

Study of Gene Action and Correlation for Grain Yield and its Attributing Characters in F₁ Generation of Bread Wheat (*Triticum aestivum* L.)

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(Received 12 August, 2022; Accepted 5 October, 2022)

ABSTRACT

Wheat is one of the most important cereal crop both in regard to its antiquity and its use as a source of human food. It is a major staple food crop of the world. The experimental materials consisted of 36 genotypes (28 F₁s + 8Parents) were sown in Randomized Block Design with 3 replications. The estimated values of additive genetic component (\hat{D}) were significant for days to 75% heading, But dominance variance (\hat{h}_i^2) was significant ear length (cm), no. of grains /ear, 1000 grain weight (g), grain yield / plant (g). In the present study, correlation coefficients for parents and F₁s at phenotypic and genotypic levels among the grain yield and other characters have been worked out. The grain yield per plant showed positive and highly significant association with no. of tillers per plant and 1000 grain weight.

Key words : Gene action, Correlation, Grain yield and Bread wheat

Introduction

Wheat is one of the most important cereal crops in terms of both its antiquity and utility as a human food source. It is an important global staple food crop. It was first cultivated between 10,000 and 15,000 B.C. in ancient Persia, Egypt, Greece, and Europe. Wheat was grown by the Swiss lake dwellers, and there are traces of its cultivation in China around 3,000 B.C. Numerous samples of ancient

wheat have been discovered in archaeological excavations. Although the grains of these samples have been carbonised, the anatomical structure has been maintained in some situations. Wheat was cultivated in India more than 5,000 years ago, according to evidence from the ancient ruins of Janno in Eastern Iraq and the excavations of Mohen - Jo - Daro in India. Wheat is mentioned extensively in ancient Indian texts. The Atharva - Veda, which is thought to have been composed between 1,500 and 500 B.C., alludes

to wheat grain. Wheat arrived in North America with Spanish missions in the 16th century, but it was not until the colonization of the prairies in the 1870s that North America became a major grain exporter. Grain output in 2 Kansas quadrupled after grain exports from Russia ended during the First World War. Bread wheat has proved worldwide and well adapted to modern industrial baking products. The centre of origin of wheat is Asia Minor. Wheat (*Triticum aestivum* L.) is belonging to poaceae family presently. Bread wheat is an allohexaploid (AABBDD). It has an interesting history and is a rare illustration of how closely related species can combine to form polyploidy in nature. Combining the tetraploid species *Triticumturgidum* var.dicoccoides (AABB) and the diploid species *Aegilopsquarosa* (DD) and then doubling the chromosomal number resulted in the evolution of bread wheat. Wheat is a remarkable gift of nature to mankind as a healthy complement for human nutritional requirements, containing 12 percent protein, 1.8 percent lipids, 1.8 percent ash, 2% reducing sugar, 59.2 percent starch, 70 percent total carbohydrates, and providing 314 kcal/100 g of food.

The first attempt to partition the genotypic variance into its components was made by Fisher (1918). He recognized three components of hereditary variance: 1) additive 2) dominance and 3) epistasis. In the presence of epistasis the estimation of additive (D), dominant (H) and non-allelic component (i, j and l) of generation mean were calculated by using six parameter model of Hayman (1958). The type of epistasis was determined only when dominance (H) and dominance \times dominance (l) were significant, when these effects had the same sign the effects were complementary while different signs indicated duplicate type of epistasis (Kearsey and Pooni, 1956). The correlation aids in determining the rela-

tive value of various yield affecting features, allowing us to identify the most essential yield components. It is nearly impossible and impractical to practice selection for a large number of characters without attempting correlation, identifying the few most essential yield components is necessary for planning and executing a good selection strategy.

