Assessing gene action utilizing Hayman's graphical approach in bread wheat (*Triticum aestivum* L.)

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ABSTRACT

A study was conducted for the assessment of gene action involved in the expression of different yield components in bread wheat by using the Hayman's graphical approach. The significant additive variance (D) and dominance variance (H_1) indicated that, expression of these traits is controlled by both additive and non-additive gene action. Among the parents, there was asymmetrical distribution of positive and negative dominant genes and preponderance of over-dominance type of gene action for all the studied traits in both F_1 and F_2 generations. Graphical regression analysis for days to 50% flowering, days to maturity, plant height, effective tillers plant^{-1}, grain number spike^{-1}, 1000-grain weight and grain yield showed negative intercepts of Wr-Vr regression line, indicating over-dominance type of gene action, therefore selection should be delayed to later generations for these traits. The cultivar DBW 14 for grain yield and NW 2036 for days to 50% flowering, days to maturity, plant height and effective tillers plant^{-1} contain maximum dominant genes in both F_1 and F_2 generations, therefore these cultivars could be used as donors in wheat breeding programme. Based on the specific combining ability effects the cross PBW343 × K8962 identified to be a superior candidate for 1000- grain weight and grain yield in F_1 generation. Therefore, it is suggested that present findings may be useful in formulating future breeding programme to develop high yielding wheat genotypes.

***Keywords*:** Bread wheat, diallel crosses, gene action, Hayman'sgraphical approach and yield

Wheat is one of the major cereal crops and is widely cultivated under different agro-climatic conditions throughout the world and provides about 20 per cent of protein to mankind. In India, wheat covers an area of 29.72 million hectares with 98.61 million tonnes production during 2017-18 (Anonymous, 2018). However, this crop offers opportunities of a quantum jump in production by accelerating its yield potential through genetic manipulation.These gains can be realized by utilizing vast and enormous magnitude of genetic variability available in the crop for which no efforts should be spared. Genetic improvement in any crop results from creating variability and selecting the desirable recombinants to be released as a variety. The genetic improvement largely depends upon the nature and magnitude of components of genetic variances involved for grain yield and its related traits. Among biometrical techniques,diallel analysis is considered as most suitable as it provides maximum information related to genetic analysis and other parameters for formulation of suitable breeding strategies. Improving quantitative traits like grain yield and its contributing traits in wheat breeding program requires a specific breeding approach due to the genetic complexity of these traits. Therefore, the recognition of these traits and the parameters, which are mainly under polygenic control, involves the use of principles of quantitative inheritance for formulating breeding approaches in wheat. Diallel analysis also gives opportunity to the plant breeders to choose the most efficient selection method by allowing them to estimate several genetic parameters. The present study was designed with the objective to draw information on nature and type of gene action controlling various yield components traits in F_1 and F_2 generations in bread wheat.

MATERIALS AND METHODS

The plant material consisted of 13 diverse bread wheat genotypes *viz*., (1) NW 1014, (2) NW 2036, (3) PBW 502, (4) PBW 343, (5) K 8962, (6) HI 1563, (7) DBW 14, (8) RAJ 3765, (9) RAJ 4120, (10) HP 1744, (11) UP 2490, (12) UP 2425 and (13) CBW 38 which were planted at main experimental station of Narendra Deva University of Agriculture and Technology, Kumarganj, Faizabad (U.P.) during *rabi* 2012-2013. The crosses among the parental lines were performed following 13×13 half diallel mating design during main season. During off-season, F_1 seed of 78 crosses were planted at IARI- Regional Research Station, Wellington, Tamil Nadu for generation advancement. In the next crop season (*rabi*, 2013-2014), the experimental material comprising 13 parents along with their 78 F_1 and 78 F_2 were evaluated following a randomized block design with three replications. Each genotype was planted in a

