Plant Archives Volume 20 No. 2, 2020 pp. 7813-7819 **e-ISSN:2581-6063 (online), ISSN:0972-5210**

STUDIES ON CHOICE OF TRAITS FOR SEED YIELD IMPROVEMENT THROUGH BREEDING IN BREAD WHEAT (*TRITICUM AESTIVUM* L.) GENOTYPES

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Abstract

A study was conducted to estimate the genetic variability of economic traits in 68 genotypes of wheat in randomized block design with three replications during *rabi* season 2018-19 at Agriculture Research Farm, Department of Genetics and Plant Breeding, Lovely Professional University, Phagwara (Punjab), India. Analysis of variance revealed that genotypes exhibited significant variation for all the characters studied. The estimate of PCV in all the traits studied were greater than those of the GCV, the close the proximity between PCV and GCV values for most of the characters indicated less influence of environment on the expression of the characters under study. Heritability for broad sense was estimated for all the characters under study and observed range from 22.58 to 96.39%. Harvest index and grain yield per plant exhibits High PCV and GCV whereas, plant height and protein content revealed high heritability coupled with high genetic advance as per cent of mean andthe charactersto be under additive genetic control and also scope of improvement through direct selection.

Key words : Heritability, genetic advance, PCV, GCV.

Introduction

Wheat (*Triticum aestivum* L.) is the most important cereal in the world and was one of the crops to be domesticated some 10000 years ago. It is a cereal grass and self-pollinated crop of the *Poaceae* family and genus *Triticum*. Wheat is a segmental allohexaploid ($2n = 6x = 42$, AABBDD) having originated in the fertile crescent area of South-Western Asia. The majority of the cultivated wheat varieties belongs to the main species of genus *Triticum* where common bread wheat (*T. aestivum*) and durum wheat (*T. durum*, $2n = 4x = 28$, AABB) make up 90% of the total world's wheat crop cultivation. 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. Wheat occupies 28% area under cereals contributing 33% of the total food grain production in the country (Rangare *et al.,* 2010). It has relatively high content of niacin and thiamine which are principally concerned in providing the special protein called 'Gluten' which provides the framework of spongy cellular texture of bread and baked products (Bhushan *et al.,* 2013). Global wheat production during 2016-17 was 760.1 million metric tons (FAO, 2017) while in India it was 99.7 million tonnes with an area coverage of 29.58 million hectares and an average productivity of 33.71 q/ ha (ICAR-IIWBR, 2018). Major wheat producing states are Punjab, Haryana, Uttar Pradesh, Bihar and Rajasthan which are located in the Indo-Gangetic Plains and accounts for 85% of total wheat production in the India.

The first basic step for any hybridization programme is the assessment of genetic variability among the available genotypes for desirable traits (Rahman *et al.,* 2016). Heritability is a technique used by the plant breeders for effectively isolating the amount of genetic variation from the total phenotypic variation (Harshawardhan *et al.* 2016). High genetic advancement

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as well as high heritability offers the better scope for selection (Johnson *et al.,* 1955). The knowledge about genetic variability, heritabilityand its other parameters help in further improving the grain yield through directed selection of component traits and their interrelationship with yield. The selection of parents becomes more difficult if the improvement is made for a polygenetically controlled complex character like grain yield. Since, efficient selection of genetically superior individuals requires adequate phenotypic variance in the base population and sufficient high heritability. Therefore, the efforts were made to study the extent of variability and possible amount of genetic gain expected to occur during the selection for yield improvement.

Materials and Methods

Experimental material and details

The experiment was carried out under Agriculture Research Farm, Department of Plant Breeding and Genetics, Lovely Professional University, Phagwara (Punjab). The experiment comprised of 68 different genotypes of wheat grown in Randomized Complete Block Design with three replications during *Rabi* 2018-19. The sowing was done by dibbling seeds in rows with row to row distance 22.5 cm, plant to plant distance 3 cm, row length is 2 m. All genotypes were sown in 5 lines each. The recommended packages of practices were adopted for optimum crop growth. Recommended dose of fertilizers (120:60:40 kg NPK ha^{-1}) and 4 irrigations were applied for better crop production.

