

# Genetic variability, correlation coefficient and path analysis of some quantitative traits in bread wheat

Bharat Bhushan<sup>1\*</sup>, Sonu Bharti, Ashish Ojha<sup>1</sup>, Manoj Pandey, Shailendra Singh Gourav, Bhudeva Singh Tyagi<sup>1</sup> and Gyanendra Singh<sup>1</sup>

Chaudhary Charan Singh University  
Meerut, Uttar Pradesh

## Abstract

A study was undertaken to estimate the genetic variability, correlation and path coefficient analysis of yield and yield contributing traits in 40 wheat cultivars grown in randomized block design with three replications at Research Farm, Department of Genetics and Plant Breeding, CCS University, Meerut, during *rabi* season 2008-09. The analysis of variance revealed that the treatments were highly significant for all the characters. The higher magnitudes of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were recorded for grain yield, biological yield, productive tillers per plant and plant height. The high heritability in broad sense was estimated for all the characters except for grain filling period and test weight. High value of heritability indicates that it may be due to higher contribution of genotypic components. High heritability coupled with high genetic advance as percent of means were recorded for plant height, harvest index, biological yield and grain yield that indicated predominance of additive gene action in the inheritance of these traits. The correlation coefficients estimate showed high direct genotypic and phenotypic correlations for the test weight, biological yield, spikelets per spike and grain filling period. While, days to heading, plant height and days to maturity showed negative correlation with grain yield. Path analysis showed that harvest index had highest direct positive effect on grain yield followed by biological yield, productive tillers per plant, spikelets per spike and test weight thereby indicated that these were main contributors to the grain yield.

**Key words:** Genetic variability, correlation coefficient, path analysis and bread wheat

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## Introduction

Wheat (*Triticum aestivum* L. em. Thell.) is a self-pollinated crop of the member of *Poaceae* family and one of the most leading cereal of many countries of the world including India. It is the most important food crop of India and is a main source of protein and energy. In India, wheat is the second most important food crop after rice both in terms of area and production. It has been described as the 'King of cereals' because of the acreage it occupies, high productivity and the prominent position it holds in the international food grain trade. It is grown in temperate, irrigated to dry and high-rain-fall areas and in warm, humid to dry, cold environments. Wheat is consumed in a variety of ways such as bread, chapatti, porridge, flour, suji etc. Wheat has relatively high content of niacin and thiamin which are principally concerned in providing the special protein called 'Gluten'. Wheat proteins are of special significance because gluten provides the framework of spongy cellular texture of bread and baked products. The record production in the country during last few years has enabled India to attain the position of being second largest producer of the wheat in the world. During 2011-2012, India area under wheat is 29.90 m ha<sup>-1</sup> with the production 93.90 million tons and productivity 3140 kg ha<sup>-1</sup>. Haryana state on the whole

has achieved a productivity level of 5.03 tons ha<sup>-1</sup> on 2.5 million hectares (Anonymous, 2012). However, the demand for wheat is expected to grow and therefore productivity increase is needed. The knowledge about genetic variability, heritability, correlation coefficients and its other parameters help in further improving the grain yield through directed selection of component traits and their interrelationship with yield. The present study was therefore conducted to estimate variability, heritability in wheat for utilization in selection programmes aimed at productivity increase of future genotypes.

## Materials and methods

The experimental material consisting 40 diverse wheat cultivars, grown in a randomized block design in three replications during 2008-09 at the Research Farm, Department of Genetics and Plant Breeding, Chaudhary Charan Singh University, Meerut. Each cultivar was grown in a single row plot of 3 meter length with row to row distance of 23 centimeter with an appropriate plant to plant distance of 5-6 centimeter in each plot. Recommended packages and practice were followed to raise the crop. The observations were recorded on various quantitative characters *viz.* days to heading, days to maturity, plant height, grain filling period, number of productive tillers per plant, number of spikelets per spike, test weight (g), harvest index (%), biological yield per plant (g) and grain yield per plant (g). Five randomly selected

<sup>1</sup> Current address: Directorate of Wheat Research, Karnal- 132 001, Haryana  
\* Corresponding author email : [bharat.nduat@gmail.com](mailto:bharat.nduat@gmail.com)

competitive plants in each row of each replication for all the characters were recorded for all the characters under study except of days to 50 per cent flowering and days to maturity which were recorded on plot basis. Further, the value of harvest index was calculated as per the formula given by Donald and Humblin (1976).

