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To Study the Genetic Veriability, Heritability and Genetic Advance for Grain Yield and its Components in Bread Wheat (*Triticum aestivum* L. em. Thell) Genotypes

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Abstract

The present investigation was carried out using 20 bread wheat genotypes at Agriculture Research Farm of B.R.D. P.G. College Deoria, (U.P.). during Rabi, 2020-2021 in Randomized Block Design (RBD) with Three replication. The data were recorded form five randomly selected plants for 14 quantitative traits Viz., Days to 50% flowering, Days to maturity, Plant height (cm), Number of productive tillers per plant, Length of spike (cm), Number of spikelets per spike, Number of grains per spike, 1000-grain weight (g), Grain yield per plant (g), Flag leaf area per plant (cm^2), peduncle length per plant (cm), Grain yield per spike (g), Biological yield per plant (g), Harvest index (%). The result of analysis of variance in respect of germplasm evaluation revealed that the mean squares due to genotypes (treatment) were highly significant for all 14 characters under study. Genotypic coefficient of variation (GCV) was recorded highest for grain yield per plant (19.14%) followed by biological yield per plant (18.97%), flag leaf area (15.88%), grain weight per spike (11.15%) and 1000-grain weight (8.29%). Days to maturity (3.44%) and days to 50% flowering (3.89%) exhibited low genotypic coefficient of variation. The phenotypic coefficient of variation (PCV) was higher in magnitude than that of genotypic coefficient of variation for all the characters under study. The highest PCV was recorded for grain yield per plant (21.28%) followed by biological yield per plant (20.74%), flag leaf area (17.78), grain weight per spike (13.72%) and harvest index (12.64). The characters viz., days to maturity (5.42%) and number of grains per spike (6.93 %) showed low phenotypic coefficient of variation. Broad sense heritability was estimated for all the characters under study. High heritability was observed for most of the traits and it was noted highest for biological yield per plant (83.60%), grain yield per plant (80.91%), flag leaf area (79.77%), grain weight per spike (66.06%) and number of productive tillers per plant (55.71%). However, days to 50% flowering (25.86 %) and number of spikelets per spike (32.73%) exhibited low estimates of heritability. The high genetic advance as per cent of mean (genetic gain) was recorded for biological yield per plant (35.73%) followed by grain yield per plant (35.48%), flag leaf area (29.22), grain weight per spike (18.68%) and 1000-grain weight (11.57%). However, days to 50% flowering (4.08%) and days to maturity (4.50%) showed low genetic gain.

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

Introduction

About wheat [*Triticum aestivum* (L.) em. Thell]; 2n = 6x = 42] is a cereal crop of the member of Gramineae (Poaceae) family and one of the most leading cereals of many countries of the world including India. It is one of the world's most common staple foods. It covers 17 per cent (one-sixth) of global cropland, feeds about 40% of the world's population and accounts for 20% of overall food calories and protein in human nutrition. 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 areas and in warm, humid to dry, cold environments (1). Wheat is a self-pollinated, monocotyledonous plant that had originated from South West Asia. There are different species of wheat, out of which only three *Triticum* species are mostly cultivated throughout the world. These are *Triticum aestivum* (bread wheat), *Triticum durum* (macaroni wheat) and *Triticum dicoccum* (emmer wheat). The bread wheat is an allohexaploid species (2n=6x=42) having AABBDD with A, B and D genome. The genetic origin of wheat is of interest; since it is a classic example of how closely related species may be combined in nature into a polyploid series. The species of Triticum and their close relatives can be divided into diploid, tetraploid and hexaploidy groups, with chromosome numbers of 2n = 14, 28 and 42, respectively, in which the basic chromosome number of Wheat is x = 7. *Triticum durum* originated thousands of years ago from a hybridization between the wild diploid Triticum monococcum (A genome donor) and the donor of the B genome which, according to morphological, geographical and cytological evidence, has been recognized as Triticum speltoides or a closely related species (2). Globally, wheat (*Triticum* species.) is grown in about 224.09 million hectares holding the position of highest acreage among all crops with annual production hovering around 794.44 million metric tons. It is necessary for a plant breeder to quantify the variability in terms of

