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Research Articles

Genetic architecture of various agromorphological and some quality traits in bread wheat (*Triticum aestivum*)

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ABSTRACT

A study was conducted for estimating genetic parameters involving 10 parents and their 45 F_1s (half diallel) of bread wheat (*Triticum aestivum* L.) der timely sown condition of north western plains zone of India during 2011-12 and 2012-13. Positive and significant values of F component were estimated for yield and its contributing traits in F_1s indicating the preponderance of dominance and positive genes in the parents involed. The estimates of h^2 were positive and significant for days to maturity (2.97), plant height (28.14), peduncle length (5.48), productive tillers (0.55), spike length (0.76), spikelets/spike (26.28), grains/spike (228.45), biological yield (149.71), grain yield (73.58), harvest index (33.15), and 1 000 grain weight (21.71). The theoretical value (0.25) of ($H_2/4H_1$) for all the traits indicated asymmetrical distribution of positive and negative genes. The proportion of dominant and recessive alleles for days to 50% flowering, days to maturity, plant height, peduncle length, productive tillers, spike length, biological yield, grain yield, harvest index and 1 000 grain weight, indicated preponderance of dominant alleles in the parents for these traits, whereas traits namely; flag leaf area, spikelets/spikes, grains/spike and gluten content, reflected more recessive alleles in the parents. Estimates of SCA effects revealed that the best cross combinations for respective traits were K 9162 × UP 2425, PBW 373 × UP 2425, K 9423 × Unnat Halna, K 9423 × HUW 560, Raj 3765 × NW 1014, K 9423 × NW 1014, NW 1014 × NW 1076, Raj 3765 × PBW, K 9423 × NW 1076, Raj 3765 × NW 1076, Raj 3765 × Unnat Halna and Unnat Halna x HUW 560 may be exploited through heterosis breeding programme to improve these traits in bread wheat. The traits showing more than 30% narrow sense heritability could be rewarding for further improvement of grain yield and gluten content in bread wheat. It may therefore be concluded that these parental lines could be used as donors for improving both the components following biparental mating or diallel selective mating system could be the best breeding methodology followed by early generation selection for improvement in these traits.

Key words: Bread wheat, Diallel cross, Gene effects, Grain yield, Hayman's apporoach

Wheat (*Triticum aestivum* L.) is one of the most important cereal crop and occupies a notable position among food grains of the world not only in terms of area and production but also in respect of its adaptation to a wider range of agro-climatic conditions. India is the second largest producer of wheat Anonymous (2014) after China. The other major wheat producing countries are Russian Federation, United States of America and Canada and these five countries together contribute more than half of the total global wheat production. The improvement in grain yield and quality traits of wheat in a sustainable way, primarily depend upon the genetic potential and inherent genetic variability that exists in the population. Among the various biometrical techniques, diallel cross analysis is most effective with proven merits for ascertaining the systematic genetic architecture of quantitative traits within a short period from all possible single crosses. Genetic analysis of wheat has shown that grain yield a highly complex trait is determined by component traits (Sajjad *et al.* 2011) and these component traits affect the yield directly or indirectly. Also, the analysis showed that genes for yield *per se* do not exits (Grafius 1959) and therefor knowledge about the nature and magnitude of gene effects of yield contributing traits and their expression is of paramount important in formulating an efficient breeding programme. The objective of the present investigation was to draw information on nature and type of gene action and contribution of different component traits to grain yield and quality attributes. The information generated would may be effectively exploited to develop an appropriate breeding programme for continued genetic improvement in wheat crop and also for developing new genotypes with higher grain yield and better nutritional quality.

