

Original Research Article

Assessing Genetic Variability and Heritability in Wheat [*Triticum aestivum* L.]

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ABSTRACT

The present investigation was conducted at Main Experiment Station (MES) of A.N.D. University of Agriculture and Technology, Kumarganj, Ayodhya (U.P.) during *Rabi* 2018-19. The study was undertaken to inheritance of grain yield and its components in ninety varieties (45 indigenous and 45 Exotic) of bread wheat along with four checks. The experiment was laid out in Augmented Block Design. The wide range of variation for different characters and comparison of means of germplasm line indicating existence of very high degree of variability for all the characters in the indigenous as well as exotic lines of wheat. Almost high to moderate estimates of broad sense heritability were recorded for tillers per plant followed by days to maturity, spikelets per spike, harvest index, test weight, days to 50% flowering, grains per spike and for the peduncle length. The characters which exhibited higher estimates of PCV and GCV were, harvest index and days to maturity. The high estimates of genetic advance in per cent of mean were recorded for harvest index, days to maturity, tillers per plant and for plant height.

Keywords

Wheat, Genetic advance, Genetic variability, Coefficient of variation, Heritability, Variability and heritability in wheat

Introduction

The common bread Wheat (*Triticum aestivum* L.) is the most important cereal crop in India and stands only second largest producer of wheat in the world after china. It is the largest staple food crop of about two billion people (36% of the world population) and an important commodity on the world grain commerce. Worldwide, wheat provides nearly 55% of the carbohydrates and 20% of the food calories consumed globally (Breiman and Graur, 1995). Sakamura reported the chromosome number sets (genomes) for each commonly recognized type. He separated wheat into three groups viz. diploids (2n=14), tetraploids (2n=28) and hexaploids (2n=42) chromosomes. Major

cultivated species of wheat include: *Triticum aestivum*, which is a hexaploid species and is widely cultivated in the world; *Triticum durum*, the only tetraploid form of wheat widely used today, and the second most widely cultivated wheat; *Triticum monococcum*, a diploid species with wild and cultivated variants; *Triticum dicoccum*, a tetraploid species.

These earliest cultivated forms were diploid (genome AA) (einkorn) and tetraploid (genome AABB) (emmer) wheat's and their genetic relationships indicate that they originated from the south-eastern part of Turkey (Heun *et al.*, 1997; Nesbitt, 1998; Dubcovsky and Dvorak, 2007).

Materials and Methods

The experiment was conducted to evaluate 90 (45 indigenous and 45 Exotic) germplasm lines with four checks (Namely WR-544, HD-3086, HD-2967 and HI-1544) in Augmented Block Design at Main Experiment Station Acharya Narendra Deva University of Agriculture and technology (A.N.D.U.A.T.)Kumarganj, Ayodhyaduring 2018-19. The experimental field was divided into 6 blocks and 19 plots in each block (15 test genotypes along with 4 checks) were accommodated. Each plot consist two rows of 2.5 m with spacing of 5 cm within the rows and 25 cm between the rows. The recommended cultural practices were followed to raise a good normal crop. The observation was recorded on 5 randomly selected plants for, days to 50% flowering, days to maturity, plant height, number of productive tillers per plant, peduncle length, spike length, number of spikelet per spike, number of grain per spike, test weight/1000-grain weight, grain yield per plant, biological yield per plant and harvest index from each plot (Except days to 50% flowering and days to maturity where data was recorded on plot basis.) respectively. Recommended cultural practices were applied to raise a good normal crop. The phenotypic and genotypic coefficients of variation which measure the magnitude of phenotypic and genotypic variation present in a particular character were computed by the formulae given by Burton and De Vane (1953). The estimation of expected genetic advance from selection $G(s)$, was obtained by the formula suggested by Robinson, Comstock, and Harvey (1949) and Genetic advance as percent of mean was classified as low, moderate and high by Robinson *et al.*, (1949). Heritability in per cent in broad sense was estimated by Singh and Choudhary (1977). Heritability values are categorized as low, moderate and high by Robinson and Comstock (1949)

Statistical analysis

The descriptive statistics including mean, range, coefficient of variability, Heritability and Genetic Advance were calculated using SPSS, Python and R language.

