

Estimation of nature and magnitude of genetic variability, heritability and genetic advance for yield and its contributing traits in wheat (*Triticum aestivum* L.)

Abstract

The present research investigation was conducted at AKS University, Satna, Madhya Pradesh during *rabi* Season of 2022. Altogether 20 wheat genotypes were grown under RBD design with three replications. In the present study various parameters of genetic variability, broad sense heritability and genetic advance estimates of wheat crop. Analysis of variance revealed that the mean sum of square showed significant due to genotypes for all the 12 characters studied. Analysis of variance for the design of experiment revealed highly significant difference for all the characters which expressed huge amount of diversity among 20 genotypes of wheat. Phenotypic coefficients of variation (PCV) were higher than genotypic coefficients of variation (GCV) for all the characters. The maximum GCV and PCV were observed for ear length (cm) (26.37 & 27.04) followed by number of productive tillers per plant (23.72 & 25.65) and test weight (21.76 & 22.57 g). The maximum value of heritability was shown by number of spikelets per ear (98.05), number of seed per spike (97.59), ear length (95.12 cm), test weight (92.99 g), biological yield per plant (91.99 g), plant height (89.86 cm), seed yield per plant (87.28 g), days to maturity (86.67) and number of productive tillers per plant (85.56). The highest genetic advance was found for number of productive tillers per plant (45.20), number of seed per spike (43.60), test weight (43.24 g), seed yield per plant (37.37 g), no of ears per plant (34.99) and number of spikelets per ear (31.49). High heritability coupled with high genetic advance for the characters number of productive tillers per plant, no of ears per plant, ear length, number of spikelets per ear, number of seed per spike, test weight and seed yield per plant which indicated that above characters were governed by additive gene action and direct selection may be useful for further improvement program.

***Key words:* wheat, genetic variability, heritability, genetic advance.**

Introduction:

Wheat (*Triticum aestivum* L.) is a self pollinated crop belongs to family gramineae. It is widely grown all over the world as food crop. Wheat is most produced cereal in the world

followed by rice and maize. China is the world's largest producer of wheat which produces more than 2.4 billion tonnes of wheat in the last 20 years, around 17% of the total wheat production. Russia is the largest exporter of wheat in the world, which exported more than 7.3 billion tonnes of wheat in 2021 (Anonymous (a) 2022-23). The top 10 wheat producing countries in the world are China, India, Russia, United States, France, Canada, Germany, Pakistan, Australia and Ukraine (Anonymous (b) 2022-23). In India, wheat is extensively cultivated in North West India, Eastern part, Central plain to some extent Southern peninsular zone. The top wheat producing states in the India are Uttar Pradesh, Punjab, Madhya Pradesh, Haryana, Rajasthan, Bihar, Gujarat, Maharashtra, West Bengal and Uttarakhand.

Genetic improvement for quantitative traits depends on the nature and amount of variability present in the genetic material and the extent to which the desirable traits are heritable (Namrata *et al.*, 2016). The knowledge about genetic variability of yield contributing characters, inter relationship among them and their relation with yield are necessary for an effective crop improvement programme (Nayak *et al.*, 2016). The genetic variability could be determined with the help of genetical parameters such as Genetic Coefficient of Variation (GCV), heritability and genetic advance (GA). GCV indicates the relative degree of genetic variability existing for different characters in a population of genotypes. (Reference)

Knowledge about heritability helps the breeders to predict the nature of the succeeding generation, to make an appropriate selection and to assess the magnitude of genetic improvement through selection (Tuhina Khatun *et al.*, 2015). In addition, high genetic advance coupled with high heritability offers the most effective condition for selection for a particular trait (Larik and Rajput, 2000). Heritability estimates provide the information on the proportion of variation that is transmissible to the progenies in subsequent generations. Genetic advance provides information on expected genetic gain resulting from selection of superior individuals. Genetic variability is the key of any crop improvement programme, this provide an opportunity for breeder to combine desired genes into novel genotype for enhancing the yield and stability of economically important plants. Germplasm serve as the most valuable natural resource for providing useful characters for developing high yielding input responding genotypes resistant to various biotic and abiotic tresses. Therefore, valuation of germplasm under the prevailing environments is essential for selecting the donor parents for the traits to be improved in breeding programme. Keeping these things in the view, the present investigation was conducted to assess

the nature and magnitude of genetic variability, heritability and genetic advance among various yield and its contributing characters of wheat.

