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Estimates of genetic parameters for grain yield, agro-morphological traits and quality attributes in bread wheat (*Triticum aestivum*)

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ABSTRACT

A study for estimating genetic parameters was carried out by involving 10 parents and their 45 F_1's planted in randomized block design (RBD) having three replications revealed significant variance for all the characters under study. The analysis of genetic components showed that significant additive and dominant components for all the traits. Positive and significant value of 'F' for yield and quality components in F_1 crosses indicated the preponderance of dominant and positive genes in the parents. The estimates of h^2 were found highly significant for number of productive tillers/ plant, flag leaf area, spike length, spikelets/ spike, biological yield/ plant, grain yield/ plant, harvest index, ash content and gluten content, whereas, non-significant values were reported for rest of the traits. The value of ($H_2/4H_1$) for all the traits indicated the asymmetrical distribution of positive and negative alleles among the parents. The proportion of dominant and recessive genes indicated presence of dominant alleles in the parents for these traits. The ratio of $h^2/H_2$for eight traits in F_1 generation revealed that more than one major gene group was responsible for controlling these traits. Estimates of SCA effects revealed that the best cross combinations namely; DBW 58/ HD 2687, DBW 58/ DBW 17, PBW 590/HD 2687, PBW 373/DBW 17, PBW 373/RAJ 3765, HD 2687/WH 711, MP 1236/PBW 373, MP 1236/HD 2687, MP 1236/PBW 590, PBW 550/HD 2687 and PBW 550/DBW 17 for respective yield components and quality traits may be exploited through heterosis breeding programme to improve these traits in wheat (*Triticum aestivum* L.). It may be concluded from the present investigation that these parental lines can be used as donors for improving both components in future by following bi-parental mating and diallel selective mating system could be the best breeding method in early segregating generations for improvement in these traits.

Key words: Diallel cross, Gene action, Quality traits, Wheat, Yield

Wheat (*Triticum aestivum* L.) is one of the most important cereal crops of the world after rice. It occupies a notable position among foodgrains of the world not only in terms of acreage and production but also for its versatility in adaptation to a wider range of agro-climatic conditions. Because of its versatility in adaption and utility in various ways, wheat is grown in more than 44 countries globally. Among the several approaches followed for the genetic analysis of quantitative characters, diallel analysis is most effective with proven merits for ascertaining the systematic genetic architecture of metric traits within a short period. The improvement in grain yield of wheat genotypes in a sustainable manner would mainly depend upon the genetic potential and desired inherent genetic variability that should exist in the population with regards to grain yield. When a population with considerable genetic variability (predominantly of additive in nature) is subjected to selection, a change in gene frequency in the progenies is a natural consequence of the process. Diallel mating design has been recognised as a useful tool for genetic analysis and used extensively by wheat breeders to analyse mating system in which a set of genotypes are inter-crossed in all possible combinations. The results obtained from diallel analysis of genetic components throw light on the presence or absence and magnitude of additive and non-additive gene action and estimates of gene action are important in launching a successful wheat breeding programme. Diallel analysis developed by Hayman (1954) provides information on genetic mechanism involved in early generation. The major objective of the present study was to generate information on gene action and magnitude of contributing yield and quality components using 10 × 10 diallel excluding reciprocals. The information generated would be effectively exploited to develop an appropriate breeding strategy for

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continued genetic improvement in wheat crop, for evolving new genotypes with desirable yield and ultimate good quality for nutritional security.

MATERIALS AND METHODS

The study material comprising ten wheat genotypes (MP 1236, PBW 550, WH 1094, PBW 590, PBW 373, RAJ 3765, DBW 58, HD 2687, DBW 17 and WH 711) was sown at Crop Research Centre, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut during *rabi* 2010-2011 for attempting crossing programme in a diallel fashion (10×10). The pedigree details and other passport data showing diversity among these genotypes are given below in Table 1.