Estimation of coefficient of variability

The genotypic coefficient of variability (GCV), phenotypic coefficient of variability (PCV) was computed following Burton and de Vane (1953).

$$GCV (\%) = \frac{\sigma_p}{\bar{x}} \times 100$$

$$PCV (\%) = \frac{\sigma_g}{\bar{x}} \times 100$$

Where,

σ_p = Genotypic Standard Mean

σ_g = Phenotypic Standard Mean

Heritability

Heritability in broad sense h^2 (b) was calculated as a ratio of genotypic variance to phenotypic variance (Robinson and Comstock 1949)

$$h^2b (\%) = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where,

h^2 (b) = Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

Heritability (h^2) in broad sense

>80% High

60-80% Moderate

<60% Low

Table.1 Estimation of heritability, genetic advance and coefficient of variability in wheat

Characters	Heritability broad sense (%)	GCV (%)	PCV (%)	Genetic Advance	GA as % means
DAYS TO 50% FLOWERING	90.563	9.971	10.478	11.161	19.548
No. SPIKELETS/SPIKE	92.874	6.170	6.402	8.904	12.249
No. GRAINS/SPIKE	86.352	10.408	11.200	4.231	19.924
PLANT HIEGHT (CM)	66.636	13.461	16.490	2.354	22.636
SPIKE LENGTH (CM)	56.375	8.843	16.571	1.852	5.482
PEDUNCLE LENGTH (CM)	82.231	2.599	2.790	5.944	4.988
TILLERS /PLANT	97.121	18.071	18.337	20.097	36.687
DAYS TO MATURITY	94.813	20.426	20.978	12.943	40.972
BIOLOGICAL YIELD/PLANT (g)	73.510	8.379	9.773	6.539	14.799
HARVEST INDEX (%)	92.110	24.410	25.434	6.768	48.260
TEST WEIGHT (g)	91.220	4.680	8.320	1.230	9.540
GRAIN YIELD/PLANT (g)	71.301	8.550	10.126	3.213	14.872

Genetic advance

The expected genetic advance under selection for the different characters was estimated as suggested by Allard, (1960).

$$G. A. = h^2 (b) \times \sqrt{\sigma_p^2} \times k$$

G. A. = Expected genetic advance

$h^2 (b)$ = Heritability in broad sense

σ_p = Phenotypic standard deviation ($\sqrt{\sigma_p^2}$)

K = Intensity of selection, the value of which is 2.06 when 5 percent of the individuals are selected from the population, as given by Lush, (1949).

Results and Discussions

Heritability, coefficient of variability and genetic advance in per cent of mean were estimated for all the 12 characters and are presented in Table 1.

High estimates of broad sense heritability (> 80%) were recorded for tillers per plant (97.12%) followed by days to maturity (94.81%), spikelets per spike (92.87%), harvest index (92.11%), test weight (91.22%), days to 50% flowering (90.56%), grains per spikes (86.35%) and for the peduncle length (82.23%). The moderate estimates of heritability (60-80%) were observed for biological yield per plant (73.51%), grain yield per plant (71.30%) and plant height (66.63%). while the low estimates of broad sense heritability (< 60%) were shown by spike length (56.37%). Present finding conformed to those of Ali *et al.*, (2008), Chaudhary *et al.*, (2015), Deoraj *et al.*, (2016) and Shashikala *et al.*, (2012).

The high estimates of genetic advance in per cent of mean (>20%) were recorded for harvest index (48.26%), days to maturity (40.972%), tillers per plant (36.68%) and plant height (22.63%). Number of grains per

spike (19.92%), days to 50% flowering (19.54%), grain yield per plant (14.87) and biological yield per plant (14.79%) showed moderate estimate for genetic advance (10-20%) in per cent of mean. While the test weight (9.54%), spike length (5.48%) and plant height (4.98%), showed low estimate of (< 10%) genetic advance in per cent of mean. These findings are confirmed with Deoraj *et al.*, (2016) and Kabir *et al.*, (2015)

The phenotypic and genotypic coefficient of variation for all the 12 characters has been given in Table 1. In general, the magnitude of phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the characters. The characters which exhibited higher estimates (> 20%) of PCV and GCV were, harvest index and days to maturity. The characters which exhibited moderate estimates 10 - 20% of PCV and GCV were tillers per plant, plant height, grains per spike days to 50% flowering and grain yield per plant. The remaining characters *viz.*, biological yield per plant, spikelets per spike, peduncle length, and test weight showed low estimates (< 10%) of PCV and GCV.

Present finding are in confirmation with Degewione *et al.*, (2013), Maurya *et al.*, (2014) and Yadav *et al.*, (2014).

In conclusion, studies on variability, heritability and genetic advance showed that tillers per plant followed by days to maturity, spikelets per spike, harvest index, test weight, days to 50% flowering, grains per spikes and for the peduncle length are having considerable importance to breeder for selection. Because of this additive variability, selection for these characters would be highly sensitive, and a superior genotype could be produced as the environment had the least impact on the speech of these characters.

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