



Assessment of gene action for morpho-physiological and biochemical trait in bread wheat (*Triticum aestivum* L.)

Priyanka Jaiswal ✉

Dept. of Genetics and Plant Breeding, LPU, Phagwara, Punjab, India.

Banshidhar

Dept. of Genetics and Plant Breeding, LPU, Phagwara, Punjab, India.

Satish Kumar Singh

Dept. of Genetics and Plant Breeding, RPCAU, Pusa Bihar, India.

Mithilesh Kumar Singh

Dept. of Genetics and Plant Breeding, RPCAU, Pusa Bihar, India.

Rabiya Parveen

Dept. of Genetics and Plant Breeding, RPCAU, Pusa Bihar, India.

ARTICLE INFO

Received : 07 February 2022

Revised : 12 May 2022

Accepted : 16 July 2022

Available online: 08.01.2023

Key Words:

Bread wheat

Duplicate gene action

Gene interaction

Grain Iron content

Grain Zinc content

ABSTRACT

The present study was undertaken with the objective to assess the nature and magnitude of gene action for various morpho-physiological and biochemical traits in two crosses namely cross BHU 31 × HD 2733 and cross, HPYT 485 × HD 2967 in wheat. The six basic generations (P₁, P₂, F₁, F₂, B₁ and B₂) obtained from these crosses (made in Rabi 2018 and 2019) were evaluated for 13 quantitative traits including yield and micronutrient traits during Rabi 2020 in compact family block design with 3 replications at Research farm, RPCAU, Pusa and data were recorded on randomly selected plants per replication of each cross for all the traits. The estimation of micronutrient in wheat grains was done by X-Ray Fluorescence Spectrometry at Harvest-plus Division, ICRISAT, Hyderabad. The result regarding gene effect indicated that in both the crosses dominance and dominance × dominance effect for grain Zinc content (-29.00 & 19.18 and -9.79 & 7.04 respectively in cross I and II) and grain Iron content (-18.16 & 12.37 and -20.29 & 12.31 respectively in cross I and II) has significant role in expression of these traits. Duplicate type of gene interaction was found predominant for grain Zinc and Iron content and almost for all the traits due to opposite sign of dominance (h) and dominance × dominance (l) gene effect which tends to cancel the effect of each other in hybrid combination therefore selection should be advanced in later generation.

Introduction

Bread wheat (*Triticum aestivum* L.), enjoyed the status of second most important food crop in India with a production of 107.2 million tons and average productivity of 3.51 t/ha from an acreage of 30.5 million hectares (Annual Report, 2019-2020, DAC&FW). Globally, it is the preferred staple food crop for a large section of world population, fulfilling nearly 20 % of daily food requirement and ranks first at global level in terms of overall production. Additionally, it is also a rich source of protein, essential dietary micronutrient, including Zinc, Iron and Manganese and Vitamins B & E (Reynolds *et al.*, 2012; Velu *et al.*, 2017). Being the

most important staple crop at global level, wheat is a better alternative for bio-fortification to circumvent hidden hunger by ensuring food & nutritional security for millions of people of poorer section bio-fortification is a sustainable solution (Bouis *et al.*, 2011). Wheat varieties with improved nutrition quality and high grain yield can help to overcome the micronutrient malnutrition among resource poor people (Velu *et al.*, 2018). Thus, development of high yielding biofortified varieties has become the first and foremost objective of wheat breeders in the contemporary context to address the question of malnutrition. Development

of such promising varieties require a comprehensive knowledge of prevalent gene action governing the concerned trait which will guide in choice of appropriate breeding procedure in the improvement of various morphophysiological and biochemical traits. The successful breeding program for developing nutrient enriched high-yielding genotypes requires screening available germplasm to identify suitable sources of higher micronutrient content. However, improvement of these complex traits which are largely under polygenic control requires specific breeding approach which could picture a clear understanding of the inheritance, nature and magnitude of genetic variance and heritability of yield and yield attributing traits. Heritability and mode of gene action are also important genetic parameter that facilitate determination of the right stage of selection whether to start it in early generation or to advance it in later generations. Apart, estimation of different component of genetic variance viz. additive, dominance and epistatic variance is helpful in deciphering the inheritance pattern of genes influencing yield and related traits. This could be achieved through Generation Mean Analysis (GMA) that helps in the estimation of different components of genetic effects namely additive effects, dominance deviations and epistatic effects in determining genotypic values of the individuals and consequently, mean genotypic values of families and generations. It is also a robust tool to determine the nature of gene interaction i.e. additive \times additive, dominance \times dominance and additive \times dominance. Scaling test provide the information on presence and absence of epistasis while the joint scaling test enable the estimation of important genetic parameters viz., mean performance, additive effects and dominance effects along with the evidence of presence and absence of epistasis. Keeping these in view, the present investigation was carried out with the objective of determining the nature and magnitude of gene action for grain yield and Zinc and Iron content in bread wheat genotypes using generation mean analysis.

