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Genetic analysis for various agromorphological and quality traits in bread wheat (*Triticum aestivum*)

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ABSTRACT

A study was made to estimate gene action and combining ability effects involving 10 diverse parents and their 45 F_1s (half diallel approach) developed and evaluated during 2012-13 and 2013-14 crop seasons, respectively. The general combining ability (GCA) estimates for bread wheat (*Triticum aestivum* L.) genotypes namely, HD 2967 (days to maturity, plant height); DBW 90 (plant height, spikelets/spike, grains/spike, grain yield); HD 2824 (plant height, spikelets/spike); HD 3095 (spikelets/spike, grains/spike, grain yield); and HD 2733 (plant height, days to maturity and grains/spike) showed favourable GCA effects. Estimates of specific combining ability (SCA) effects revealed that cross combinations DBW 90 × HD 2733, HD 3095 × RAJ 4246, PBW 435 × HD 2824, PBW 435 × RAJ 4246 and HD 2967 × RAJ 4246 showed high and significant SCA effects, and thus might be exploited through heterosis breeding to improve these traits. Significant values of additive (D) and dominance (H_1) variance for six traits (plant height, grains/spike, spikelets/spike, 1000-grain weight, gluten content and grain yield) indicated that expression of these traits is controlled by both additive and non-additive type of gene action. Positive and significant values of h^2 for plant height, grains/spike, spikelets/spike, 1000-grain weight and grain yield; indicated preponderance of dominance component. Average degree of dominance $(H_1/D)^{1/2}$ was more than unity in most of the F_{15} for grains/spike, spikelets/spike, 1000-grain weight, gluten content and grain yield, thereby indicating the preponderance of over-dominance gene action. Positive and significant values of F-test indicated the preponderance of dominance and positive genes in the expression of these traits. The proportionate distribution of dominant and recessive alleles indicated presence of dominant alleles in the parents. Regression analysis indicated that days to maturity, plant height, grains/spike, 1000-grain weight, gluten content and grain yield were governed by dominance gene action. Genotype HD 3095 contained maximum dominant genes for days to maturity, spikelets/spike; while HD 2967 for plant height, grains/spike, 1000-grain weight and HD 2824 for gluten content and grain yield that thus these could be utilized as donors for bi-parental mating or diallel selective mating system for improvement in these traits.

Key words: Combining ability, Genetic components, Regression analysis, Wheat, Yield, Quality traits

Wheat (*Triticum aestivum* L.) is a predominant cereal crop and India is second largest wheat producing nation after China. The other major wheat producing countries include Russian Federation, United States of America and Canada and these five countries together contribute more than half of the global wheat production (Singh *et al.* 2010). The major aim of any wheat breeding programme is to create new genetic variability and gather information about the genetic architecture of component traits that are polygenic in nature and also influenced by the environmental factors. Improvement in grain yield is feasible only by improving component traits, knowing their gene action and combining ability effects among the parents with wider adaptability. In addition, general combining ability (GCA) gives the information about additive and additive × additive gene action; whereas specific combining ability (SCA) provides information about the non-allelic interaction and dominance gene action. The choice of parental lines and planned hybridization programme are the two factors for deciding breeding programme. Improvement in desired traits is feasible through planned strategy and making selection process based on target traits. The major objective of the present investigation was to generate material and information on nature and type of gene action, identify the best combining parents on the basis of their general and specific combining ability and contribution of major components to grain yield and quality traits to develop future genotypes.

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MATERIALS AND METHODS

The base material consisted of 10 diverse genotypes of bread wheat namely, PBW 435, HD 2967, MP 3336, MP 4010, DBW 90, HD 2824, HD 3095, RAJ 4246, NW 5038 and HD 2733 was planted at Crop Research Centre, SVBPU&T, Meerut during *rabi* 2012-2013 for attempting crosses following 10 × 10 half diallel system (excluding reciprocals). In the next crop season (*rabi* 2013-2014), complete set of experimental material (10 parents and their 45 F_1s) was planted in a randomized block design (RBD) having three replications. Seeds of each of the parental line and also F_1s were dibbled in two-row plot of 2 m length maintaining spacing of 10 cm among the plants within a row and 23 cm between the rows. All the standard agronomical practices were followed to raise normal crop. Observations were recorded on randomly selected plants from each replication for seven traits namely; days to maturity, plant height (cm), number of spikelets/spike, number of grains/spike, 1000-grain weight (g), grain yield/ plant and gluten content (%). The analysis of variance was estimated following Panse and Sukhamte (1967). Diallel analysis was carried out by method described by Mather and Jinks (1982) and genetic parameters were estimated by method described by Hayman (1954). The combining ability analysis was done following method-II, model-I as suggested by Griffing (1956).