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phenotypic coefficients of variation (PCV) and genotype coefficients of variation (GCV), heritability and genetic advance. The knowledge of nature and magnitude of genetic variance controlling yield and yield components is a prerequisite for improvement of yield in any crop. Therefore, the first step in any crop improvement programme is to assess the extent of variability in the base populations under study. Information on the magnitude of variability and extent, to which desirable characters are heritable, is important for planning of breeding programme and ascertaining the scope of its improvement. whereas estimate of heritability and genetic advance are useful in inferring the genetic factors. When heritability, which measures the genetic link of a trait in the population, is high, it should be relatively straight forward to improve that trait. In an experiment, genetic advance estimates provide an estimate of the improvement in the mean performance of the selected clusters over the base populations.

Materials and Methods

The field experiment under present investigation was conducted during rabi 2021-22 at Agriculture Research Farm of Baba Raghav Das Post Graduate College Deoria (U.P.). Geographically, this College is situated in the east part of Uttar Pradesh, India. The site of experiment is located at 26.5°N latitude, 83.79°E longitude and 68 meter (223 feet) above the mean sea level. The climate of district Deoria is semi-arid with hot summer and cold winter nearly 80% of total rain fall is received during the monsoon (only up to September) with a few showers in the winter. The experiment was laid out in Randomized Block Design (RBD) with 3 replications, each replication and each genotype sown in two rows of five meters length spaced at 2.5m from row to row and 10 cm form plant to plant. The recommended package of practices was adopted for raising the healthy crop. Observations for all the traits were recorded on five randomly selected plants of each entry in reach replication while observation for days to 50 per cent heading and days to maturity were recorded on plot basis.

Statistical analysis : To test the difference among the genotypes, the analysis of variance was worked out separately for each character as per method suggested by (3) and using standard statistical procedure given by (4). Genotypic coefficient of variation (GCV) and Phenotypic coefficient of variation (PCV) were calculated as per the standard formula suggested by (5). Heritability (h^2) was calculated in broad sense by using the following formula given by. Genetic Gain (GG) is the Genetic Advance (GA) is the expressed as per cent of mean. It was estimated by using the formula of (6,7).

Results and Discussion

The Analysis of variance (ANOVA) indicated that the mean sum of squares due to genotypes were highly significant for all the traits viz., days to 50 per cent flowering, days to maturity, plant height, peduncle length, flag leaf area, number of productive tillers per plant, ear length, number of spikelets per spike, number of grains per spike, grain weight per spike, 1000-grains weight, biological yield per plant, grain yield per plant and harvest index. The mean sum of squares due to replication showed non-significant differences for all the traits under study indicating good homogeneity among replications. Mean sum of square from analysis of variance for various traits are given in Table-1.

Genotypic coefficient of variation (GCV) was recorded highest for grain yield per plant (19.14%) followed by biological yield per plant (18.97%), flag leaf

Table-1 : Analysis of variance of Randomized Block Design for 14 characters of wheat Germplasm.

S. No.	Character	Source of variation		
		Replication (df=2)	Genotype (df=19)	Error (df=38)
1.	Days to 50% flowering	1.61	52.45**	25.62
2.	Days to maturity	73.24	73.89**	24.41
3.	Plant height (cm)	13.64	127.76**	41.42
4.	Peduncle length (cm)	3.07	30.93**	10.54
5.	Flag leaf area (cm^2)	8.80	62.03**	4.83
6.	Number of productive tillers per plant	0.06	0.50**	0.10
7.	Ear length (cm)	1.30	1.18**	0.46
8.	Number of spikelets per spike	2.12	2.89**	1.17
9.	Number of grains per spike	12.45	11.56**	4.15
10.	Grain weight per spike (g)	0.03	0.12**	0.01
11.	1000-grains weight (g)	2.50	54.71**	15.43
12.	Biological yield per plant (g)	5.18	50.54**	3.10
13.	Grain yield per plant (g)	0.24	13.61**	0.99
14.	Harvest index (%)	80.14	74.11**	26.71

* Significant at P = 0.05%, ** Significant at P = 0.01%

Table-2 : Estimates of Heritability and Genetic Advance in 20 germplasm lines of wheat.