Materials and Methods:

The experimental materials comprising of 20 genotypes were grown in a randomized block design with three replications at the Research farm of Department of Genetics and Plant Breeding, Faculty of Agriculture Science and Technology, AKS University, Satna, M.P. during rabi 2022. Each plot consisted of two row plots of 1m length with a spacing of 30 cm X 20 cm were 2 seed per hill were dropped manually later on plant per hill was maintained after thinning. Recommended dose of fertilizers (NPK-120:60:60 Kg/Ha) were applied for raising healthy and uniform crops. The data was collected for some morphological traits i.e. .days to 50% flowering, plant height (cm.), days to maturity, number of productive tillers per plant, no of ears par plant, ear length (cm.), number of spikelets per ear, number of seed per spike, test weight (g), biological yield per plant (g), harvest index (%) and seed yield per plant (g.)were taken from five randomly selected plants from middle row of each entry in each replication.

The analysis of variance for the design of the experiment was carried out according to the procedure outlined by Panse and Sukhatme (1967). The mean of i^{th} trait was measured by dividing the total of all observations ($\sum X_{ij}$) by their number and was denoted by X_i . The range was estimated as the differences between the least and the greatest value of a series of observations of accessions. The genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and environmental coefficient of variation (ECV) was computed following Burton and de Vane (1953). Heritability in broad sense (h^2) was calculated using the formula suggested by Burton and de Vane (1953). Genetic advance was calculated by the method suggested by Johnson *et al.* (1955). All the statistical analysis done by statistical software developed by Popat *et al.* 2020

$$\text{Mean: } X_i = \frac{(\sum X_{ij})}{j=1}$$

Where \bar{X} = Mean of the i^{th} trait, X_{ij} = the value of j^{th} observations of i^{th} trait, n = number of observations.

GCV & PCV:

Genotypic standard deviation (σ_g)

$$\text{GCV} = \frac{\text{Phenotypic standard deviation } (\sigma_p)}{\text{Mean } \bar{X}}$$

$$\text{PCV} = \frac{\text{Phenotypic standard deviation } (\sigma_p)}{\text{Mean } \bar{X}}$$

Heritability:

$$h^2 = \frac{\sigma^2_g}{\sigma^2_g + \sigma^2_e}$$

or

$$h^2 = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Expected genetic advance:

$$\text{G.A.} = \frac{\sigma^2_g}{\sigma^2_p} \cdot K \cdot \sigma^2_p$$

$$= h^2 \cdot K \cdot \sigma^2_p$$

Where,

K = Selection differential at 5% selection intensity (2.06).

Genetic advance as per cent of mean (G.A.%)

$$\text{G.A.}\% = \frac{\text{Genetic advance}}{\bar{X}} \times 100$$

Results and discussion:

Analysis of variance for the design of experiment has presented in table 1. The results revealed highly significant difference for all the characters which expressed huge amount of diversity among 20 genotypes of wheat. Non significant difference due to replications were observed for days to 50% flowering, plant height (cm), days to maturity, biological yield per plant (g), harvest index (%) and seed yield per plant (g). These results are in conformity with Bhushan *et. al* (2013), Singh *et al.* (2018), Aliyu Usman Ibrahim (2019), Seyoum and Sisay (2021), Khinchiet. *al* (2022) and Ahmad and Gupta (2023).

