

Estimation of Heritability and Genetic Variability in Hexaploid Wheat (*Triticum aestivum* L.)

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ABSTRACT

The field experiment was carried out during Rabi season in 2019-20, 2020-21 at Mata Gujri College, Fatehgarh Sahib's Experimental Farm, Department of Agriculture. Experimental materials comprising 15 F1s using half diallel mating design involving six parents were grown in randomized block design. High heritability estimates involving broad sense along with high genetic advance as a percent of mean was observed for number of grain plant⁻¹, harvest index (%), plant height (cm) and grain yield plant⁻¹ (g). The high genotype coefficient of variation (GCV) and phenotype coefficient of variation (PCV) were observed for grain yield/plant and test weight whereas, moderate values for PCV and GCV was recorded for no. of spikelets spike⁻¹, no. of grain spike⁻¹, and spike length (cm) indicating prevalence of genetic variability, which can successfully be used for improvement of seed yield genetically in wheat.

Keywords: Genetic advance, Genetic variability, Genotype, Harvest index, Heritability.

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INTRODUCTION

Triticum aestivum L. is commonly known as bread wheat. In India, it is staple food crop after rice. It belongs to the Gramineae family. Mostly cultivated species are hexaploid (*T. aestivum*) (2n=4x=42) otherwise diploid (*T. monococcum*) (2n=14) called einkorn wheat, tetraploid (*T. durum*) (2n=4x=28) called macaroni wheat and octoploid as (*Triticale*) (2n=56) (Jatav *et al.*, 2013). Bread wheat is allohexaploid in nature and origin from South West Asia. The flower of wheat is small, bracteates, sessile, incomplete, hermaphrodite (consists of male and female reproductive organs within the same flower), zygomorphic and incomplete. Wheat is a caryopsis type of fruit (Singh *et al.*, 2015). Wheat is a self-pollinated, cleistogamous, annual, and C₃ plant. From warm, humid to dry, cold environments and from irrigated to dry and high rainfall areas required for wheat (Verma *et al.*, 2013). 9.75 mha (32%) largest area share by Uttar Pradesh, followed by (18.75%) Madhya Pradesh, (11.48%) Punjab, (9.74%) Rajasthan, (8.36%) Haryana and (6.82%) Bihar. In the states as Jharkhand (51%), Madhya Pradesh (27%) and Rajasthan (13%) major expansion in wheat area was observed. Uttar Pradesh also stands first in production, followed by Punjab, Haryana, and Madhya Pradesh. In India, the production and average yield of wheat is 29 mha, 106.21 mt and 3500 kg/ha, respectively (Anonymous, 2019). Heritability is the ratio of genotypic variance to phenotypic variance. The magnitude of genetic variability useful in crop improvement. Genetic variability is divided into genotypic, phenotypic and environmental component of variation. Phenotypic consist both genotypic and environmental variability, also called total variability. The GCV means genotypic component of variance consists heritable part of the total variability, its magnitude on yield and its component characters influences the selection breeder adopted this strategy. Palkar *et al.* (2019) showed that 28 genotypes of maize were identified high genetic divergences which are further used in hybridization program as parent, suggested to be crossed in diallel fashion to obtain superior cross combinations. Solanke *et al.* (2013) studied genetic divergence for days to 50% tussling, 50% silking,

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maturity days, plant height (cm), cob length, girth, no. of grain per cob and grain yield.

MATERIALS AND METHODS

Experimental material consisting of six parents (HD 1981, PBW 343, CPAN 3004, RAJ 2184, PBW 154 and PBW 65) were collected from the Indian Institute of Wheat and Barley Research (IIWBR) New Delhi, India. The study was conducted for yield and yield-related parameters. The experiments were conducted at Experimental Farm, Mata Gujri College, Fatehgarh Sahib, during Rabi season of 2019-20 and 2020-21. All 6 parents crossed in half diallel mating design as per the method suggested by Hayman, 1954 and Griffing, 1956. The experimental trail was conducted with three replications in two rows with spacing of 22.5 cm row to row and 5.6 cm within plants in a randomized block design (RBD). The recommended agronomic package of practices was adopted to raise a good crop. From each replication for recording the observations five competitive plants were randomly selected for all the characters which were recorded under on replication basis as well as plant basis. From the sampled plants of each replication average of the data was used for various statistical analyses of different characters. The observations were recorded on days to booting, heading, anthesis, maturity days, no. of productive tiller per plant, plant height (cm), spike length (cm),

peduncle length (cm), no. of spikelets/spike, no. of grain/spike, no. of grain/plant, test weight (g), grain yield/plant (g), biological yield/plant (g) and harvest index (%) respectively.

