Estimation of nature and magnitude of genetic variability, heritability and genetic advance among various yield and its contributing characters of wheat (*Triticum aestivum* L.)

Abstract

Thepresent research investigationwas conducted atInstructional farm of AKS University, Satna, Madhya Pradesh during *rabi* Seasonof 2022. The experimental material for the present research trial comprised of 20diverse genotypes of wheat collected from different sourcesthroughthehelpfromDepartmentofGenetics&PlantBreeding,Facultyof AgricultureScience,AKSUniversity,Satna(M.P.). This experiment was conducted by using Randomized Block Design with three replications. Five plants were chosen aimlessly from every genotype in each replication.The arbitrarily chosen plants were labelled for recording perceptions on different yield contributing characters viz. 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.).

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 (g) (21.76 & 22.57). The maximum value of heritability was shown by number of spikelets per ear (98.05), number of seed per spike (97.59), ear length (cm.) (95.12), test weight (g) (92.99), biological yield per plant (g) (91.99), plant height (cm.) (89.86), seed yield per plant (g.) (87.28), days to maturity (86.67) and number of productive tillers per plant (85.56). 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 (g) (43.24), seed yield per plant (g.) (37.37), no of ears par 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 par plant, ear length (cm.), 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.

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 third most produced cereal in the world after 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, 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 estimates and genetic advance (GA). GCV indicates the relative degree of genetic variability existing for different characters in a population of genotypes.

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 perticular 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 progamme, 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 available germplasm of wheat with the objectives: to estimate the nature and magnitude of genetic variability, heritability and genetic advance among various yield and its contributing characters of wheat (*Triticum aestivum* L.).

Materials and Methods:

Thepresent research investigationwas conducted atInstructional farm of AKS University, Satna, Madhya Pradesh during *rabi* Seasonof 2022.Thealtitude of Satna is 317 meters above mean sea level and the latitude of Satna,MadhyaPradesh,Indiais24.579716,andthelongitudeis80.832176. The experimental material for the present research trial comprised of 20diverse genotypes of wheat collected from different sourcesthroughthehelpfromDepartmentofGenetics&PlantBreeding,Facultyof AgricultureScience,AKSUniversity,Satna(M.P.). This experiment was conducted by using Randomized Block Design with three replications.Five plants were chosen aimlessly from every genotype in each replication.The arbitrarily chosen plants were labeled for recording perceptions on different yield contributing characters viz. 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.).

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 $X_{i.}$Therange 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

Mean: $$X_i = \frac{1}{N} (\sum_{j=1} X_{ij})$$

Where $\bar{X}$ = Mean of the ith trait, X_{ij} = the value of jth observations of ith trait, n = number of observations.

GCV & PCV:

$$GCV = \frac{\text{Genotypic standard deviation } (\sigma g)}{\text{Mean } \bar{X}}$$

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

Heritability:

$$h^2 = \frac{\sigma^2 g}{\sigma^2 g + \sigma^2 e}$$

or

$$h2 = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Expected genetic advance:

$$G.A. = \frac{\sigma^2 g}{\sigma^2 p} K. \sigma^2 p$$

$$= h^2.K. \sigma^2 p$$

Where,

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

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

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

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), Khinchi et 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. The result of table 2 of days to 50% flowering revealed that it ranged from 80 to 93 days with grand 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 grand 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 grand mean value 5.36. The GCV & PCV values for this trait were 23.72 & 25.65 respectively. No of ears par 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 (cm.) 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 variation15.59. The range of this trait was from 33.30 to 61.25 with its grand 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 (g)showed the range from 3.0 to 8.4 with its grand mean 5.53. The GCV & PCV for this trait was 21.76 and 22.57.Biological yield per plant (g) ranged from 33.25 to 58.36. The grand mean was 46.10. The GCV & PCV were 14.08 and 14.68 respectively.Harvest index (%) exhibited the range from 17.77 to 45.63 with its grand mean value 29.68. The GCV was 14.06 and the PCV was 16.99 for this trait.Seed yield per plant (g.) showed range from 6.80 to 19.40 with its grand mean value 13.67. 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 findings has also been reported by Bhushan *et. al* (2013), Singh et al. (2018), Aliyu Usman Ibrahim (2019), Seyoum and Sisay (2021), Khinchi et 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 (cm.) (95.12), test weight (g) (92.99), biological yield per plant (g) (91.99), plant height (cm.) (89.86), seed yield per plant (g.) (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 (cm.). 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 (g) (43.24), seed yield per plant (g.) (37.37), no of ears par 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 (cm.) (8.51).High heritability coupled with high genetic advance for the characters 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) 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), Singh et al. (2018), Aliyu Usman Ibrahim (2019), Seyoum and Sisay (2021), Khinchi et 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, no of ears par plant, ear length (cm.), number of spikelets per ear, number of seed per spike, test weight (g) and seed yield per plant (g.) 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 RK (2023). Genetic Variability, Heritability and Genetic Advance for Yield and Yield Associated Traits in Bread Wheat (*Triticum aestivum* L.). *Ann Agric Crop Sc.*; 8(1): 1125:1-3.