In the following crop season (*rabi* 2011-2012), experimental material comprising total 55 genotypes (10 parental line and 45 F_1's) was planted in a Randomized Block Design (RBD) having three replications. Each of the parental lines and crosses were raised by dibbling seeds in two rows plot of 3m length at spacing of 10cm between plants. Row to row spacing of 25cm was maintained. All the recommended agronomic practices were followed to raise good crop. Observations were recorded on ten randomly selected competitive plants in each of three replications for fourteen different characters namely days to 50% flowering, days to maturity, number of productive tillers/plant, plant height, flag leaf area, spike length, spikelets/spike, grains/spike, 1000-grain weight (g), biological yield/plant (g), grain yield/plant (g), harvest index, ash content and gluten content. The data were analyzed for analysis of variance model suggested by Panse and Sukhatme (1969). Components of genetic parameters were calculated as per the methods given by Hayman (1954). The combining ability analysis was done following method 2 -model I of Griffing (1956a).The expectations in biometrical scale for various statistics were worked out following Hayman (1954) approach.

The genetic components studied included; D (variation due to genetic effects), H_1 (variation due to dominant 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) mean degree of dominance$(H_1/D)^{½}$, (ii) proportion of genes with positive and negative effects in the parents $[H_2/4H_1]$, (iii) proportion of dominant and recessive genes in the parents, F being insignificantly different from zero $[(4DH_1)$ ½ + F/ $(4DH_1)$ ½ - F] and (iv) number of groups of genes which control the character and exhibit dominance $[h_2/H^2]$ were also worked out.

RESULTS AND DISCUSSION

The results obtained for testing the significance of variance among the treatments by "F" test and mean squares and other parameters are presented (Table 2). 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 characters under study. Parents vs hybrid also showed highly significant differences for all the characters except days to maturity and grains/spike. This revealed that the significant variability exists in present set of material that allowed us for further partitioning of genetic effects. The understanding of variation and genetic architecture of a population is of considerable importance in formulating the efficient breeding programme. The estimated values of all the genetic components of variation (D, H_1, H_2, h^2, F and E) along with standard errors and related parameters are presented (Table 3).

The estimates of additive genetic variance (D) were highly significant for all the traits under study indicating the predominance of additive gene action in the inheritance of these traits. The dominance components (H_1 and H_2) were also found highly significant for all the traits, viz days to 50% flowering, days to maturity, number of productive tillers/plant, plant height, flag leaf area, spike length, spikelets/spike, grains/spike, 1000-grain weight, biological yield/plant, grain yield/plant, harvest index, ash content and gluten content in F_1 generation.

This showed higher magnitude of dominance components for all the characters. The estimates of H_1 were

Table 1 Pedigree and other passport details of parental lines used for present study

Parent	Parentage/pedigree	Area of adoption	Production condition	Source/origin
MP1236	GW276/PBW429/HI1077	CZ	IR,LS	JNKVV, Jabalpur
PBW550	WH 594/RAJ 3814//W 495	NWPZ	IR,TS	PAU, Ludhiana
PBW590	WH 594/RAJ 3814//W 485	NWPZ	IR,LS	PAU, Ludhiana
PBW373	ND/VG 1944//KAL/BB/3/YACO'S'4/VEE#5'S'	NWPZ	IR,LS	PAU, Ludhiana
DBW58	ATTILA/3*BCN//BAV92/3/TILHI	NWPZ	IR,TS	DWR, Karnal
DBW17	CMH 79A.95/3*CNO79//RAJ 3777	NWPZ	IR,TS	DWR, Karnal
RAJ3765	HD 2402/VL 639	NW/NEPZ	IR,LS/VLS	RAU, Rajasthan
HD2687	CPAN 2009/HD 2329	NWPZ	IR,TS	IARI, New Delhi
WH1094	WH337/HD2285//URES/BOW	NWPZ	IR,LS	CCSHAU, Hisar
WH711	S 308/ CHR//KAL	NWPZ	IR,TS	CCSHAU, Hisar

NEPZ=North Eastern Plains Zone; NWPZ=North Western Plains Zone; CZ=Central Zone; IR=Irrigated; TS=Timely sown;LS=Late Sown; and VLS=Very Late Sown

Table 2 Analysis of variance for 14 agromorphological and quality traits in bread wheat