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single row plot of 3m length with a spacing of 23 and 10 cm between rows and between plants in a row, respectively for parents and F_1s. However, the F_2 generation of each cross was planted in five rows of 3m length and spacing as mentioned above. All the recommended agronomic practices were adopted to raise a good crop. The observations were recorded on five randomly selected plants in parents, 10 plants in F_1 generation and 20 plants in F_2 generation for days to 50% flowering, days to maturity, plant height (cm), number of effective tillers plant^{-1}, grains number spike^{-1}, 1000-grain weight (g) and grain yield plant^{-1}(g). Diallel analysis was carried out as described by Mather and Jinks, 1982.The genetic parameters and graphical analysis (Wr-Vr) was done according to the Hayman (1954) approach using Windostat version 9.2. Information about gene action was obtained by plotting the covariance of each array against its variance. The slope and position of the regression line fitted to the array points within the limiting parabola indicated the degree of dominance and the presence or absence of gene interaction. The position of regression line on Wr-Vr graph provides information about the average degree of dominance which are as follows: (1) When the regression line passes through the origin, it indicates dominance (D=H_1), (2) When it passes above the origin and cut the Wr-axis, it shows partial dominance (D>H_1), (3) When it passes above the origin, cutting Wr-axis and touching the limiting parabola, it suggests no dominance and (4) when it passes below the origin, cut the Vr-axis, it indicates presence of over dominance.Where, D = variation due to genetic effects, H_1= variation due to dominance genetic effects, h^2 = overall dominance 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 $[(4D H_1)^{0.5}+F]/[(4DH_1)^{1/2}–F]$ and (iv) number of groups of genes controlling the traits and exhibited dominance (h^2/H_2) to work out gene action for various traits under study.

The estimates of these components of genetic variation were determined using following formulae as suggested by Hayman (1954a)

$$\hat{D} = V_0L_0 - \hat{E}$$

$$\hat{F} = 2V_0L_0 - 4 W_0L_{01} - \frac{2(n-2)\hat{E}}{n}$$

$$\hat{H}_1 = V_0L_0 + 4 V_0L_1 - 4W_0L_0 - \frac{(3n-2)\hat{E}}{n}$$

$$\hat{H}_2 = 4V_1L_1 - 4V_0L_1 - 2\hat{E}$$

$$h^2 = 4 \left(ML_1 - ML_0\right)^2 - \frac{4(n-1)\hat{E}}{n^2}$$

The statistics in the above formula may be explained as here under.

V_0L_0 = Variance of parents
V_r = Variance of rth array
V_1L_1 = Mean variance of the array
W_r = The covariance between the parents and their offspring in the rth array.
W_0L_1 = Mean of covariance between the parents and their arrays
V_0L_1 = The variance of the means of arrays.

Testing of hypothesis

1. Uniformity of (W_r-V_r) would indicate the validity of the hypothesis as postulated by Hayman (1954a) with ungrouped randomization, this may be tested by using the formula mentioned below`:

$$t^2 = \frac{n-2}{4} \times \frac{(Var.Vr-Var.Wr)^2}{(Var.VrxVar.Wr) - Cov^2(Vr.Wr.)}$$

With (n-2) degree of freedom where n is the number of parents. Significance of t^2 indicates the failure of the hypothesis.

1. Regression coefficient (b)

$$b = \frac{Cov(WrVr)^{\frac{1}{2}}}{VarVr(n-2)}$$

$$SE (b) = \frac{\left(Var\ Wr - b\ Cov\ WrVr\right)^{1/2}}{Var\ Vr(n-2)}$$

Now the significance of b from zero and unity can be tested as follows:

H0 : b = 0

= (b-0) / SE (b)

and H0 : b =1

= (1-b) / SE (b)

These values are tested against table value of t for n-2 degree of freedom.

Standard error of estimates

In order to estimate the accuracy of the above components of variance, the terms of main diagonal of the matrix given by Hayman (1954a) with common multipliers S^2 was used, where.

$S^2 = (1/2) [Var (Wr- Vr)]$

The formula being

S.E. ($\hat{D}$) = $\pm[S^2 (n^5 + n^4)/n^5]^{0.5}$

S.E. ($\hat{F}$) = $\pm [S^2 (4n^5 + 20n^4 - 16 n^3 + 16 n^2) /n^5)^{0.5}$

S.E. ($\hat{H}_1$) = $\pm [S^2 (n^5 + 41 n^4 - 12 n^3 + 4n^2)/n^5]^{0.5}$

S.E. ($\hat{H}_2$) = $\pm [S^2 (36 n^4/n^5)^{0.5}$

S.E. ($\hat{h}^2$) = $\pm [S^2 (16n^4 + 16n^2 - 32 n + 16)/n^5]^{0.5}$

S.E. ($\hat{E}$) = $\pm [S^2 (n^4/n^5)]^{0.5}$

After testing the significance of the components of variation, the related statistics of components of variance was calculated by using the above formulas.