Materials and Methods

The present investigation "Assessment of gene action and correlation in F_1 generation of bread wheat (*Triticum aestivum* L.)" was carried out at Crop Research Farm, Nawabganj, Chandra Shekhar Azad University of Agriculture and Technology, Kanpur-208 002 (U.P.) during Rabi, 2018-20. This area falls in sub-tropical climatic zone. The soil type is sandy loam. The annual rainfall is about 1270 mm. The climate of district Kanpur is semi-arid with hot summer and cold winter. The present investigation comprised of 28 F_1 s developed by crossing 8 lines viz., K - 9107, HD - 2733, HD - 2888, WH - 1218, K - 1313, DBW - 187, HD - 3086 and DBW - 107 (depicted in Table 1) following half diallel mating design (Jinks, 1954) and Hayman (1954a, 1954b). The experimental materials consisted of 36 genotype (28 F_1 s + 8 Parents) were sown in Randomized Block Design with three replications in timely sown (TS) condition. The entries were sown in a single row plot of 3 m length with inter and intra-row spacing of 23 cm and 10 cm, respectively. Recommended agronomic practices were adopted to raise a good crop.

Results and Discussion

Gene action

The estimate of all the components of variation namely D^* , H^*_1 , H^*_2 , F^* , h^2 and E^* along with their

Table 1. Details of genotypes

S.No.	Genotype	Species	Pedigree	Place of origin
1.	K-9107	<i>T.aestivum</i>	K-8101/K68	CSA, Kanpur
2.	HD-2733	<i>T.aestivum</i>	ATTILA/3/HUITLE(HUI)/(CARC)CARCOMUN//CHEN/(CHTO)CHORLITO/4/ATTILA	IARI, New Delhi
3.	HD-2888	<i>T.aestivum</i>	C306/ <i>T. sphaerococcum</i> // HW	IARI, New Delhi
4.	WH-1218	<i>T.aestivum</i>	KA/NAC//TRCH/3/VORB	CCS, Hisar
5.	K-1313	<i>T.aestivum</i>	HUW468/K9107	CSA, Kanpur
6.	DBW-187	<i>T.aestivum</i>	NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2* PASTOR/5/KACHU/6/KACHU	IIWBR, Karnal
7.	HD-3086	<i>T.aestivum</i>	DBW14/HD-2733//HUW468	IARI, New Delhi
8.	DBW-107	<i>T.aestivum</i>	TUKURU/INQLAB	IIWBR, Karnal

standard errors and related statistics as presented in the Table 2. The estimated values of additive genetic component (D^*) were significant for days to 75% heading, number of tillers per plant and days to maturity remaining other traits (D^*) were non - significant, But dominance variance (H^*) was significant for days to 75 % heading (days), days to maturity (days), ear length (cm), no. of grains /ear, 1000 grain weight (g), grain yield / plant (g) characters which were studied. Relatively magnitude of component was higher than that of (D^*) component values for most of the characters under study indicating role of both additive and dominance gene action with prevalence of dominant gene action. Similar findings were also reported by Rabbani *et al.* (2011) and Ahmad *et al.* (2016). However, the non-additive component was more prominent than additive component for all the traits based on average degree of dominance (more than unity for almost all characters).

The estimates of average degree of dominance expressed $(H^*/D^*)^{0.5}$ were higher than unity for most the traits. It revealed that there was over dominance effect for these traits. The value of positive and negative gene proportion ($H^*_2 / 4 H^*_1$) was less than 0.25 for all the characters indicating that the distribution of positive and negative alleles was asymmetrical in the parents. Similar findings were also reported by Farhad *et al.* (2011) and Sandeep *et al.* (2018) for number of tillers. Ratio of (h^2/ H^*_2) was obtained more than unity for three characters those are number of tillers per plant, ear length and no. of spikelet's per ear indicating that more than one gene group were involved to control the expression of these characters. If the value was less than unity, it indicated the frequent involvement of single gene group for inheritance of traits and it may be due to complementary gene interaction causing depression in the ratio.