RESULTS AND DISCUSSION

Analysis of variance (ANOVA) indicated significant differences for most of the traits (Table 1) namely days to maturity, plant height, spikelets/spike, grains/spike, 1000-grain weight and grain yield in parents and in hybrids, whereas plant height, spikelets/spike, grains/spike, 1000-grain weight and grain yield in parents vs. hybrids, indicated the presence of considerable amount of genetic variability in the present set of experimental material and therefore further genetic analysis would be meaningful. The presence of high magnitude of genetic variability in present set of material might be due to the fact that parental genotypes selected for this study were of diverse nature as they were developed for different agro-climatic zones and conditions of the country and F_1s were developed by crossing among these 10 diverse genotypes following half diallel mating design.

The analysis of variance for combining ability was done for all the seven traits (Table 2). General and specific combining ability variances and effects were estimated with a view to decipher the genetic architecture of the traits under study. Significant variances for general and specific combining ability indicated the importance of both additive and non-additive gene action for all the traits except gluten content. Griffing (1956) reported that general combining ability (GCA) has been equated with additive gene action and specific combining ability (SCA) with non-additive gene action.

The estimated value of σ^2g was higher than its σ^2s

Table 1 Analysis of variance for various agromorphological and quality traits in bread wheat

Source of variation	DF	Days to maturity	Plant height	Spikelets/ spike	Grains/ spike	Grain yield	Gluten content	1000 grain weight
Replication	02	0.26	0.27	0.25	0.32	1.26	0.42	3.84
Treatments	54	2.14**	31.28**	1.14**	10.19**	9.85**	0.16	3.58**
Parents	09	4.52**	66.84**	1.89**	13.56**	7.11**	0.23	4.75**
Hybrids	44	1.70**	22.31**	0.88**	8.18**	3.75**	0.15	2.38*
Parents Vs F1s	01	0.16	105.46**	5.96**	68.40**	302.73**	0.18	45.96**
Error	108	0.76	0.73	0.10	1.15	0.78	0.15	1.58
Total	164	1.21	10.78	0.44	4.12	3.77	0.16	2.27

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

Table 2 Analysis of variance of combining ability for various traits in bread wheat

Source of variance	DF	Days to maturity	Plant height	Spikelets/ spike	Grain / spike	1000 grain weight	Gluten content	Grain yield
GCA	9	3.60**	53.74**	1.04**	11.05**	1.25*	0.10	2.68**
SCA	45	0.14	1.76**	0.25**	1.87**	1.18**	0.04	3.40**
Error	108	0.25	0.24	0.03	0.38	0.53	0.05	0.26
Estimated component of variance due to								
σ^2g		0.28	4.46	0.08	0.89	0.06	0.02	0.20
σ^2s		0.12	1.52	0.22	1.49	0.66	0.01	3.14
σ^2g/σ^2s		2.33	2.93	0.37	0.59	0.09	2	0.063
$(\sigma^2s/\sigma^2g)^{1/2}$		0.65	0.58	1.66	1.29	3.32	0.71	3.96

*Significant at 5% probability level; **Significant at 1% probability level, gca, general combining ability; sca, specific combining ability; σ^2g/σ^2s, ratio of gca variance to sca variance; $(\sigma^2s/\sigma^2g)^{0.5}$, degree of dominance for days to maturity and plant height which indicated the predominance of additive gene action as the ratio of σ^2g/σ^2s was more than unity while remaining traits namely, spikelets/spike, grains/spike, 1000-grain weight, gluten content and grain yield showed preponderance of non-additive type of gene action. The value of average degree of dominance (σ^2s/σ^2g) for days to maturity, plant height and gluten content indicated partial dominance, whereas spikelets/spike, grains/spike, 1000-grain weight and grain yield showed over-dominance. Singh *et al.* (2012), Singh *et al.* (2014), Kumar *et al.* (2015), Kumar *et al*. (2016c) and Gautam *et al.* (2016) reported similar pattern for different yield contributing traits in wheat.

