GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE FOR YIELD COMPONENT AND QUALITY TRAITS IN SPRING WHEAT (*TRITICUM AESTIVUM* L.)

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ABSTRACT

A field study was carried out involving 10 parents and 45 F_1's planted in RBD having three replications during 2011-2012. The analysis of genetic variability, heritability and genetic advance for fourteen quantitative traits *viz.*, days to 50% flowering, days to maturity, number of productive tillers/ plant, plant height, flag leaf area, spike length, spikelets/ spike, grains/ spike, 1000-grain weight, biological yield/ plant, grain yield/ plant, harvest index, ash content and gluten content. The maximum values of pcv and gcv were recorded for flag leaf area, while the minimum for days to maturity. High heritability coupled with high genetic advance was observed for flag leaf area, grain yield/ plant and biological yield/ plant. The high heritability coupled with moderate genetic advance for grains/ spike, number of productive tillers/ plant, plant height, ash content and spike length were recorded while for traits like 1000-grain weight, days to 50% flowering, gluten content, spikelets/ spike and days to maturity high heritability coupled with low genetic advance was observed.

INTRODUCTION

Wheat belongs to family Poaceae and Triticum genera. Spring wheat or bread wheat (Triticum aestivum L.), which comes under aestivum species, is the most common and widely grown wheat at global level as well as in India. . Other wheat like Triticum durum, Triticum dicoccum are also grown in a limited areas for their some special significance in developing products for human consumption. Wheat flour is the main product of wheat produce, by which various kinds of human foods are being developed. Wheat straw is a main byproduct which is a major bulk source of animal feed in the country like India.

According to Fisher (1918), the continuous variation exhibited for quantitative traits with which most of the plant breeders have to deal with, includes the heritable and non-heritable components. The heritable component is the consequence of genotypes and the non- heritable part is mainly due to environmental factors. As it is very difficult to assess the genotypes directly, it is possible only through the assessment of phenotypic expression in the existing material. These traits for which variability present should be highly heritable as the progress through selection depends on heritability and genetic advance of the trait. An estimate of genetic advance along with heritability is helpful in assessing the reliability of character for selection. Therefore, the study of phenotypic variability for various traits under investigation is of great importance. It is known that the improvement of the genetic architecture of

yield must be based on a more intensive study of individual quality and yield components.

As for more cereal crops, the studies regarding the new varieties for bread wheat are being conducted and the selection continues to be the basic breeding method. The effectiveness of the selections of both yield, which is a quantitative trait, and the yield contributing characters depend on the genetic variability, heritability and genetic advance. It is necessary to a successful breeding programmes the presence of genetic variability plays a vital role. It is true that the more diverse crop plants, the greater chance of exploiting to generate productive recombinants and broad variability in segregating generations during genetic improvement (Mohammadi and Prasanna, 2003). The genetic parameters studies in segregating population of bread wheat is also studied by Bergale *et al.* (2002), Pawar *et al.* (2003), Gollen *et al.* (2011), Kumar *et al.* (2014) Meena *et al.* (2014) and Yadawad *et al.* (2015). Keeping this view, the present study was conducted to study genetic variability, heritability and genetic advance for yield component and quality traits in spring wheat *(Triticum aestivum* L.)

MATERIALS AND METHODS

The study material comprising ten wheat genotypes namely MP 1236, PBW 550, WH 1094, PBW 590, PBW 373, RAJ 3765, DBW 58, HD 2687, DBW 17 and WH 711 was sown at Crop Research Centre, Sardar Vallabhbhai Patel University of

Agriculture and Technology, Meerut during *rabi* 2010-2011 for attempting of crossing programme in a diallel fashion (10 × 10). The pedigree details and other pass port data showing diversity among these genotypes are given below in Table 1.

Following season (*rabi* 2011-2012) experimental material comprising total 55 genotypes (10 parental line and 45 F_1's) was planted in a Randomized Block Design (RBD) having three replications. Each of the parental lines and crosses were sown by hand dibbling method in two rows plot (3m length keeping 25cm spacing between row and 10cm between plants). All the recommended agronomic practices were followed to raise good crop and for proper expression of material. Observations were recorded on 10 randomly selected competitive plants in each of three replications fourteen different characters namely days to 50% flowering, days to maturity, number of productive tillers per plant, plant height (cm), flag leaf area (cm^2), spike length (cm), spikelets per spike, grains per spike, 1000-grain weight (g), biological yield per plant (g), grain yield per plant (g), harvest index (%), ash content (%) and gluten content (%).

Statistical analysis

Statistical analysis was done on the mean values of 10 competative plants per treatment in each of three replications for 14 characters. The statistical software (WINDOSTAT version 8.0) was used to work out analysis of variance and genotypic & phenotypic coefficient of variation, heritability, genetic advance and the statistical methods adopted were as follows.