The results of range, coefficient of variation and (CV) character wise presented in table 2. The consolidated results revealed that, in general phenotypic coefficient of variation were higher than genotypic coefficient of variation for all the characters under study. days to 50% flowering ranged from 80 to 93 days with mean value of 86.26. The genotypic and phenotypic coefficients

of variation for this trait were 3.48 and 3.92 respectively. Plant height ranged from 91.30 to 113.90 cm with mean 104.90. The GCV & PCV for this trait was 4.35 and 4.59 respectively. Days to maturity showed range from 120 to 145 days with mean of 129.08. The genotypic coefficient of variation was 3.86 whereas; the phenotypic coefficient of variation was 4.15 for this trait. Number of productive tillers per plant showed the range from 2.90 to 7.90 with its mean value 5.36. The GCV & PCV values for this trait were 23.72 & 25.65 respectively. Number of ears per plant exhibited the range from 3.40 to 7.90 with grand mean 5.41. GCV & PCV for this trait were 18.79 & 20.80 respectively. Ear length showed the range from 3.2 to 10.5 cm. The grand mean of this trait was 6.88. The GCV & PCV were 26.37 & 27.04 respectively. Number of spikelets per ear showed genotypic coefficient of variation 15.44 and the phenotypic coefficient of variation 15.59. The range of this trait was from 33.30 to 61.25 with its mean value 44.48. Number of seed per spike has ranged from 22.30 to 48.36 and the grand mean was 34.78. The GCV & PCV of this trait were 21.42 & 21.69. Test weight showed the range from 3.0 to 8.4 with its mean 5.53. The GCV & PCV for this trait was 21.76 and 22.57. Biological yield per plant ranged from 33.25 to 58.36 g. The grand mean was 46.10g. The GCV & PCV were 14.08 and 14.68 respectively. Harvest index exhibited the range from 17.77 to 45.63 per cent with its mean value 29.68 per cent. The GCV was 14.06 and the PCV was 16.99 for this trait. Seed yield per plant showed range from 6.80 to 19.40g with its grand mean value 13.67g. The GCV & PCV were 19.41 and 20.78 respectively. Overall results of estimation of genetic parameter revealed that, the sufficient variability present among the genotypes, which provides ample scope for further breeding program. The similar finding has also been reported by Devi *et.al.*(2013) Bhushan *et. al* (2013), Singh *et al.* (2018), Aliyu Usman Ibrahim (2019), Seyoum and Sisay (2021), Khinchiet. *al* (2022) and Ahmad and Gupta (2023).

Heritability in broad sense was computed for all the character under study and has been presented in table 3. The heritability values ranged from 68.48 to 98.05. The maximum value of heritability was shown by number of spikelets per ear (98.05 %). Including the character number of spikelets per ear (98.05%) total nine characters showed estimates of high heritability *viz.*, number of seed per spike (97.59), ear length (95.12), test weight (92.99), biological yield per plant (91.99), plant height (89.86), seed yield per plant (87.28), days to maturity (86.67) and number of productive tillers per plant (85.56). Genetic advance for all the traits under study estimated and presented in table 3. The expected genetic advance in per cent of means ranged from 6.36 for days to 50% flowering to 52.99 for ear length. High estimates of genetic advance

in per cent of means were found for number of productive tillers per plant (45.20), number of seed per spike (43.60), test weight (43.24), seed yield per plant (37.37), number of ears per plant (34.99) and number of spikelets per ear (31.49). Three characters showed low genetic advance in percentage of mean *viz.*, days to 50% flowering (6.36), days to maturity (7.41) and plant height (8.51). High heritability coupled with high genetic advance for the characters number of productive tillers per plant, number of ears per plant, ear length, number of spikelets per ear, number of seed per spike, test weight (g) and seed yield per plant (g.) which indicated that above characters were governed by additive gene action and direct selection may be useful for further improvement program. Similar findings have also been reported by Ullah *et al.* (2011), Bhushan *et al.* (2013), Nukasani *et al.* (2013), Kumar *et al.* (2014), Devi & Lal (2016), Singh *et al.* (2018), Aliyu Usman Ibrahim (2019), Seyoum and Sisay (2021), Khinchiet *al.* (2022) and Ahmad and Gupta (2023).