RESULTS AND DISCUSSION

Diallel analysis technique as developed and illustrated by Hayman (1954) provides information in early generations on genetic mechanism involved in the inheritance of character.The diallel analysis was carried out for seven yield components by adopting analytical approach in terms of component of genetic variance along with standard error and related parameters, and is presented in table 1. The additive genetic variance (D) was found highly significant for three traits *viz.*, days to 50% flowering, plant height and grain number spike^{-1}, indicating that the expression of these traits is control by additive type of gene action in both F_1 and F_2 generations. Similarly, additive type of gene action in the expression of days to 50% flowering was reported by Nayeem (1994); for plant height and grain number spike^{-1} by Kumar *et al.* (2017); for plant height by Kumar *et al.* (2016a). The estimates of dominance components(H_1) were also found significant for days to 50% flowering, days to maturity, plant height, grain number spike^{-1}, 1000-grain weight and grain yield plant^{-1} in both F_1 and F_2 generations, and for number of effective tillers plant^{-1} in F_2 generations,indicating that the expression of these traits is controlled by the dominance type of gene action. In previous study, dominance type of gene action for the inheritance of days to 50% flowering and days to maturity was reported by Nayeem (1994); for plant height, grain number spike^{-1}, and grain yield plant^{-1} by Kumar *et al.* (2017); for effective tillers plant^{-1}, by Kumar *et al.*(2016a). However, dominance component (H_1) was more predominant than additive component (D) for all the traits under study. Present results indicated that both additive and dominance types of gene action is involved in the expression of these quantitative traits. These findings were also supported by the earlier results (Dayal *et al.*, 2003 and Singh *et al.*, 2014) for various yield components in wheat. Since the proportion of alleles with +ve and –ve effects in parents *i.e.* $H_2/4H_1$ is less than 0.25, there is asymmetry of +ve and –ve alleles *i.e.* there are unequal allelic frequencies at all loci.). Asymmetrical distribution of positive and negative genes among the parents were also reported by Nayeem (1994) for days to 50% flowering and days to maturity; Singh *et al.* (2014) for plant height, Kumar *et al.* (2016a) for number of effective tillers plant^{-1}, grain number per spike and Kumar *et al.* (2017) for 1000-grain weight and grain yield per plant in wheat.

The estimates of average degree of dominance ($H_1/D)^{1/2}$ were found more than unity for days to 50% flowering, days to maturity, plant height, number of effective tillers plant^{-1}, grain number spike^{-1}, 1000-grain weight and grain yield plant^{-1} in both F_1 and F_2 generations,indicating the preponderance of over dominance type of gene action. Present results were also supported by Kumar *et al.* (2016a) for days to 50% flowering, days to maturity, plant height, number of effective tillers plant^{-1}, grain number spike^{-1}, 1000-grain weight and grain yield plant^{-1}.

The proportion of dominant and recessive alleles among the parents were more than unity for grain numberper spike and 1000-grain weight in both F_1 and F_2 generations and for plant height in F_1 generation, while for days to 50% flowering in F_2 generation, indicating that there is more of dominant alleles than recessive alleles in the parents for these traits. Similar finding was also supported by Kumar *et al.* (2016a) for days to 50% flowering, plant height and 1000-grain weight,while by Kumar *et al.* (2017) for grain number spike^{-1} in F_1 generation. However, the ratio of dominant to recessive alleles among the parents was less than unity for days to maturity, number of effective tillers plant^{-1} and grain yield plant^{-1} in both F_1 and F_2 generations and for days to 50% flowering in F_1 generation,whereas for plant heightin F_2 generations, reflecting more of recessive alleles than dominant alleles in the parents for these traits.

Since the estimates of ratio for number of gene groups controlling the traits to exhibit dominance (h^2/H_2) was more than unity for grain yield plant^{-1} in both F_1 and F_2 generations,there was involvement of more than one major gene groups in inheritance of these traits. Whereas, for days to 50% flowering, days to maturity, plant height, number of effective tillers plant^{-1}, grain number spike^{-1} and 1000-grain weight,this ratio was less than unity in both F_1 and F_2 generations thus indicating the involvement of single gene group. Similarly, for grain number spike^{-1} (Kumar *et al.,* 2015),days to 50% flowering, days to maturity, plant height and grain yield (Kumar *et al.,* 2016a) reported the involvement of single gene group in inheritance of these traits.