The results obtained for GCA effects of the parents, indicated that none of the parent was a good general combiner for all the seven traits (Table 3). While there were numbers of parents possessing high GCA for individual or combination of traits. For example, genotype PBW 435 for plant height; HD 2967 for days to maturity and plant height; DBW 90 for plant height, spikelets/spike, grains/spike and grain yield; HD 2824 for plant height and spikelets/spike; HD 3095 for spikelets/spike, grains/spike and grain yield and HD 2733 for plant height, days to maturity and grains per spike had good favourable GCA effects. Findings reported by Kumar and Maloo (2012), Yao *et al.* (2014), Singh *et al*. (2014), Kumar *et al.* (2015), Kumar *et al*. (2016c) and Gautam *et al.* (2016) in wheat confirm this study results. Based on the above results, it is clear that some of the parents are good general combiner and therefore can be used for improving multiple traits simultaneously. Griffing (1956) reported that high GCA effects are mostly due to additive gene effects or additive × additive interaction effects. Therefore, breeders might utilize the good general combiners in specific breeding programme for improvement of grain yield in wheat.

The results based on estimates of SCA effects (Table 5) revealed that the combinations namely, MP 4010 × HD 3095 and DBW 90 × HD2733 exhibited high but negative significant SCA effects which is desirable for plant height (semi-dwarf plant type) along with positive effects on grain yield. Similarly, cross combination (HD 3095 × RAJ 4246) showed significant and high positive SCA effects for spikelets/spike and grains/spike along with positive effects on grain yield; while combination PBW 435 × HD 2824 showed that positive and significant SCA effects for 1000 grain weight and also had positive effects on grain yield; PBW 435 × RAJ4246 had high positive and significant SCA effects for gluten content along with positive effects for grain yield; and HD 2967× RAJ 4246 showed significant SCA effects for grain yield with desirable and significant effects onplant height and grains per spike. These combinations may be further exploited through heterosis breeding to improve trait of interest in wheat crop. Reports by Kumar and Maloo (2012), Yao *et al.* (2014), Singh *et al*. (2014), Kumar *et al.* (2015), Kumar *et al.* (2016c), Kumar *et al.* (2016d) and Gautam *et al.* (2016) for different yield components and gluten contain in wheat were confirmatory.

The results indicated that the best crosses involved all three types of parental combinations (high × high, high × low and low × low) based on their respective GCA effects for the traits under study. Therefore it is evident that high specific combiners are not always due to high general combiners but may occur due to low × low or high × low parental GCA effects also. However, in self-pollinated crops like wheat, the additive × additive type of epistasis is fixable in later generations. In view of the above, efforts may be made for obtaining transgressive segregants through planned hybridization and producing more potent homozygous lines. Crosses involving high × low parental GCA effects in respect of different traits may be utilized for obtaining transgressive segregants in the next generations resulting from dominance gene interaction.

The estimated values of all the genetic components of variance (D, H_1, H_2, h^2, F and E) alongwith standard

Table 3 Estimates of general combining ability effects for various traits in bread wheat

Trait parents	Days to maturity	Plant height	Spikelets/ spike	Grains/ spike	1000 grain weight	Gluten content	Grain yield
PBW 435	-0.03	-0.95**	0.04	0.31	-0.47*	-0.10	-0.46**
HD 2967	-0.64**	-0.50**	-0.15**	-0.69**	-0.29	0.08	-0.36*
MP 3336	0.13	-0.76**	-0.28**	-0.68**	0.16	-0.05	-0.10
MP 4010	0.27	2.22**	-0.39**	-1.10**	0.35	-0.18**	-0.50**
DBW 90	0.27	-2.48**	0.54**	1.61**	-0.42*	0.11	0.79**
HD 2824	0.44**	-1.07**	0.25**	0.00	-0.15	0.09	0.22
HD 3095	0.33*	2.96**	0.30**	1.47**	0.39	0.05	0.78**
RAJ 4246	-0.01	1.74**	-0.25**	-0.72**	-0.03	-0.04	-0.29*
NW 5038	0.49**	2.04**	-0.13**	-0.71**	0.34	0.01	-0.19
HD 2733	-1.26**	-3.22**	0.07	0.50**	0.12	0.03	0.11
Gi	0.31**	0.31**	0.11**	0.38**	0.45**	0.14**	0.32**
Gi-Gj	0.47**	0.46**	0.17**	0.57**	0.67**	0.21**	0.47**