Conclusions and suggestions:

There is ample scope of improvement as the experimental material of 20 genotypes of wheat showed huge amount of variability. The phenotypic coefficients of variation were higher than genotypic coefficients of variation which indicates that this is due to environmental factors. The characters number of productive tillers per plant, number of ears per plant, ear length, number of spikelets per ear, number of seed per spike, test weight and seed yield per plant showed high heritability along with high genetic advance, so it was concluded that direct selection may be useful for further improvement program of these traits.

References:

Ahmad, A. and Gupta, R. K. (2023). Genetic Variability, Heritability and Genetic Advance for Yield and Yield Associated Traits in Bread Wheat (*Triticum aestivum* L.). *Ann. Agric. Crop Sci.* 8(1): 1125:1-3.

Aliyu Usman Ibrahim (2019). Genetic variability, correlation and path analysis for yield and yield components in F₆ generation of wheat (*Triticum aestivum* L. em. Thell.). *J. Agril. and Vet. Sci.* 12(1): 17-23.

Anonymous (a) (2022-23) <https://www.weforum.org/agenda/2022/08/top-10-countries-produce-most-wheat/>

Anonymous (b) 2022-23 <https://www.world-grain.com/media/photos/154-world-s-top-wheat-producing-countries>.

Bineeta Devi & G.M. Lal (2016), Evaluation of some exotic Rice (*Oryza Sativa* L.) genotypes for yield and yield component traits with reference to Allahabad Agro-climatic condition. *Rice Genomics and Genetics* 7(3): 1-8
Bineeta Devi., Pankaj Kumar., G.M. Lal and Deepshikha Singh. (2013) Genetic parameters and Character Association among Yield and its Component Characters in Wheat (*Triticum astivum* L.). Proceeding of International Conference on Health, Environment and Industrial Biotechnology: 95-98, November, 2013

Bhushan, B., Bharti, S., Ojha, A., Pandey, M., Gourav, S.S., Tyagi, B.S. and Singh, G. (2013). Genetic variability, correlation coefficient and path analysis of some quantitative traits in bread wheat. *J. Wheat Res.* 5(1) :21-26.

Burton, G.W. and de Vane, E.H. (1953). Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agron. J.*, 45: 478-481.

Khinchi Pooja, Jaiswal H.K. and Sharma Aarti (2022). Analysis of genetic variability, heritability and genetic advance for yield & yield associated traits in wheat. *The Pharma Innovation Journal* 11(5): 1105-1109.

Kumar N., Markar S. and Kumar V. (2014). Studies on heritability and genetic advance estimates in timely sown bread wheat (*Triticum aestivum* L.). *Biosci. Dis.*, 5(1): 64-69.

Nayak, R., Singh, V.K., Singh, A., Singh, P.K., (2016). Genetic variability, character association and path analysis of rice genotypes. *Ann. Plant and Soil Res.* 18(2): 161-164.

Nukasani, V., Potdukhe, N.R., Bharad, Swati, Deshmukh, Shradha and Shinde, S. M. (2013) Genetic variability, correlation and path analysis in wheat. *J. Wheat Res.* 5(2): 48-51.

Panse, V.G. and Sukhatme, P.V. (1967). *Statistical Methods for Agricultural Workers*. ICAR, New Delhi.

- Seyoum Endashaw Girma and Sisay Alemnesh (2021). Estimation of genetic variability, heritability and genetic advance in bread wheat (*Triticum aestivum* L.). *Int. J. Res. Studies in Agril. Sci.* 7 (9):2454–6224.
- Singh, G., Kumar, P., Kumar, R., Gangwar, L.K. (2018). Genetic diversity analysis for various morphological and quality traits in bread wheat (*Triticum aestivum* L.). *J. Applied and Natural Sci.* 10(1):24-29.
- Tuhina-Khatun, M., Hanafi, M.M., Rafii Yusop, M., Wong, M.Y., Salleh, F.M., Ferdous, J., (2015). Genetic variation, heritability, and diversity analysis of upland rice (*Oryza sativa* L.) genotypes based on quantitative traits. *BioMed research international*, 7.(page number)
- Ullah K., Khan S. J., Muhammad I., Muhammad T. and Muhammad S. (2011). Genotypic and phenotypic variability, heritability and genetic diversity for yield components in bread wheat (*Triticum aestivum* L.) germplasm. *Afr. J. Agric. Res.* 6(23):5204-5207.

