



Research Article

GENERATION MEAN ANALYSIS FOR MORPHO-PHENOLOGICAL TRAITS IN BREAD WHEAT (*Triticum aestivum* L.)

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Abstract- The study was carried to investigate the inheritance of gene action for various morpho-phenological traits in bread wheat at the Haryana Agricultural University, Hisar during *rabi* 2013-14 and 2014-15. A set of six generations (P₁, P₂, F₁, F₂, B₁ and B₂) of each two cross combinations (P 12210/Raj MR 1 and P 12231/Raj MR 1) was grown in the compact family block design in three replications and the morpo-phenological traits such as plant height, biomass *per* plant, harvest index, days to heading and days to maturity were observed. High values of PCV, GCV, heritability and genetic advance were observed for all the traits in the study. The results regarding gene effects indicated that plant height, days to heading and days to maturity were predominantly governed by additive gene effects, while biomass *per* plant and harvest index were predominantly governed by dominance gene effects. Components of genetic variances indicated additive variance for days to heading and days to maturity and dominance variance for biomass *per* plant, while both additive and dominance components of genetic variance were important for plant height and harvest index. Thus, it is suggested to perform selection in early generations for phenological traits like days to heading and days to maturity while selfing for few generations required before selection in remaining traits.

Keywords- Inheritance, Variability, Heritability, Selection, Bread Wheat.

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Introduction

Wheat is the second most important cereal crop after rice grown under diverse agro-climatic conditions. Wheat improvement program deals with development of high yielding varieties. Moreover, phenological traits play a vital role in the wheat yield improvement program as many researchers have been reported that wheat yield is considerably affected by sowing date and maturity time [1]. Thus, the knowledge of gene action helps in the choice of appropriate breeding procedure in improvement of these traits to develop high yielding varieties. In earlier reports Sood [2] observed preponderance of non-additive gene action for days to maturity while, Sood *et al.* [3] reported the presence of additive gene action for this trait. Munir *et al.* [4] reported that days to heading was controlled by additive genes. Shrikant *et al.* [5] reported that both additive and dominance gene effects were prevalent for harvest index. Akhtar and Chowdhary [6] indicated that additive or additive × additive gene effects were more prevalent for plant height while dominance or dominance × dominance effects was noticed prevalent for biomass *per* plant. Thus, in order to reach on the consensus of gene action the genetic studies required to be conducted over the wide range of genetic material, environmental conditions and other factors influencing inheritance.

Haluver and Miranda [7] have presented extensive review on evaluating methods of genetic components and showed that there are several advantages of generation mean analysis. It is relatively simple and statistically reliable [8]. Moreover, the errors are inherently smaller in generation mean analysis as it is based on means which are estimated with greater precision than variances. Thus, the present study was undertaken to study genetic variability parameters and inheritance pattern of different morpho-phenological traits in bread wheat using generation mean analysis.

Materials and Methods

Three diverse parents P 12210, P 12231 and Raj MR 1 were used to develop six generations *i.e.* P₁, P₂, F₁, F₂, B₁ and B₂ in two cross combinations [Table-1]. A set of these generations *i.e.* P₁, P₂, F₁, F₂, B₁ and B₂ of each two crosses were evaluated in Compact Family Block Design with three replications, during *rabi* 2013-2014 and 2014-2015 in the Department of Genetics and Plant Breeding, CCSHAU, Hisar. Among the treatments, the non segregating generations, *viz.*, parents P₁, P₂, and F₁ were grown in single row of 3m length. The segregating F₂ generation was grown in ten rows of 3m row length and backcrosses B₁ and B₂ were grown in four rows of 3m length. The row to row and plant to plant distance was maintained 23 cm and 10 cm, respectively. All recommended package of practices were followed to raise the healthy crop. Five plants from each non-segregating P₁, P₂ and F₁ generations were selected. Whereas, 20 plants from each backcross generation and 50 plants from F₂ generation were selected for observing data on plant height (cm), biomass *per* plant (g), harvest index, days to heading and days to maturity.