Material and Methods

In this investigation, six basic generations viz., P₁, P₂, F₁, F₂, B₁ and B₂ were generated from 4 diverse

parents BHU31, HPYT 485, HD2967 and HD2733 for micronutrient content which were selected & procured from department of Plant Breeding and Genetics, RPCAU, Pusa Samastipur, Bihar. The parents were crossed as following cross-I (BHU 31 \times HD 2733) and cross-II (HPYT 485 \times HD 2967) in which BHU31 and HPYT485 were used as female parent having high grain Zn & Fe content, while HD2733 and HD2967 were used as male parent having low grain Zn & Fe content but higher yield. The crosses were made during *Rabi* 2018 and the F₁ seeds were grown during *Rabi* 2019 to obtain F₂ seeds and backcrossed with both parents to generate B₁ and B₂ which were shown along with F₁ in *Rabi* 2020 for evaluation.

Statistical Analysis

The adequacy of additive \times dominance model for different trait in each cross was tested using scaling test (A, B, C and D) as suggested by Mather, 1949 and elaborated by Mather and Jinks, 1982 and Joint scaling test (Cavalli 1952; Mather and Jinks 1982; Ceballos 1996). The significance of scales were tested using 't' test and chi square (χ^2) respectively. The gene effects of various morpho-physiological and biochemical traits of each cross were estimated by generation mean analysis. Three parameter model (Jink and Jones, 1958; Manivannan, 2014) was applied to estimate gene effect of traits in absence of epistasis, whereas in the presence of non-allelic interaction test analysis was done by six parameter model (Hayman, 1958; Manivannan, 2014). The significance of the mean value of a particular parameter was tested against its corresponding standard error, via a Student's t-test, as suggested by Mather and Jinks (1982) and Uzokwe *et al.* (2017).

Results and Discussion

In any crop improvement programme, genotypic value of the lines used as parent as well as those that are selected as promising lines for a defined trait is very crucial. The relative contribution of additive, dominant and epistatic effects in governing a trait provides information on genotypic values of the individuals and, consequently, mean genotypic values of families and generations. In this research investigation, generation mean analysis was done to determine the prevalence as well as the relative contribution of different gene

actions in governing expression of various morpho-physiological and biochemical trait in bread wheat. Analysis of variance and mean performance of various morpho-physiological and biochemical traits of each generation are presented in table 1 and 2. Mean sum of square showed significant difference among the generations for all traits under study indicated the presence of variability for these traits. In cross-I (BHU31 \times HD2733) mean performance of F_1 was higher than both parent for days to 50% flowering(84.87 days), plant height(93.04 cm), spike length(12.35 cm) and number of tillers per plant(7.53). Mean performance of F_2 was higher than F_1 for most of traits except chlorophyll content(53.80), plant height(92.94 cm) and spike length(11.55 cm). In cross-II (HPYT485 \times HD 2967), mean performance of F_1 was higher than both parent for chlorophyll content(57.24), plant height(95.60 cm), spike length (11.82 cm), number of tillers per plant(7.20) and harvest index(45.62%). Similar result was reported by Ljubicic *et al.*, 2016, for spike length and by Said *et al.*, 2014, for chlorophyll content, which indicate hybrid vigour of these traits. The performance of F_2 was higher than F_1 for most of traits except chlorophyll content, plant height, spike length, number of tillers per plant and harvest index. Mean performance of F_1 for grain Zinc (29.25 ppm and 29.03 ppm resp.) and Iron content (38.13 ppm and 37.80 ppm resp.) was in between the parental performances in both the crosses, while, it was lower than both parent for rest of traits under study for both the crosses. To determine the nature and magnitude of gene action of various morpho-physiological trait along with grain Zinc and Iron content, generation mean analysis was carried out using data recorded from six basic generations of cross-I (BHU 31 \times HD 2733) and cross-II (HPYT 485 \times HD 2967) the values of scaling and joint scaling tests and estimates of six parameters *viz.*, m, d, h, i, j and l for different traits are present in table 3,4 and 5. Information of these six parameters are essential for proper selection of breeding methodology. The scaling test showed that at least one of the scales i.e. A, B, C and D were significant for plant height(A:-11.34, D: 10.10), spike length(A:-2.10,B:-1.00,D:1.49), number of tillers per plant(A:-3.13,B:-1.66,D:1.76), number of grains per spike(A:-25.94,B:-18.88,D:21.32), 1000-grain weight(B:-12.37,D:6.45), harvest index(C:-

11.79), canopy temperature(B:-3.05,C:-9.06), grain Zinc(A:-5.52, B:-3.16, D:5.24) and Iron content(A:-4.72, D: 2.70) in cross-I (BHU 31 \times HD 2733) which indicate the presence of epistasis for these traits. Further χ^2 value of joint scaling test was also found significant for these traits *viz.* plant height(20.09), spike length(15.58), number of tillers per plant(107.03), number of grains per spike(129.04), 1000-grain weight(29.91), harvest index(15.06), canopy temperature(34.79), grain Zinc(41.01) and Iron content(34.77) except days to maturity(7.60). In cross-II (HPYT485 \times HD 2967) inter-allelic interactions were observed for number of tillers per plant, grain Zinc content and grain Iron content on the basis of scaling and joint scaling test.