The mean performance of individual genotypes was embayed for statistical analysis. Analysis of variance to test the significance for each character was carried out as per methodology given by Panse and Sukhatme (1967). Genotypic and phenotypic coefficients of variation (GCV and PCV) were calculated by the formula given by Burton (1952), heritability in broad sense ( $h^2$ ) by Burton and Vane (1953) and genetic advance given by Johnson *et al.* (1955).

Correlation coefficient and path coefficient was worked out as method suggested by Al-Jibouri *et al.* (1958) and Dewey and Lu (1959), respectively.

### Results and discussion

The analysis of variance (Table 1) revealed that the treatments were highly significant for all the characters and highest value was estimated for biological yield followed by plant height and grain yield while, spikelets per spike was lowest. This suggested that the genotypes selected were genetically variable and considerable amount of variability existed among them. Similar finding were reported by Bergale *et al.* (2001), Dwivedi *et al.* (2002), Asif *et al.* (2004) and Tripathi *et al.* (2011).

**Table 1.** The analysis of variance (ANOVA) for 10 characters in bread wheat

Character	DF	DH	DM	PH	GFP	NT/P	NS/S	TW	HI	BY/P	GY/P
Replication	2	2.91	3.28	7.35	2.12	0.98	1.05	4.55	0.55	1.16	0.63
Treatment	39	28.31**	20.78**	127.09**	19.36**	23.58**	8.72**	23.34**	33.63**	182.31**	43.28**
Error	78	12.68	13.69	3.16	8.37	1.31	2.53	4.14	0.89	2.39	1.21

\*\* Significant at 1% level, Where, DH: days to heading, DM: days to maturity, GFP: grain filling period (days), PH: plant height, NT/P: number of tillers per plant, NS/S: number of spikelets per spike, TW: test weight (g), HI: harvest index BY/P: biological yield per plant and GY/P: Grain yield per plant.

**Table 2.** Estimates of mean, coefficient of variation, heritability and genetic advance for 10 characters in wheat

Sr. Characters	General	Coefficient of variation		Herita- bility	Genetic advance
	mean	GCV	PCV		
1. Days to heading	89	7.53	7.12	94.38	13.14
2. Days to maturity	124	3.22	3.08	77.51	17.33
3. Plant height	96.53	10.23	8.39	97.63	28.42
4. Grain filling period	31.48	4.85	3.37	67.33	6.42
5. Productive tillers per plant	7.83	13.01	11.28	78.42	9.01
6. Spikelets per spike	18.23	8.41	7.53	84.22	8.53
7. Test weight	38.89	7.02	6.21	73.05	16.43
8. Harvest index	43.15	6.53	6.12	91.56	21.28
9. Biological yield	53.24	13.17	12.48	89.50	34.54
10. Grain yield	20.78	15.29	13.69	78.88	27.63

The genotypic (GCV) and phenotypic (PCV) coefficients of variation were observed in the experimental material for all the characters studied (Table 2). The higher magnitudes of GCV and PCV were recorded for grain yield, biological yield, productive tillers per plant and plant height. However, number of spikelets per spike, days to heading, test weight, harvest index, grain filling period and days to maturity exhibited least genotypic and phenotypic coefficient of variation. On an average, the higher magnitude of GCV and PCV were recorded for grain yield (13.69 and 15.29), biological yield (12.48 and 13.17), productive tillers per plant (11.28 and 13.01) and plant height (8.39 and 10.23), respectively, suggesting

sufficient variability are available and thus exhibited scope for genetic improvement through selection for all these traits.

These findings were agreement with Dwivedi *et al.* (2002), Yausaf *et al.* (2008) and Tripathi *et al.* (2011). These values alone are not helpful in determining the heritable portion of variation. The proportion of genetic variability which is transmitted from parents to all spring is reflected by heritability (Lush, 1949). The high heritability in broad sense estimated for all the characters except for grain filling period and test weight. Among these plant height recorded highest estimates followed by days to heading, harvest index, biological yield, spikelets per spike, grain

yield, productive tillers per plant and days to maturity (Table 2). High value indicates that heritability may be due to higher contribution of genotypic components. Similar results for high heritability estimates were reported by Panwar and Singh (2002), Nibalkar *et al.* (2002), Asif *et al.* (2004), Joshi and Mahal (2004) Riba dia *et al.* (2007), Payal *et al.* (2007), Rasal *et al.* (2008), Yausaf *et al.* (2008), Molla and Thomas (2011) and Tripathi *et al.* (2011). Moderate heritability was found grain filling period and test weight. Similar result was also reported by Rahman *et al.* (2008).