Table 1: Estimates of genetic parameters and other related statistics for grain yield and yield components in bread wheat

Genetic parameter	Days to 50% flowering		Days to maturity		Plant height (cm)		Effective tillers per plant		Grain number per spike		1000-grain weight (g)		Grain yield per plant (g)	
	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
Additive variance (D)	6.31** ±1.70	6.34** ±1.72	1.41 ±0.58	1.43± 0.70	86.14** ±17.54	86.28** ±17.96	0.51 ±0.19	0.51 ±0.53	5.19** ±10.83	48.88** ±5.94	0.52 ±2.59	0.67 ±3.24	1.05 ±1.81	1.01 ±1.77
Dominance variance (H₁)	18.90** ±3.31	19.60** ±3.35	7.56** ±1.13	7.73** ±1.36	154.95** ±34.16	164.13** ±34.99	1.70 ±0.38	3.38** ±1.04	120.81** ±21.10	71.24** ±11.57	33.58** ±5.75	44.27** ±6.31	26.24** ±3.52	25.97** ±3.45
Overall dominance effects (h²)	2.15* ±1.82	1.84 ±1.84	0.45 ±0.62	1.27 ±0.75	16.40** ±18.80	20.55** ±19.25	0.47 ±0.21	0.47 ±0.21	8.99** ±11.61	27.26** ±6.37	4.10** ±3.16	2.46* ±3.47	43.78** ±1.94	40.95** ±1.90
Average degree of dominance (H₁/D)^½	1.73	1.75	2.31	2.32	1.34	1.37	1.81	1.81	4.82	3.81	8.00	8.07	4.98	5.04
Proportion of dominant genes with +/- effects (H₂/4H₁)	0.22	0.22	0.22	0.23	0.21	0.21	0.22	0.22	0.21	0.21	0.22	0.22	0.23	0.22
Proportion of dominant and recessive genes {(4DH₁)^½+F/(4DH₁)^½-F}	0.80	1.05	0.93	0.97	1.31	0.30	0.89	0.89	1.37	1.17	1.17	1.30	0.82	0.89
Number of groups of genes control the traits and exhibited dominance (h²/H₂)	0.12	0.10	0.06	0.17	0.12	0.14	0.30	0.30	0.08	0.44	0.13	0.06	1.78	1.76
Heritability (ns) %	53	43	36	33	52	51	46	30	18	22	14	12	19	21

*Note: *, ** significant at 5% & 1% probability levels, respectively*

Table 2: Top five superior cross combination having significant and desirable specific combining ability (SCA) effects for grain yield and yield component in bread wheat

| Character	Best crosses in F_1	SCA effects in F_1	GCA effects of parents P_1	P_2	Type of parental combination	Type of gene action in F_1
Days to 50% flowering	NW 1014 × PBW 343	-4.36**	-1.11**	4.18**	High × Low	Non additive
	NW 1014 × PBW 502	-3.49**	-1.11**	2.65**	High × Low	Non additive
	NW 2036 × PBW 343	-3.49**	-0.64**	4.18**	High × Low	Non additive
	UP 2490 × UP 2425	-3.29**	-0.55**	-0.44**	High × High	Additive
	DBW 14 × HP 1744	-3.09**	-0.29**	-0.57**	High × High	Additive
Days to maturity	HP 1744 × UP 2490	-2.84**	-0.11	0.31**	Average × Low	Non Additive
	K 8962 × RAJ 4120	-2.53**	0.35**	0.53**	Low × Low	Non additive
	DBW 14 × UP 2425	-2.51**	-0.22*	0.42**	High × Low	Non additive
	NW 2036 × HI 1563	-2.35**	-1.49**	0.53**	High × Low	Non additive
	DBW 14 × CBW 38	-2.09**	-0.22*	0.00	High × Low	Non additive
Plant height (cm)	DBW 14 × UP 2490	-12.31**	-6.20**	4.44**	High × Low	Non additive
	DBW 14 × CBW-38	-10.56**	-6.20**	1.08**	High × Low	Non additive
	PBW 343 × UP-2490	-10.12**	-7.43**	4.44**	High × Low	Non additive
	PBW 343 × K 8962	-7.80**	-7.43**	4.95**	High × Low	Non additive
	DBW 14 × HP 1744	-7.60**	-6.20**	-1.44**	High × High	Additive
Effective tillers plant[-1]	NW 1014 × HP 1744	1.38**	0.66**	-0.35**	High × Low	Non additive
	PBW 343 × DBW 14	1.19**	1.04**	-0.24**	High × Low	Non additive
	NW 1014 × UP 2425	1.11**	0.66**	-0.15**	High × Low	Non additive
	NW 1014 × UP 2490	1.07**	0.66**	0.05*	High × High	Additive
	PBW 343 × HI 1563	0.95**	1.04**	-0.34**	High × Low	Non additive
Grains number spike[-1]	UP 2490 × CBW 38	11.68**	0.72**	-0.41**	High × Low	Non additive
	PBW 343 × K 8962	10.26**	-0.39**	-4.55**	Low × Low	Non additive
	NW 2036 × UP 2490	9.72**	1.21**	0.72**	High × High	Additive
	UP 2490 × UP 2425	9.55**	0.72**	1.05**	High × High	Additive
	PBW 502 × K 8962	9.06**	-0.19	-4.55**	Low × Low	Non additive
1000-grain weight (g)	PBW 343 × K 8962	5.65**	0.62**	-2.02**	High × Low	Non additive
	PBW 502 × K 8962	5.40**	0.57**	-2.02**	High × Low	Non additive
	PBW 502 × HI 1563	4.65**	0.57**	-0.17	High × Low	Non additive
	UP 2490 × UP 2425	4.57**	0.21	-0.06	Low × Low	Non additive
	RAJ 3765 × UP 2425	3.75**	0.40**	-0.06	High × Low	Non additive
Grain yield per plant (g)	PBW 343 × K 8962	6.03**	0.77**	-1.79**	High × Low	Non additive
	UP 2490 × CBW 38	5.18**	0.41**	-1.05**	High × Low	Non additive
	PBW-343 × HI 1563	5.13**	0.77**	-0.82**	High × Low	Non additive
	NW 2036 × UP 2490	4.56**	-0.80**	0.41**	Low × High	Non additive
	PBW 502 × K 8962	3.83**	0.39**	-1.79**	High × Low	Non additive