Anova

The analysis of variance for the experimental design was based on the model suggested by Pance and Sukhatme (1969).

$P_{ijk} = \mu + v_{ij} + Bk = e_{ijk}$

(i, j = 1...,t; k = 1...................................b)

Where,

P_{ijk} = the phenotype of ijk^{th} observation

μ = the population mean

v_{ij} = the progeny effect

b_k = the block effect

e_{ijk} = the error term for ijk^{th} observation

The significance of variance in treatments/genotypes for different characters was tested by F test at 5% and 1% level of probability. The observed value of 'F' is compared with the table value 'F' for the error and treatment degree of freedom. If the observed value of 'F' is more than the value of table, It is considered to be significant and vice-versa.

GCV and PCV

GCV% = (σ^2g/ $\bar{x}$) x 100

PCV% = (σ^2p/ $\bar{x}$) x100

where,

σ^2g = genotypic standard deviation
σ^2p = phenotypic standard deviation
$\bar{x}$ = general mean of the characters

The estimate of GCV and PCV were classified as low, medium and high (Sivasubramanian and Madhavamenon, 1973)

> 25%	:	High
10-25%	:	Moderate
< 10%	:	Low

Heritability

Heritability, in narrow sense, was calculated by the following formula suggested by Crumpacker and Allard (1962), which is based on the component analysis :

$$\hat{h}^2 = \frac{1/4\hat{D}}{1/4\hat{D} + 1/4\hat{H}_1 + 1/4\hat{F} + \hat{E}}$$

Where

$\hat{h}^2$ = estimate of heritability coefficient and $\hat{D}$, $\hat{H}$, $\hat{F}$ and $\hat{E}$ are the same components as explained earlier.

Heritability % in narrow sense = $\hat{h}^2$ x 100 .

The estimates of heritability in narrow sense were arbitrarily categorized according to Robinson (1965).

> 30%	:	High
10-30%	:	Moderate
< 10%	:	Low

Genetic advance

The genetic advance was calculated by the formula given by Robinson *et al*. (1949) as: G.A. = $K \times \hat{h}^2 \times \sigma^2_{ph}$ and, Genetic advance as percent of mean of the character

G.A. (%) = $\frac{G.A.}{\bar{X}}$ × 100

Where,

G.A.	=	Estimate of genetic advance,
K	=	Selection differential at 5 per cent selection intensity, *i.e.* 2.06,
s^2_{ph}	=	phenotypic standard deviation,
$\hat{h}^2$	=	estimate of heritability coefficient,
$\bar{x}$	=	mean of the character concern

The range of genetic advance as percent of mean is classified as suggested by (Johnson *et al.,* 1955a).

> 20%	:	High
10-20%	:	Moderate
< 10%	:	Low

RESULTS AND DISCUSSION

The estimates of coefficient of variation, (i) genotypic coefficient of variation (gcv) and (ii) phenotypic coefficients of variation (pcv) along with general mean, range and mean square for all the 14 characters are given in Table 2.

Analysis of variance for the experiment and for parents and F_1s showed highly significant differences among the treatments (55) for all the 14 characters (Table 2). Parents (10) and F_1s (45) also showed high significant differences for all the characters. This revealed that the significant variability exists among present set of material which allowed for conducting

Table 1: Pedigree and other passport data of parental lines used for study.

Parent	Parentage/pedigree	Area of adoption	Production condition	Source/origin
MP1236	GW276/PBW429/HI1077	CZ	IR,LS	JNKVV, M.P.
PBW550	WH 594/RAJ 3814//W 495	NWPZ	IR,TS	PAU, Ludhiana
WH1094	WH337/HD2285//URES/BOW	NWPZ	IR,LS	HAU, Hisar
PBW590	WH 594/RAJ 3814//W 485	NWPZ	IR,LS	PAU, Ludhiana
PBW373	ND/VG 1944//KAL/BB/3/YACO'S'4/VEE#5'S'	NWPZ	IR,TS/LS	PAU, Ludhiana
RAJ3765	HD 2402/VL 639	NW/NEPZ	IR,LS/VLS	RAU, Rajasthan
DBW58	ATTILA/3*BCN//BAV92/3/TILHI	NWPZ	IR,TS	DWR, Karnal
HD2687	CPAN 2009/HD 2329	NWPZ	IR,TS	IARI, New Delhi
DBW17	CMH 79A.95/3*CNO79//RAJ 3777	NWPZ	IR,TS	DWR, Karnal
WH711	S 308/ CHR//KAL	NWPZ	IR,TS	HAU, Hisar