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

Table 4 Estimates of genetic components and related parameters for various traits in bread wheat

Genetic parameters	Days to maturity	Plant height	Spikelets/ spike	Grains/ spike	Grain yield	Gluten content	1000 grain weight
D	1.256*	22.040*	0.598*	4.144*	2.106*	0.026*	1.045*
SE	0.089	0.508	0.075	0.370	0.526	0.012	0.331
H_1	-0.083	5.783*	0.986*	7.350*	10.369*	0.064*	3.253*
SE	0.189	1.082	0.159	0.788	1.119	0.025	0.706
H_2	-0.001	4.751*	0.765*	4.882*	8.284*	0.052*	2.706*
SE	0.160	0.920	0.135	0.670	0.951	0.021	0.600
F	0.064	5.877*	0.495*	2.711*	3.265*	0.014	1.351
SE	0.204	1.173	0.172	0.854	1.213	0.027	0.765
h^2	-0.069	13.834*	0.775*	8.893*	39.866*	0.005	5.872*
SE	0.107	0.616	0.090	0.448	0.636	0.014	0.401
E	0.251*	0.241	0.034	0.377*	0.263	0.053*	0.540*
SE	0.027	0.153	0.023	0.112	0.158	0.004	0.100
$(H_1/D)^{1/2}$	0.256	0.512	1.285	1.332	2.219	1.575	1.764
$H_2/4H_1$	0.003	0.205	0.194	0.166	0.200	0.206	0.208
$(4DH_1)^{1/2}+F/ (4DH_1)^{1/2}-F$	1.220	1.704	1.951	1.651	2.074	1.429	2.157
h^2/H_2	65.174	2.912	1.012	1.822	4.813	0.099	2.170
r	0.421	0.984	0.680	0.837	0.809	0.842	0.375

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

error and related parameters are presented (Table 4). The additive genetic variance (D) was found significant for all seven traits thereby indicating the predominance of additive gene action in the inheritance of these traits. Whereas, dominance component was significant for six traits (plant height, grains/spike, spikelets/spike, 1000-grain weight, gluten content and grain yield) indicating the predominance of dominance gene action in the inheritance of these traits as revealed in the F_1 generation. The estimates of H_1 were higher than the estimates of H_2 for all the seven traits under study indicating the unequal allelic frequencies at relevant loci in the populations. These results indicate that both (additive and dominance) type of gene action played important role in the inheritance of these traits. Reports by Singh *et al.* (2008), Singh *et al.* (2012), Yao *et al.* (2014), Singh *et al.* (2014), Kumar *et al.* (2015) and Kumar *et al.* (2016d) for different yield component and gluten content in wheat supported our study. The analysis of variance components indicated that both additive and dominance variance are significant for all the seven traits, indicating that the expression of these traits is governed by both (additive and dominance) type of gene actions but predominance of dominance components were predominant for the traits under study. Significant additive and dominance genetic variance were also reported by Singh *et al*. (2012), Singh *et al*. (2014), Kumar *et al*. (2015) and Kumar *et al.* (2016d). Estimates of positive and significant F-component of genetic variance for plant height, grains/spike, spikelets/spike and grain yield in F_1 crosses indicated the role of dominant and positive alleles in the parents for improving these traits. The positive and significant estimates of h^2 for the traits (plant height, grains/spike, spikelets/spike, 1000-grain

Table 5 Best cross combination for significant SCA effects for various traitsinbread wheat

Trait	Best cross	SCA effects	GCA effects		Gene action
			P_1	P_2	
Days to maturity	HD 2967 × RAJ 4246	-0.75	-0.64**	-0.01	Non additive
Plant height	DBW 90 × HD 2733	-1.40**	-2.48**	-3.22**	Additive
Spikelets/spike	HD 2824 × NW 5038	1.07**	0.25**	-0.13**	Non additive
Grains/spike	HD 3095 × Raj 4246	2.59**	1.47**	-0.72**	Non additive
Gluten content	PBW 435 × Raj 4246	0.45**	-0.10	-0.04	Non additive
1000 grain weight	PBW 435 × HD 2824	1.61**	-0.47*	-0.15	Non additive
Grain yield	HD 2967 × Raj 4246	2.52**	-0.36*	-0.29*	Non additive

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

weight and grain yield), also indicated dominance of genetic components in F_1crosses. Whereas, non-significant values recorded for remaining traits indicated partial dominance. The environmental component (E) were significant for days to maturity, 1000-grain weight, gluten content and grains per spike, indicating thereby that these traits are under the influence of environmental factors. Earlier reports by Yao *et al.* (2014), Singh *et al.*(2014), Kumar *et al.* (2015) and Kumar *et al.* (2016d) are confirmatory.