Observations recorded

Observations on yield and yield attributing characters were recorded, leaving border plants in each replication. Taken out five random plants from each entry of genotype of replications and tagged for data recording. Data was recorded on whole plot basis for Days to 50% heading, Days to maturity and canopy temperature whereas plant height (cm), peduncle length (cm), number of productive tillers plant^{-1}, number of spikelet's ear^{-1}, ear length (cm), ear weight (g), number of ears plant^{-1}, number of grains ear^{-1}, 1000-grain weight (g), biological yield plant^{-1}(g), grain yield plant^{-1} (g), harvest index (%) and chlorophyll content from individual tagged plant.

Statistical Analysis

The data obtained in respect of all the characters has been subjected to: Analysis of variance (Panse and Sukhatme, 1952), Heritability (Hanson *et. al.,* 1956) and Genetic advance (Johnson *et. al.,* 1955). The phenotypic and genotypic coefficients of variation in per cent were computed by the following formulae given by Burton (1952).

ANOVA

Skeleton of ANOVA for completely randomized block design

Source ofvariation	d.f.	Sum of square	Mean sum of square	F cal. value	Expected mean squares
Replication	(r-1)	RSS	RMS	RMS/EMS	-
Genotype	(g-1)	GSS	GMS	GMS/EMS	$\sigma^2 e + r\sigma^2 g$
Error	(r-1)(g-1)	ESS	EMS	-	$\sigma^2 e$
Total	(rg-1)	TSS	-	-	-

Where,

r = Number of replications

g = Number of genotypes

d.f. = Degree of freedom

RSS = Replication sum of square

GSS = Genotype sum of square

ESS = Error sum of square

TSS = Total sum of square

RMS = Replication mean sum of square

GMS = Genotypic mean sum of square

EMS = Error mean sum of square = $\sigma^2 e$

$= \sigma^2 g$ Genotypic variance

Test of significance

If the variance ratio (or) F-calculated value [Vt / EMS] of treatment was greater than the F table value at 5% and 1% level of significance the variance between treatments was considered to be significant. If the F calculated value is less than F tabulated value, the difference between treatments was considered to be non-significant.

Genetic variability

(i) Mean: Mean is the average value of the character in a sample, *i.e.*, it is the average of all the observations on a character in sample

$$\text{Grand mean } (\overline{X}) = \frac{\sum Xi}{N}$$

Where,

$(\overline{X}) =$ Grand mean or over all mean of the observation

$\sum Xi$ = Sum of all observations; [i= 1, 2, 3,……n.]

N = Number of observations

(ii) Range: It was taken as the difference between the highest and lowest mean value for each character. It is the simple measure of variability and gives an idea of the dispersion or spread of the observations in a sample.

Range = Xn– X1

Where, Xn= Highest mean value of character

X1 = Lowest mean value of character

(iii) Coefficient of variation (CV %): Genotypic and phenotypic coefficient of variation was computed, using formula given by Burton (1952).

Genotypic coefficient of variation (GCV %) =

$$\frac{\sigma^2 g}{\overline{}} \times 100$$

Phenotypic coefficient of variation (PCV %) =

$$\frac{\sigma^2 p}{\overline{}} \times 100$$

Where,

$\sqrt{\sigma^2 g} =$ Genotypic standard deviation

$\sqrt{\sigma^2 p} =$ Phenotypic standard deviation

$\overline{X} =$ General mean of particular character

(iv) Standard error of mean (SEM): Standard error of mean was calculated by following formula

$$SEm\pm = \sqrt{\frac{EMS}{r}} \qquad SE_{diff} = \sqrt{\frac{2EMS}{r}}$$

Where,

SEm± = Standard error of means

SE_{diff} = Standard error of difference

(v) Coefficient of variation (CV): A measurement of variance which is independent of the unit of measurement is provided by the standard deviation expressed as percentage of mean. This is known as coefficient of variation (CV).

$$C.V. = \frac{\sqrt{EMS}}{GM} \times 100$$

CD at 5% prob. Level = $SE_{diff} \times t_{5\%}$ table value

Where,

C.V. % = Coefficient of variation

GM= Grand mean

C.D. = Critical difference

$t_{5\%}$ = t, table value 5% probability level at error d.f.