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Table 1: Analysis of variance for 12 characters in 20 genotypes of wheat

Sr. No.	Characters	Mean sum of squares		
		Replications d.f. = 2	Treatment d.f. = 19	Error d.f. = 38
1	Days to 50% flowering	1.51	29.56***	2.44
2	Plant height (cm)	1.43	65.08***	2.35
3	Days to maturity	1.86	78.59***	3.83
4	Number of productive tillers per plant	2.04**	5.13***	0.27
5	Number of ears per plant	1.43**	3.33***	0.23
6	Ear length (cm)	0.82*	10.04***	0.16
7	Number of spikelets per ear	25.85***	142.49***	0.93
8	Number of seed per spike	6.94*	168.01***	1.37
9	Test weight (g)	5.52***	4.45***	0.10
10	Biological yield per plant (g)	1.13	130.12***	3.67
11	Harvest index (%)	1.41	60.32***	8.02
12	Seed yield per plant (g)	0.35	22.18***	1.02

Significant. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Table 2. Estimation of genetic parameters for 12 characters in 20 genotypes of wheat

Sr. No.	Traits	Range		Mean \pm SEM	CD @ 5%	GV	PV	GCV	PCV	CV@ %
		Min.	Max.							
1	Days to 50% flowering	80	93.	86.26	2.58	9.03	11.48	3.48	3.92	1.81
2	Plant height (cm)	91.30	113.90	104.90	2.53	20.90	23.26	4.35	4.59	1.46
3	Days to maturity	120	145	129.08	3.23	24.92	28.75	3.86	4.15	1.51
4	Number of productive tillers per plant	2.90	7.90	5.36	0.86	1.61	1.89	23.72	25.65	9.74
5	Number of ears per plant	3.40	7.90	5.41	0.79	1.03	1.26	18.79	20.80	8.90
6	Ear length (cm)	3.20	10.50	6.88	0.67	3.29	3.46	26.37	27.04	5.97
7	Number of spikelets per ear	33.30	61.25	44.48	1.60	47.18	48.12	15.44	15.59	2.17
8	Number of seed per spike	22.30	48.36	34.78	1.93	55.54	56.91	21.42	21.69	3.36
9	Test weight (g)	3.00	8.40	5.53	0.54	1.44	1.55	21.76	22.57	5.97
10	Biological yield per plant (g)	33.25	58.36	46.10	3.16	42.15	45.82	14.08	14.68	4.15
11	Harvest index (%)	17.77	45.63	29.68	4.68	17.43	25.45	14.06	16.99	9.54
12	Seed yield per plant (g)	6.80	19.40	13.67	1.67	7.05	8.07	19.41	20.78	7.41

Table 3 Estimation of heritability and genetic advance 12 characters in 20 genotypes of wheat

Sr. No.	Characters	Heritability (%) (h^2)	Genetic advance (GA)	Genetic Advance as % mean (GAM)
1	Days to 50% flowering	78.70	5.49	6.36
2	Plant height (cm)	89.86	8.92	8.51
3	Days to maturity	86.67	9.57	7.41
4	Number of productive tillers per plant	85.56	2.42	45.20
5	No of ears par plant	81.68	1.89	34.99
6	Ear length (cm)	95.12	3.64	52.99
7	Number of spikelets per ear	98.05	14.01	31.49
8	Number of seed per spike	97.59	15.16	43.60
9	Test weight (g)	92.99	2.39	43.24
10	Biological yield per plant (g)	91.99	12.82	27.82
11	Harvest index (%)	68.48	7.11	23.98
12	Seed yield per plant (g)	87.28	5.11	37.37