



Short Communication

## Genetic architecture of yield and quality traits in wheat (*Triticum aestivum* L.)

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### Abstract

The aim of this study was to investigate gene effects and genetic variability by generation mean analysis for some yield and quality traits in three diverse crosses of wheat (JW 3288 × HD 8864, MP 3269 × GW 173 and JW 3020 × GW 366). The parents  $P_1$  and  $P_2$  and  $F_1$ ,  $F_2$ ,  $BC_1$  and  $BC_2$  populations were grown in a randomized complete block design with three replications during 2017-2018 crop seasons. Both additive and non-additive gene effects were involved in the expression of days to ear emergence, plant height, days to maturity, number of grains per spike, grain yield, flour recovery, husk content, protein content, lysine content and amylose content. The epistatic interaction was observed for all the ten traits in said crosses. In general, magnitude of dominance effect ( $h$ ) has a greater value than additive effect ( $d$ ) in all the traits. Digenic interaction indicated complex nature of inheritance means non-additive gene action. The improvement by selection in early generation could be advisable.

**Key words:** Gene action, epistasis, generation mean analysis, six parameter model, yield and quality components, bread wheat

Generation mean analysis is a simple but useful technique for estimating gene effects for a polygenic trait, its greatest merit lying in the ability to estimate epistatic gene effects such as additive × additive, dominance × dominance and additive × dominance effects. Since genetic information obtained from multiple generations is more reliable than that based on one generation, six populations ( $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$ ,  $BC_1$  and  $BC_2$ ) from different generations were considered sufficient to give detailed genetic information for the employed genotypes (Singh and Singh, 1992). This

study was carried out to investigate heritability of yield and quality components and to determine appropriate selection.

Six homozygous and genetically diverse varieties of wheat JW 3288, HD 8864, MP 3269, GW 173, JW 3020 and GW 366 were chosen for building up the experimental materials. The experimental material used for the present investigation comprised of the parents ( $P_1$  and  $P_2$ ), the  $F_1$ 's,  $F_2$ 's and the back crosses with both the parents ( $B_1$  and  $B_2$ ) of each of the three crosses viz., JW 3288 × HD 8864 (cross 1), MP 3269 × GW 173 (cross 2) and JW 3020 × GW 366 (cross 3). The above mentioned diverse varieties of wheat were sown in crossing nursery for making desired cross combinations ( $F_1$ 's) were made. Harvested seeds of each diverse parent and their  $F_1$ 's were kept separately for sowing during next year. During *rabi* the hybrid seeds ( $F_1$ 's) of five cross combinations were raised to make the back crosses ( $BC_1$ ,  $BC_2$ ) and  $F_2$ . In addition, fresh  $F_1$ 's were also made to make 6 generations for analysis. All the  $F_1$  populations were planted in two rows,  $F_2$ 's in six rows and  $BC_1$  and  $BC_2$  in 4 rows of 3 meter length spaced 25 cm apart, at Regional Agricultural Research Station Sagar Madhya Pradesh, India. The experimental set was planted under black soil having pH of 7.5-7.8 in a Compact Family Block Design in three replications. Five randomly selected plants from parents and  $F_1$  generation, and 20 each from back crosses and  $F_2$  generations in replications were tagged before flowering. The data were first subjected to analysis of variance separately

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for each cross. Genetic analysis was done by using a six-parameter model (Hayman, 1958) after applying the scaling test suggested by Hayman and Mather (1955).

The estimates of the six-parameter model from generation mean analysis showed that additive as well as non-additive gene effects were important for all the traits. However, the magnitude of dominance effect (h) was greater than additive effect (d). The expectation of A, B and C. scaling tests tend towards zero in the absence of interactions. If there is a significant deviation from zero, then it is assumed that epistasis may play an important role. It could be visualized from the table under reference that for most of the characters, the additive-dominance model was found inadequate. The scaling test (Table 1) revealed that epistasis had a predominant role in the expression of all the traits except in flour recovery (cross I).

The estimates of gene effects for 10 characters of three crosses used for determining the genetic architecture have been presented in Table 2. The dominance gene effect (h) was of greater importance as compared to additive gene effect (d) in the inheritance of days to ear emergence, plant height, days to maturity, husk content, and amylose content in all the three crosses. Similar results were also obtained for the character flour recovery in cross 3, protein content in cross 1 and lysine content in cross 1 and cross 3, respectively. The parameter of 'd' provides a combined estimate of the parameters 'i' and 'j'. This combined estimate 'd' is considered as the sufficient measure of additive gene action. Comparison of estimates of gene effects with respect to magnitude as well as significance revealed that additive gene effect (d) was of greater importance compared to the dominance (h) gene effects for plant height in cross II and grain yield per plant in all the three crosses. Thus, selection for those two characters will be effective in early segregating generations.