Presence or absence of epistasis was sorted out by scaling and joint scaling test. Traits for which additive-dominance model was adequate three parameters *viz.* m (mean value), d (additive effect) and h (dominance effect) were estimated and estimates are presented in table 5. In cross-I (BHU31 \times HD2733), three parameter model (Jink and Jones, 1958; Manivannan, 2014) was used to estimate gene effects for days to 50% flowering, chlorophyll content and grain yield per plant, while, in cross-II (HPYT485 \times HD 2967), it was applicable to days to 50% flowering, chlorophyll content, plant height, spike length, days to maturity, number of grains per spike, 1000-grain weight, harvest index, canopy temperature and grain yield per plant. Estimates of gene effect from three parameter model exhibited the preponderance of additive gene effect for grain yield per plant in cross-I (BHU31 \times HD2733) and for chlorophyll content, spike length, days to maturity, number of grains per spike, 1000-grain weight and grain yield per plant in cross-II (HPYT485 \times HD 2967). These findings suggested that the additive gene effect plays a major role in quantitative expression of these traits. Similar findings were reported by Ljubicic *et al.*, 2016 for number of grains per spike, Usman *et al.*, 2013 and Kumar *et al.*, 2013 for spike length. For the improvement of these traits selection would be effective in early segregating generations. In cross-I (BHU31 \times HD2733) along with additive gene effect, dominance gene effect played significant role in expression of grain yield per plant with higher magnitude than that for additive effect.

Table 1: ANOVA for Morpho-physiological and biochemical traits in wheat crosses BHU 31 × HD 2733 and HPYT 485 × HD2967

Source	df	Mean sum of squares												
		Days to 50% flowering	Chlorophyll content (SPAD)	Plant height (cm)	Spike length (cm)	Number of tillers/plant	Days to maturity	Number of grains per spike	1000-grain weight	Harvest Index (%)	Canopy temperature (°C)	Grain Zinc content (ppm)	Grain Iron content (ppm)	Grain yield per plant (g)
BHU 31 × HD 2733														
Replication	2	0.02	0.03	0.54	0.05	0.02	0.42	0.31	0.02	0.23	0.5	0.01	0.02	0.04
Generation	5	13.39**	3.17*	18.09**	1.30**	1.36**	7.38**	135.41**	32.60**	5.09**	3.30**	32.44**	27.47**	4.60**
Error	10	0.24	0.78	0.39	0.16	0.08	0.39	0.36	0.05	0.31	0.14	0.06	0.1	0.1
HPYT 485 × HD 2967														
Replication	2	0.17	0.63	0.05	0.00	0.07	0.04	0.04	0.15	0.5	0.26	0.00	0.02	0.13
Generation	5	3.66**	3.36**	7.74**	1.42**	2.15**	6.73**	9.96**	7.22**	2.93**	1.83**	30.47**	16.09**	3.97**
Error	10	0.3	0.22	0.43	0.03	0.03	0.47	0.21	0.13	0.24	0.09	0.11	0.19	0.08

* and ** indicate significance at 1% and 5% respectively.

Table 2: Per se performance of six generations in two crosses of bread wheat

Cross		Generations					
		P ₁	P ₂	F ₁	F ₂	B ₁	B ₂
Days to 50% flowering							
BHU 31 × HD 2733	Mean	81.93	82.53	84.87	85.17	84.47	85.33
HPYT 485 × HD 2967	Mean	81.93	82.67	79.53	81.68	81.40	82.33
Chlorophyll content (SPAD)							
BHU 31 × HD 2733	Mean	54.91	56.30	54.29	53.80	54.69	53.35
HPYT 485 × HD 2967	Mean	56.47	55.47	57.24	54.95	54.86	54.51
Plant height (cm)							
BHU 31 × HD 2733	Mean	91.95	90.53	93.04	92.94	86.83	88.95
HPYT 485 × HD 2967	Mean	90.93	92.60	95.60	91.81	93.27	92.20
Spike length (cm)							
BHU 31 × HD 2733	Mean	10.95	10.68	12.35	11.55	10.60	11.01
HPYT 485 × HD 2967	Mean	10.96	11.36	11.82	11.58	10.83	11.21
Number of tillers/plant							
BHU 31 × HD 2733	Mean	6.53	6.67	7.53	6.75	5.47	6.27
HPYT 485 × HD 2967	Mean	6.67	6.73	7.20	6.50	5.13	5.27
Days to maturity							
BHU 31 × HD 2733	Mean	128.40	130.87	126.53	128.78	130.13	130.07
HPYT 485 × HD 2967	Mean	125.47	127.40	125.67	125.12	124.67	128.53
Number of grains per spike							