Table 2. Estimates of variance components and related parameters for nine characters in a set of 8 parent diallelcross of breadwheat

Characters	Variance component					Related parameter (genetic ratio)				
	D^*	H^*_1	H^*_2	F [*]	h^2	E^*	$(H^*/D^*)^{0.5}$	$(H^*/4H^*)$ $F^*1(4DH^*)^{0.5}F^{-1}$	$(h^2/H^*)^2$	
Days to heading (days)	45.48012**	39.12236**	36.05670**	-19.01443	0.09214	0.33726	0.927	0.230	0.632	0.003
SE±	3.58169	8.23378	7.16338	8.46320	4.80407	1.19390				
Days to maturity (days)	32.11896**	19.11177**	17.6870**	-13.05846	2.03850	0.36278	0.771	0.231	0.583	0.115
SE±	2.31511	5.32209	4.63021	5.47038	3.10522	0.77170				
Plant height (cm)	42.15541	188.48840	164.58000	-3.00317	8.36014	1.89340	2.115	0.218	0.967	0.051
SE±	37.01770	85.09822	74.03539	87.46940	49.65128	12.33923				
No. of tillers /plant	6.22597**	19.79629**	16.47749**	-11.95735	25.04786**	1.23173*	1.783	0.208	0.300	1.520
SE±	1.56746	3.60337	3.13493	3.70377	2.10242	0.52249				
No. of spikelet's/ear	0.78116	2.29641	1.84479	-1.23271	2.00954	1.62963**	1.715	0.201	0.370	1.089
SE±	0.72128	1.65812	1.44256	1.70432	0.96744	0.24043				
Length of ear (cm)	-0.07524	1.64499**	1.75715**	-0.47381	2.62057**	0.32762**	4.676	0.267	0.195	1.491
SE±	0.12740	0.29287	0.25480	0.30103	0.17088	0.04247				
No. of grains/ear	10.56993	83.99191**	71.31957**	-0.20804	8.12058	8.69370*	2.819	0.212	0.993	0.114
SE±	9.44765	21.71875	18.89530	22.32392	12.67199	3.14922				
1000 grain weight (g)	5.37169	34.42637**	33.76140**	3.31030	15.85250*	2.58396	2.532	0.245	1.277	0.470
SE±	3.68466	8.47048	7.36931	8.70650	4.94217	1.22822				
Grain yield /plant(g)	5.90326	24.86555*	21.86498*	-9.53784	13.34932*	1.13207	2.052	0.220	0.435	0.611
SE±	3.11755	7.16679	6.23510	7.36648	4.18152	1.03918				

*Significantat 5% level; **Significantat 1% level

Correlation coefficients analysis

The term “correlation” describes a relationship between two variables in which the values of one variable change when the values of the other variable change. Thus, by assessing the degree of association between two characters, correlation can be used to discover how two characters differ from one another or whether two of these characters are related. The correlation study, from breeder point of view, is concerned mainly with two aspects: 1.) It can be useful in selecting the plants for such characters which are not easily observed. 2.) Selection for one character invariably affects a number of other characters too. The significance of phenotypic coefficient was tested against ‘r’ values from ‘r’ Table of Fisher and Yates (1938)¹ for (n-2) degree of freedom where ‘n’ is number of treatments.

In the present study, correlation coefficients for parents and F₁s at phenotypic and genotypic levels

among the grain yield and other characters and also among the other characters themselves have been worked out. The results obtained are presented in Table 3A and 3B. Phenotypic correlation coefficient results are represented as under here:

Days to 75% heading

Days to heading showed positive correlated with number of tillers per plant (0.1688), days to maturity (0.7861), and grain yield per plant (0.1609) while it was negative for ear length (-0.0803), 1000 grain weight (-0.0594).