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

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 50% flowering, days to maturity, plant height, number of effective tillers plant[-1], grain number spike[-1], 1000-grain weight and grain yield plant[-1] in both F_1 and F_2 generations. The present results were also supported by Chowdhry *et al.* (2002) and Kumar *et al.* (2016b) for
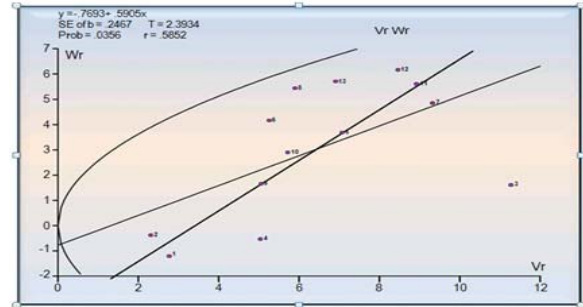
plant height, grain number per spike[-1], 1000-grain weight and grain yield plant[-1]; Farshadfar *et al.* (2013) for plant height and 1000-grain weight; Kumar *et al.* (2017) for days to maturity and grain numberper spike in bread wheat.

It is inferred from the graphical illustrations (Fig. 1) that the parents that were closer to the origin possessed maximum dominant genes and therefore the cultivar NW 2036 contains more of dominant genes for days to 50%
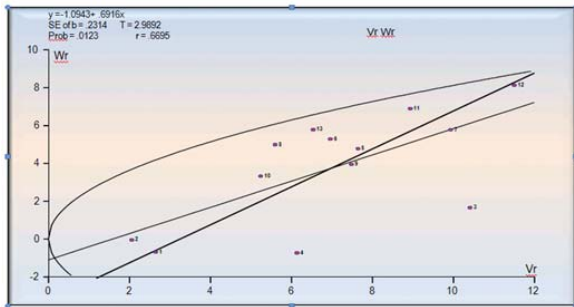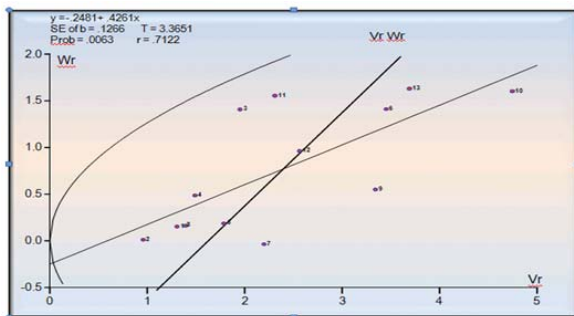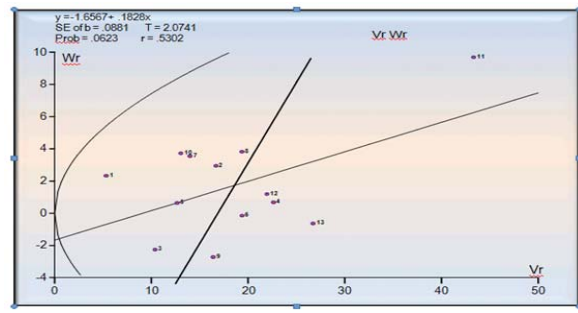
a (F_1)