Source of variation	DF	Days to 50% flowering	Days to maturity	Productive tillers/ plant	Plant height	Flag leaf area	Spike length	Spikelets/ spike	Grains/ spike	1000-grain weight	Biological yield	Grain yield	Harvest index	Ash content	Gluten content
Replication	2	1.82	1.04	0.09	1.21	7.81	0.02	0.08	2.55	1.43	5.76	1.39	4.42	0.012	0.02
Treatments	54	30.99**	7.67**	2.40**	119.78**	106.24**	1.03**	1.19**	68.97**	19.66**	83.78**	24.34**	27.60**	0.052**	0.32**
Parents	9	70.80**	13.91**	3.38**	305.35**	142.36**	1.40**	3.74**	115.44**	29.64**	61.05**	45.91**	63.02**	0.063**	0.31**
crosses	44	23.27**	6.56**	1.23**	83.86**	92.90**	0.92**	0.37**	61.01**	15.72**	85.15**	17.06**	16.28**	0.046**	0.29**
Parent vs. crosses	1	12.41**	0.34	44.81**	30.20**	367.70**	2.63**	14.76**	1.31	103.21**	227.67**	150.47**	207.29**	0.214**	1.75**
Error	108	0.87	0.76	0.38	1.64	3.32	0.08	0.10	3.93	4.55	2.62	1.49	8.66	0.011	0.04
Total	164	10.80	3.04	1.04	40.53	37.26	0.39	0.46	25.33	9.49	29.38	9.01	14.84	0.025	0.13

*,**Significant at (P=0.05) and (P=0.01), respectively.

higher than the value of H_2 for all characters indicating unequal allelic frequencies at relevant loci in the population. These results indicated that both additive and dominant gene action played important role in the inheritance of these traits. Such findings of additive and dominant effects were also reported by Sheikh *et al.* (2000), Kashief and Khaliq (2003), Singh *et al.* (2003), Ahmad *et al.* (2006), Dere and Yildirin (2006), Nazeer *et al.* (2010), Ahmad *et al.* (2011), Nazeer *et al.* (2011), Badieh *et al.* (2012) and Singh *et al.* (2014) for different characters related to yield and yield components in wheat.

The values of 'F' were positive and significant for days to 50% flowering, plant height, spikelets/spike, grains/spike, grain yield/plant, harvest index and ash content in F_1 combinations that indicated the role of dominant and positive alleles in the parents for improving these characters. Similar findings were also found by Singh *et al.* (2003) and Dere and Yildirin (2006). The estimates of h^2 were reported to be significant and positive for number of productive tillers/plant, flag leaf area, spike length, spikelets/spike, biological yield/plant, grain yield/plant, harvest index, ash content and gluten content, which indicated dominance of genetic component in F_{1s}. Whereas, non-significant values observed for remaining the characters indicated partial dominance of genetic component. Sheikh *et al.* (2000), Khan and Habib (2003) and Adel *et al.* (2013) reported similar findings for most of the characters as given in the present study.

The estimates for degree of dominance $(H_1/D)^{1/2}$ were found to be more than unity in F_1 generation for the characters namely, number of productive tillers/plant, flag leaf area, spike length, spikelets/spike, grains/spike, biological yield per plant, harvest index, ash content and gluten content that indicated the existence of over dominance. While the degree of dominance for characters, viz days to 50% flowering, days to maturity, plant height, 1000 grain weight and grain yield/plant was less than unity which revealed partial dominance. The findings of over dominance and partial dominance for individual traits are in conformity with those of Sheikh *et al.* (2000), Khan and Habib (2003), Singh *et al.* (2003), Dere and Yildirin (2006), Akram *et al.* (2009), Ahmad *et al.* (2011), Hussain *et al.* (2012) and Adel *et al.* (2013). 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 characters, viz days to 50% flowering, days to maturity, number of productive tillers/plant, plant height, flag leaf area, spike length, spikelets/spike, grains/spike, 1000-grain weight, biological yield/plant, grain yield/plant, harvest index, ash content and gluten content indicated asymmetrical distribution of positive and negative genes/alleles in the parents. Similar findings were also reported by Dhayal *et al.* (2003) in wheat crop.