The estimates of heritability are more advantageous when expressed in terms of genetic advance. Johnson *et al.* (1955) suggested that without genetic advance the estimate of heritability will not be practical value and emphasized the concurrent use of genetic advance along with heritability. Hanson (1963) stated that heritability and genetic advance are two complementary concepts. Based on this consideration, high heritability coupled with high genetic advance as percent of mean were registered for plant height, harvest index, biological yield and grain yield indicated predominance of additive gene action in the expression of these traits.

High heritability coupled with moderate genetic advance were observed for days to heading and days to maturity indicated predominance of additive and non-additive gene action in the expression of these characters therefore,

these characters can be improved by mass selection and other breeding methods based on progeny testing. Similar results in wheat were also reported by Kisana *et al.* (1982), Pawar *et al.* (2002), Prasad *et al.* (2006), Kamboj (2007), Payal *et al.* (2007), Sen and Toms (2007) and Tripathi *et al.* (2011).

Correlation coefficient analysis measure ten natural relations between various plant characters and determine the component characters on which selection can be used for genetic improvement in yield. The breeder is always concerned for the selection of superior genotype on the basis of phenotypic expression. However, for the quantitative characters, genotypes are influenced by environment, thereby effecting the phenotypic expression. Information regarding the nature and extent of association of morphological character would be helpful in developing suitable plant type, in addition to the improvement of yield a complex character for which direct selection is not effective.

The correlation coefficient estimated (Table 3) highest direct genotypic and phenotypic correlation was observed in the test weight (1.18, 0.37), biological yield (0.77, 0.10) spikelets per spike (0.59, 0.26) and grain filling period (0.36, 0.06). While days to heading (-0.47, -0.11), plant height (-0.36, 0.07) and days to maturity (-0.31, 0.15) has direct negative correlation with grain yield.

**Table 3.** The estimates of genotypic and phenotypic correlation coefficient among 10 characters in bread wheat

Characters	r	Days to heading	Days to maturity	Plant height	Grain filling period	Productive tillers	Spikelets per spike	Test weight	Harvest index	Biological yield	Grain yield
Days to heading	rg	1.00	0.06	-0.15	0.19	-0.21	-0.42*	-0.18	0.11	0.61**	-0.47*
	rp	1.00	0.11	-0.24	0.21	-0.15	-0.12	-0.46*	-0.19	-0.09	-0.11
Days to maturity	rg		1.00	0.21	0.19	0.13	-0.28	0.21	0.01	1.17**	-0.31*
	rp		1.00	-0.59*	0.03	0.17	-0.13	0.08	0.13	0.12	0.15
Plant height	rg			1.00	0.41*	0.03	0.17	0.44*	0.91**	0.18	-0.36*
	rp			1.00	0.10	-0.21	0.16	0.11	0.25	-0.14	-0.07
Grain filling period	rg				1.00	-0.49*	-0.42*	-0.49*	0.50*	0.12	0.36*
	rp				1.00	-0.16	-0.30	-0.20	-0.07	-0.01	0.06
Productive tillers	rg					1.00	0.75**	1.10**	0.19	0.27	0.77*
	rp					1.00	0.67*	0.42*	0.13	0.03	0.10
Spikelets per spike	rg						1.00	0.75**	-0.05	-0.42*	0.59*
	rp						1.00	0.69*	-0.52*	0.11	0.26
Test weight	rg							1.00	0.60*	0.68**	1.18**
	rp							1.00	0.22	0.32*	0.37*
Harvest index	rg								1.00	0.90**	0.16
	rp								1.00	0.07	-0.07
Biological yield	rg									1.00	1.08**
	rp									1.00	-0.30
Grain yield	rg										1.00
	rp										1.00

Where, r = correlation coefficient; rg and rp are genotypic and phenotypic correlation coefficients; \*, \*\* significant at 5% & 1% probability levels, respectively.