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MATERIALS AND METHODS

The base material consists 10 diverse genotypes of bread wheat (Raj 3765, K 9162, PBW 373, K 9423, K 7903, Unnat Halna, NW 1014, HUW 560, NW 1076 and UP 2425) was planted at Crop Research Centre, SVBPU&T, Meerut during *rabi* 2011-12 for attempting crossing in a 10x10 diallel fasion excluding reciprocals. In the next crop season (i.e. *rabi* 2012-13), experimental material consisted total 55 genotypes (10 parents and their 45 F_1s) was sown in a randomized block design with three replications. Seeds of each of the parental lines and also F_1s were dibbled in two row plot of 2 m length maintaining spacing of 10 cm among plants within a row and 23 cm between rows. All the standard agronomical practices were followed to raise normal crop. Observations were recorded on days to 50% flowering, days to maturity, plant height (cm), number of productive tillers per plant, flag leaf area (cm^2), spike length (cm), number of spikelets per spike, number of grains/spike, 1 000-grain weight (g), biological yield/plant (g), grain yield/plant (g), harvest index (%) and gluten content (%). For flag leaf area (cm^2), length and the maximum width of flag leaf was measured and the area was calculated using formula suggested by Muller (1991) as flag leaf area = leaf length × maximum leaf width ×correction factor (0.74). Components of genetic parameters were calculated following Hayman, (1954). The analysis of variance were estimated following Panse and Sukhamte (1967). The combining ability analysis was done following method-II, model-I by Grifing (1956a). The expectations in biometrical scale for various statistics were worked out following Hayman (1954) approach. Where, D = variation due to genetic effects, H_1= variation due to dominance genetic effects, H_2= proportion of +/-genes, F= mean covariance of additive and dominance effects, h^2= overall dominance effects and E= variation attributed to environmental effects. Related statistics of components of variance included (i) average degree of dominance $(H_1/D)^{1/2}$, (ii) proportion of genes with positive and negative effects in the parents ($H_2/4\ H_1$), (iii) proportion of dominant and recessive genes in the parents, F being in-significantly different from zero $[(4D\ H_1)^{0.5} + F/(4D\ H_1)^{1/2} - F]$ and (iv) number of groups of genes control the traits and exhibited dominance (h_2/H_2) to work out gene action for various traits under study.

RESULTS AND DISCUSSION

The results obtained for significance of variance among the treatments was tested by "F" test and are presented alongwith mean squares and other parameters (Table1). The variance due to treatments were further partitioned into their orthogonal components namely, parents, hybrids and parents vs hybrids. The "F" test indicated that variance due to treatments was highly significant for all the traits under study. Also, parents vs hybrids showed highly significant differences for all the traits exccept days to 50 % flowering and flag leaf area. Whereas, variance due to parents and hybrids were found highly significant for all the traits except grains per spike. The results revealed sufficient genetic variability in the present set of material that allowed us to further partion genetic effects. The estimated value of all the genetic components of variation (D, H_1, H_2, h^2, F and E) along with standard error and related parameters are presented (Table 3). The non significant value of t^2 for all the traits in F_1s combinations are presented (Table 2) indicated the validity of hypothesis. Significant value of t^2 indicated the failure of one or more assumptions that might be due to sampling error. Non-significant value of regression coefficient from unity suggested absence of gene interaction. The absence of gene interaction in bread wheat has also been reported by Pooranchand (1999), Mehta *et al.* (2000) and Singh *et al.* (2012).

The additive genetic variance were significant for nine traits (plant height, peduncle length, number of productive

Table 1 Analysis of variance for fourteen agro-morphological traits and grain yield in bread wheat

