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**Dinesh Kumar**

Department of Genetics and  
Plant Breeding, A.N.D.U.A.T.,  
Kumarganj, Ayodhya, Uttar  
Pradesh, India

**Shivam Dubey**

Department of Genetics and  
Plant Breeding, A.N.D.U.A.T.,  
Kumarganj, Ayodhya, Uttar  
Pradesh, India

**Virendra Bahadur**

Department of Genetics and  
Plant Breeding, A.N.D.U.A.T.,  
Kumarganj, Ayodhya, Uttar  
Pradesh, India

**Ankaj Tiwari**

Department of Genetics and  
Plant Breeding, A.N.D.U.A.T.,  
Kumarganj, Ayodhya, Uttar  
Pradesh, India

**Vinod Singh**

Department of Genetics and  
Plant Breeding, A.N.D.U.A.T.,  
Kumarganj, Ayodhya, Uttar  
Pradesh, India

**Corresponding Author:**

**Virendra Bahadur**

Department of Genetics and  
Plant Breeding, A.N.D.U.A.T.,  
Kumarganj, Ayodhya, Uttar  
Pradesh, India

## Estimation of Genetic variability, Heritability and Genetic advance in Wheat (*Triticum aestivum* L. em. Thell) under sodic soil

**Dinesh Kumar, Shivam Dubey, Virendra Bahadur, Ankaj Tiwari and Vinod Singh**

### Abstract

The present investigation was carried out during *Rabi* 2017-18 at Main Experiment Station Research Farm of Acharya Narendra Deva University of Agriculture and Technology, Narendra Nagar, Kumarganj, Ayodhya (U.P.) with the objectives of estimating genotypic variability, heritability, genetic advance and associations among yield and yield-related characters of *Triticum aestivum*. The variation due to blocks was highly significant for flag leaf area, plant height, spike length, tillers per plant, peduncle length, biological yield per plant, grain yield per plant, 1000-grain weight and harvest index. The highest estimates of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was observed in case of peduncle length (PCV 14.04 %, GCV = 13.88%) followed by flag leaf area (cm<sup>2</sup>) (PCV=11.77%, GCV=11.50%). The high heritability was recorded in peduncle length (cm) (97.69%) followed by flag leaf area (cm<sup>2</sup>) (95.54%), biological yield per plant (g) (93.83%), spike length (cm) (92.10%), and plant height (cm) (91.88%). The highest value of genetic advance was shown by peduncle length (cm) (28.26%), and flag leaf area (cm<sup>2</sup>) (23.17%). The high estimates of heritability coupled with high genetic advance were found in peduncle length (cm) and flag leaf area (cm<sup>2</sup>) both traits were regulated by additive gene effect. That region the selection of genotypes based on two characteristics are more useful and effective for genetic improvement of genotype.

**Keywords:** Variability, heritability, genetic advance, *Triticum aestivum*

### Introduction

Wheat (*Triticum aestivum* L. em. Thell., 2n=42) 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 (Mollasadeghi *et al.*, 2011) [8]. 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 (Shashikala, 2006) [11]. 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. Wheat is consumed in a variety of ways such as bread, chapati, porridge, flours and 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. Wheat is classified into two major types: (1) the hexaploid bread wheat (2n = 6x = 42, AA BB DD) and (2) the tetraploid durum wheat (2n = 4x = 28, AA BB). Currently, at the global level, bread wheat accounts for 95% of all the wheat produced. Based on growth habit, wheat is classified into spring wheat and winter wheat, covering about 65 and 35% of the total global wheat production area, respectively (Braun *et al.* 2010; Braun and Săulescu, 2002) [9].

Wheat is more nutritive as compared to the other cereals. It has a good nutrition profile with 12.1 per cent protein, 1.8 per cent lipids, 1.8 per cent ash, 2.0 per cent reducing sugars, 6.7 per cent pentose's, 59.2 per cent starch, 70 per cent total carbohydrates and provides 314K cal/100g of food. It is also a good source of minerals and vitamins *viz.*, calcium (37 mg/100g), iron (4.1 mg/100g), thiamine (0.45mg/100g), riboflavin (0.13mg/100g) and nicotinic acid (5.4mg/100mg). The development of an effective plant breeding program is dependent upon the existence of genetic variability. The efficiency of selection largely depends upon the magnitude of genetic variability present in the plant population. Thus, the success of genetic improvement in any character depends on the nature of variability present in the gene pool for That character.