Aliyu Usman Ibrahim (2019). Genetic variability, Correlation and Path analysis forYield and yield components in F6 generation of Wheat (Triticum aestivumEm. Thell.). Journal of Agriculture and Veterinary Science. Volume 12,Issue1Ver. I, 17-23.

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

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

Bhushan,B.,Bharti,S., Ojha,A.,Pandey, M.,Gourav,S.S., Tyagi,B.S. andSingh, G. (2013) enetic variability, correlation coefficient and path analysisofsomequantitativetraitsinbreadwheat.*J.WheatRes*. 5(1) :21-26.

Burton,G.W.anddeVane,E.H.(1953).Estimatingheritabilityintallfascue(*Fastucaarundinacea*) from replicated clonal material. *Agron. J.*, **45**: 478-481.

Johnson, H.W., Robinson, H.F. and Comstock, R.E. (1955). Estimates of geneticandenvironmentalvariabilityinsoybeans.*Agron.J*.**47**:314-318.

Khinchi Pooja, Jaiswal HK 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. andKumar V.(2014). Studies on heritability and geneticadvance estimates in timely sown bread wheat (Triticum aestivum L.).*Biosci.Dis.*,**5**(1):64-69.

Larik, A.S., Rajput, L.S., 2000. Estimation of selection indices in *Brassica juncea* L. and *Brassica napus* L. Pakistan Journal of Botany 32(2), 323–330.

Namrata, Sharma, H., Ranwah, B.R., Bisen, P., 2016. Variability Assessment and Path Coefficient Analysis in Groundnut (Arachis hypogaea L.) Genotypes in Sub- Humid Southern Plains of Rajasthan. Trends in Biosciences 9, 642–646.

Nayak, R., Singh, V.K., Singh, A., Singh, P.K., 2016. Genetic variability, character association and path analysis of rice genotypes. Annals of Plant and Soil Research 18(2), 161–164.

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

Panse,V.G.andSukhatme,P.V.(1967).StatisticalMethodsforAgriculturalWorkers. ICAR, NewDelhi.

Popat Raj, Patel Rumit and Parmar Dinesh (2020). Variability: Genetic VariabilityAnalysisforPlantBreedingResearch.Rpackageversion0.1.0.https://CRAN.R-project.org/package=variability.

Seyoum Endashaw Girma and Sisay Alemnesh (2021). Estimation of GeneticVariability,HeritabilityandGeneticAdvanceinBread Wheat(Triticumaestivum L.).InternationalJournalofResearchStudiesinAgriculturalSciences(IJRSAS). 7 (9):2454–6224.

Singh G, Kumar P, Kumar R, Gangwar L.K. (2018). Genetic diversity analysis forvarious morphological and quality traits in bread wheat (*Triticum aestivum*L.).Journalof AppliedandNaturalScience.;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.

Ullah K., Khan S. J., Muhammad I., Muhammad T.and Muhammad S. (2011).Genotypic and phenotypic variability, heritability and genetic diversity foryield components in bread wheat (*Triticum aestivum* L.) germplasm. Afr. J.Agric.Res.**6**(23)**:**5204-5207.

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	1.5167	29.5649***	2.4465
2	Plant height (cm.)	1.437	65.088***	2.359
3	Days to maturity	1.867	78.592***	3.832
4	Number of productive tillers per plant	2.0482**	5.1312***	0.2734
5	No of ears par plant	1.4352**	3.3373***	0.2322
6	Ear length (cm.)	0.8295*	10.0496***	0.1688
7	Number of spikelets per ear	25.857***	142.490***	0.939
8	Number of seed per spike	6.941*	168.010***	1.371
9	Test weight (g)	5.5295***	4.4565***	0.1093
10	Biological yield per plant (g)	1.130	130.129***	3.672
11	Harvest index (%)	1.419	60.326***	8.025
12	Seed yield per plant (g.)	0.3512	22.1807***	1.0277

Signifcant. 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		Grand Mean	Critical Difference (CD) 5%	Genotypic variance	Phenotypic variance	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	No of ears par 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 (%) (h2)	Genetic advance (GA)	Genetic Advance as % means
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