Estimation of phenotypic and genotypic coefficients of variation

The phenotypic and genotypic coefficients of variation in per cent were computed by the following formulae given by Burton (1952).

PCV (%) = (Phenotypic standard deviation) / Mean × 100 (or) $\frac{\sqrt{V_g}}{\overline{X}} \times 100$

$$\text{GCV (\%)} = \frac{\text{Genotypic standard deviation}}{\text{Mean}} \times 100$$

(or) $\frac{\sqrt{V_p}}{\overline{X}} \times 100$

Where,

PCV or V_g = Phenotypic coefficient of variation

GCV or V_p= Genotypic coefficient of variation

$\overline{X} =$ General mean of character

The PCV and GCV value are ranked as Low (0-10%), Moderate (10-20%), High (>20%).

(vi) Heritability: Heritability in per cent in broad sense was estimated by the method given by Hanson *et al.,* (1956).

$$h^2(BS) = \frac{\text{Genotypic variance}}{\text{Phenotypic variance}} \times 100$$

(or) $\frac{V_g}{V_p} \times 100$ (or) $\frac{\sigma^2 g}{\sigma^2 p} \times 100$

Heritability value are categorized as low, moderate and high (Robinson *et al.,* 1949) and are given below: - Low (0-30%), Moderate (30-60%), High (>60%).

(vii) Genetic advance: Improvement in the mean genotypic value of selected plants over the parental population is known as genetic advance. Expected genetic advance (GA) was calculated by the method suggested by Johnson *et al.,* (1955)

GA(s) = $k \times h^2 \times \sigma_p$

Where,

k = Selection differential in standard deviation units which is 2.06 for 5% selection intensity,

h^2 = Heritability in broad sense, and

$\sigma_p =$ Phenotypic standard deviation

Genetic advance as percentage of Mean: -This was expressed by following formula:

Genetic advance (as % of mean) = $\frac{GA}{\overline{\ }} \times 100$

Where,

GA = Genetic advance

$\overline{X} =$ Mean

GA was categorized asLow (0-10%), Moderate (10-20%), High (>20%).

Results and Discussion

Analysis of variance

Analysis of variance indicated that the mean sum of squares due to genotypes were significant for all the characters revealed that there was considerable genetic variability amongst the material under study. There is no significant variation for replication which shows that error due to environmental error was less. The result from the analysis of variance of all character under the study have been given in Table 1. Similar kind of results were also found by Tiwari *et al.,* (2017), Kumar *et al.* (2019).

Range and Mean

Table 2 reveals that, Days to 50% heading ranged from 90.67 to 125.00 days with a general mean of 108.58 days. Days to maturity ranged from 149.67 to 167.33 days with a general mean of 155.12 days. Plant height ranged from 88.87 to 148.73 cm with a general mean of 108.57 cm. Peduncle length ranged from 88.87 to 47.73 cm with a general mean of 37.34 cm. No. of productive tillers per plant ranged from 12.20 to 22.40 cm with a general mean of 17.04cm. No. of productive tillers per plant ranged from 12.20 to 22.40 cm with a general mean of 17.04cm. No. of spikelet's per ear ranged from 15.20 to 24.93 with a general mean of 19.71. Ear length ranged from 9.42 to 13.58 cm with a general mean of 11.08 cm. Ear weight ranged from 2.35 to 4.16 g with a general mean of 3.23 g. Number of ears per plant ranged from 12.73 to 23.87 with a general mean of 18.12. Number of grains per ear ranged from 45.87 to 81.27 with a general mean of 64.95. 1000-grain weight ranged from 36.73 to 60.06 g with a general mean of 48.32 g. Biological yield per plant ranged from 68.17 to 164.33 g with a general mean of 114.03 g. Harvest index ranged from 15.30 to 38.58 g with a general mean of 26.35g. Chlorophyll content ranged from 33.08 to 47.15 with a general mean of 40.63. Canopy temperature ranged from 18.20 to 22.37 with a general mean of 20.15. Protein content ranged from 9.67 to 15.54 with a general mean of 12.91. Grain yield per plant ranged from 17.25 to 40.31 with a general mean of 29.24.