a (F_2)

b (F_1)
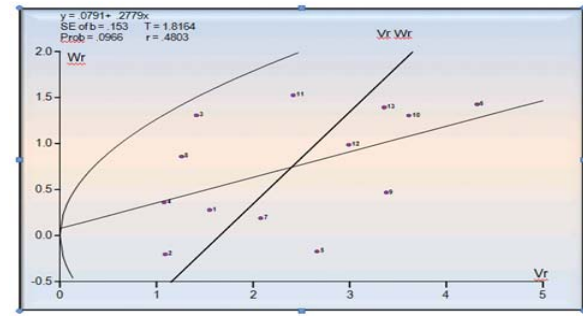
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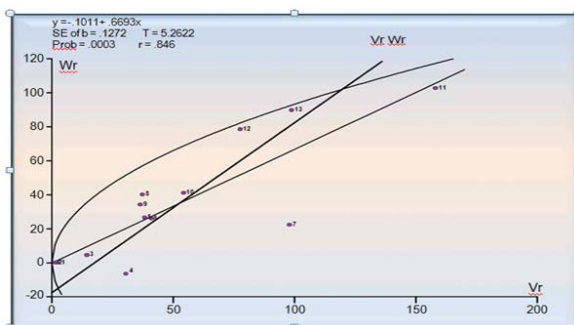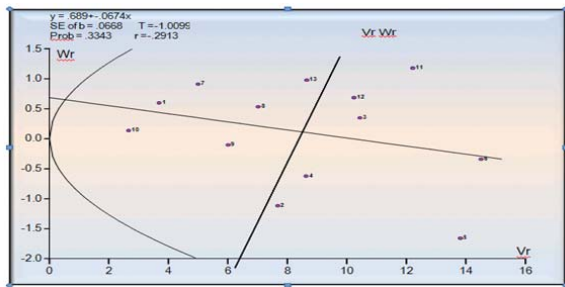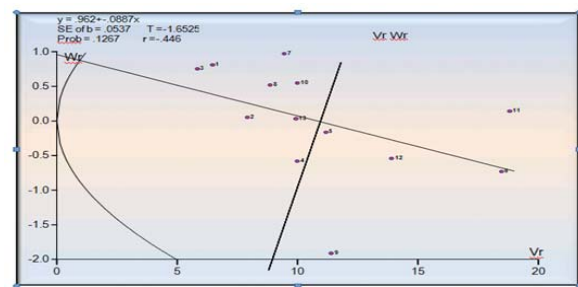