The estimates of average degree of dominance $(H_1/D)^{1/2}$ were recorded as more than unity in F_1 crosses for the five traits namely; grains/spike, spikelets/spike, 1000-grain weight, gluten content and grain yield, thus indicated the preponderance of over-dominance gene action, whereas days to maturity and plant height showed partial dominance due to average degree of dominance that was less than unity but greater than zero. Average degree of dominance in wheat was reported by Kumar *et al.* (2015) and Kumar *et al.* (2016d).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 days to maturity, plant height, grains/spike, spikelets/spike, 1000-grain weight, gluten content and grain yield in F_1 crosses that had indicated asymmetrical distribution of positive and negative genes among the parents. Farooq *et al.* (2011), Kumar *et al.* (2015) and Kumar *et al.* (2016d) also reported similar results in wheat.

The estimates of the ratio of dominant and recessive alleles among the parents was more than unity for days to maturity, plant height, grains/spike, spikelets/spike, 1000-grain weight, gluten content and grain yield that indicated the role of more dominant alleles in the parents for these traits. Nazeer *et al.* (2011), Kumar *et al.* (2015) and Kumar *et al.* (2016d) also reported similar findings.

The estimates of ratio for number of gene groups was more than one for six traits (days to maturity, plant height, grains/spike, spikelets/spike, 1000-grain weight and grain yield) thereby indicated involvement of more than one major gene groups in inheritance of these traits. Whereas, this ratio was less than unity for the quality trait (gluten content) and that indicated the involvement of single gene group and the same has earlier been reported by Kumar *et al.* (2015) and Kumar *et al.* (2016d).

The present findings indicated that both additive (fixable) and non-additive (non-fixable) components of genetic variances were involved in governing the inheritance of most of the traits under study. Therefore, bi-parental mating and/or diallel selective mating of the selects in