Where, NEPZ = North Eastern Plain Zone; NWPZ = North Eastern Plain Zone; CZ = Central Zone; LS = Late Swon; VL = Very late swon; IR = Irrigated and TS = Timely swon

Table 2: Estimates of Mean square, Mean, Range, PCV, GCV, Heritability and genetic advance for 14 traits in wheat

Traits	MS (P)	MS (C)	MS (T)	Mean	Range	PCV (%)	GCV (%)	Heritability (%)	GA	Gen.adv as % of mean (5%)
DTF	70.80**	23.27**	30.99**	91.98	82.66-96.66	3.59	3.45	80.21	6.26	6.81
DTM	13.91**	6.56**	7.67**	139.64	135.33-142.00	1.25	1.09	63.84	2.71	1.94
NPTP	3.38**	1.23**	2.40**	8.77	5.76-10.63	11.72	9.35	31.84	1.35	15.37
PH	305.35**	83.86**	119.78**	91.02	76.53-103.66	7.04	6.89	79.33	12.67	13.92
FLA	142.36**	92.90**	106.24**	41.26	28.78-53.15	14.87	14.20	61.05	11.52	27.92
SL	1.40**	0.92**	1.03**	9.25	8.14-10.45	6.82	6.07	52.27	1.03	11.13
SS	3.74**	0.37**	1.19**	19.81	17.30-20.80	3.45	3.04	26.34	1.10	5.53
GS	115.44**	61.01**	68.97**	53.96	46.46-64.90	9.38	8.63	57.50	8.83	16.36
GW	29.64**	15.72**	19.66**	39.17	33.12-46.82	7.91	5.73	58.87	3.35	8.55
BY	61.05**	85.15**	83.78**	40.90	33.73-54.33	13.32	12.72	68.82	10.23	25.01
GY	45.91**	17.06**	24.34**	20.52	14.76-28.30	14.71	13.45	62.28	5.20	25.35
HI	63.02**	16.28**	27.60**	50.20	42.14-56.32	7.71	5.01	9.47	3.36	6.70
AC	0.063**	0.046**	0.052**	1.541	1.180-1.800	10.215	7.598	11.47	0.179	11.643
GC	0.31**	0.29**	0.32**	8.94	8.18-9.49	4.06	3.44	48.14	0.54	6.00

DTF = Days to 50% flowering, DTM = Days to maturity, NPTP = Number of productive tillers/plant, PH = Plant height, FLA = Flag leaf area, SL = Spike length, SS = Spikelets / spike, GS = Grains / spike, GW = 1000 grain weight, BY = Biological yield per plant, HI = Harvest index, AC = Ash content, GC = Gluten content and CGY = Correlation with grain yield per plant, P = Parents, C = Crosses, T = Treatments; * & ** Significant at 5 and 1 probability level, respectively

further genetic analysis.

A thorough screening of the material studied under present investigation revealed (Table 2) sufficient variability for all the 14 characters viz; days to 50% flowering (82.00-96.00), days to maturity (135.33-142.00), number of productive tillers per plant (5.76-10.63), plant height (76.53-103.66), flag leaf area (28.78-53.15), spike of length (8.14-10.45), spikelets per spike (17.30-20.80), grains per spike (46.46-64.90), 1000-grain weight (33.12-46.82), biological yield per plant (33.73-54.33), grain yield per plant (14.76-28.30), harvest index (42.14-56.32), ash content (1.180-1.800) and gluten content (8.18-9.49). Such type of variability were also reported by Bergale *et al.* (2002), Pawar *et al.* (2003), Chandrashekhar and Kerketta (2004), Gollen *et al.* (2011) and Meena *et al.* (2014).

The genotypic and phenotypic variability are of little meaning as they do not have any clear limit or ceiling, and at the same time, the categorization of the genotypic and phenotypic variability, as low or high, is difficult, rendering them unsuitable for comparison of two populations with desired precision when expressed in absolute values. To overcome this difficulty, the genotypic and phenotypic coefficients of variation which are free from the unit of measurement, can be conveniently employed for making comparison between populations and

for different metric traits of population. Results from the present study showed highest percentage of gcv for flag leaf area (14.20) followed by grain yield per plant (13.45) and biological yield per plant (12.72) which indicated moderate % of gcv. However, for rest of characters the gcv was less than 10.