Trait	Replication (df=2)	Treatment (df=54)	Parents (df=9)	Hybrids (df=44)	Parents vs Hybrids (df=1)	Error (df=108)	Total (df=164)
Days to 50% flowering	0.16	40.69**	16.51	46.39**	7.77*	1.61	42.46
Days to maturity	1.76	13.73**	5.20**	15.26**	23.28**	0.82	16.31
Plant height	15.68*	72.93**	129.42**	58.09**	217.37**	4.44	93.05
Peduncle length	0.75	23.17**	30.85**	21.17**	42.37**	0.99	24.91
Flag leaf area	4.12	123.54**	58.79**	139.02**	25.24*	4.48	132.14
Productive tillers/plant	0.14	0.48**	0.66**	0.35**	4.28**	0.07	0.69
Spike length	0.28	0.80**	1.29**	0.58**	5.93**	0.20	1.28
Spikelets/spike	2.17	10.94**	4.95*	7.84**	201.21**	2.26	15.37
Grains/spike	14.98	51.26**	28.11	17.45	1747.15**	18.21	84.45
Biological yield/plant	11.18	104.14**	98.83**	81.65**	1141.02**	7.47	122.79
Harvest index	0.31	13.43**	8.62**	10.94**	166.44**	2.20	21.14
1 000 grain weight	1.12	18.30**	17.57**	6.16**	559.01**	1.72	70.54
Grain yield/plant	0.67	68.34**	140.49**	49.39**	252.55**	1.53	15.94
Gluten content	0.08	0.38**	0.33	0.39**	0.24	0.20	0.66

*, ** Significant at 5 and 1% probability level, respectively.

Table 2 Estimates of genetic component and related parameters for agro-morphological traits in bread wheat

Genetic parameter	Days to flowering	Days to maturity	Plant height	Peduncle length	Flag leaf area	Productive tillers/plant	Spike length	Spikelets/ spike	Grains/ spike	Biological yield	Grain yield	Harvest index	Test weight	Gluten content
D	4.98	1.45	41.59*	9.96*	18.11*	0.19*	0.36*	0.89*	3.31	30.43*	5.28*	46.32*	2.15	0.04
SE	3.79	1.00	3.93	1.35	8.09	0.02	0.04	0.35	2.11	8.38	2.33	4.58	1.36	0.02
H_1	63.45*	20.39*	80.56*	23.79*	99.25*	0.23*	0.32*	6.98*	28.93*	135.09*	22.35*	104.00*	13.26*	0.10*
SE	8.08	2.14	8.36	2.87	17.22	0.05	0.08	0.75	4.49	17.85	4.97	9.75	2.90	0.04
H_2	57.86*	18.00*	66.77*	21.17*	85.68*	0.22*	0.29*	6.92*	28.85*	110.80*	17.34*	70.01*	12.39*	0.09*
SE	6.87	1.82	7.11	2.44	14.63	0.04	0.07	0.64	3.81	15.17	4.22	8.28	2.46	0.04
F	8.72	2.69	42.36*	7.36*	-18.44	0.04	0.1	-1.84	-2.40	44.02*	9.90	72.30*	1.02	-0.11
SE	8.76	2.32	9.07	3.11	18.66	0.05	0.09	0.82	4.87	19.35	5.38	10.57	3.14	0.05
h^2	0.84	2.97*	28.14*	5.48*	2.79	0.55*	0.76*	26.28*	228.45*	149.71*	73.58*	33.15*	21.71*	0.008
SE	4.59	1.22	4.76	1.63	9.79	0.02	0.04	0.43	2.55	10.15	2.82	5.54	1.65	0.02
E	0.53	0.28	1.55	0.33	1.49	0.03*	0.07*	0.75*	6.05*	2.51	0.57	0.50	0.72	0.06*
SE	1.15	0.30	1.18	0.41	2.44	0.00	0.01	0.10	0.63	2.52	0.70	1.38	0.41	0.007
$(H_1/D)^{1/2}$	3.57	3.74	1.39	1.54	2.34	1.09	0.93	2.77	2.9	2.10	2.05	1.49	2.48	1.51
$H_2/4H_1$	0.22	0.22	0.20	0.22	0.21	0.23	0.23	0.25	0.24	0.20	0.19	0.16	0.23	0.25
$(4DH_1)^{1/2}+F/(4DH_1)^{1/2}-F$	1.65	1.65	2.15	1.62	0.64	1.19	1.34	0.45	0.78	2.04	2.67	3.17	1.21	0.09
h^2/H_2	0.01	0.16	0.42	0.25	0.03	2.53	2.56	3.76	7.91	1.35	4.24	0.47	1.75	0.08
r	0.31	0.51	0.91	0.94	0.79	0.78	0.78	0.92	0.78	0.39	-0.62	0.75	-0.07	0.84
h^2 (ns)	5.78	10.70	26.30	31.72	52.24	51.30	50.30	34.92	17.94	15.04	3.78	18.19	20.73	45.00