Epistatic interactions (i, j and l) were significant in the cross 1 (days to ear emergence), cross II and cross 3 (plant height) cross 2 (days to maturity), cross 3 (no. of grains/spike), cross 2 and 3 (grain yield per plant), cross 2 and 3 (grain yield per plant,) cross II (flour recovery) cross I and II (protein content), cross 1 and 3 (lysine content) and cross II and III (amylose content). The results for plant height and other characters are in accordance with the previous findings of Ilker (2010), Khattab et al. (2010), Tonk et al. (2011), Golestani et al. (2012), Hassan and El-Said (2014).

**Table 1.** Scaling test for different traits in wheat

Scale	Days to ear emergence	Plant height (cm)	Days to maturity	No. of grains/spike	Grain yield/plant (g)	Flour recovery (g)	Husk content (g)	Protein content (%)	Lysine content (mg/g)	Amylose content (%)
<b>Cross 1: JW 3288 x HD 8864</b>										
A	9.33**+2.51	26.80**+1.49	8.67**+2.65	12.43**+3.81	3.76**+1.04	2.33**+1.09	-4.20**+1.59	-3.30**+1.09	-1.33+1.15	1.13+1.19
B	-8.67**+2.15	25.46**+2.15	7.00**+1.82	-36.33**+1.79	3.97**+2.06	1.10+1.74	1.66**+1.25	-4.90**+1.25	3.00**+1.14	7.50**+1.18
C	-13.00**+5.14	50.76**+2.89	-4.00**+2.56	-39.57**+6.54	28.73**+2.33	3.77+2.57	-4.80**+1.66	7.67**+1.26	-1.73**+1.28	2.77**+1.29
<b>Cross 2: MP 3269 x GW 173</b>										
A	10.33**+1.40	16.60**+2.14	8.33**+2.63	-14.17**	+2.10	25.47**+0.41	-5.77**+48.72	6.60**+0.71	-1.93**+0.38	-1.03+0.16
B	11.33**+3.03	41.07**+1.35	13.33**+1.41	-18.27**+1.72	14.70**+1.26	-7.80**+1.47	8.47**+0.62	-5.27**+0.21	1.43**+0.21	-1.03+0.34
C	-22.67**+5.43	8.60**+0.93	-9.00**+2.94	-53.37**+3.87	24.27**+0.93	-15.90**+2.36	14.33**+3.01	-3.80**+1.58	-1.67+1.30	-5.57**+1.41
<b>Cross 3: JW 3020 x GW 366</b>										
A	8.34**+1224	-23.23**+1.58	25.00**+4.05	-8.43**+1.91	4.60**+1.34	-10.23**+1.30	7.73**+0.70	6.56**+0.19	2.50**+0.14	2.83**+0.33
B	-8.34**+2.63	-9.87**+1.89	18.60**+4.40	-32.31**+2.25	16.53**+2.20	-8.80**+1.37	7.76**+0.71	5.73**+0.15	-2.17**+0.19	1.76+0.56
C	-3.67+1.30	22.00**+2.67	55.67**+4.65	50.00+6.52	87.40**+4.48	-20.23**+3.55	15.17**+1.85	7.03**+1.39	-2.40**+0.17	1.00**+0.76