Coefficients of Variation Estimation

Burton and Devane (1953) suggested a formula for the estimation of the coefficient of variation for different traits.

$$\text{GCV (\%)} = (\sqrt{g^2/X}) * 100$$

$$\text{PCV (\%)} = (\sqrt{p^2/X}) * 100$$

$$\text{ECV (\%)} = (\sqrt{e^2/X}) * 100$$

PCV = Phenotypic coefficient of variation

GCV = Genotypic coefficient of variation

X = Average of character

$\sqrt{g^2}$ = Genotypic variance

$\sqrt{p^2}$ = Phenotypic variance

$\sqrt{e^2}$ = Environmental variance

Magnitude of coefficient of variation high (> 20%), Moderate (20% - 10%) and low (< 10%).

Estimation of Broad Sense Heritability

Heritability is the ratio of genotypic variance to the phenotypic variance (total variance). Hanson *et al.* (1956) suggested formula for estimation as follows:

$$h^2 (bs) \% = (g^2 / p^2) * 100$$

$h^2 (bs)$ = heritability in broad sense,

$\sqrt{g^2}$ = Genotypic variance,

$\sqrt{p^2}$ = Phenotypic variance

Johnson *et al.* (1955) categorized heritability values as low (<30%), moderate (30 - 60%), and high (>60%).

Estimation of Genetic Advance

Genetic advance is the average improvement in the genotypic value of selected plants over the parental or base population. Johnson *et al.* (1955) suggested formula to calculate expected genetic advance (GA)

$$GA = K.h^2.p$$

GA = Genetic advance

K = Constant value

2.06 at 5 % level of selection intensity.

h^2 = Heritability of the trait

p = Phenotypic standard deviation

Estimation of Genetic advance as Percentage of Mean

Formula for calculation as follows

$$\text{GA as percentage of mean} = \frac{\text{Genetic Advance}}{\text{General Mean}} \times 100$$

Johnson *et al.* (1955) classified range of genetic advance as percent of mean as

GA > 20 percent High

GA = 10 – 20per cent Moderate

GA < 10 percent Low

RESULTS AND DISCUSSIONS

Genetic Variability

The results of genetic variability are shown in Table 1. The highest value of GCV (17.52) shown by grain yield/plant followed

by number of grain/plant (16.63), number of productive tillers (14.77), harvest index (13.34) and biological yield (11.96). Similarly, for PCV highest value (18.42) shown by grain yield/plant followed by the number of grain/plant (16.82), number of productive tillers (16.29), harvest index (13.82) and biological yield (13.30). And values of ECV are lower for each trait as compared to GCV and PCV as the highest value of ECV (6.86) shown by the number of productive tillers followed by spike length (6.06), number of spikelets per spike (5.87), biological yield (5.83) and grain yield per plant (5.70). The genetic variability in the population plays important role for making selection effective. The values of GCV were close to PCV values and higher to this shows variability due to genotype or genetic factors. But smaller values of ECV for these traits showed effect of environment or non-genetic factors is less on phenotype than genetic factor and here, phenotypic selection to yield is expected.

High estimates of PCV and GCV was depicted by grain yield per plant followed by grains/plant, tillers/plant, harvest index (HI), and biological yield per plant, respectively. For yield traits high coefficient of variability have observed by Tripathi *et al.* (2011), Majumder *et al.* (2008), Bayisa *et al.* (2020) and Fikre *et al.* (2018).

The values of PCV and GCV for heading and maturity days were very high to ECV showed that no effect of environmental changes on the expression of these traits produces favorable changes. Similarly, for yield traits, values of GCV are highest to PCV and ECV shown that no effect of environmental factors on trait development and genetic variability arises due to the fixable effect of genes. That is useful for direct selection of traits.

Heritability also estimated from existence of variability and its transmission to the offsprings not ensure if, selection on the basis of phenotypic performance.

Heritability

Heritability estimates evaluate effect of heritable and on heritable factors in phenotypic variation and aids in selection. Heritability estimates and genetic advance together are must useful for selection than heritability alone as suggested by Johnson *et al.* (1955). Wright (1921) derives symbol h^2 for heritability; it stands for the corresponding ratio of standard deviation. Heritability is a ratio of genotypic values and phenotypic values. The term heritability used to specify the genetic portion of the total variability by Allard (1960). Heritability can be divided into broad and narrow sense heritability based on gene action. Broad-sense heritability (h^2b includes additive, dominant and epistatic gene action and narrow-sense (h^2n) includes only additive action. Heritability estimates provide an indication of the expected response to selection in segregating populations, and in theory, Values of h^2b and h^2n varies from 0 to 1. High estimates indicate how well the evaluation of the parents will predict what the progenies will be like with a particular combination of breeding material and technique of evaluation (Jones, 1986).