**Table 4.** Direct and indirect effects of different characters on grain yield per plant in bread wheat

Trait	Days to heading	Days to maturity	Plant height	Grain filling period	Productive tillers	Spikelets per spike	Test weight	Harvest index	Biological yield	Grain yield
Days to heading	-0.79	0.11	0.11	0.23	0.17	0.23	0.18	-0.20	0.21	0.24
Days to maturity	-0.65	-0.76	0.24	-0.14	0.18	0.28	-0.26	0.01	0.22	0.38
Plant height	0.15	0.13	-0.63	-0.20	0.07	-0.09	-0.19	-0.46	-0.19	-0.33
Grain filling period	0.05	0.04	0.08	-0.21	-0.08	0.11	-0.10	0.11	0.10	-0.06
Productive tillers	0.29	-0.28	0.05	0.58	1.40	-1.04	-1.42	-0.26	0.89	-0.16
Spikelets per spike	-0.18	-0.16	0.10	-0.32	0.34	0.59	0.42	-0.03	-0.43	0.04
Test weight	-0.03	0.21	0.10	-0.14	0.37	0.23	0.30	0.19	-0.33	0.14
Harvest index	0.11	-0.04	0.83	1.33	0.63	0.18	2.14	3.33	0.56	-2.61
Biological yield	0.16	0.16	0.26	-0.16	0.29	0.28	0.50	-0.07	1.46	0.27
Grain yield	-0.87	0.17	0.41	0.17	0.17	0.23	0.27	-0.01	0.21	0.24

Residual effects = 0.028

Further, genotypic correlation coefficients were higher in negative than the corresponding phenotypic correlation coefficient which might be due to marking on modifying effect of environment. High genotypic correlation also suggests that there is inherent relationship between the characters studied. Direct non-significant genotypic correlation was observed for harvest index. Thus selection for higher yield on the basis of above characters would be reliable. Similar findings were also reported by Dwivedi *et al.* (2002), Lad *et al.* (2005), Khan *et al.* (2005), Ayccek and Yldrm (2006), Prasad *et al.* (2006), Payal *et al.* (2007), Dharamandra and Singh (2010), Tripathi *et al.* (2011), El-Mohsen (2012) and Singh *et al.* (2012).

When characters having direct bearing on yield are selected, their associations with other characters are to be considered simultaneously as this will indirectly affect the yield. The result of correlation coefficient implied that significant positive correlation at both level were recorded for test weight with biological yield and days to heading, days to maturity and harvest index at genotypic level while negatively correlated for spikelets per spike at genotypic level.

Harvest index positively correlated with the plant height, grain filling period and test weight while, spikelets per spike negatively associated at genotypic level (Table 4). Test weight was positively correlated with the productive tillers per plant and spikelets per spike while, plant height at genotypic level showed negatively significant correlation among days to heading and grain filling period. Spikelets per spike had positive and significant correlation with the productive tillers per plant at both genotypic and phenotypic levels. Productive tillers per plant had negative and significant correlation for grain filling period, but showed positive and significant association with the plant height while, plant height had negative and significant correlation with days to maturity.

These findings were in agreement with the results of Ashfaq *et al.* (2003), Shukla *et al.* (2005), Prasad *et al.* (2006), Raiz-ud-Din *et al.* (2010) and Tripathi *et al.* (2011). However, these results were in disagreement with finding of Burio *et al.* (2004), who observed that harvest index had positive effect with plant height.

Shrivastava and Sharma (1976) suggested that only direct yield component should be used for path analysis. Path harvest index (3.33) had highest direct positive effect on grain yield followed by biological yield (1.46), productive tillers per plant (1.40), spikelets per spike (0.59) and test weight (0.30) indicated main contributors to grain yield. Similar findings were also reported by Esmail (2001), Lad *et al.* (2003), Ayccek and Yldm (2006), Payal *et al.* (2007) and Tripathi *et al.* (2001). Gupta *et al.* (2007) observed the highest contribution towards grain yield with biological yield, harvest index, test weight and spikelets per spike. However, days to heading (-0.79), days to maturity (-0.76), plant height (-0.63) and grain filling period (-0.21) had direct negative effect on grain yield per plant. However, the negative effects were in agreement with the results of Bhutta *et al.* (2005) and Singh *et al.* (2012).

This type of relationship is due to manifold effect of gene(s). It therefore becomes very difficult to partition such effects by selecting particular characters that are so related. Information obtained from correlation study cannot reflect or give complete idea about the contributors of each character. Therefore, it is important to establish the genetic basis of correlation before initiating breeding programme aimed at yield improvement through component traits. Path coefficient analysis is however, more useful for partitioning of direct and indirect causes of correlation and also enables breeders to compare the component factors on the basis of their relative contributors.

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