BHU 31 × HD 2733	Mean	59.47	51.87	51.01	52.80	42.27	42.00
HPYT 485 × HD 2967	Mean	57.27	57.93	53.67	53.58	56.40	56.07
1000-grain weight (g)							
BHU 31 × HD 2733	Mean	45.78	45.90	40.82	43.34	43.05	37.17
HPYT 485 × HD 2967	Mean	43.91	44.55	41.25	41.67	41.15	41.05
Harvest Index (%)							
BHU 31 × HD 2733	Mean	42.47	43.49	44.47	40.78	42.62	41.67
HPYT 485 × HD 2967	Mean	43.94	44.46	45.62	43.52	42.73	43.54
Canopy temperature (°C)							
BHU 31 × HD 2733	Mean	21.37	22.83	22.49	20.03	20.83	21.13
HPYT 485 × HD 2967	Mean	23.19	22.07	24.43	23.76	23.35	23.11
Grain Zinc content (ppm)							
BHU 31 × HD 2733	Mean	33.13	24.03	29.25	29.37	28.43	25.06
HPYT 485 × HD 2967	Mean	33.73	24.70	29.03	28.65	30.05	25.96
Grain Iron content (ppm)							
BHU 31 × HD 2733	Mean	42.81	34.21	38.13	37.93	38.11	35.05
HPYT 485 × HD 2967	Mean	42.10	35.67	37.80	38.72	37.99	35.99
Grain yield per plant							
BHU 31 × HD 2733	Mean	23.65	22.01	20.71	21.64	21.25	20.06
HPYT 485 × HD 2967	Mean	21.64	23.63	20.29	22.04	20.85	21.90

Table 3: Scaling and joint scaling test for Morpho-physiological and biochemical trait in cross I (BHU 31 × HD 2733)

Traits	Scaling test				Joint Scaling test				Epistasis
	A	B	C	D	m	d	h	χ^2 value (3 d.f)	
Days to 50% flowering	2.13	-2.73	0.46	0.53	85.05**	-2.89**	-0.22	3.89	-
Chlorophyll content (SPAD)	0.19	-3.89	-4.57	-0.43	54.65**	0.16	-1.27	4.40	-
Plant height (cm)	-11.34**	-5.66	3.19	10.10**	89.86**	0.19	2.71*	20.09**	Present
Spike length (cm)	-2.10**	-1.00*	-0.113	1.49**	10.66**	0.25*	1.45**	15.58**	Present
Number of tillers/plant	-3.13**	-1.66**	-1.26	1.76**	6.25**	-0.18*	0.63**	107.03**	Present
Days to maturity	5.33**	2.73	2.80	-2.63	129.87**	-1.30*	-2.36*	7.60	Present
Number of grains per spike	-25.94**	-18.88**	-2.18	21.32**	53.05**	3.89**	-3.95**	129.04**	Present
1000-grain weight (g)	-0.50	-12.37**	0.03	6.45**	44.92**	1.06	-4.48**	29.91**	Present
Harvest Index (%)	-1.70	-4.61	-11.79**	-2.73	42.18**	0.15	0.93	15.06**	Present
Canopy temperature (°C)	-2.18*	-3.05*	-9.06**	-1.91	21.24**	-0.08	0.77*	34.79**	Present
Grain Zinc content (ppm)	-5.52**	-3.16**	1.80	5.24**	28.35**	4.53**	0.58*	41.01**	Present
Grain Iron content (ppm)	-4.72**	-2.24	-1.56	2.70**	38.27**	4.25**	-0.66*	34.77**	Present
Grain yield per plant (g)	-1.86	-2.60	-0.54	1.96	22.60**	0.91**	-2.15**	5.98	-

*and **: Significance at 5% and 1% respectively.

Table 4: Scaling and joint scaling test for Morpho-physiological and biochemical trait in cross II (HPYT 485 × HD 2967)

Traits	Scaling test				Joint Scaling test				Epistasis
	A	B	C	D	m	d	h	χ^2 value (3 df)	
Days to 50% flowering	1.33	2.46	3.06	-0.36	82.57**	-0.46	-2.72**	2.17	-
Chlorophyll content (SPAD)	-3.98	-3.68	-6.62	0.52	55.31**	0.46	0.75	4.92	-
Plant height (cm)	0	-3.8	-7.5	-1.85	91.36**	-0.58	3.45	4.86	-
Spike length (cm)	-1.12	-0.75	0.35	1.11	11.07**	-0.23	0.65*	6.51	-
Number of tillers/plant	-3.60**	-3.40**	-1.80*	2.60**	6.35**	0.02	-0.14	81.51**	Present
Days to maturity	-1.80	4.00	-3.73	-2.96	126.33**	-1.21	-0.77	4.70	-
Number of grains per spike	1.86	0.53	-8.20	-5.30	57.38**	-0.23	-3.98**	2.94	-
1000-grain weight (g)	-2.85	-3.70	-4.27	1.14	43.48**	-0.18	-2.97**	4.41	-
Harvest Index (%)	-4.10	-2.98	-5.56	0.76	43.28**	-0.25	1.74	6.87	-
Canopy temperature (°C)	-0.93	-0.29	0.90	1.06	22.58**	0.57*	1.81**	1.50	-
Grain Zinc content (ppm)	-2.66**	-1.81	-1.90	1.28	28.95**	4.39**	-0.06	12.83**	Present
Grain Iron content (ppm)	-3.92**	-1.48	1.49	3.45**	38.75**	3.08**	-1.12**	17.11**	Present
Grain yield per plant (g)	-0.22	-0.12	2.32	1.33	22.79**	-1.05**	-2.44**	1.46	-