Hence, an insight into the magnitude of variability present in the gene pool of a crop species is of paramount importance to a plant breeder for starting a judicious plant breeding program (Farshadfar *et al.* 2013). The presence of genetic variability in a population can be divided into heritable and non-heritable variation. Heritability in general term is the ratio of genetic variance to the total variance i.e. phenotypic variance is known as heritability. The concept of heritability is associated with the relative influence of the heredity and environment. Heritability is of two types i.e. broad sense and narrow sense heritability. Broad-sense heritability estimates the ratio of total genetic variance, including additive, dominance, and epistatic variance, to the phenotypic variance, while heritability in narrow sense estimates only the additive portion of the total phenotypic variance (Raiz and Chowdhry, 2003) [12]. Knowledge about heritability helps the plant breeder in predicting the behavior of successive generations and making desirable selections, which is one of the important tools in crop improvement. Genetic advance will be more effective in prediction of efficiency under selection. Therefore, genetic advance is another important parameter, assisting the plant breeders in the selection program. The estimates of genetic advance help in understanding the type of gene action involved in the expression of various quantitative characters. High values of genetic advance are indicative of additive gene action whereas low values are indicative of non-additive gene action.

### Materials and Methods

The present investigation was carried out during *Rabi* 2017-18 at Main Experiment Station Research Farm of Acharya Narendra Deva University of Agriculture and Technology, Narendra Nagar, Kumarganj, Ayodhya (U.P.). This place is situated between 26<sup>o</sup>.47' N latitude, 82<sup>o</sup>.12' E longitude and at an altitude of 113 m above the mean sea level. The climate of district Ayodhya is semi arid with hot summer and cold winter. Nearly 80% of total rainfall is received during the monsoon (only up to September) with a few showers in the winter. The soil type of experimental site was reclaimed salt affected soil (pH = 7.9) EC = 0.36 rich in potash and low in organic carbon, nitrogen and phosphorus. The experiment of present investigation was conducted to evaluate the ninety six wheat germplasm lines along with four checks (namely WR-544, SONALIKA, GE-366 and HD-3086.) in Augmented Block. These genotypes exhibited a wide spectrum of variation for various agronomical and morphological characters. The experimental field was divided into six blocks equal size and twenty plots in each block sixteen test genotypes. Each plot consisted of two rows of 2.5 m length with spacing of 5 cm within the rows and 25 cm between the rows. The recommended cultural practices will be followed to raise a good normal crop. The observation was recorded on 5 randomly selected plants from each plot except days to 50% flowering and days to maturity where data will be recorded on plot basis. The experiment was conducted to evaluate ninety six germplasm lines with four checks under reclaimed salt affected soil and irrigated condition, following Augmented Block Design.

### Results and Discussion

Analysis of variance for augmented design was carried out for eleven characters to test the significance of differences among various treatments (checks) and has been presented in Table-1. The variation due to blocks was highly significant for flag

leaf area, plant height, spike length, tillers per plant, peduncle length, biological yield per plant, grain yield per plant, 1000-grain weight and harvest index however the differences among the blocks were not significant for remaining characters. The differences among the four check varieties were found to be highly significant for the spike length.

The estimates of genotypic and phenotypic coefficient of variation for eleven characters of wheat genotypes evaluated are presented in Table-2 and Fig.1. The highest estimates of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was observed in case of peduncle length (PCV 14.04 %, GCV = 13.88%) followed by flag leaf area (cm<sup>2</sup>) (PCV=11.77%, GCV=11.50%), can be considered as moderate because of being very close to 10%. Four characters exhibited low estimates (< 10%) of PCV as well as GCV. The lowest estimates of PCV and GCV were observed for days to maturity (PCV=1.66%, GCV=1.43%) followed by days to 50% flowering (PCV=2.99 %, GCV=2.61%) and plant height (cm) (PCV=5.14 %, GCV=4.93 %) spike length (cm) (PCV=9.60 %, GCV=9.21%) and grain yield per plant (g) (PCV=9.50 %, GCV=7.81%). Similar results were observed by Bergale *et al.* (2001) [2], Arya *et al.* (2005) [3], Paul *et al.* (2006) [4], Yadav *et al.* (2006), Siddharthan and malik (2007), and Tripathi *et al.* (2015).