Table-1 Parentage/source of plant material used in study

Generations	Pedigree		Collection Centre
	Cross A	Cross B	
P ₁	P 12210 [W462/UJEE/KOEL/3/PEG/HRL/BUC]	P 12231 [WBL1*2/K1RITAT]	HAU, Hisar-Haryana
P ₂	Raj MR 1 [AUS 15854/J-24]	Raj MR 1 [AUS 15854/J-24]	RAS, Jaipur-Rajasthan
F ₁	P 12210/Raj MR 1	P 12231/Raj MR 1	
F ₂	P 12210/Raj MR 1	P 12231/Raj MR 1	
B ₁	P 12210*2/Raj MR 1	P 12231*2/Raj MR 1	
B ₂	P 12210/2* Raj MR 1	P 12231/2* Raj MR 1	

Analysis of variance was carried out as per method described by Little and Hill [9]. The coefficients of genotypic and phenotypic variation were calculated by the formula given by Burton and Devane [10]. Heritability percentage in broad sense and genetic advance as percent of mean was calculated for each character as per formula and standard procedure prescribed by Singh and Chaudhary [11].

$$\text{Heritability in broad sense } (H^2) = [\sigma^2_g / \sigma^2_P] \times 100$$

Genetic advance (as percentage of mean)

$$G.A.(%) = [(k \cdot H^2 \cdot \sigma^2_P) / \bar{F}_2] \times 100$$

Where, k = selection differential constant (2.06 at 5% selection intensity); H²= heritability in broad sense; σ^2_g = Genotypic variance; σ^2_P = Phenotypic variance and \bar{F}_2 = mean of F₂.

The components of genetic variances and heritability in narrow sense for generations were calculated by the formulae of Mather and Jinks [8] given below.

$$D = 4V_{F_2} - 2(V_{B_1} - V_{B_2})$$

$$H = 4(V_{B_1} + V_{B_2} - V_{F_2} - V_E)$$

$$E = 1/4(V_{P_1} + V_{P_2} + 2V_{F_1})$$

$$\text{Heritability in narrow sense } (h^2) = \left[\frac{D/2}{D/2 + H/4 + E} \right] \times 100$$

Where: D – additive genetic variance; H – dominance genetic variance; E –

environmental component of variance.

For estimation of gene effects joint scaling test outlined by Cavalli [12] was applied to six generations P₁, P₂, F₁, F₂, B₁ and B₂ to fit three parameter model accordingly given in Dabholkar [13]. It consists of estimating the parameters m, (d) and (h) using weighted least squares method. The test of goodness of fit was calculated by Chi-square test (as given below) and the characters with significant chi-square values were further analyzed by using six parameter model.

$$\chi^2 \text{ at } (n - p) \text{ d. f.} = \sum_{i=1}^n (O_i - \hat{E}_i)^2 W_i$$

Where, O_i = observed mean of ith generation, \hat{E}_i = expected mean of ith generation, W_i = weight of information of ith generation, n = number of generations and p = number of parameters estimated.

Results and Discussion

Analysis of variance showed that the progenies were highly significant for all the characters in both the crosses [Table-2]. This suggested that the genotypes selected were genetically variable and considerable amount of variability generated in their filial generations, which facilitate possibility of selection in a breeding programme. Similarly, many scientists also reported high variability in the filial and backcross generations of wheat [14-16]. The significant variation due to year × progenies for plant height, biomass per plant and harvest index revealed that different progenies behaved differently over the different years, for these traits.

Table-2 Analysis of variance for various traits in bread wheat during the years 2013-14 and 2014-15 for both the crosses

Source of variation	Crosses†	Year (df=1)	Replications (df=4)	Progenies (df=5)	Progenies × year (df=5)	Residual (df=20)
Plant height	I	57.2*	8.4	89.9**	29.5*	9.9
	II	37.1*	1.1	83.5**	42.7*	12.2
Biomass per plant	I	251.5**	1.2	75.6**	24.5*	7.6
	II	155.3**	5.7	55.0**	71.9*	3.9
Harvest index	I	48.6	35.4	55.4*	128.0**	18.2
	II	153.1	40.7	99.6*	50.5**	18.5
Days to heading	I	225.0**	0.2	13.0**	0.1	0.2
	II	225.0**	0.1	15.4**	0.1	0.2
Days to maturity	I	36.0**	0.1	62.6**	0.1	0.4
	II	36.0**	0.1	36.3**	0.1	0.1

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

† I and II representing the different crosses P 12210/Raj MR 1 and P 12231/Raj MR 1, respectively

In general, all the traits in the study had high genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) followed by high heritability and genetic advance [Table-3], suggested selection may be practiced for improvement of these

traits provided there was high additive genetic variance. Similar findings were also reported for plant height [17]; for days to heading and days to maturity [4, 18]. While, Yaqoob [19] showed low variability and heritability estimates for days to maturity.