**Table 2.** Estimation of different types of gene action in three crosses of wheat

Characters	Cross	m	d	h	i	j	l	Type of interaction
Days to ear emergence	C <sub>1</sub>	78.37**+0.43	3.66**+0.64	3.67**+2.31	13.67**+2.10	9.00**+0.91	-14.3**+3.97	D
	C <sub>2</sub>	79.00**+1.25	1.67+1.25	49.50**+5.34	42.33**+5.18	-1.50+1.25	-62.00**+6.97	D
	C <sub>3</sub>	75.34**+0.33	3.66**+0.74	8.34**+2.21	3.67**+3.00	7.34**+1.81	-3.67+4.47	-
Plant height (cm)	C <sub>1</sub>	82.73**+1.29	-3.47**+1.61	11.52**+1.04	1.79+1.68	1.98+1.02	-44.3**+3.55	D
	C <sub>2</sub>	79.07+0.59	-10.57**+0.60	54.88+2.80	49.07**+2.67	13.23**+0.67	-11.73**+3.79	D
	C <sub>3</sub>	82.46**+0.38	-1.2+0.46	-53.80**+1.82	-33.00**+1.79	-7.18**+0.57	83.10**+2.48	D
Days to maturity	C <sub>1</sub>	145.00**+1.00	1.37+1.49	20.83**+5.37	-17.60**+4.98	3.17+2.10	-21.67**+3.05	D
	C <sub>2</sub>	146.33**+0.33	-2.33**+0.47	30.3**+2.03	27.67**+1.63	-3.00+0.66	-48.33**+3.46	D
	C <sub>3</sub>	147.00**+1.00	-1.67+1.49	-14.80**+5.30	-18.00**+4.90	3.10+2.10	-26.67**+3.05	C
No. of grains/spike	C <sub>1</sub>	65.73**+0.75	6.40**+1.21	16.62**+3.99	17.59**+3.86	23.88**+1.52	9.03+6.04	-
	C <sub>2</sub>	69.20**+0.72	-3.53**+1.29	51.75**+8.54	-3.93**+3.38	2.55+3.88	7.50+6.46	-
	C <sub>3</sub>	91.57**+2.11	8.90**+0.57	-6.60+2.64	-86.73**+8.52	14.43**+0.73	14.47**+8.82	D
Grain yield/plant (g)	C <sub>1</sub>	37.60**+0.53	5.50**+0.74	-6.60**+2.04	-22.20**+2.58	-10.45**+0.79	-13.63**+3.80	-
	C <sub>2</sub>	32.33**+0.29	-14.93**+0.75	-30.90**+2.05	-36.33**+1.90	-17.73**+0.81	49.40**+3.55	D
	C <sub>3</sub>	34.43**+0.62	9.53**+0.94	17.83**+3.33	20.33**+3.10	10.56**+0.97	33.27**+5.12	C
Flour recovery (g)	C <sub>1</sub>	89.70**+0.64	1.23+0.81	8.28**+2.75	1.59+1.27	1.89+0.49	4.13+4.34	-
	C <sub>2</sub>	88.20**+0.58	2.67**+0.73	9.25**+2.89	1.19+2.83	3.02**+0.75	9.22**+3.77	C
	C <sub>3</sub>	87.40**+0.57	-2.09+0.85	9.25**+2.89	-1.93+0.77	-1.72+2.86	17.83**+4.23	C
Husk content (g)	C <sub>1</sub>	16.00**+0.15	3.00**+0.23	3.70**+0.79	-1.93+0.77	2.39**+0.28	3.33+7.78	-
	C <sub>2</sub>	18.83**+0.47	-1.50+0.44	-5.50**+2.11	-2.27+2.08	-1.93**+0.46	-7.79**+2.67	D
	C <sub>3</sub>	16.00**+0.42	-1.19+0.32	-9.12**+1.85	-3.67+1.78	-2.02**+0.38	-7.83**+2.33	C
Protein content (%)	C <sub>1</sub>	15.57**+0.12	-1.13+0.19	-11.48**+0.65	-12.39**+0.62	1.88**+0.22	20.23**+0.99	D
	C <sub>2</sub>	13.23**+0.12	2.11**+0.19	1.35**+0.06	-3.40**+0.65	3.17**+0.21	6.60**+0.96	-
	C <sub>3</sub>	14.23**+0.08	-2.57**+0.09	1.66+0.35	-2.73+0.40	3.08**+0.12	-7.57**+0.54	-
Lysine content (mg/g)	C <sub>1</sub>	4.20**+0.06	1.80**+0.07	5.43**+0.27	11.93**+0.27	-2.53**+0.08	-6.13**+0.37	D
	C <sub>2</sub>	3.20**+0.06	-1.23+0.11	2.50+0.33	1.47+0.31	-1.23**+0.11	-1.87+0.52	-
	C <sub>3</sub>	3.40**+0.06	3.13**+0.15	2.23**+0.38	2.73**+0.31	2.33**+0.31	-3.07**+0.50	D
Amylose content (%)	C <sub>1</sub>	13.40**+0.03	1.00+0.15	3.88**+0.38	4.80+0.33	3.68**+0.12	10.90**+0.73	C
	C <sub>2</sub>	10.27**+0.08	1.87**+1.18	10.98**+0.81	7.27+0.49	1.88**+0.19	8.96**+0.82	C
	C <sub>3</sub>	13.37**+0.12	-1.03+0.23	-7.79**+0.69	8.39**+0.67	1.53**+0.25	6.79**+1.09	D

C<sub>1</sub> = JW 3288 × HD 8864, C<sub>2</sub> = MP 3269 × GW 173, C<sub>3</sub> = JW 3020 × GW 366, D = duplicate; C = complimentary type of epistasis  
\*, \*\*, 5% and 1% significant level, respectively

Additive × additive and dominance × dominance type epistatic gene effects were significant for spike length and grain number per spike in MP 3269 × GW 173 and JW 3020 × GW 366, although no gene effects were significant for these traits in the JW 3288 × HD 8864 cross. Erkul et al. (2010), Tonk et al. (2011), Koumber and El-Gammaal (2012) found that additive, dominance and epistatic gene effects were significant for these traits.

The complementary gene action was observed in cross 3 for days to maturity, grain yield per plant and husk content cross 2 and 3 for flour recovery and cross 1 and 2 for amylose content and that can be utilized for gene fixation through conventional breeding

methods. The duplicate type of gene action was recorded for, majority of the traits under study where (h) and (l) effect had opposite signs. Thus it indicated that non-fixable gene effects are expressing that particular traits *i.e.*, greater role of non-additive gene effects in such cases.

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