The estimates of broad sense heritability ( $h^2_{bs}$ ) and genetic advance in per cent of mean for different characters are given in Table – 2 and Fig.1. The highest estimate of heritability in broad sense was recorded by peduncle length (cm) (97.69%) followed by flag leaf area (cm<sup>2</sup>) (95.54%), biological yield per plant (g) (93.83%), spike length (cm) (92.10%), plant height (cm) (91.88%), exhibited high estimates of heritability (>75%). The characters exhibiting moderate estimates (>50 to <75%) of heritability broad sense ( $h^2_{bs}$ ) in per cent of mean was recorded 97.69 for plant height (cm) and 95.54 for flag leaf area (cm<sup>2</sup>) while the lowest value 7.16 for tiller per plant and 46.28 for harvest index (%). Similar results were observed by Singh *et al.* (2010), Yadav *et al.* (2006) [5], Potdukhe *et al.* (2013), and Arya *et al.* (2005) [3],

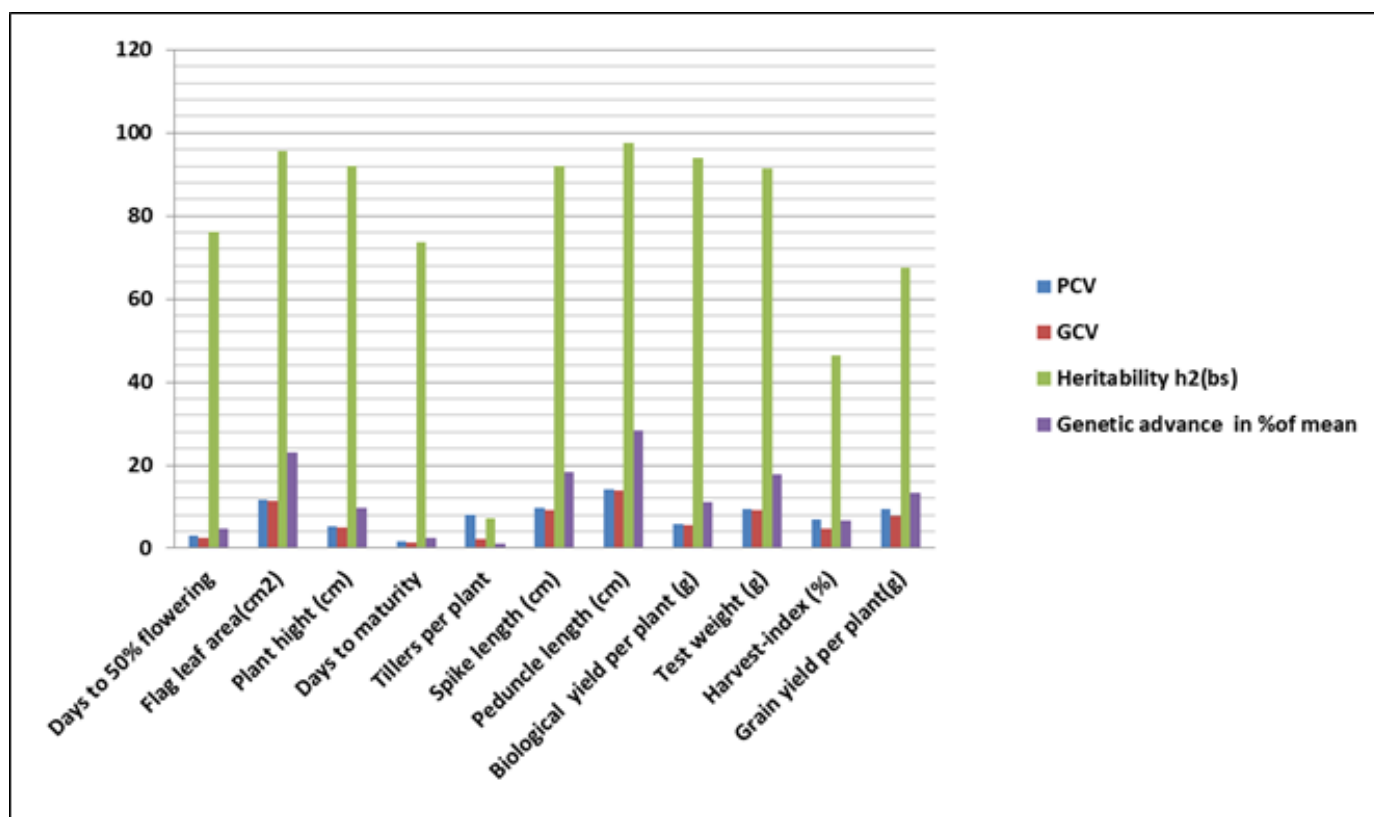
The highest value of genetic advance (Ga.) at 5% of mean was shown by peduncle length (cm) (28.26%), while tiller per plant (1.18%) had lowest value for this parameter. The characters exhibiting high estimates (>20%) of genetic advance in per cent of mean were recorded for peduncle length (cm) (28.26%), and flag leaf area (cm<sup>2</sup>) (23.17%). The characters exhibiting moderate estimates (>10%) of genetic advance in per cent of mean were spike length (18.21%) and test weight (17.79%). The lower estimates of genetic advance (<10) resulted in cases of days to maturity (2.52%), days to 50% flowering (4.69%), harvest index (6.70%) and plant height (9.74%). High estimates of heritability coupled with high genetic advance were found in peduncle length (cm) and flag leaf area (cm<sup>2</sup>) both traits were regulated by additive gene effect. That region the selection of genotypes based on these two characters are more useful and effective for genetic improvement of genotypes. Similar results were observed by Arya *et al.* (2005) [3], Bergale *et al.* (2001) [2] and Yadav *et al.* (2011) [5].