The ratio $[(4DH_1)^{½} + F/ (4DH_1)^{½} - F]$ that indicates the proportion of dominant and recessive alleles among the parents was more than one for 12 characters, viz days to 50% flowering, days to maturity, number of productive tillers/plant, plant height, flag leaf area, spike length, spikelets/spike, grains/spike, 1000-grain weight, grain yield/plant, harvest index and ash content. This indicates about accumulation of desired alleles in the parents for these characters. Whereas, this ratio was less than unity for only two characters namely, biological yield/plant and gluten content, reflecting role of more recessive alleles in the parents for these two characters and similar findings have been reported by Nazeer *et al.* (2011).

The ratio of h^2/H_2 (number of gene groups) was more than one for eight characters, viz number of productive tillers/plant, flag leaf area, spikelets/spike, 1000-grain weight, biological yield/plant, grain yield/plant, harvest index and gluten content indicating involvement of more than one major gene groups for controlling inheritance pattern of these traits. However for rest of the characters the ratio of h^2/H_2less than unity that indicated the

Table 3 Estimates of genetic components and other parameters for 14 agro-morphological and quality traits in wheat

Genetic parameter	Days to 50% flowering	Days to maturity	Productive tillers/ plant	Plant height	Flag leaf area	Spike length	Spikelets/ spike	Grains/ spike	1000 grain weight	Biological yield	Grain yield	Harvest index	Ash content	Gluten content
Additive variance (D)	23.31**	4.38**	1.00**	101.24**	46.32**	0.44**	1.21**	37.18**	8.38**	19.46**	14.81**	18.14**	0.017**	0.09**
SE	0.889	0.353	0.179	3.347	4.448	0.049	0.080	2.805	0.611	2.262	0.845	2.882	0.007	0.026
Dominance variance (H_1)	9.43**	3.63**	1.64**	37.49**	57.97**	0.67**	1.45**	44.26**	6.84**	37.31**	11.32**	44.58**	0.075**	0.19**
SE	1.891	0.752	0.381	7.124	9.468	0.103	0.171	5.972	1.300	4.816	1.798	6.135	0.014	0.056
Proportion of +/- genes (H_2)	6.66**	3.12**	1.46**	29.98**	47.85**	0.58**	0.84**	35.92**	6.11**	28.57**	9.04**	19.62**	0.050**	0.18**
SE	1.607	0.639	0.324	6.055	8.046	0.088	0.145	5.075	1.105	4.093	1.528	5.214	0.012	0.047
Mean covariance of additive and dominance effects (F)	9.77**	1.55	0.67	49.12**	8.68**	0.14	1.68**	17.58**	0.89	-17.88	6.79**	39.84**	0.036**	-0.01
SE	2.050	0.816	0.413	7.722	10.262	0.112	0.185	6.473	1.409	5.220	1.949	6.650	0.015	0.060
Overall dominance effects (h^2)	1.53	-0.05	5.87**	3.79**	48.13**	0.34**	1.94**	-0.29	13.08**	29.73**	19.68**	26.33	0.027**	0.23**
SE	1.076	0.428	0.217	4.053	5.386	0.059	0.097	3.397	0.739	2.740	1.023	3.490	0.008	0.032
Environmental (E)	0.29	0.25	0.13	0.54	1.13	0.03	0.03	1.30	1.50	0.89	0.49	2.86	0.004	0.01
Mean degree of dominance	0.64	0.91	1.28	0.61	1.12	1.23	1.10	1.09	0.90	1.39	0.87	1.57	2.076	1.46
Pro. of genes with +/- effects	0.18	0.21	0.22	0.20	0.21	0.22	0.14	0.20	0.22	0.19	0.209	0.11	0.167	0.24
Pro. of dom. & recessive genes	1.98	1.48	1.71	2.33	1.18	1.30	4.45	1.55	1.13	0.50	1.71	5.68	2.972	0.88
No. of gene groups	0.23	-0.01	4.03	0.13	1.01	0.59	2.31	-.01	2.14	1.04	2.18	1.34	0.541	1.24

*,**Significant at (P=0.05) and (P=0.01), respectively.