*and **: Significance at 5% and 1% respectively

Table 5: Estimates of three parameters (m, d& h) for Morpho-physiological and biochemical trait in two crosses of bread wheat cross-I (BHU 31 × HD 2733) and cross-II (HPYT 485 × HD 2967)

S. No.	Traits	Crosses	m	d	h
1	Days to 50% flowering	BHU 31 × HD 2733	86.3**	-3.3	-3.1
		HPYT 485 × HD 2967	81.57**	-0.37	2.50
2	Chlorophyll content (SPAD)	BHU 31 × HD 2733	54.73**	-0.70	-3.27
		HPYT 485 × HD 2967	57.02	0.50*	-8.50
3	Plant height (cm)	HPYT 485 × HD 2967	88.07	-0.83	7.43
4	Spike length (cm)	HPYT 485 × HD 2967	13.39**	-0.20*	-5.69
5	Days to maturity	HPYT 485 × HD 2967	120.50**	-0.97*	13.30
6	Number of grains per spike	HPYT 485 × HD 2967	47.00**	-0.33*	19.67
7	1000-grain weight (g)	HPYT 485 × HD 2967	46.51**	-0.32*	-14.11
8	Harvest Index (%)	HPYT 485 × HD 2967	45.72**	-0.26	-8.71
9	Canopy temperature °C	HPYT 485 × HD 2967	0.56**	-3.68	3.35
10	Grain yield per plant (g)	BHU 31 × HD 2733	26.76**	0.82**	-14.45*
		HPYT 485 × HD 2967	25.30**	-1.00*	-8.01

*and **: Significance at 5% and 1% respectively.

Table 6. Estimates of six parameters (m, d, h, i, j & l) for Morpho-physiological and biochemical trait in two crosses of bread wheat cross-I (BHU 31 × HD 2733) and cross-II (HPYT 485 × HD 2967)

S. No.	Traits	Crosses	m	d	h	i	j	l	Epistasis
1	Days to 50% flowering	HPYT 461 × HD 2733	75.99**	-3.40**	27.40*	10.47	1.33	-23.00*	D
2	Spike length (cm)	HPYT 461 × HD 2733	14.57**	0.41**	-9.70**	-3.89**	0.22	8.44**	D
		BHU 31 × HD 2967	10.07**	-0.05	3.35	0.95	1.15*	-3.04*	—
3	Number of tillers	HPYT 461 × HD 2733	8.87**	-0.74	-10.13**	-2.34**	-1.47**	8.33**	C
		BHU 31 × HD 2967	13.53**	0.07	-20.33**	-6.47**	0.40	14.33**	D
4	Days to maturity	HPYT 461 × HD 2733	113.83**	-3.23**	33.38*	15.14*	-2.30	-22.41*	D
		BHU 31 × HD 2967	124.50**	-0.44	7.05**	4.07*	5.64	-1.33	-
5	Grains per spike	BHU 31 × HD 2967	70.37**	0.63	-45.90**	-11.40**	-0.07	-29.60**	D
6	Thousand grain weight (g)	HPYT 461 × HD 2733	37.46**	-0.94	9.49	4.40**	-2.10	-5.66	-
7	Harvest index (%)	BHU 31 × HD 2967	41.28**	-0.95	10.37	2.93	6.69*	-6.82**	-
8	Canopy temperature °C	BHU 31 × HD 2967	25.05**	-0.29*	-3.04	-3.38*	0.76	0.92	-
9	Grain Zinc content (ppm)	HPYT 461 × HD 2733	35.93**	6.08**	-17.05**	-5.94**	-4.40**	10.77**	D
		BHU 31 × HD 2967	32.68**	4.07**	-12.43*	-3.97	-3.02**	8.10*	D
10	Grain Iron content (ppm)	HPYT 461 × HD 2733	43.10**	4.15**	-13.51**	-4.81**	-6.14**	7.31**	D
		BHU 31 × HD 2967	43.24**	3.40**	-13.21*	-3.85	-3.81**	8.98**	D
11	Grain yield per plant (g)	BHU 31 × HD 2967	25.67**	-0.18	-7.73	-1.95	-2.94*	2.98	-

*and **: Significance at 5% and 1% respectively.

Table 7: Estimate of heritability and genetic advance as percentage of mean for morpho-physiological and biochemical traits in four crosses of bread wheat

