite breeding material is the fundamental element in plant breeding [4]. Hence breeding wheat genotypes with diverse genetic base is needed to achieve self-efficiency and sustainability. Enhancement in yield in most situations is more effectively fulfilled on the basis of performance of yield components, which are closely associated with grain yield [1]. In order to achieve this target one should be aware of genetic makeup and nature of gene action involved in controlling plant responses to different environments. Additive gene effects determine heritability of the trait in question and thus, is the crucial factor that decides whether this trait will appear similarly in the progeny or not. This is important in increasing the diversity of agriculturally important crops and enhancing the genetic base.

Therefore, the present investigation has been conducted to determine the gene action for yield and its components using line x tester mating design in bread wheat.

2. MATERIALS AND METHODS

The present investigation was undertaken at the Norman E. Borlaug Crop Research Centre of Govind Ballabh Pant University of Agriculture and Technology, Pantnagar, India in *Rabi* 2010-12. Twelve lines of wheat and three testers were crossed in a line x tester mating scheme to produce 36 crosses (Table 1). These crosses were then evaluated along with the parents and 2 checks, *viz.* UP 2338 and PBW 343. The experiment was laid out in a Randomized Block Design (RBD) with three replications. Each plot consisted of two rows of 1 m length with a row to row distance of 23 cm. The plant to plant distance was maintained at 10 cm. The observations were recorded for twelve characters *viz.* days to 75% heading, days to maturity, flag leaf area, plant height at maturity, number of effective tillers per plant, spike length, number of spikelets per spike, number of grains per spike, 1000 grain weight, biological yield, grain yield per meter and harvest index.

Covariance of full sibs and covariance of half sibs were calculated from the expectations of mean squares as follows:

$$\text{Cov. H.S.}_{\text{(line)}} = \frac{M_l - M_{lt}}{rt}$$

$$\text{Cov. H.S.}_{\text{(tester)}} = \frac{M_t - M_{lt}}{lt}$$

Cov.H.S.$_{(average)}$ =

$$\frac{1}{r(2lt-1-t)}\left[\frac{(1-1)(M_l)+(t-1)(M_t)}{1+t-2}-M_{lt}\right]$$

Cov.(F.S.)= $\dfrac{(M_l-M_e)+(M_t-M_e)+(M_{lxt}-M_e)}{3r}$ +

$$\frac{6\,r\,Cov.H.S.-r(1+t)\,Cov.H.S.}{3r}$$

Where,

M_l = MS line (female)

M_t = MS tester (male)

M_{lxt} = MS line x tester

M_e = error mean sum of square

Var. gca   = Cov.H.S. $\left[\dfrac{1+F}{4}\right]$ Var.A

Therefore,

Var.A. = Cov.H.S.; if F=0

Var.A. = 2Cov.H.S.; if F=1

Var. sca = $\left[\dfrac{1+F}{2}\right]^2$ Var D

Therefore,

Var.D.= Var.sca; if F =1

All analysis was done using standard statistical formulae and procedures.

3.   RESULTS AND DISCUSSION

Analysis of Variance indicated highly significant differences among the genotypes for all the characters (Table 2). The variance due to hybrids was also significant for all the characters studied suggesting the generation of good amount of variability among the hybrids and also the possibilities of identifying the superior hybrids from the study.

The estimates of variance due to gca (σ^2gca) and sca (σ^2sca) for various characters are given in Table 3. Days to

75% heading, flag leaf area plant height and spike length were governed by partial dominance, whereas all other characters *viz.* days to maturity, number of effective tillers per plant, spike length, number of spikelets per spike, number of grains per spike, 1000 grain weight, grain yield per meter, biological yield and harvest index were governed by overdominance.

The degree of dominance based on the ratio of sca and gca variances from line x tester analysis pointed out that additive gene effects occurred for days to 75% heading, flag leaf area, plant height and spike length. In all the other characters pre-dominance of non-additive gene action was observed.

The line x tester analysis pointed out that (Table 4) additive gene effects occurred for days to 75% heading, flag leaf area, plant height and spike length. In all the other characters pre-dominance of non-additive gene action was observed. These findings were in general agreement with [2], [3], [5] and [7].

4.   REFERENCES

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Table 1: Parents mated in line x tester scheme.

Lines	
L_1	ATTILA*2/STAR
L_2	MILAN /3/PAT24 /ALD/DOVE /BUC
L_3	SERI.LB// KAUZ/ HEVO/3/ AMAD
L_4	VL 858
L_5	UP 2672
L_6	QLD 33
L_7	QLD 39
L_8	UP2706
L_9	PBW 574
L_{10}	UP 2647
L_{11}	CAL /NH //H567 .71 /3 /SERI /4/CAL /NH/ H567.7/5/…
L_{12}	UP2338*2 /4/ SNZ / TRAP# /3/ KAUZ*2 /TRAP / /KAUZ
Testers	
T_1	PBW 550
T_2	UP 2584
T_3	K 9107

Table 2: Analysis of variance for different characters

Sl. no.	Characters	Mean Squares Source of variation		
	d.f.	Replication 2	Treatment 50	Error 100
1.	Days to heading	5.81	2.53**	0.85
2.	Days to maturity	2.13	7.62**	2.35
3.	Flag leaf area	17.28	117.72**	6.94
4.	Plant height	9.68	162.34**	5.39
5.	Tillers per plant	2.05	17.38**	1.05
6.	Spike length	0.62	3.80**	0.19
7.	No. of spikelets per spike	1.12	4.05**	0.59
8.	No. of grains per spike	1.76	124.51**	2.58
9.	1000 grain weight	1.47	81.46**	2.03
10.	Grain yield per meter	3.88	3967.45**	2087.16
11.	Biological yield	741.96	3199.79**	748.18
12.	Harvest index	4.66	100.51**	8.81

* and **significant at 5% probability level and at 1% probability level, respectively

Table 3. General and specific combining ability variances.

Sl. NO.	Characters	σ^2gca	σ^2sca	σ^2gca/ σ^2sca(ratio)	$(\sigma^2$sca/ σ^2gca$)^{1/2}$ Mean degree of dominance
1.	Days to heading	0.169	0.02	8.45	0.35
2.	Days to maturity	0.11	1.92	0.05	4.17
3.	Flag leaf area	21.43	7.14	3.01	0.57
4.	Plant height	38.55	8.22	4.68	0.45
5.	Tillers per plant	0.177	3.77	0.05	4.61
6.	Spike length	1.04	0.04	26	0.2
7.	No. of spikelets per spike	0.66	0.90	0.73	1.16
8.	No. of grains per spike	5.24	29.10	0.18	2.35
9.	1000 grain weight	0.26	15.45	0.02	7.71
10.	Grain yield per meter	125.88	960.59	0.13	2.76
11.	Biological yield	51.01	474.05	0.11	3.04
12.	Harvest index	2.72	40.82	0.06	3.87

Table 4: Gene effects for different characters as revealed by line x tester cross analysis.

Gene effects	Characters
Additive	Days to 75% heading, flag leaf area, plant height and spike length.
Non-additive	Days to maturity, tillers per plant, no. of spikelets per spike, no.of grains per spike, 1000 grain weight, grain yield per meter, biological yield and harvest index,