Gene action for seed yield and its component trait in Bread Wheat (*Triticum aestivum*) (L.) em. Thell]

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Abstract:
A biometrical experiment designed involving a total 16 parents out of which 12 used as female and 04 as male parent with respect to analyze the combing ability in bread wheat. Based upon finding ,it is concluded that non additive gene action is more important than additive type of gene action. The variances due to specific combining ability (sca) were found to be considerably higher than that of general combining ability (gca) for all the characters indicating greater importance of non-additive type of gene action thus, the heterosis breeding may be a good choice. Variety WH542 and HD2285 was found to be good general combiners for most of the yield contributing traits like spike length, 1000 grain weight etc.and so the crosses involving these parents have better chances to get better segregants after judicious selection.

Key words: Non-additive gene action,gca,sca Bread wheat, combining ability,seed yield

Introduction

Wheat is the prime 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 B. Skoynand et.al. 2000. Therefore, development of new improved wheat cultivars with high genetic potential for yield and its related traits has become a prime 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 M.S Mukhtar et al.2002. 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,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.

Material and Methods

The experimental material consisted of 16 genetic diverse lines in total out of which 12 lines used as female parents and 4 as testers. These were crossed in L x T fashion and in this way their possible $48F_1$ were obtained. The F_1 crosses were selfed and thus, F_2 generation was obtained. The F_1 crosses were made following hand emasculation and pollination. The final trial conducted with all 16 parents their possible $48F_1$ and $48F_2$ cross combinations. These were grown in randomized block design with three replications. The plot size for F_1s was double row of 2m length and for F_2s 6row of 2m length. The inter and intra row spacing was 25cm and 10cm, respectively. The double row of standard check PBW343 was also sown after each 5 plots. The observations were recorded on 10 and 30 competitive plants selected randomly from each plot for twelve quantitative traits namely heading, maturity, grain filling period, plant height, flag leaf area, spike length, grains per spike, grain weight per spike,1000 grain weight, biological yield, harvest index and yield per plant. The mean values of each genotype were subjected to combining ability analysis by line x tester method as suggested by Kempthorne (1957).

Results and Discussion

The results indicated significant differences among the parents for general combining ability (gca) and crosses for specific combining ability (sca) effects for all the characters studied(**Table1**). Though the gca and sca components of variance were significant for all the characters under study, the variance due to sca was found to be considerably higher than that of gca for all the characters, indicating greater importance of non additive gene action and thus suggested heterosis breeding may be useful. Similar results have been reported by Cifei Aydogan Esra and Koksal Yagdi (2010), Dhadhal *et.al*.(2008). A ranking of desirable parents on the basis of gca effects is presented in **(Table2)**. For seed yield, the genotypes appeared as good general combiners were WH542, PBW459, UP2425, HD2402, NW1012, PBW373 and PBW435. Among the parents, WH542, UP2425, PBW459, HD2285 and PBW373 were found to be good general combiners for other yield contributing traits like thousand grain weight, grains per spike, grains weight per spike etc. So the crosses obtained from these parents may give an opportunity to get better recombinants for yield improvement. Genotype K9107 was found to be the promising general combiners for early maturity and dwarfness. Study further revealed that genotypes like UP2425, K9006, UP 2338 were also good general combiners for early maturity. Variety like PBW459, NW1012, PBW435, HUW206, UP2425 were promising general combiners for the traits like biological yield and harvest index.

Specific combining ability effects estimates revealed very wide range of variation for all the characters. Few crosses in each specific trait shortlisted on the basis of high specific combining ability effects (sca) **(Table 3).** Results revealed that the crosses showed highest values of sca effect for yield, also showed the high value of sca effects in most of the yield contributing traits indicating true to type relationship. Twelve outstanding crosses shortlisted on the basis of highest yield per plant **(Table 4)** . Cross combinations like PBW459 x RAJ3777, K9006 x UP2425,HD2285 x UP2425 and NW1012 x UP2425 are the prominent crosses as these crosses efficiently combine most of the yield contributing traits. It genetically infers that yield advantage is due to non additive type of gene action and so heterosis breeding will be rewarding. Similar results have been reported by Cifei Aydogan Esra and Koksal Yagdi (2010), Subhaschandra et al.(2010). Shrma et al. (1992), Babu and Kumar (1995), Sharma and Tandan (1997).