### Conclusion

The variation due to blocks was highly significant for flag leaf area, plant height, spike length, tillers per plant, peduncle length, biological yield per plant, grain yield per plant, 1000-grain weight and harvest index however the differences among the blocks were not significant for remaining

characters. The differences among the four check varieties were found to be highly significant for the spike length. The highest estimates of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was observed moderate in case of peduncle length followed by flag leaf area (cm<sup>2</sup>) selection may be possible in these two characters. High

heritability coupled with high genetic advance were found in peduncle length (cm) and flag leaf area (cm<sup>2</sup>), that's region the selection of genotypes based on these two characters are more useful and effective for genetic improvement of genotypes.



**Fig 1:** Phenotypic (PCV) and genotypic (GCV) coefficient of variation, heritability in broad sense (h<sup>2</sup>b) and genetic advance in per cent of mean for 11 characters in *Triticum aestivum*.

**Table 1:** Analysis of variance of augmented design for 11 characters in wheat genotype.

Characters	d.f.	Days to 50% flowering	Flag leaf area (cm <sup>2</sup> )	Plant height(cm)	Days to maturity	Tillers per plant	Spike length (cm)	Peduncle length (cm)	Biological yield per plant (g)	Grain yield per plant(g)	Test weight (g)	Harvest index (%)
Block (ignoring Treatments)	5	14.780**	15.700**	115.384**	4.248*	0.229	17.729**	76.429**	172.958**	69.877**	25.556**	29.833**
Treatment(eliminating blocks)	99	6.321**	12.460**	13.103**	4.716**	0.178	2.336**	12.360**	25.273**	5.624*	17.948**	5.646
Checks	3	16.375**	8.141**	7.529**	9.264**	0.484	3.474**	11.823**	12.728**	14.358**	51.315**	12.053*
Checks+Var vs. Var.	96	6.007**	12.595**	13.278**	4.574**	0.169	2.300**	12.377**	25.666**	5.351*	16.905**	5.446
Error	15	1.408	0.477	1.263	1.095	0.156	0.184	0.265	1.208	2.202	1.243	3.382
Block(eliminating Check +Var.)	5	0.876	1.360	0.100	0.947	0.088	0.636*	1.235**	3.740*	3.348	1.802	3.252
Entries(ignoring Blocks)	99	7.023**	13.184**	18.926**	4.883**	0.186	3.199**	16.158**	33.820**	8.984**	19.148**	6.988
Checks	3	16.375**	8.141**	7.529**	9.264**	0.484	3.474**	11.823**	12.728**	14.358**	51.315**	12.053*
Varieties	95	6.802**	12.724**	18.415**	4.757**	0.171	2.765**	13.698**	23.267**	7.713**	17.260**	6.878
Checks vs. Varieties	1	0.019	71.990**	101.660**	3.675	0.683	43.621**	262.878**	1099.588**	113.637**	101.936**	2.286
Error	15	1.408	0.477	1.263	1.095	0.156	0.184	0.265	1.208	2.202	1.243	3.382
Ci – Cj	1	1.460	0.850	1.383	1.288	0.487	0.528	0.633	1.352	0.527	0.841	0.514
BiVi– BiVj	1	3.577	2.081	3.388	3.155	1.192	1.294	1.551	3.313	1.395	2.226	1.360
BiVi– BjVj	1	3.999	2.327	3.788	3.527	1.333	1.447	1.734	3.704	1.559	2.489	1.521
Ci– Vi	1	3.054	1.777	2.893	2.694	1.018	1.105	1.325	2.829	1.179	1.882	1.149

**Table 2:** Estimates of general mean, range, phenotypic (PCV) and genotypic (GCV) coefficient of variation, heritability in broad sense ( $h^2_b$ ) and genetic advance in per cent of mean for 11 characters in *Triticum aestivum*.