S.No.	Trait	Crosses	$h^2_{(bs)}$ %	$h^2_{(ns)}$ %	GAM (5%)
1	Days to 50% flowering	BHU 31 \times HD 2733	85.90	59.70	5.54
		HPYT 485 \times HD 2967	83.00	60.00	9.05
2	Chlorophyll content (SPAD)	BHU 31 \times HD 2733	71.00	39.03	9.92
		HPYT 485 \times HD 2967	70.00	55.00	10.24
3	Plant height (cm)	BHU 31 \times HD 2733	93.00	65.17	20.13
		HPYT 485 \times HD 2967	76.00	52.00	13.68
4	Spike length(cm)	BHU 31 \times HD 2733	80.49	54.20	11.97
		HPYT 485 \times HD 2967	72.00	51.00	12.13
5	Number of tillers/plant	BHU 31 \times HD 2733	78.00	41.00	20.96
		HPYT 485 \times HD 2967	51.00	40.00	15.52
6	Days to maturity	BHU 31 \times HD 2733	75.11	36.00	3.82
		HPYT 485 \times HD 2967	86.00	42.00	8.20
7	Number of grains per spike	BHU 31 \times HD 2733	84.00	40.00	9.26
		HPYT 485 \times HD 2967	82.00	60.00	18.20
8	1000-grain weight (g)	BHU 31 \times HD 2733	91.30	50.31	11.90
		HPYT 485 \times HD 2967	80.00	67.00	12.16
9	Harvest Index (%)	BHU 31 \times HD 2733	70.00	30.00	10.03
		HPYT 485 \times HD 2967	76.00	37.00	6.21
10	Canopy temperature (°C)	BHU 31 \times HD 2733	89.00	44.00	10.58
		HPYT 485 \times HD 2967	85.00	67.10	10.08
11	Grain Zinc content (ppm)	BHU 31 \times HD 2733	94.00	72.00	13.58
		HPYT 485 \times HD 2967	94.00	50.00	8.58
12	Grain Iron content (ppm)	BHU 31 \times HD 2733	87.00	55.00	7.01
		HPYT 485 \times HD 2967	78.00	36.00	5.59
13	Grain yield per plant (g)	BHU 31 \times HD 2733	87.00	62.00	16.51
		HPYT 485 \times HD 2967	89.10	40.00	11.92

role in expression of number of grains per spike with higher magnitude of dominance gene effect in cross BHU31 \times HD2733. Similar findings were reported by Abedi *et al.*, 2015 and Dvojkojic *et al.*, 2010 for preponderance of dominance gene effect in governing number of grains per spike. Among inter-allelic interactions additive \times additive and dominance \times dominance gene action was observed with higher magnitude of dominance \times dominance in cross BHU31 \times HD2733. Similar results were reported by Erkul *et al.*, 2010; Ljubcic *et al.*, 2016 and Ninghot *et al.*, 2016 for presence of dominance \times dominance gene interaction in influencing number of grains per spike. For expression of trait 1000-grain weight dominant gene effect along with all three epistatic interactions with higher magnitude of dominance \times dominance was observed in cross BHU31 \times HD2733. Similar finding was reported by Mohamed *et al.*, 2014 for 1000 grain weight. Additive and dominance gene effect with higher

magnitude of dominance gene effect was observed in expression of Canopy temperature in cross BHU31 \times HD2733. Among the epistatic interaction only additive \times additive gene effect was observed. Additive and dominance gene action played role in expression of Grain Zinc content but due to higher magnitude of dominance gene effect preponderance of dominance gene action was observed in expression of trait in both crosses, BHU31 \times HD2733 and HPYT485 \times HD 2967. Among the inter-allelic interactions additive \times additive and dominance \times dominance both interaction was found in cross BHU31 \times HD2733 while in cross HPYT485 \times HD 2967 only dominance \times dominance was observed. Similar results were reported by Gaddameedi *et al.*, 2018 and Amiri *et al.*, 2020 for grain Zinc content. All the three types of gene action is found contributing in governing expression of grain Zinc content thus for improvement of this trait reciprocal recurrent selection will be very effective. In expression of

grain Iron content additive and dominance gene action played role in expression of this trait but due to higher magnitude of dominance gene effect preponderance of dominance gene action was observed in both crosses, BHU31 \times HD2733 and HPYT485 \times HD 2967. Among epistatic interaction, higher magnitude of dominance \times dominance gene effect suggests for preponderance of dominance \times dominance effect in expression of grain Iron content in both crosses. Similar result was reported by Gaddameedi *et al.*, 2018. Higher magnitude of non-additive gene interaction of dominant nature in expression of grain Iron content indicates that for improvement of this trait recurrent selection for specific combining ability will be more effective. Further, non-additive gene action also disfavours selection in early generations thus selection for this trait should be delayed in later generation.

Heritability and genetic advance are two important genetic parameters that guides a breeder in devising a crop improvement programme. The estimates of heritability and genetic advance are presented in table 7. In the present study broad sense heritability as well as narrow sense heritability were recoded to be high in both crosses while the genetic advance as percent of mean was low both crosses for days to 50% flowering. Thapa *et al.*, (2019) reported similar findings for low genetic advance of days to 50% flowering. This indicate that days to 50% flowering is governed by genes that are predominantly non additive in nature. For chlorophyll content and harvest index broad sense heritability was high and narrow sense heritability was moderate in both crosses while the genetic advance as percent of mean was low to moderate in both crosses. For plant height broad sense heritability as well as narrow sense heritability was high in cross BHU31 \times HD2733 while the genetic advance as percent of mean was moderate to high. For spike length, broad sense heritability, narrow sense heritability and genetic advance as percent of mean were moderate to high in both crosses. Similar observations were reported by Kumar *et al.*, 2017 and Tilahun *et al.*, 2020 for high genetic advance of plant height and spike length. These findings indicate that genes governing spike length are mostly additive in nature. Thus indirect selection for higher yield based on spike length would be rewarding and effective. For number of