*, ** Significant at 5 and 1% probability level, respectively.

tillers per plant, flag leaf area, spike length, number of spikelets/spike, biological yield/plant, grain yield/ plant and harvest index) indicating the predominance of additive gene action in the inheritance of these traits. Whereas, dominance component was significant for the traits (days to 50% flowering, days to maturity, plant height, peduncle length, flag leaf area, productive tillers per plant, spike length, number of spikelets/spike, number of grains/spike, biological yield/plant, grain yield/plant, harvest index, 1 000 grain weight and gluten content) in F_1 generation. This showed higher magnitude of dominance components for all the traits. The estimates of H_1 were higher than the estimates of H_2 for all the traits under study indicating the unequal allelic frequencies at relevant loci in the populations. These results indicated that both additive and dominance gene action played important role in the inheritance of these traits. Similar findings of additive and dominant effects were also reported by Dayal *et al.*(2003), Singh *et al.* (2003, 2008, 2012, 2014), Ahmad *et al.* (2006), Dere and Yildrin (2006), Nazeer *et al.* (2011), Badeih *et al.* (2012), Yao *et al.* (2014), Farooq *et al.* (2015) and Kumar *et al.* (2015) for different traits related to yield and yield component in wheat. The analysis of variance components indicated that both additive and dominance variance are significant for almost all the trait under study, indicating that the expression of all these traits is controlled by both additive and dominance (non-additive) gene action. However, dominance components were predominent for all the traits under study. Similar to this significant additive and dominace genetic variation was reported by Farhad *et al.* (2011), Singh *et al.* (2012, 2014), Farooq *et al.* (2015) and Kumar *et al.* (2015). Positive and significant value of F component of genetic variance for the traits namely plant height, peduncle length, biological yield/plant and harvest index in F_1 cross combinations indicated possible role of dominant and positive alleles in the parents for improving these traits. Similar finding were also reported by Singh *et al.* (2003, 2008), Dere and Yildrin (2006), Farooq *et al.* (2015) and Kumar *et al.* (2015). The estimates of h^2 were positive and significant for days to maturity, plant height, peduncle length, productive tillers/plant, spike length, number of spikelets/spike, number of grains/ spike, biological yield/plant, grain yield/plant, harvest index and 1 000 grain weight, indicated dominance of genetic components in F_1s. Whereas, non-significant values were observed for remaining traits that indicated partial dominance of genetic components. Khan and Habib (2003), Adel and Ali (2013), Farooq *et al.* (2015) and Kumar *et al.* (2015) also reported similar findings. The environmental component (E) were significant for five traits and

Table 3 Estimates of regression parameters for yield and its components traits in bread wheat

Trait	b	SEb	b-o/SEb	b-1/SEb	T^2	r
Days to 50% flowering	0.726	0.765	-0.950	0.358	7.56	0.32
Days to maturity	0.316	0.187	-1.688	3.652	2.74	0.51
Plant height	1.111	0.169	-6.564	-0.657	1.88	0.92
Peduncle length	0.621	0.076	-8.215	5.009	14.12	0.95
Flag leaf area	0.478	0.131	-3.643	3.973	5.82	0.79
Productive tillers/ plant	0.888	0.250	-3.546	0.449	0.33	0.78
Spike length	0.729	0.201	-3.634	1.348	0.13	0.78
Spikelets/spike	0.496	0.071	-7.024	7.151	25.66	0.93
Grains/spike	0.318	0.088	-3.611	7.744	22.57	0.79
Biological yield/ plant	0.366	0.302	-1.211	2.097	0.05	0.39
Grain yield/plant	-0.420	0.183	2.289	7.744	2.29	-0.63
Harvest index	1.138	0.352	-3.232	-0.392	3.34	0.75
1000 grain weight	-0.081	0.406	0.199	2.659	0.16	-0.07
Gluten content	0.74	0.168	-4.39	1.57	0.48	0.84