S. No.	Characters	Min.	Max.	Mean	Var Environmental	ECV	Var Genotypical	GCV	Var Phenotypical	PCV	h^2 (Broad Sense)	Genetic Advancement 5%	Gen.Adv as % of mean 5%
1.	Days to 50% flowering	70.00	82.00	76.60	25.627	6.6	8.942	3.899	34.569	7.666	25.868	3.133	4.085
2.	Plant height (cm)	110.00	124.00	118.00	41.427	7.6	28.781	6.335	70.207	9.894	40.994	7.076	8.355
3.	Peduncle length (cm)	76.24	78.10	84.69	10.549	7.2	6.797	5.779	17.346	9.233	39.184	3.362	7.453
4.	Flag leaf area (cm^2)	39.84	51.10	45.11	4.835	8	19.065	15.885	23.9	17.786	79.771	8.034	29.227
5.	Ear length (cm)	20.31	35.02	27.49	0.46	7.801	0.241	5.64	0.701	9.626	34.329	0.592	6.807
6.	Number of productive tillers per plant	4.60	6.20	5.40	0.105	6.001	0.132	6.731	0.237	9.018	55.719	0.558	10.35
7.	Ear length (cm)	7.26	9.72	8.70	1.175	5.999	0.572	4.186	1.746	7.315	32.739	0.891	4.934
8.	Number of spikelets per spike	15.20	19.30	18.07	24.413	4.187	16.494	3.442	40.907	5.42	40.32	5.312	4.502
9.	Days to maturity	31.40	39.60	37.13	4.152	5.488	2.47	4.233	6.622	6.93	37.3	1.977	5.325
10.	Grain weight per spike (cm)	1.42	2.13	1.72	0.019	7.997	0.037	11.158	0.056	13.728	66.065	0.321	18.683
11.	Biological yield per plant (g)	35.00	50.00	43.65	3.101	8.4	15.815	18.97	18.916	20.746	83.606	7.491	35.731
12.	1000-grain test weight (g)	15.40	32.57	20.96	15.434	9	13.095	8.29	28.529	12.236	45.901	5.05	11.57
13.	Grain yield per plant (g)	7.32	15.52	10.71	0.993	9.301	4.207	19.148	5.199	21.288	80.91	3.801	35.481
14.	Harvest Index (%)	41.98	60.19	51.58	26.718	10.021	15.797	7.706	42.515	12.641	37.157	4.991	9.676