tillers per plant, broad sense heritability was high and narrow sense heritability was moderate and the genetic advance as percent of mean was moderate in first cross. For days to maturity broad sense heritability was high and narrow sense heritability as well as genetic advance was low. For number of grains per spike broad sense heritability and narrow sense heritability was moderate to high while the genetic advance as percent of mean was low to moderate. For 1000- grain weight and grain yield per plant, broad sense heritability was high and narrow sense heritability was moderate to high while the genetic advance as percent of mean was moderate. Kumar *et al.*, 2017 reported similar results for moderate genetic advance of 1000-grain weight and grain yield per plant. These findings indicate that genes governing 1000- grain weight and grain yield per plant are mostly additive in nature. Thus these traits could be an important parameter for indirect selection for higher yield. For canopy temperature, grain Zinc content and grain Iron content broad sense heritability was high and narrow sense heritability was moderate to high while the genetic advance as percent of mean was low to moderate. Similar result was reported by Amiri *et al.*, 2018 and 2020 for high broad sense heritability and moderate narrow sense heritability of grain Zinc and Iron content. These findings indicate that genes governing canopy temperature, grain Zinc content and grain Iron content are mostly non additive in nature. However, for these traits high heritability coupled with high genetic advance as percent of mean indicated for preponderance of additive gene action thus progress through selection would be rapid and rewarding. Further, the non-additive gene action in governing these traits are expected to be of additive \times additive types.

High heritability coupled with low to moderate genetic advance as percent of mean indicated for slow progress through selection and preponderance of non-additive gene action or high environmental influence on trait expression, which could be exploited through selection in later generation. The findings suggested for prevalence of non-additive gene action in expression of days to 50 % flowering, chlorophyll content, number of tillers per plant, days to maturity, number of grains per spike, 1000 grain weight, harvest index, canopy temperature, grain Zinc content, grain Iron content

and grain yield per plant. Thus selection for these traits should be practiced.

Conclusion

In both the crosses dominance and dominance \times dominance effect played a significant role in the expression of both grain Zinc content and grain Iron content. Duplicate type of gene interaction was found predominant for grain Zinc and Iron content

and almost for all the traits due to opposite sign of dominance (h) and dominance \times dominance (l) gene effect which tends to cancel the effect of each other in hybrid combination therefore selection should be practiced in advance generation.

Conflict of interest

The authors declare that they have no conflict of interest.

References

- Abbasi, S., Baghizadeh, A., Mohammadi-Nejad, G., and Nakhoda, B. (2014). Genetic analysis of grain yield and its components in bread wheat (*Triticum aestivum* L.). *Annual Research & Review in Biology*. 3636-3644.
- Abedi, J., Baghizadeh, A., and Mohammadi-Nejad, G. (2015). Genetic analysis for some of morphological traits in bread wheat under drought stress condition using generations mean analysis. *Journal of Stress Physiology & Biochemistry*. 11(2).
- Amiri, R., Bahraminejad, S., Cheghamirza, K., and Arzani, A. (2020). Genetic analysis of iron and zinc concentrations in bread wheat grains. *Journal of Cereal Science*. 95: 103077.
- Bouis, H. E., Hotz, C., McClafferty, B., Meenakshi, J. V., & Pfeiffer, W. H. (2011). Biofortification: a new tool to reduce micronutrient malnutrition. *Food and nutrition bulletin*, 32(1_suppl1), S31-S40.
- Cavalli L. L. (1952). An analysis of linkage in quantitative inheritance (ed. E. C. R. Reive and C. H. Waddington), pp 135–144. HMSO, London.
- Ceballos H. (1996). Manual de genética cuantitativa y mejoramiento genético. Universidad Nacional de Colombia, Palmira. pp. 337.
- Dvojkovic, K., Drezner, G., and Novoselovic, D. (2010). Estimation of some genetic parameters through generation mean analysis in two winter wheat crosses. *Periodicum biologorum*. 112(3): 247-251.
- Erkul, A., Aydin, U. N. A. Y., and Konak, C. (2010). Inheritance of yield and yield components in a bread wheat (*Triticum aestivum* L.) cross. *Turkish Journal of Field Crops*. 15(2): 137-140.
- Fethi, B. (2010). Epistasis and genotype-by-environment interaction of grain yield related traits in durum wheat. *Journal of Plant Breeding and Crop Science*. 2(2): 024-029.
- Gaddameedi, A., Ravikiran, K. T., Mohammed, R., Phuke, R. M., Sadaiah, K., Kishor, P. K., and Kumar, A. A. (2018). Inheritance studies on grain iron and zinc concentration and agronomic traits in sorghum [*Sorghum bicolor* (L.) Moench]. *Journal of Cereal Science*. 83: 252-258.
- Hayman, B.I. (1958). The separation of epistasis from additive and dominance variation in generation means. *Heredity*, 12, 371-391.
- India. Ministry of Agriculture and Farmers Welfare, Government of India. Department of Agriculture, Cooperation & Farmers Welfare (2020). Annual report 2019-2020. New Delhi. Krishi Bhawan. 252p.
- Jinks, J. L., and Jones, R. M. (1958). Estimation of the components of heterosis. *Genetics*. 43(2): 223.
- Johnson, H.W., Robinson, H.F. and Comstock, R.E. (1955). Estimates of genetic and environmental variability in soybeans, *Agronomy Journal*, 47, 314-318.
- Kearsey, M. J. & Pooni, H. S. (1996) The genetical analysis of quantitative traits. 1st ed. Chapman and Hall, London, pp 46.
- Kumar, P., Yadava, R. K., Gollen, B., and Sheoran, O. P. (2013). Gene effects for different traits of spike morphology in wheat (*Triticum aestivum*). *Indian Journal of Agricultura Sciences*, 83(7), 748-757.
- Ljubicic, N. D., Petrovic, S. R., Dimitrijevic, M., and Hristov, N. S. (2016). Gene actions involved in the inheritance of yield related traits in bread wheat (*Triticum aestivum* L.). *Emirates Journal of Food and Agriculture*, 477-484.
- Manivannan N. 2014. TNAUSTAT-Statistical package. In: <https://sites.google.com/site/tnaustat>
- Mather, K. (1949). Biometrical Genetics: The study of continuous variation. Methuen and Company Limited, London.
- Mather K. and Jinks I.L. (1982). Biometrical Genetics. 3th ed. Chapman and Hall, London, pp 65-83.
- Mohamed, N. E. M. (2014). Genetic control for some traits using generation mean analysis in bread wheat (*Triticum*