Number of tillers per plant

Number of tillers per plant showed positive and non-significant correlation with days to maturity (0.0881), ear length (0.0999) and significant correlation with grain yield per plant (0.8007). It had negative and non-significant correlation with no. of

Table 3A. Genotypic correlation for nine characters in a set of 8 parents diallel cross of bread wheat

Attributes	Days to 75% heading (days)	Days to maturity (days)	Plant height (cm)	No. of tillers/ plant	No. of spikelet's/ ear	Ear length (cm)	No. of grains/ ear	1000 grain weight (g)	Grain yield/ plant (g)
Days to 75 % heading (days)	1.0000	0.8057	0.2055	0.1951	0.1917	-0.1205	0.3271	-0.0914	0.1838
Days to maturity (days)		1.0000	0.3700	0.0978	0.2013	-0.0053	0.2524	-0.0456	0.1065
Plant height (cm)			1.0000	-0.2334	0.3150	0.1075	0.2231	0.0252	-0.2891
No. of tillers / plant				1.0000	-0.3040	0.2036	-0.1912	0.1851	0.7808
No. of spikelet's/ear					1.0000	-0.0414	0.7763	-0.5463	-0.3802
Ear length (cm)						1.0000	-0.1181	0.0502	0.1283
No. of grains/ear							1.0000	-0.5380	-0.2299
1000 grain weight (g)								1.0000	0.3052
Grain yield/Plant (g)									1.0000

Table 3B. Phenotypic correlation for nine characters in a set of 8 parents diallel cross of bread wheat

Attributes	Days to 75% heading (days)	Days to maturity (days)	Plant height (cm)	No. of tillers/ plant	No. of spikelet's/ ear	Ear length (cm)	No. of grains/ ear	1000 grain weight (g)	Grain yield/ plant (g)
Days to 75 % heading (days)	1.0000	0.7861**	0.2039*	0.1688	0.0694	-0.0803	0.2153*	-0.0594	0.1609
Days to maturity (days)		1.0000	0.3547**	0.0881	0.1109	0.0195	0.1841	-0.0176	0.0973
Plant height (cm)			1.0000	-0.1898 *	0.1263	0.0585	0.1387	0.0077	-0.2569**
No. of tillers / plant				1.0000	-0.1452	0.0999	-0.1402	0.4077**	0.8007**
No. of spikelet's/ear					1.0000	0.6698**	0.8053**	-0.1813	-0.1482
Ear length (cm)						1.0000	0.4786**	0.0403	0.0905
No. of grains /ear							1.0000	-0.2738**	-0.1483
1000 grain weight (g)								1.0000	0.4952**
Grain yield/Plant (g)									1.0000

*Significant at 5% level; **Significant at 1% level

grains / ear (-0.1402), no. of spikelet's per ear (-0.1452) and significant correlation with plant height (-0.1898) in F₁ generation.

Plant height (cm)

Plant height showed positive and non-significant correlation with ear length (0.0585) and significant correlation with days to maturity (0.3547), days to 75% heading (0.2039) while negative and significant correlation with no. of tillers/ plant (-0.1898), grain yield per plant (-0.2569).

Days to maturity

Days to maturity showed positive and non-significant correlation with number of spikelet's per ear (0.1109), number of grains per ear (0.1841) and ear length (0.0195) and significant correlation with days to 75% heading (0.7861), plant height (0.3547).

Ear length (cm)

Ear length showed negative and non-significant correlation with days to 75 % heading (-0.0803) in F₁ generation while positive and significant correlation with no. of spikelet's per ear (0.6698), no. of grains per ear (0.4786).

Number of spikelet's per ear

Number of spikelet's per ear showed positive and significant correlation with ear length (0.6698), number of grains per ear (0.8053). Negative and non-significant correlation observed for 1000 grain weight (-0.1813), grain yield per plant (-0.1482), no. of tillers per plant (-0.1452).

Number of grains per ear

Number of gains per ear showed positive and highly significant correlation with ear length (0.4786), no. of spikelet's per ear (0.8053). Negative and significant value observed for 1000 grain weight (-0.2738).

1000-grain weight (g)

1000-grain weight showed positive and highly significant correlation with grain yield per plant (0.4952), no. of tillers per plant (0.4077). It had negative and significant correlation with no. of grains / ear (-0.2738).