nonsignificant for other eight traits. However, its value was much lower than that of D or H_1 components for all traits. The traits showing significant environmental components included productive tillers/plant, spike length, number of spikelets/spike, number of grains/spike and gluten content. It may be concluded from the above results that these traits are under the influence of environmental factors. Singh *et al.* (2003, 2014) and Yao *et al.* (2014) also reported that non additive type of gene effects are important for number of productive tillers per plant. Farooq *et al.* (2010) and Singh *et al.* (2014) reported that additive gene action played a predominant role in the inheritance of plant height and peduncle length.

The estimates of average degree of dominance expressed as $(H_1/D)^{1/2}$ were found to be more than unity in F_{1s} cross combinations for the traits namely, days to 50% flowering, days to maturity, plant height, peduncle length, flag leaf area, productive tillers/plant, number of spikelets/spike, number of grains/spike, biological yield/plant, grain yield/plant, harvest index, 1 000-grain weight and gluten content, indicating the preponderance of over dominance gene action. Whereas, the average degree of dominance for spike length was found less than unity and greater than zero indicated partial dominance. Similar findings for dominance and partial dominance for different yield contributing traits in wheat were reported by Singh *et al.* (2003), Khan and Habib (2003), Dere and Yildrin (2006), Hussain *et al.* (2012), Adel and Ali (2013) and Kumar *et al.* (2015). The proportion of genes with positive and negative effects in the parents $(H_2/4H_1)$ was found less than its theoretical value (0.25) for all the traits in F_1 combinations indicated asymmetrical distribution of positive and negative genes in the parents. Similar finding were also reported by Dayal *et al.* (2003), Singh *et al.* (2003), Farooq *et al.* (2011, 2015) and Kumar *et al.* (2015).

The estimates of the ratio showing proportion of dominant and recessive alleles among the parents was more than unity for 10 traits namely (days to 50 % flowering, days to maturity, plant height, peduncle length, productive tillers/plant, spike length, biological yield/plant, grain yield/plant, harvest index and 1 000 grain weight) indicated role of more dominant alleles in the parents for these traits. Whereas, this ratio was less than one for the traits namely, flag leaf area, number of spikelets per spikes, number of grains per spike and gluten content, reflecting the role of more recessive alleles in the parents for these traits and similar findings were reported by Gill *et al.* (1986), Nazeer *et al.* (2011), Farooq *et al.* (2015) and Kumar *et al.* (2015).

The estimates of ratio for number of gene groups was more than one for seven traits (number of productive tillers/plant, spike length, number of spikelets/spike, number of grains/spike, biological yield/plant, grain yield/plant and

Table 4 Best cross combination the basis of significant sca effects for 14 traits in bread wheat

Trait	Best cross	SCA	GCA		Nature of gene action
			P_1	P_2	
Days to 50 % flowering	K-9423 × HUW-560	-5.44**	-0.36	0.59**	Non additive
Days to maturity	K-9162 × UP-2425	-3.56**	-0.38**	-0.36*	Additive
Plant height	K-9423 × Unnat-halna	-6.38**	3.15**	-1.62**	Non additive
Peduncle length	NW-1014 × NW-1076	4.58**	0.89**	0.47**	Additve
Flag leaf area	Raj-3765 × PBW-373	10.67**	-0.93**	-5.82**	Non additive
Productive tillers/plant	Raj-3765 × NW-1014	0.60**	-0.22**	-0.06	Non additive
Spike length	K-9162 × UP-2425	0.65**	-0.14*	0.09	Non additive
Spikelets/spike	K-9423 × NW-1076	2.79**	0.70**	0.69**	Additive
Grains/spike	PBW-373 × UP-2425	5.13*	0.11	-021	Non additive
Biological yield/plant	PBW-373 × UP-2425	10.86**	-1.35**	0.19	Non additive
Grain yield/plant	K-9423 × NW-1014	4.01**	0.19	0.09	Non Additive
Harvest index	Raj-3765 × NW-1076	8.85**	-2.23**	0.65**	Non additive
1000-grain weight	Raj-3765 × Unnat-halna	3.59**	-0.82**	-1.40**	Non additive
Gluten content	Unnat-halna × HUW 560	0.54*	-0.36**	-0.33**	Non additive