area (15.88%), grain weight per spike (11.15%) and 1000-grain weight (8.29%). Days to maturity (3.44%) and days to 50% flowering (3.89%) exhibited low genotypic coefficient of variation. The phenotypic coefficient of variation (PCV) was higher in magnitude than that of genotypic coefficient of variation for all the characters under study. The highest PCV was recorded for grain yield per plant (21.28%) followed by biological yield per plant (20.74%), flag leaf area (17.78), grain weight per spike (13.72%) and harvest index (12.64). The characters viz., days to maturity (5.42%) and number of grains per spike (6.93%) showed low phenotypic coefficient of variation. Broad sense heritability was estimated for all the characters under study. High heritability was observed for most of the traits and it was noted highest for biological yield per plant (83.60%), grain yield per plant (80.91%), flag leaf area (79.77%), grain weight per spike (66.06%) and number of productive tillers per plant (55.71%). However, days to 50% flowering (25.86 %) and number of spikelets per spike (32.73%) exhibited low estimates of heritability. The high genetic advance as per cent of mean (genetic gain) was recorded for biological yield per plant (35.73%) followed by grain yield per plant (35.48%), flag leaf area (29.22), grain weight per spike (18.68%) and 1000-grain weight (11.57%). However, days to 50% flowering (4.08%) and days to maturity (4.50%) showed low genetic gain Table-2 and Fig-2. The presence of adequate genetic variability is essential and its consideration combined with heritability (broad sense) may play a significant role in analysis the relative contributions of genetic and non-genetic factors to the total phenotypic variation in a population. To obtain a clear picture about the variability in all the genotypes, the variability was further partitioned into phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV). In the present investigation, phenotypic coefficient of variation (PCV) is marginally higher than the respective genotypic coefficient of variation (GCV) for all the characters indicating negligible influence on the characters by the environmental fluctuations. The grain yield per plant depicted highest genotypic coefficient of variation followed by biological yield per plant, flag leaf area, grain weight per spike and 1000-grain weigh while highest phenotypic coefficient of variation (PCV) was observed for grain yield per plant followed by biological yield per plant, flag leaf area, grain weight per spike and harvest index. The magnitude of GCV and PCV were low for days to maturity. Similar results were reported by (8,9,10). The coefficient of variation indicated only the extent of variability existing for various traits but does not give any information regarding heritable portion of it. Amount of high or moderate heritability accompanied with high or moderate genetic advance indicate additive gene

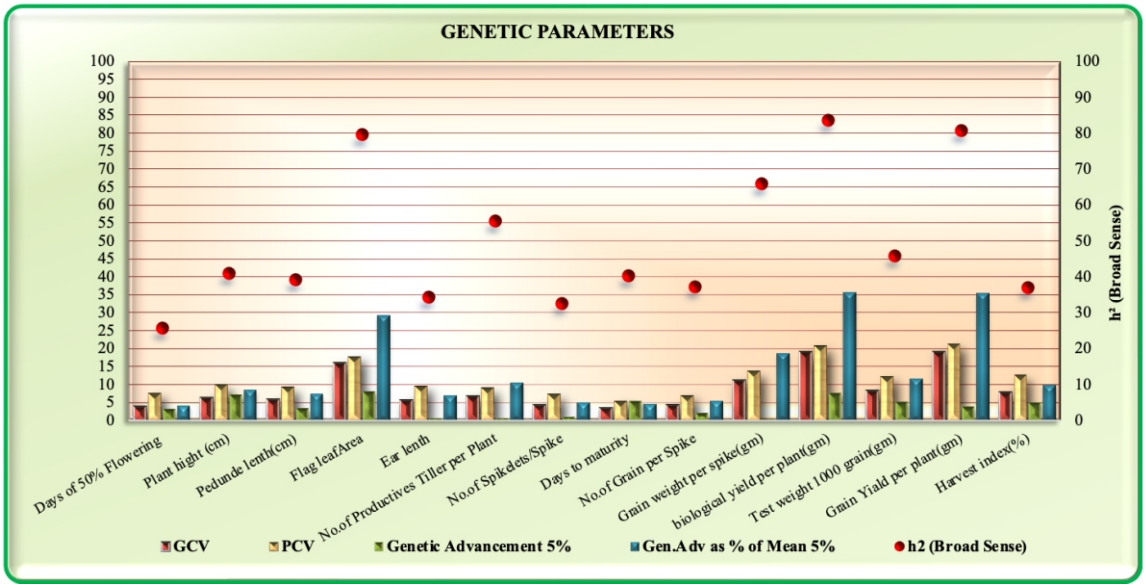

Fig.-1 : Graphical presentation of genetics parameters.

action involved in the inheritance of concerned traits, hence selection may be effective. The heritability estimates in broad sense were quite high for most of the characters indicating the strong genetic nature for all the traits under study. The higher heritability implied that selection for most of the traits might be effective in this set of genotypes. The high heritability estimates coupled with high genetic gain for biological yield per plant, grain yield per plant, flag leaf area and grain weight per spike indicated that all these characters are governed by additive gene action and as such are expected to exhibit improvement for such traits by direct selection. These observations are in agreement with the earlier reports of (8,11,12).

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