In Table 2. high estimates of broad sense heritability were recorded for the characters; number of grain per plant (97.65) followed by harvest index (93.23), plant height (91.39) and grain yield/plant (90.44). Similar results for these traits have also been reported (Singh & Kumari, 2006). High GCV estimates showed by grain yield per plant, grain per plant, tillers/plant, and harvesting

Table 1: General mean and genetic variability in bread wheat (*Triticum aestivum* L.)

Characters	Days to booting	Days to heading	Days to anthesis	Days to maturity	No. of productive tillers	Plant height (cm)	Peduncle length (cm)	Spike length (cm)	Number of spikelet/ per spike	Number of grain/ spike	Number of grain/ plant	Test weight (g)	Harvest index	Biological Yield/ Plant(g)	Grain yield/ plant (g)
General Mean	84.60	96.43	102.48	129.18	10.88	102.89	35.65	10.85	20.45	45.29	488.43	41.85	56.01	36.40	20.36
var (p)	3.07	5.59	5.39	8.28	3.14	26.96	6.67	1.13	4.50	19.14	6752.48	13.22	59.93	23.45	14.07
var (g)	2.12	4.74	3.28	6.65	2.58	24.64	4.49	0.70	3.06	15.60	6593.95	9.66	55.87	18.95	12.72
var (e)	0.95	0.84	2.11	1.63	0.56	2.32	2.18	0.43	1.44	3.54	158.53	3.56	4.06	4.50	1.34
PCV	2.07	2.45	2.27	2.23	16.29	5.05	7.24	9.80	10.38	9.66	16.82	8.69	13.82	13.30	18.42
GCV	1.72	2.26	1.77	2.00	14.77	4.82	5.95	7.70	8.55	8.72	16.63	7.43	13.34	11.96	17.52
ECV	1.15	0.95	1.42	0.99	6.86	1.48	4.14	6.06	5.87	4.15	2.58	4.51	3.60	5.83	5.70

Table 2: Genetic advance and heritability in hexaploid wheat (*Triticum aestivum* L.)

Characters	Days to booting	Days to heading	Days to anthesis	Days to maturity	No. of productive tillers	Plant height (cm)	Peduncle length (cm)	Spike length (cm)	Number of spikelet/ spike	Number of grain per spike	No. of grain per plant	Test weight (g)	Harvest index	Biological Yield/ Plant(g)	Grain yield/ plant (g)
h ² (Broad Sense)	69.13	84.88	60.89	80.32	82.26	91.39	67.38	61.77	67.97	81.52	97.65	73.05	93.23	80.81	90.44
Genetic Advancement 5%	2.50	4.13	2.91	4.76	3.00	9.78	3.58	1.35	2.97	7.35	165.30	5.47	14.87	8.06	6.99
Genetic Advancement 1%	3.20	5.30	3.73	6.10	3.85	12.53	4.59	1.73	3.81	9.42	211.84	7.01	19.05	10.33	8.96

index it pointing to the simple mass selection useful for the improvement of these characters. In earlier studies, high h^2_b means heritability in broad sense observed (Bhoite *et al.*, 2008; Tsegaye *et al.*, 2012; Tazeen & Naqvi, 2009).

The estimates of genetic advance give the genetic gain that can be expected by selection for a character. The GA at 5% level of significance ranged from number of grain per plant (165.30) followed by harvest index (14.87), plant height (9.78), biological yield (8.06), number of grain per spike (7.35) to grain yield per plant (6.99). The genetic advance is expressed in percent of mean $G_s\%$. The $G_s\%$ at 5% level of significance was found to be maximum for grain yield/plant followed by grains per plant, tillers per plant, harvest index (HI) and biological yield/plant. Such characters also showed high heritability estimates, similar findings Farooq *et al.* (2019), Naik *et al.* (2015) and Oguz *et al.* (2011).

Here, high value of genetic advance and heritability shown by most of the traits as number of grain yield/plant, harvest index, biological yield/plant and tillers/plant. All these traits are governed by additive genes and for improvement of such traits selection will be rewarding.

CONCLUSION

From above study, it is concluded that grain yield/plant showed high GCV, PCV and days to booting showed low GCV, PCV. High genetic advance (GA) and heritability (h^2) was revealed by no. of grains/plant. Due to effect of additive gene action, genotypic values are high. For further breeding programs, the genotypes with high genotypic values are used. These traits are useful for direct selection in further hybridization programs.

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