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

1 000 grain weight) indicated involvement of more than one major gene groups that are responsible for inheritance of these traits. Whereas, this ratio was less than unity for the traits (days to 50% flowering, days to maturity, plant height, peduncle length, flag leaf area, harvest index and gluten content) indicated the involvement of single gene groups in the inheritance of these traits. Similar findings were also reported by Singh *et al*. (2003) and Kumar *et al.* (2015).

The general combining ability is primarily a function of additive and additive × additive gene action, whereas specific combining ability is owing to non-allelic intrection and overdominance. The narrow-sense heritability was moderate for flag leaf area (52.24), productive tillers/plant (51.30), spike length (50.30), gluten content (45.00), spikelets/spike (34.92) and peduncle length (31.72) (Table 2). Therefore, early generation selection for these traits will be rewarding. Khiabani *et al.* (2015) reported high estimates of narrow sense heritability for spikelets/spike, spike length, peduncle length, Singh *et al.* (2014) also reported high estimates of narrow sense heritability for spike length and Yao *et al*. (2011) and Farooq *et al.* (2015) for peduncle length.

The trait wise estimates of SCA effects (Table 4) revealed that the cross combination K 9162 x UP 2425 exhibited desired highest negative significant SCA effects for days to 50% flowering (early flowering type) alongwith highest positive effects for spike length; cross PBW 373 × UP 2425 exhibited positive significant SCA effects for grains per spike and biological yield per plant; K 9423 × Unnat Halna exhibited highest negative significant SCA effects for plant height; K 9423 × HUW 560 exhibing highest significant SCA effects for days to 50% flowering; Raj 3765 × NW 1014 showed highest positive significant SCA effects for plant height; K 9423 × NW 1014 showed highest positive significant SCA effects for grain yield/plant. Combinations namely NW 1014 × NW 1076 for peduncle length; Raj 3765 × PBW for flag leaf area; K 9423 × NW 1076 for number of spikelets /spike; Raj 3765 × NW 1076 for harvest index; Raj 3765 × Unnat Halna for 1 000-grain weight and Unnat Halna × HUW 560 for gluten content exhibited high positive and significant SCA effects for individual trait. These combinations may be further exploited through heterosis breeding to improve trait (s) of interest in wheat crop. Such reports for SCA/GCA effects were also reported by Yao *et al.* (2014), Singh *et al*. (2014), Khiabani *et al.* (2015) and Kumar *et al.* (2015) for different yield and its contributing traits in bread wheat.

The traits which showed dominance or non-additive type of gene effects, might be improved by intermating the most desirable segregates followed by selection. Whereas, traits that exhibited predominance of non-additive gene effects would require maintaining considerable heterozygosity through mating of selected plant in early segerigating generations to attain maximum genetic gain. Therefore, few cycles of recurrent selection followed by pedigree breeding would be effective for the improvement of grain yield.

It may be concluded that both additive and non-additive component of genetic variances were involved in governing the inheritance of the almost all the quantitative traits including grain yield in the present set of material. Generation advancement of selected F_1s crosses showing highest SCA effects and further hybridization involving parents with good GCA into multiple cross combinations might improve yield and quality. Therefore, biparental mating and/or diallel selective mating would be useful to exploit both additive and non additive gene effects. The traits that showed high narrow sense heritability can play greater role for additive genetic components therefore selection for these traits in early generation would be effective. Therefore, findings of the present investigation could help in formulating future breeding programme to develop the high yielding and better quality wheat genotypes for food and nutritional security.

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