Grain yield per plant (g)

Grain yield per plant showed positive and highly significant correlation with 1000 grain weight

(0.4952), no. of tillers per plant (0.8007). It had negative and significant correlation with plant height (-0.2569).

In general, genotypic correlation coefficients in the F₁ generation were higher than phenotypic correlation coefficients, indicating a significant inherent relationship between different pairs of traits in the wheat genotype. This suggests that the phenotypic expression of correlation was less attributable to improvement effects. In the present study, the grain yield per plant showed positive and highly significant association with no. of tillers per plant and 1000 grain weight. Similar findings were also reported by Iftikhar *et al.* (2012) and Mecha *et al.* (2017) for grain yield per plant. From the perspective of the breeder, this is a positive indication of crop improvement.

Acknowledgement

Authors are highly grateful to the Department of Genetics and Plant Breeding, Chandra Shekhar Azad University of Agriculture and Technology, Kanpur, Uttar Pradesh, India for providing logistic support necessary to conduct the research work.

References

- Ahmad, I., Mahmood, N., Khaliq, I. and Khan, N. 2016. Genetic analysis for five important morphological attributes in wheat (*Triticum aestivum* L.). *JAPS: Journal of Animal & Plant Sciences*. 26(3).
- Fisher, R. A. and Yates, F. 1938. *Statistical Tables for Biological, Agricultural and Medical Research*. 5 Aufl. Oliver and Boyd. Edinburg.
- Fisher, R. A. 1918. The correlation between relatives on the supposition of mendelian inheritance. *Trans. R. Soc. Edinb.* 53 : 399-433.
- Farhad, Ahmad, Saleem, Khan, Abdul, Latif, Hakim, Khan, Ayub, Khan and Akhtar, N. 2011. Genetics of yield and related traits in bread wheat over different planting dates using diallel analysis. *African J. of Agril. Res.* 6(6): 1564-1571.
- Hayman, B.I. 1954a. The theory of analysis of diallel crosses II. *Genetics*. 43 : 789-809.
- Hayman, B.I. 1954b. The analysis of variance of diallel tables. *Biometrics*. 10 : 235-244.
- Hayman, B.I. 1957. Interaction heterosis and diallel crosses. *Ibid.* 42 : 336-355.
- Hayman, B.I. 1958. The separation of epistatic from additive and dominance variation in generation means. *Hereditiy*. 12 : 371- 390.
- Iftikhar, R., Khaliq, I., Ijaz, M. and Rashid, M. A. R. 2012. Association analysis of grain yield and its compo-

- nents in spring wheat (*Triticum aestivum* L.). *American Eurasian Journal of Agricultural and Environmental Sciences*. 12(3) : 389-392.
- Jinks, J. L. 1954. The analysis of continuous variation in a diallel cross of *Nicotiana rustica* varieties. *Genetics*. 39: 767-788.
- Jinks, J. L. A. 1955. Survey of the genetical basis of heterosis in a variety of diallel crosses. *Heredity*. 9: 223-238.
- Kearsey, M. J. and Pooni, H. S. 1956. *The Genetical Analysis of Quantitative Traits*. Chapman and Hall: London.
- Mecha, B., Alamerew, S., Assefa, A., Dutamo, D. and Assefa, E. 2017. Correlation and path coefficient studies of yield and yield associated traits in bread wheat (*Triticum aestivum* L.) genotypes. *Adv Plants Agric Res*. 6(5) : 128-136.
- Rabbani, G., Mahmood, A., Shabbir, G., Shah, K. N. and Ud-din, N. 2011. Gene action in some yield attributes of bread wheat under two water regimes. *Pak. J. Bot.* 43(2): 1141-1156.
- Sandeep Kumar, Pradeep Kumar, Arya, V. K., Ravi Kumar and Kerkhi, S. A. 2018. Estimates of genetic components and regression analysis for grain yield and various morphological traits in bread wheat (*Triticum aestivum* L.). *Journal of Applied and Natural Science*. 10(1): 6-11.
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