Table-3 Parameters of genetic variability, heritability and genetic advance for various traits in both the crosses during years 2013-14 and 2014-15

Traits	Crosses*	Genotypic Coefficient of Variance	Phenotypic Coefficient of Variance	Heritability in broad sense	Genetic Advance (as per cent of mean)
Plant height	I	17.3	18.5	93.7	33.6
	II	14.9	15.9	93.5	28.9
Biomass per plant	I	35.3	36.9	84.9	64.8
	II	31.7	37.3	95.7	55.7
Harvest index	I	55.6	59.6	90.2	74.2
	II	56.0	62.1	93.3	76.4
Days to heading	I	27.3	28.5	83.7	23.6
	II	29.3	30.5	85.7	25.6
Days to maturity	I	30.1	32.6	79.8	38.2
	II	32.1	34.6	82.8	40.2

* I and II representing different crosses P 12210/Raj MR 1 and P 12231/Raj MR 1, respectively.

Present study revealed that the plant height was governed by additive gene effect in majority of the cases [Table-4]. In cross P 12231/Raj MR 1 during year 2014-15 the plant height was governed by dominance gene action. Gene interactions were mostly non-significant for this trait. Thus, due to the predominant role of additive effect selection in early generation will be effective for plant height. Similar, results were reported by Haleem [20], while Tonk *et al.* [21] reported both additive and dominance

effect with additive × additive and dominance × dominance interaction. Ahmad *et al.* [22] are also opined that dominant effect was the most contributor factor to the inheritance of majority of traits in spring wheat.

For biomass per plant, both additive and dominance were significant, but the dominance component was in negative direction in majority of the crosses [Table-4]. In respect to epistatic interactions, additive × additive and additive × dominance were

significant in majority of the crosses. This indicated that selection should be delayed to later generations for biomass *per* plant. Kularia and Sharma [23] also reported both additive and dominance gene actions and suggested biparental mating approach to get best combination with fixable genes. In present study harvest index was governed by additive and dominance types of gene actions. The non fixable dominance × dominance type of epistatic interaction was more important as it was significant in majority of the crosses. Shrikant *et al.* [5] studied the inheritance of harvest index and observed both additive and dominance gene effects were significant but epistasis was absent in the study. Inamullah *et al.* [24] reported that the additive component was significant for harvest index.

Present study revealed that the days to heading and days to maturity were governed

by additive gene effect in majority of the cases [Table-4]. Additive × additive type of gene interaction was mostly significant for these traits. Thus, due to the predominant role of additive effect and additive × additive interaction selection in early generation will be effective for days to heading and days to maturity. Similarly, Kathiria *et al.* [25] found that both additive as well as dominance gene effects were involved in the inheritance of days to heading and maturity with preponderance of additive gene effects. Also, Sood *et al.* [3] observed that the additive dominance model was found to be adequate for days to maturity, and reported the presence of additive gene effect for this trait. Munir *et al.* [4] reported that days to heading was controlled by additive genes coupled with high heritability. While, Sood [2] observed preponderance of dominance gene action for days to maturity.

Table-4 Gene effects for various traits in bread wheat for both the crosses during years 2013-14 and 2014-15