Highest percentage of phenotypic coefficients of variation (pcv) was observed for flag leaf area (14.87) followed by grain yield per plant (14.71) biological yield per plant (13.32), number of productive tillers per plant (11.72) and ash content (10.215) which showed moderate % of phenotypic coefficients of variation (pcv). However, for rest of characters the phenotypic coefficients of variation was less than 10%. Further, the present findings revealed that the estimates of pcv were in general slightly higher than their corresponding gcv for all the characters studied which indicated the influence of environment on expression of these characters. Similar findings were reported by Pawar *et al.* (2003), Dharmendra and Singh (2010), Kumar *et al.* (2010), Kumar *et al.* (2011), Kumar *et al.* (2014) and Meena *et al.* (2014).

The estimates of heritability in narrow sense were arbitrarily categorized according to Robinson (1965) in three major groups, namely, high heritability (above 30%), moderate generally (above 10% and less than 30) and low heritability

(below 10%).

In the present investigation high estimates of heritability % in narrow sense were observed for days to 50% flowering (80.21), plant height (79.33), biological yield per plant (68.82), days to maturity (63.84), grain yield per plant (62.28), flag leaf area (61.05), 1000-grain weight (58.87), grains per spike (57.50), spike length (52.27), gluten content (48.14) number of productive tiller/plant (31.67). Similar findings were also reported by Kumar *et al*. (2002), Hassani *et al*. (2005), Nagarajan *et al*. (2007), Saxena *et al*. (2007), Kumar *et al*. (2011), Yadav *et al*. (2011) and Meena *et al*. (2014).

Thus, the material under study appeared to be promising. High heritability values for quantitative characters are always preferred by the breeders as generally the characters with high heritability estimates are comparatively less affected by the environment and these estimates, thus, enable him to base his selection reliable on phenotypic expression of these characters in individual plants. Hence selection made on the basis of phenotypic expression of these characters days to 50% flowering, days to maturity, number of productive tillers per plant, plant height, flag leaf area, spike length, spikelets per spike, grains per spike, biological yield/ plant, harvest index, grain yield per plant, ash content and gluten content, could be relied upon, in the present material. High heritability estimates for these characters indicated might be due to the presence of additive or additive x additive gene effects. This indicates that, if these traits may be subjected to mass or progeny or family selection or any selection scheme, aimed at exploiting additive (fixable) genetic variance, a widely adapted genotype could be developed, possessing good quality and productivity.

Heritability denotes transmissibility of a character from parent to off-springs. Higher the heritability of a character, more effective will be the selection. Hanson (1963) reviewed the utility of heritability in biometrical studies and pointed out that heritability estimates are influenced by method of estimation, generation of study, sample size and environment while utility of heritability estimates depends on their reliability in predicting process under selection.

The estimates of genetic advance as % of mean for all 14 characters are presented in table 2. Therefore, genetic advance as % of mean is more important for observing the genetic gain. In the present investigation high % of (>20%) genetic advance was observed for flag leaf area (27.92), grain yield per plant (25.35) and biological yield per plant (25.01). This findings is in accordance to Kamboj R. K. (2010) and Kumar *et al*. (2014).

Moderate genetic advance was observed for grains per spike (16.36), number of productive tillers per plant (15.37), plant height (13.92), ash content (11.643) and spike length (11.13). Similar findings were also reported by Saxena *et al*. (2007) and Kumar *et al*. (2014).

High heritability coupled with high genetic advance was observed for flag leaf area, grain yield per plant and biological yield per plant. However high heritability coupled with moderate genetic advance was recorded for grains per spike, number of productive tillers per plant, plant height, ash content and spike length. It indicated that heritability might be due to

additive gene effects and direct selection of these traits may be effective. 1000-grain weight, days to 50% flowering, gluten content, spikelets per spike and days to maturity showed high heritability coupled with low genetic advance which indicated non-additive gene action and selection for such traits may not be rewarding. The harvest index had low heritability coupled with low genetic advance. It indicates that the traits are highly influenced by environmental effects and selection would be ineffective. These findings were in agreement with those of Chandra *et al*. (2010), Shankarrao, *et al*. (2010), Yadav *et al*. (2011), Binod Kumar *et al*. (2013), Kumar *et al*. (2014), Meena *et al*. (2014) and Yadawad *et al*. (2015) for different traits.

The genetic advance in a trait is a product of the heritability and selection differential expressed in terms of phenotypic standard deviation of the trait concerned. For comparison of the different attributes, it is better to express it as a percentage of mean. Heritability values in conjunction with selection differential are more effective as they indicate the expected genetic gain resulting from selection. In view of Hanson (1963), heritability and genetic advance are two complementary concepts.Genetic advance, though not an independent entity but has an added advantage over heritability as a guiding factor to the breeders in the selection programme where the character is to be improved through series of selection in segregating generations. Johnson *et al*. (1955) stated that without genetic advance, the estimates of heritability would not be of practical importance based on phenotypic expression and emphasized the concurrent use of genetic advance along with heritability

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