Genotypic and phenotypic coefficient of variation

The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed in the experimental material for all the characters studied (Table 2). The PCV was higher than GCV for all the characters indicating that the visible variation in the expression of traits was not only due to varying influence of environment. High PCV with moderate GCV were observed in harvest index (21.55, 14.98) and grain yield per plant (20.14, 15.37). Moderate value of PCV and GCV were recorded in plant height (12.45, 11.02), ear weight (15.23, 10.31), No. of grains per ear (12.25, 10.66), biological yield (18.15, 13.55) and protein content (11.37, 11.17). Moderate PCV with low GCV was observed in peduncle length (13.04, 8.82), No. of productive tillers per plant (16.82, 8.10), No. of spikelet's per spike (10.27, 8.48), No. of ears per plant (17.14, 9.42) and 1000 grain weight (11.39, 7.74). Low PCV and GCV were recorded in days to 50% heading (5.90, 5.74), days to maturity (2.54, 2.22), ear length (9.38, 7.62), chlorophyll content (9.48, 5.28) and canopy temperature (6.25, 4.03). These results are in conformity with the earlier which finding Chimdesa *et al.,* (2017); Rani *et al.* (2018) observed high PCV and moderate GCV for grain yield and harvest index suggesting sufficient variability are available and thus exhibited scope for genetic improvement through selection for all these traits. 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 springs is reflected by heritability.

Heritability

Heritability is a measure of the extent of phenotypic variation caused by the additive gene action. Heritability for broad sense was estimated for all the characters under study and presented in Table 2. and observed range from

Table 1: Analysis of variance for grain yield and its components in wheat.

		Mean sum of squares								
Source of variation	**D.F.**	**Days to 50% heading**	**Days to maturity**	**Plant height (cm)**	**Peduncle length (cm)**	**Number of productive tillers per plant**	**Number of spikelets per ear**	**Ear length (cm)**	**Ear weight (g)**	**Number of ears per plant**
Replication	2	4.78	9.37	101.93	27.50	15.53	0.64	0.27	0.20	18.27
Genotypes	67	118.83**	39.30**	468.71**	45.39**	12.02**	9.69**	2.51**	0.46**	15.46**
Error	134	2.14	3.70	39.55	12.88	6.31	1.31	0.37	0.13	6.73
CV	-	1.35	1.24	5.79	9.61	14.75	5.80	5.46	11.21	14.32

		Mean sum of squares							
Source of variation	**D.F.**	**Number of grains per ear**	**1000-grain weight(g)**	**Biological yield per plant (g)**	**Harvest index (%)**	**Chlorophyll content**	**Canopy temperature**	**Protein Content (%)**	**Grain yield per plant (g)**
Replication	2	1.10	27.72	470.56	3.32	30.17	2.35	0.11	43.80
Genotypes	67	159.08**	58.31**	905.92**	63.42**	24.37**	2.91**	6.31**	75.10**
Error	134	15.38	16.31	189.78	16.67	10.04	0.93	0.08	14.48
CV	-	6.04	8.36	12.08	15.50	7.81	4.78	2.15	13.01

**=significant at 5% and 1% level of probability.

Table 2: Genetic parameters of variation for grain yield and its components in Wheat.