- aestivum* L.). *International Journal of Plant & Soil Science*,3(9),1055-1068.
- Ninghot, C. J., Boratkar, M.V., Thawari, S. B. and Potdukhe, N. R. (2016). Generation Mean Analysis for Yield and Yield Components in Wheat (*Triticum aestivum* L.). *International Journal of Genetics*. 8 (4): 204-206.
- Ninghot, C. J., Boratkar, M. V., Thawari, S. B., & Potdukhe, N. R. (2016). Generation mean analysis for yield and yield components in Wheat (*Triticum aestivum* L.).*International Journal of Genetics*,4 (8), 204-206.
- Raikwar, R. S. (2019). Genetic architecture of yield and quality traits in wheat (*Triticum aestivum* L.), *Indian J. Genet.*,79(1),100-103.
- Reynolds, M., Foulkes, J., Furbank, R., Griffiths, S., King, J., Murchie, E. and Slafer, G. (2012). Achieving yield gains in wheat. *Plant, Cell & Environment*, 35(10): 1799-1823.
- Robinson, H. F., Cornstock, R.E., and Harvey, P.M. (1949). Estimates of heritability and degree of dominance in corn. *Agronomy Journal*,41, 353-359.
- Said, A. A. (2014). Generation mean analysis in wheat (*Triticum aestivum* L.) under drought stress conditions. *Annals of Agricultural Science*,59(2),177–184.
- Thapa, R. S., Sharma, P. K., Pratap, D., Singh, T., and Kumar, A. (2019). Assessment of genetic variability, heritability and genetic advance in wheat (*Triticum aestivum* L.) genotypes under normal and heat stress environment. *Indian Journal of Agricultural Research*,53(1),51-56.
- Tilahun, B., Habtamu, T., and Tesfaye, L. (2020). Genetic variability, heritability and genetic advance among bread wheat genotypes at Southeastern Ethiopia. *Agriculture, Forestry and Fisheries*, 9,128-134.
- Uzokwe VNE, Asafo-Adjei B, Fawole I, Abaidoo R, Odeh IOA, Ojo DK, Daxshiell K and Sanginga N.(2017). Generation mean analysis of phosphorus-use efficiency in freely nodulating soybean crosses grown in low-phosphorus soil. *Plant Breeding* 136(2): 139– 146. doi: 10.1111/pbr.12453
- Usman, I., and Muhammad, K. (2013). Genetic study of quantitative traits in spring wheat through generation means analysis. *American-Eurasian Journal of Agricultural & Environmental Sciences*,13(2),191-197.
- Velu, G., Singh, R. P., Crespo-Herrera, L., Juliana, P., Dreisigacker, S., Valluru, R., and Joshi, A. K. (2018). Genetic dissection of grain zinc concentration in spring wheat for mainstreaming biofortification in CIMMYT wheat breeding. *Scientific Reports*,8(1),1-10.
- Velu, G., Singh, R. P., Huerta, J., & Guzmán, C. (2017). Genetic impact of Rht dwarfing genes on grain micronutrients concentration in wheat. *Field Crops Research*, 214, 373-377.
- Velu, G., Tutus, Y., Gomez-Becerra, H. F., Hao, Y., Demir, L., Kara, R., and Cakmak, I. (2017). QTL mapping for grain zinc and iron concentrations and zinc efficiency in a tetraploid and hexaploid wheat mapping populations. *Plant and Soil*,411(1-2), 81-99.

Publisher's Note: ASEA remains neutral with regard to jurisdictional claims in published maps and figures.