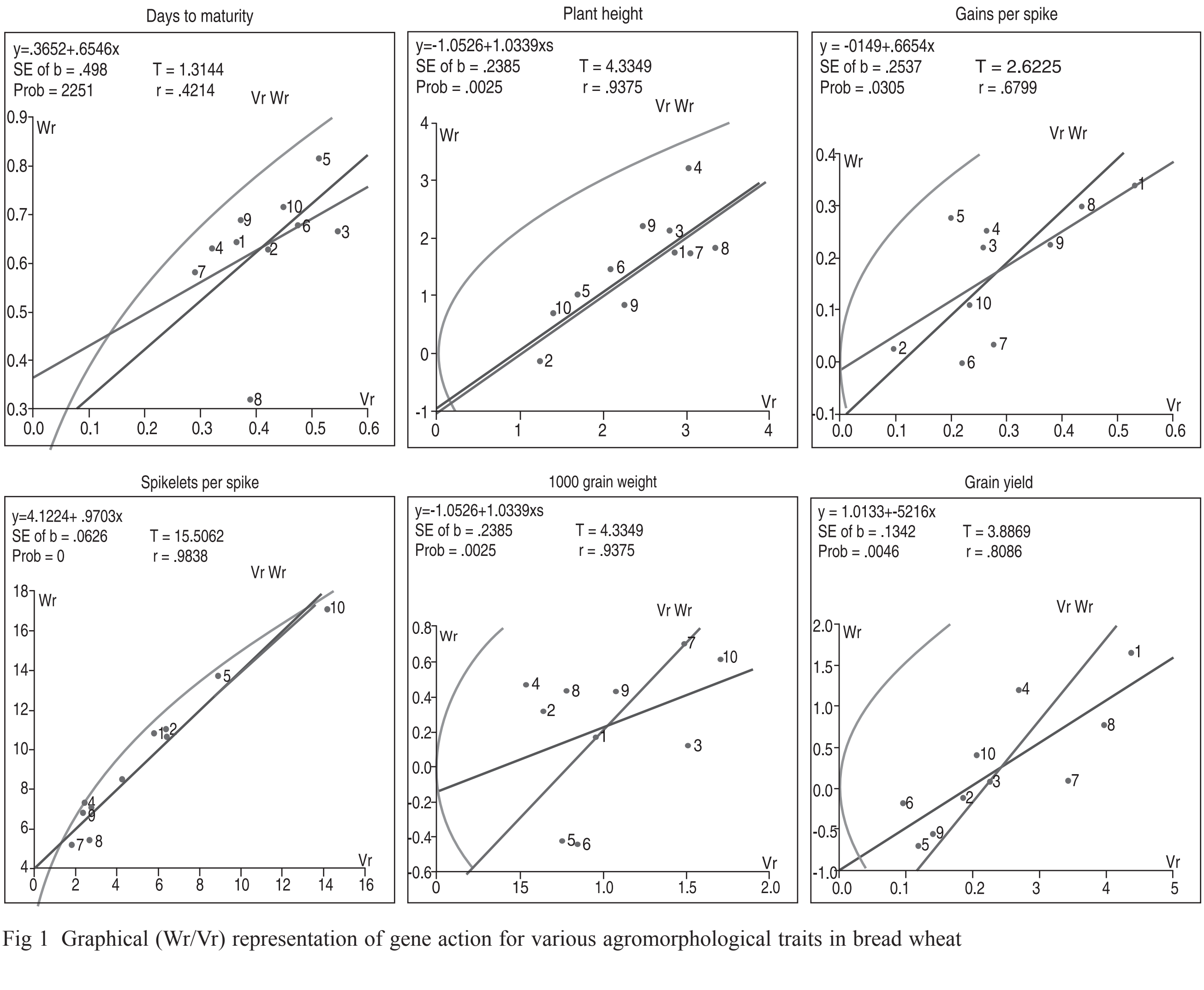

Fig 1 Graphical (Wr/Vr) representation of gene action for various agromorphological traits in bread wheat

different cycles to exploit both additive and non-additive gene effects could be useful in the improvement of these traits in wheat.

The graphical representation of Wr-Vr graphs (Fig 1) also supported the results and indicated the over dominance type of gene action, as the regression line cuts Wr-axis just below the origin for days to maturity, plant height, grains/spike, 1000-grain weight, gluten content and grain yield, whereas positive intercepts of Wr-Vr regression line supported complete dominance for spikelets per spike. Findings for different yield components reported by Nazeer *et al.* (2011), Farshadfar *et al.* (2013), Yao *et al*. (2014), Kumar *et al.* (2016a) and Kumar *et al.* (2016b) in wheat were in line with our results.

It is indicated from the graphical illustrations that parents that were closer to the origin possessed maximum dominant genes and therefore HD 3095 contains more of dominant genes for days to maturity and spikelets/spike; while HD 2967 holds good for plant height, grains/spike and 1000-grain weight; and HD 2824 for gluten content and grain yield. Our results were in confirmation to the reports of Farshadfar *et al.* (2013), Kumar *et al.* (2016a) and Kumar *et al.* (2016b) for different yield components in wheat. Whereas, parents being farthest from the origin point of graph contained more of recessive genes and therefore, DBW 90 contained maximum recessive genes for days to maturity; MP 4010 for plant height; HD 2733 for spikelets/spike and 1000-grain weight; PBW 435 for grains/spike and grain yield; MP 3336 for gluten content.

Based on the above findings, it may be concluded that both additive (fixable) and non-additive (non-fixable) components of genetic variances were involved in the expression of majority of the traits in the present set of study material. Since the parental lines used are mostly recently released varieties, this set could serve as base material for developing future genotypes having higher yield and better farmer's acceptance for grain quality. Generation advancement of selected F_1 crosses showing high SCA effects and further hybridization involving parents with good GCA into multiple combinations would bring improvement in yield and quality traits. Besides, for better exploitation of both the additive and non-additive component of variation, advance generation material may be advanced following pedigree method. Whereas, in other cases bi-parental mating for obtaining superior segregants may be followed. Considering the results of regression analysis, it might be concluded that for traits, viz days to maturity, plant height, number of grains/spike, 1000-grain weight, gluten content and grain yield that were largely governed by non-additive gene action, delayed selection to later generations may be rewarding while selecting better performing genotypes highlighting these traits. In summary, the results obtained, material generated and findings from the present investigation could be very useful in formulating breeding programme to develop high yielding and better quality wheat genotypes and would there by ensure food and nutritional security for the country.

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