Characters	**Range**		**Mean**	**Co-Variance**		**Heritability broad Sense (%)**	**Genetic advance**	**GA % mean**
	Min.	**Max.**		**GCV**	**PCV**			
Days to 50% heading	90.67	125.00	108.58	5.74	5.90	94.79	12.51	11.52
Days to maturity	149.67	167.33	155.12	2.22	2.54	76.25	6.20	4.00
Plant height (cm)	88.87	148.73	108.57	11.02	12.45	78.34	21.81	20.09
Peduncle length(cm)	30.60	47.73	37.34	8.82	13.04	45.70	4.58	12.28
No. of productive tillers per plant	12.20	22.40	17.04	8.10	16.82	23.17	1.37	8.03
No. of spikelets per ear	15.20	24.93	19.71	8.48	10.27	68.14	2.84	14.42
Ear length(cm)	9.42	13.58	11.08	7.62	9.38	66.09	1.42	12.77
Ear weight(g)	2.35	4.16	3.23	10.31	15.23	45.83	0.46	14.38
Number of ears per plant	12.73	23.87	18.12	9.42	17.14	30.20	1.93	10.66
Number of grains per ear	45.87	81.27	64.95	10.66	12.25	75.70	12.40	19.10
1000-grain weight(g)	36.73	60.06	48.32	7.74	11.39	46.19	5.24	10.84
Biological yield per plant(g)	68.17	164.33	114.03	13.55	18.15	55.71	23.76	20.83
Harvest index (%)	15.30	38.58	26.35	14.98	21.55	48.31	5.65	21.45
Chlorophyll content	33.08	47.15	40.63	5.28	9.48	31.00	2.46	6.05
Canopy temperature	18.20	22.37	20.15	4.03	6.25	41.57	1.08	5.36
Protein content (%)	9.67	15.54	12.91	11.17	11.37	96.44	2.92	22.59
Grain yield per plant (g)	17.25	40.31	29.24	15.37	20.14	58.25	7.07	24.17

22.58 to 96.39%. High heritability (above 60%) was observed for days to maturity (94.79%), days to 50% heading (76.25%), plant height (78.34%), No. of spikelets per spike (68.14%), ear length (66.09%), No. of grains per ear (75.70%) and protein content (96.44%). The moderate heritability (30-60%) was observed for traits like peduncle length (45.70%), ear weight (45.83%), No. of ears per plant (30.20%), 1000 grain weight (46.19%), biological yield per plant (55.71%), harvest index (48.31%), chlorophyll content (31.00%), canopy temperature (41.57%) and grain yield per plant (58.25%). The low heritability (below 30%) was observed for No. of productive tillers per plant (23.17%). These results are in conformity with the Avinashe (2015); Arya *et al.,* 2017; Rajput (2018).

Genetic Advance as % of mean

Genetic advance as percentage of mean is presented in table 2 and observed range from 4.10% to 24.06%. The highest genetic advance as percentage of mean (above 20%) (at 1% selection intensity) was recorded for plant height (20.09%), biological yield per plant (20.83%), harvest index (21.45%), protein content (22.59%) and grain yield per plant (24.17%). Moderate genetic advance as percentage of mean (10-20%) was recorded for days to 50% heading (11.52%), peduncle length (12.28%), No. of spikelet's per plant (14.42%), ear length (12.77%), ear weight (14.38%), No. of ears per plant (10.66%), No. of grains per ear (19.10%) and 1000-grain weight (10.84%). Low genetic advance as percentage of mean (below 10%) was recorded for days to maturity (4.00%), No. of productive tiller per plant (8.03%), chlorophyll content (6.05%) and canopy temperature (5.36%). Similar findings were observed by Sharma *et al.* (2018); Rajput (2018); Singh *et al.* (2019); Verma *et al.* (2019).

The estimates of high heritability (broad sense) and high genetic advance indicate that improvement in these traits could be possible by direct selection. High heritability coupled with moderate genetic advance was observed for plant height and protein content indicating predominance of non-additive gene action and presence of G × E interaction, simple selection may not be rewarding. In such cases, hybridization followed by selecting desirable segregants will be better option. Similar findings were observed by Singh *et al.* (2019); Verma *et al.* (2019).

Conclusion

Analysis of variance indicated that the mean sum of squares due to genotypes were significant for all the characters revealed that there was considerable genetic variability amongst the material under study. Hence it can be concluded that in wheat; traits like harvest index and grain yield per plant having high magnitude of PCV and moderate GCV, whereas plant height and protein content having high heritability and genetic advance as percent of mean, suggesting sufficient variability are available and thus exhibited scope for genetic improvement through selection for all these traits.

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