c (F_1)
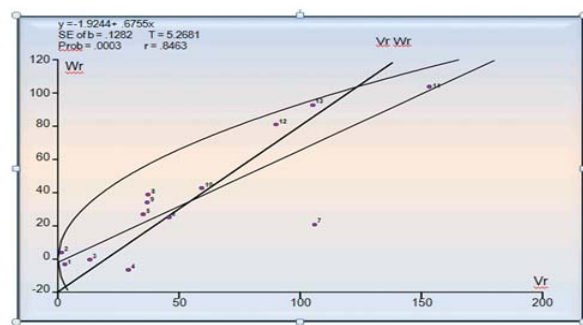
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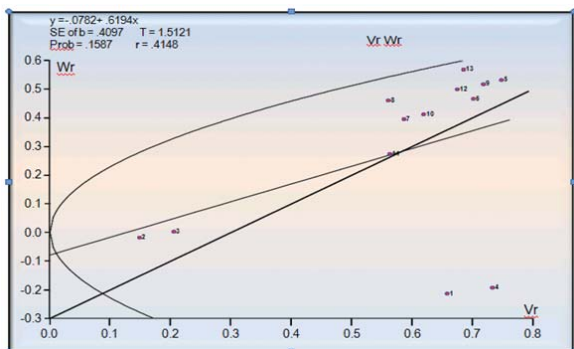
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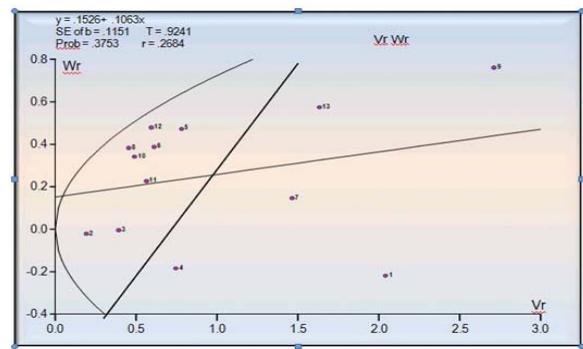
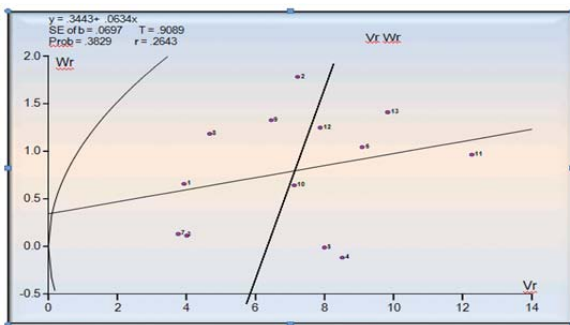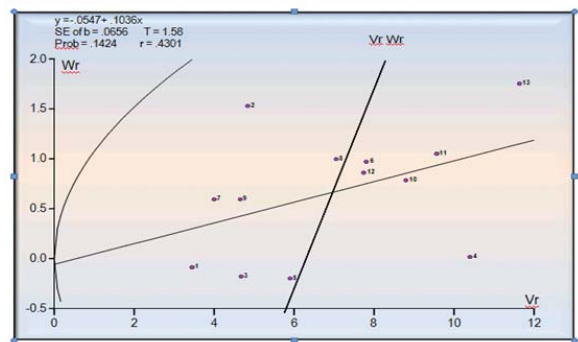d (F_2)
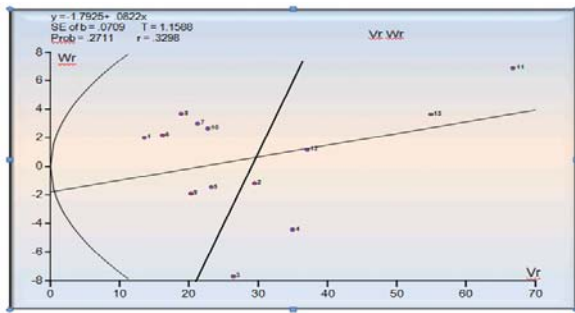
e (F₁)

e (F₂)

f (F₁)

f (F₂)

g (F₁)

g (F₂)

flowering, plant height, number of effective tillers plant^{-1}; NW 1014 for grain number spike^{-1} and grain yield plant^{-1} in both F_1 and F_2 generations. Whereas, the cultivar NW 2036 in F_1 and PBW 343 in F_2 for days to maturity, HP 1744 in F_1 and NW 2036 in F_2 for 1000-grain weight possessed maximum dominant genes.

The cultivar being farthest from the origin contained more recessive genes and therefore, PBW 502 in F_1 and UP 2425 in F_2 generation contained maximum recessive genes for days to 50% flowering; HP 1744 in F_1 and HI 1563 in F_2 generation for days to maturity, UP 2490 in both F_1 and F_2 generations for plant height and grain numberper spike; K 8962 in F_1 and RAJ 4120 in F_2 generation for number of effective tillers plant^{-1}; K 8962 in F_1 and HI 1563 in F_2 generation for 1000-grain weight; UP 2490 and CBW 38 for grain yield plant^{-1} in both F_1 and F_2 generations. The present findings were also

supported by the earlier results of various researchers (Farshadfar *et al.,* 2013; Kumar *et al.,* 2016b and Kumar *et al.,* 2017) for grain yield and its contributing traits in bread wheat.

The value of narrow-sense heritability estimates were found moderate to lower for almost all the traits under study in both F_1 and F_2 generations (Table 1).The narrow-sense heritability was moderate for days to 50% flowering (53% and 43%), days to maturity (36% and 33%), plant height (52% and 51%), number of effective tillers plant^{-1} (46% and 30%) whereas low for grain number spike^{-1} (18% and 22%), 1000-grain weight (14% and 12%) and grain yield plant^{-1} (19% and 21%) in F_1 and F_2 generations respectively. Therefore, the selection in early generation for these yield components will be rewarding. Singh *et al.* (2014) also reported moderate estimates of narrow sense heritability for days to 50%

flowering and plant height while low for grain number spike[-1], 1000-grain weight and grain yield plant[-1]; Kumar *et al.*(2016a) also reported moderate estimates of narrow sense heritability for number of productive tillers plant[-1] in F_1 generation in wheat.