Traits	Cross	m	d	h	i	j	l	Chi-square value
Plant height	I	95.72**	12.83**	14.05	6.39	25.93**	-3.79	22.93**
	II	92.88**	4.99**	3.48	-	-	-	2.24
	III	87.29**	4.63*	-4.11	0.41	4.00	33.21**	58.21**
	IV	90.89**	2.18	16.93*	11.86*	-3.63	-6.23	10.34*
Biomass <i>per</i> plant	I	48.22**	4.85*	-19.48**	21.65**	-12.70**	6.08	68.30**
	II	42.33**	6.33	-25.80**	23.80*	11.33	14.00	24.85**
	III	48.18**	11.95**	-40.99**	39.49**	21.57**	45.25**	109.72**
	IV	33.90**	0.48	8.06**	-	-	-	6.49
Harvest index	I	47.01**	80.01*	-0.21	-0.23	1.90**	4.10*	15.22**
	II	48.21**	5.01	22.20*	0.16	0.09	6.10*	10.18*
	III	45.0**	20.00*	6.00	-	-	-	3.04
	IV	56.01**	3.24	-32.02*	-0.38	1.41	2.70*	8.18*
Days to heading	I	94.72**	16.63**	4.25	6.39*	15.23**	-6.79	12.93**
	II	92.88**	6.85**	2.18	12.2**	2.13	3.61	32.24**
	III	96.29**	5.88*	3.11	2.41	5.01	13.21**	28.21**
	IV	97.89**	12.18**	6.93*	10.56*	-4.63	-2.23	11.24*
Days to maturity	I	126.51**	10.12**	1.49	8.79**	0.63	-6.23	53.12**
	II	129.83**	11.90**	4.26*	2.01	6.69**	2.24	9.36*
	III	130.15**	9.98**	-2.45	4.91*	2.03	5.28*	21.14**
	IV	135.33**	8.38**	-3.50	6.63**	1.02	-2.00	11.02*

m - mean; d - additive component; h - dominance component; i - additive × additive interaction; j - additive × dominance interaction and l - dominance × dominance

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

†: I, II, III and IV representing cross P 12210/Raj MR 1 during 2013-14, P 12210/Raj MR 1 during 2014-15, P 12231/Raj MR 1 during 2013-14 and P 12231/Raj MR 1 during 2014-15, respectively.

Table-5 Components of variance for various traits in bread wheat for both the crosses during year 2013-14 and 2014-15

Characters	Crosses*	Additive genetic variance (D)	Dominance genetic variance (H)	Environmental variance (E)	Heritability (%) in narrow sense
Plant height	I	224.49	173.52	18.85	88.00
	II	100.70	37.64	8.49	91.90
	III	143.44	75.84	12.21	69.70
	IV	17.47	172.74	14.63	13.10
Biomass <i>per</i> plant	I	10.93	62.16	6.44	18.60
	II	16.01	66.16	8.36	22.90
	III	22.68	49.40	38.40	5.87
	IV	44.28	25.09	10.25	57.30
Harvest index	I	22.86	417.52	69.78	6.20
	II	64.24	72.08	15.37	25.60
	III	13.08	241.24	26.06	4.30
	IV	1.12	19.03	1.61	0.50
Days to heading	I	0.87	5.57	1.09	14.90
	II	6.99	4.25	0.95	54.80
	III	1.29	4.47	0.75	25.70
	IV	1.12	5.66	1.26	10.70
Days to maturity	I	4.39	3.02	1.21	82.80
	II	7.20	5.48	1.13	67.20
	III	0.92	2.59	0.63	26.50
	IV	1.98	1.34	0.90	38.80

*I, II, III and IV representing cross P 12210/Raj MR 1 during 2013-14, P 12210/Raj MR 1 during 2014-15, P 12231/Raj MR 1 during 2013-14 and P 12231/Raj MR 1 during 2014-15, respectively.

Results regarding components of genetic variance showed that both additive and dominance genetic variances were prevalent over the crosses and years for plant height and biomass *per* plant [Table-5]. Therefore, selection for this trait may be

deferred for a few generations to reduce the dominance gene action. Similarly, Ojaghi and Akhundova [26] and Meena *et al.* [27] reported both additive and dominance variance for plant height however the magnitude of additive variance

was higher in these studies. In the present study, the magnitude of additive genetic variance was higher than the dominance genetic variance in majority of the crosses for harvest index, days to heading and days to maturity [Table-5]. This revealed the ample scope of selection for these traits. Similarly, Khan [28] and Abd El-Rahman [29] showed that the magnitude of additive genetic variance was higher than dominance genetic variance for days to heading and days to maturity. In contradiction, higher dominance variance was reported by Singh *et al.* [30] and Akhtar and Chowdhary [6] for harvest index and by Moussa [31] for days to heading and days to maturity.

Conclusion

In conclusion, almost all the traits showed high variability, heritability and genetic advance indicated better opportunities for selection. Further, components of gene effects and variances showed that additive component was important for days to heading and days to maturity. This suggested selection would be effective from early generations for these traits. Whereas, both additive and dominance component were important for remaining traits *i.e.* plant height, biomass *per* plant and harvest index indicated that selection may be deferred up to few generations of selfing to reduce dominance component.

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