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Table 1. Analysis of variance (ANOVA) for 12 metric traits in wheat

Sources	Generation	DF	HD (I)	MT (II)	GFP (III)	PHT (IV)	FLA (V)	SL (VI)	Gr/sp (VII)	Grw/sp (VIII)	1000GW (IX)	BY (X)	HI (XI)	Y/PL (XII)
Replication	F_1	2	49.77	36.77	0.46	103.18	30.73	15.09	256.18	0.625	75.35	1417.55	10.86	174.88
	F_2		29.05	23.88	2.42	143.23	41.03	6.28	152.58	0.285	37.05	3152.83	380.18	183.03
Male	F_1	3	7.47	51.31**	90.27**	28.99**	87.28**	6.41**	339.43**	0.775**	36.49**	3681.17**	317.67**	1879.83**
	F_2		44.99**	98.98**	43.41**	100.14**	250.53**	6.50**	119.12**	1.035**	242.19**	296.99**	989.39	367.67**
Female	F_1	1	23.65**	61.53**	52.98**	109.79**	229.23**	5.29**	395.99**	0.605**	39.95**	7089.34**	218.55**	2053.83**
	F_2	1	6.06**	24.37**	42.73	192.29**	180.47**	3.44**	246.35**	0.692**	79.46**	5135.55**	543.73	805.77**
Male x Female	F_1	3	19.73**	25.18**	24.35**	84.98**	17.20**	5.39**	39.65**	0.144**	13.33**	4624.32**	87.66**	823.17**
	F_2	3	9.05**	22.59**	40.93**	221.13**	113.36**	3.05**	333.36**	1.415**	194.33**	322.32**	688.01	578.24**
Error	F_1	9	2.70	4.39	5.69	14.36	7.49	0.41	16.50	0.032	2.39	174.86	15.66	17.14
	F_2	4	1.31	3.26	4.56	16.59	5.90	0.37	17.03	0.033	2.85	89.94	661.41	16.20

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

Abbreviation:

I.Heading II. Maturity III.Grain filling period IV.Plant height (cm) V.Flag leaf area (cm2) VI. Spike length (cm)

VII. Grains per spike VIII.Grain weight per spike (g) IX. 1000 grain weight (g) X. Biological yield (g) XI. Harvest index XII. Yield per plant (g)

Table2- List of Good General Combiners on the basis of combining ability estimates

Characters	Good General Combiners F_1	F_2	Common in F_1 and F_2
Heading	K9107K9006	UP2338 HD2285UP2425PBW459	Nil
Maturity	RAJ3777 K9107NW1012	UP2425 HUW206 K9006 K9107	K9107
Grain filling period WH542	HD2285 PBW 459 PBW373 UP2338 K9006	HUW206 K9107 K9006 UP2338 PBW459 PBW373	K9006 UP2338 PBW459 PBW373
Plant height (cm)	PBW443 NW1012	PBW373 RAJ 3777 PBW459 PBW443	PBW443
Flag leaf area (cm2) NW1012	UP2338 PBW373 PBW435 HUW206 HD2285	WH542 K9107 PBW373 HD2402 HUW206 HUW468	PBW373 HUW206
Spike length (cm) HUW206	UP2338 WH542 PBW373 NW1012 HD2285 PBW343 HUW468	WH542 HD2402 PBW435 HD2285	WH542 HD2285
Grains per spike HD2402	UP2425 PBW459 K9006 PBW373 PBW 435	RAJ3777 K9006 PBW443 NW1012 HD2285	K9006
Grains weight per spike (g)	UP2425 K9006 PBW373 HD2402 PBW435 HD2285	WH542 PBW443 PBW373 NW1012 HUW468	PBW373
1000 grain weight (g) HD2285	WH542 HD2402 HUW206 HD2285	WH542 PBW443 PBW373 PBW435 PBW343	WH542 HD2285
Biological yield (g) Harvest index PBW435	WH542 PBW459 PBW373 NW1012 PBW435 UP2425 PBW459 HD2402 NW1012 HUW206	UP2425 K9006 NW1012 PBW435 HUW468 HUW206	NW1012 PBW435 HUW206
Yield per plant (g) HD2402	WH542 UP2425 PBW459 PBW373 NW1012 PBW435 HUW206 HD2285	WH542 PBW459 K9006 HD2402 NW1012 HUW468	WH542,PBW459, HD2402, NW1012

Table 3. Promising crosses with desirable sca effect in F1 and F2 generations.