The specific combining ability provides information about the non-allelic interaction and dominance gene action. Therefore we selectedtop five crossesout of 78 cross combinations which exhibited significant specific combining ability effects for grain yield and various component traits in F_1generation. In the present study, the specific combining ability effects (Table 2) revealed that the best cross NW 1014 ×PBW 343 exhibited highest negative and significant specific combining ability effects for days to 50% flowering (early flowering type);HP 1744 × UP 2490 for days to maturity (early maturity type);DBW 14 ×UP 2490 for plant height (short plant type) in F_1 generation. Similarly, the cross NW 1014 ×HP 1744 exhibited highest positive and significant specific combining ability effects for number of effective tillers plant[-1]; UP 2490 ×CBW 38 for number of grains spike[-1]; PBW 343 × K 8962 for 1000-grain weight and grain yield in F_1 generation. These individual crosses may be further exploited through heterosis breeding to improve trait(s) of interest in wheat. Present findings were also supported by Kumar *et al.* (2016a) for days to flowering, plant height, number of productive tillers plant[-1], and grain yield; Kumar *et al.*(2017) for days to maturity, 1000-grain weight and grain yield in bread wheat.

In the present study, best combinations mostly involved high × low and low × low general combiners for the studied characters whereas, rarely high × high general combiners were involved for best combinations (Table 2). Similar findings were also reported by Singh *et al*. (2012) and Kumar and Maloo (2012). Thus, it is evident that high specific combiners are not always obtained between high general combiners but may occur between low × low or high × low general combiners. This might be probably due to the presence of dominant and epistatic gene interactions.The gene action in F_1 against all the traits can be due to non-additive type of gene action because in F_1 most of the dominance alleles at most loci will express in F_1which is heterozygous and also the genotypes used in this study are released varieties having desirable gene combinations..

In general, specific combining ability effects do not make any significant contribution in the improvement of self-pollinated crops except where there is possibility of commercial exploitation of heterosis. Breeder's interest normally, vests in obtaining transgressive segregants through crosses in order to produce homozygous lines in self-pollinated crops. Therefore,

crosses involving high × low general combiners for different characters may be utilized for obtaining transgressive segregants in the next generation resulting from dominance gene interaction.

The present study demonstrates that both additive (fixable) and non-additive (non-fixable) components of genetic variances were involved in governing the inheritance of almost all the quantitative traits in both F_1 and F_2 generations. Therefore, bi-parental mating and/ or diallel selective mating which may allow inter-mating of the selects in different cycles and exploit both additive and non-additive gene effects could be useful in the genetic improvement of bread wheat.The Hayman's graphical approach for days to 50% flowering, days to maturity, plant height, number effective tillers plant[-1], grain number spike[-1], 1000-grain weight and grain yield plant[-1] showed negative intercepts of Wr-Vr regression line supported an over-dominant type of gene actionand, therefore selection should be delayed to later generations for these traits. Those traits exhibiting dominance or non-additive type gene effect, methods which will exploit non-additive gene actions, such as restricted recurrent selection by way of inter-mating the most desirable segregants followed by selection or multiple crosses or bi-parental mating in early segregating generations could be promising for genetic improvement. The traits which show predominance of non-additive gene effects indicates that the improvement of such trait would be difficult, as simple pedigree method of breeding will not be able to fix the superior lines in the early generations. In such situation, maintaining considerable heterozygosity through mating of selected plants in early segregating generations could attain maximum gain. Therefore, few cycles of recurrent selection followed by pedigree breeding will be effective and useful for the improvement of yield in such cases in the present material.The cultivar DBW 14 holds maximum dominant genes for grain yield plant[-1], whereas NW 2036 contain maximum dominant genes for days to 50% flowering, days to maturity, plant height and number of effective tillers plant[-1] in both F_1 and F_2 generations.Therefore these cultivars could be used as donors for multiple traits in wheat breeding programme. Generation advancement of selected F_1 crosses showing highest SCA effects and further hybridization involving parents with good GCA into multiple cross combinations might improve grain yield. Therefore, biparental mating and/or diallel selective mating would be useful to exploit both additive and non-additive gene effects. Diallel selective mating system is a good technique, which delays quick fixation of gene complexes, and permits break down of linkage, general fostering of recombination and concentration of favorable gene complexes into central gene pool by a

series of multiple crosses.The specific combining ability effects revealed that the cross UP 2490 × CBW 38 could be an excellent candidate for improving grain yield in both F_1 and F_2 generations. Therefore, it is suggested that present findings are useful in formulating future breeding programme to develop high yielding wheat genotypes.

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