Characters	Grand mean	Range		Coefficient of variation (%)		Heritability $h^2_{(bs)}$	Genetic advance in % of mean
		Min.	Max.	PCV	GCV		
1. Days to 50% flowering	81.09	75.87	88.125	2.99	2.61	76.15	4.69
2. Flag leaf area( $cm^2$ )	27.83	21.38	32.04	11.77	11.50	95.54	23.17
3. Plant height (cm)	76.73	65.44	86.69	5.14	4.93	91.88	9.74
4. Days to maturity	122.13	118.21	127.21	1.66	1.43	73.59	2.52
5. Tillers per plant	5.11	4.35	5.95	8.03	2.14	07.16	1.18
6. Spike length (cm)	15.85	12.87	19.45	9.60	9.21	92.10	18.21
7. Peduncle length (cm)	23.95	17.39	33.08	14.04	13.88	97.69	28.26
8. Biological yield per plant (g)	77.25	63.96	86.72	5.75	5.57	93.83	11.11
9. Test weight (g)	40.35	29.58	49.23	9.44	9.03	91.48	17.79
10. Harvest-index (%)	35.63	29.83	41.64	7.03	4.78	46.28	6.70
11. Grain yield per plant(g)	27.51	21.81	33.34	9.50	7.81	67.59	13.23

## Reference

1. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybean. *Agron. J* 1955;47:477-483.
2. Bergale S, Billore M, Holkar AS, Ruwali KN, Prasad SVS. Genetic variability, diversity and association of quantitative traits with grain yield in bread wheat (*Triticum aestivum* L.). *Madras Agril. J* 2001;7/0:457-461.
3. Arya VD, Pawar IS, Lamba RA. Genetic variability, correlation and path analysis for yield and quality traits in bread wheat. *Haryana Agril. Uni. J Res* 2005;35(1):59-63.
4. Paul M, Qureshi SH, Shah MJ, Roshan Zamir GS. Path coefficient and correlation of yield and yield associated traits in candidate bread wheat (*Triticum aestivum* L.) lines. *Pakistan J Agril. Res* 2006;19(4):12-15.
5. Yadav DK, Pawar IS, Sharma GR, Lamba RAS. Evaluation of variability parameters and path analysis in bread wheat. *Nat. J Plant Improvement* 2006;1:86-89.
6. Siddharthan SP, Malik VK. Character association and path analysis in wheat (*Triticum aestivum* L.). *Agril. Sci. Digest* 2007;22(4):255-257.
7. Tripathi GP, Parde NS, Zate DK, Lal GM. Genetic variability and heritability studies on bread wheat (*Triticum aestivum* L.). *Int. J Plant Sci* 2015;10(1):57-59.
8. Mollasadeghi V, Valizadeh M, Shahryari R, Imani AA. Evaluation of end drought tolerance of 12 wheat genotypes by stress indices. *Middle-East J. Sci. Res* 2011;7:241-247.
9. Braun HJ, Atlin G, Payne T. Multi-location testing as a tool to identify plant response to global climate change. In: Reynolds, M.P. (Ed.), *Climate Change and Crop Production*. CABI Publishers, Wallingford, UK, 2010, 115-138.
10. Braun HJ, Saulescu NN. *Breeding Winter and Facultative Wheat*. FAO Plant Production and Protection Series. FAO, Rome 2002.
11. Shashikala SK. *Analysis of Genetic Diversity in wheat* (Thesis). University of Agricultural Sciences, Dharwad 2006.
12. Riaz R, Chowdhry MA. Estimation of variation and heritability of some physio-morphic traits of wheat under drought condition. *Asian J Plant Sci* 2003;2:748-755.
13. Singh P, Narayanan SS. *Biometrical Techniques in Plant Breeding*. New Delhi, India: Kalyani Publishers 1999.
14. Mollasadeghi V, Shahryari R. Important morphological markers for improvement of yield in bread wheat. *Advances Environ. Biol* 2011;5(3):538-542.