Trait	Promising crosses having significant sca effect
Heading	K9006xUP2425(-1.86 in F_1 and -1.82 in F_2) NW1012XWH542(-1.75 in F_1 and -1.07 in F_2) PBW343xWH542 (-7.06in F_1 and-0.49in F_2)
Maturity	K9006x UP2338(-2.41in F_1 and -5.88 in F_2) PBW373xWH542(-2.44xin F_1 and -2.47in F_2)
Plant height (cm)	HD2285xWH542(-7.15in F_1 and -8.06 in F_2) PBW343xWH542(-4.15 in F_1 and-7.06 in F_2) HUW468xUP2425(-6.46in F_1 and-3.92 in F_2)
Grain filling period	K9006xUP2425(4.17 in F_1 and 6.52 in F_2) PBW373xUP2425(4.00in F_1 and 2.94 in F_2) PBW443xUP2338(3.03in $F_1$and 4.80 in F_2)
Flag leaf area (cm2)	PBW443xWH542(11.76 in $F_1$and 3.76 in F_2) PBW459xUP2425 (5.69 in F_1 and 6.82 in F_2)
Spike length (cm)	HUW206x UP2425(1.43 in F_1 and 1.01 in F_2) HUW468 xWH542 (0.99 in F_1 and 0.85 in F_2)
Grains per spike	HD2402xUP2425 (14.04 in F_1 and 20.01 in F_2) PBW373xWH542 (14.51 in F_1 10.90 in F_2) PBW459xRAJ 3777 (11.96in F_1 and 12.17 in F_2)
Grain weight per spike (g)	K9006xUP2425 (1.05 in F_1 and 0.54 in F_2) HUW468xWH542(0.96in F_1 and 0.17 in F_2) K9107xUP2338(0.79in F_1 and 0.58 in F_2)
1000 grain weight (g)	HD2402xWH542 (11.97 in F_1 and7.28 in F_2) HUW206xWH542(11.22 in $F_1$and 6.48 in F_2) PBW435xRaj3777(6.38 in F_1 and 7.87 in F_2)
Biological yield (g)	PBW459xRAJ3777 (70.38 in F_1 and 23.67 in F_2) K9006xUP2425 (37.65 in F_1 and 26.46 in F_2) NW1012xUP2425(45.82 in F_1 and30.71 in F_2)
Harvest index	HUW206xWH542(10.63 in F_1 and 65.42 in F_2)
Yield per plant (g)	PBW459xRAJ3777 (32.70 in F_1 and 11.27 in F_2 K9006xUP2425 (16.68 in F_1 and 14.99 in F_2) PBW373xWH542 (16.08 in F_1 and 15.18 in F_2)

Table 4 - Prominent crosses of breeding value for grain yield and their performance with respect to GCA and SCA Effects in bread wheat

Cross combination	GCA effect P1	GCA effect P2	SCA effect	Significant sca effects in other traits
PBW459xRAJ3777	16.52**	-6.05**	32.70**	IV,VI,VII,VIII, IX,X
PBW459xUP2425	16.52**	7.81**	13.97**	V,VI,XI
PBW373xWH542	13.61**	4.48**	16.08**	II,VII,VIII,XI
NW1012xUP2425	9.74**	7.81**	16.19**	III,VII,VIII,X
PBW435xWH542	7.45**	4.48**	19.98**	II,VII,X
HD2285xUP2425	3.41**	7.81**	18.41**	IV,VI,X
K9006xUP2425	1.81**	7.81**	16.68**	I,III,IV,V,VII,VIII,IX,X
HUW206xUP2425	5.45**	7.81**	11.17**	III,VIII,IX,X
HD2402xWH542	6.99**	4.48**	10.74**	III,VIII,IX,X
PBW373xUP2425	13.61**	7.81**	-2.52	I,III,V,VI,VIII,IX,XI
HD2402xUP2425	6.99**	7.81**	2.27	X,VII,VIII
HUW206xWH542	5.45**	4.48**	7.04**	X,VI,VIII,X,XI

Abbreviation:

I.Heading	II. Maturity	III.Grain filling period	IV.Plant height (cm)	V.Flag leaf area (cm2)
VI. Spike length (cm)		VII. Grains per spike	VIII.Grain weight per spike (g)	
IX. 1000 grain weight (g)		X. Biological yield (g)	XI. Harvest index	XII. Yield per plant (g)

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