Table 4 Trait-wise best cross combination based on significant SCA effects in desirable direction

Character	Cross combination	SCA effects	GCA effects		Nature of gene action
			P_1	P_2	
Days to 50% flowering	DBW 58/HD 2687	–1.96**	–0.84*	–0.97**	Additive
Number of tillers/plant	DBW 58/HD 2687	1.87**	–0.84*	–1.36**	Non-additive
Biological yield/plant	DBW 58/DBW 17	8.08**	–0.84*	–0.97**	Non-additive
Grain yield/plant	DBW 58/DBW 17	3.93**	–0.84*	–0.97**	Additive
Days to maturity	MP1236/PBW590	–2.33**	0.34	–0.31	Additive
1000 grain weight	MP 1236/PBW 373	2.06	0.34	4.22**	Additive
Harvest index	MP 1236/HD 2687	5.27**	0.34	–1.36**	Non-additive
Flag leaf area	PBW 590/HD 2687	6.47**	–0.31	–1.36**	Non-additive
Spike length	PBW 373/DBW 17	0.71**	4.22**	–0.97**	Non-additive
Spikelets/spike	PBW 373/RAJ 3765	0.77**	4.22**	0.52**	Non-additive
Ash content	PBW 550/HD 2687	0.231**	–0.11	–1.36**	Non-additive
Gluten content	PBW 550/DBW 17	0.64**	–0.11	–0.97**	Non-additive
Grains/spike	HD 2687/WH 711	6.67**	–1.36**	–1.60**	Non-additive
Plant height	WH 1094/PBW 590	–8.41**	0.10	–0.31	Additive

presence of at least one major gene or gene group in controlling these traits. Similar findings were also reported from made done by Singh *et al.* (2003).

The traits wise (Table 4) estimates of SCA effects revealed that the cross combinations DBW 58/HD 2687 exhibited highest negative significant SCA effects for days to 50% flowering (early flowering type) with highest positive effect for number of productive tillers/plant; MP 1236/PBW 590 exhibiting highest negative SCA effects for plant height; DBW 58/DBW 17 exhibiting highest positive significant effects for biological yield and grain yield. The other cross combinations exhibiting highest positive significant only for single character wise PBW 590/HD 2687 for flag leaf area; PBW 373/DBW 17 for spike length; PBW 373/RAJ 3765 for spikelets/spike; HD 2687/WH 711 for grains/spike; MP 1236/PBW 373 for 1000-grain weight; MP 1236/HD 2687 for harvest index; PBW 550/HD 2687 for ash content and PBW 550/DBW 17 for gluten content. These individual crosses or their combinations may be exploited in heterosis breeding programme to improve involved traits in wheat. Such type findings of SCA/GCA effects were also reported by Singh *et al.* (2014) for different characters related to yield and yield components in wheat.

The estimates of nature and magnitude of gene action and selection of suitable parents and crosses is a prerequisite in order to propose a systematic and effective breeding programme as well as utilization of suitable parents and crosses in further breeding programme for rapid and sequential improvement in a targeted crop. The general combining ability (gca) is primarily a function of additive and additive × additive gene action, whereas specific combining ability (sca) is owing to non-allelic interaction and over dominance.

It may be concluded that the preponderance of both additive (fixable) and non-additive (non-fixable) components of genetic variance appeared important in the expression of almost all the traits in present set of material. Since the parental lines used are mostly recently released varieties that could serve as base material for development of new genotypes having higher yield and better farmer's acceptance for grain quality. Generation advancement of selected F_1 crosses showing highest SCA effects and further hybridization involving parents with good GCA into multiple cross combination may improve yield and quality. Besides, for exploitation of both the additive and non-additive component of variation, advance generation material may be handled through pedigree method of selection. Whereas, in other case bi-parental mating for obtaining superior segregants may be followed. Therefore, findings of present investigation and information generated will help in formulating breeding programme to develop of high yielding and better quality wheat genotypes for food and nutritional security.

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