

Original Research Article

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Genetic Variability, Heritability in Wheat (*Triticum aestivum* L.) Genotypes

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ABSTRACT

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Information on the extent of genetic variability and heritability as well as correlation among agronomical important traits is a requirement to design a suitable plant breeding method. The present research was conducted at ANDUAT, Ayodhya, India during the 2018-19 main crop growing season. The experimental material consisted of 80 wheat genotypes tested in augmented block design with three checks. Eleven agronomic traits were included in the investigation. Highly significant differences were revealed among wheat genotypes for all traits studied, suggesting the possibility of improving wheat for these traits. Peduncle length and Biological yield per plant showed the highest phenotypic and genotypic coefficients of variations and genetic advance, whereas, Spike length, days to maturity and tiller per plant had the lowest values. Peduncle length exhibited highest heritability value of 97.12% while tiller per plant showed minimum value of 17.04%. Hence, these traits could be considered as suitable selection criteria for the development of high yielding wheat varieties.

Introduction

Bread wheat (*Triticum aestivum*) is an important food crop for more than one third of the population. The demand of wheat is increasing day by day due to increasing the population. India is second largest wheat producing nation in the world after China and account for more than 13.06 percent of the world's wheat grain production. The Directorate of Economics and Statistics estimates that the India's wheat production

2017-2018 will be 99.87 million metric tons. Wheat Production last year was 102.19 million tons which share 15% of total food grain production in 2018-19. This year's 106.21 estimated million tons could represent an increase of 7.7 million tons or a 1.06% in wheat production around the globe. Ways to sustain increasing productivity should be explored, it is now realized that sustaining as well as increasing productivity may be essential. The knowledge of factors responsible for high yield has been rendered

difficult as yield is complex character (Singh *et al.*, 2010). Grain yield is a complex trait and highly influenced by many genetic factors and environmental fluctuations. In plant breeding programme successful selection depends on the information on the genetic variability in base population. The estimates of genotypic coefficient of variation (GCV) reflect the total amount of genotypic variability present in material. However, the proportion of this genotypic variability which is transmitted from parents to progeny is reflected by heritability. Lush (1949) gave the concept of broad sense heritability. It determines the efficiency with which we can utilize the genotypic variability in a breeding programme.

The genotypic variance and its components are influenced by the gene frequencies. Because the frequencies of genes differ from one population to another, estimates of heritability also vary from one population to another for a given character. Burton (1952) suggested the genetic variation along with heritability estimates would give a better idea about the expected efficiency of selection thus a character possessing high GCV along the high heritability will be valuable in selection programme.

Heritability alone does not provide any indication of how much genetic change will come from choosing individual genotypes. Hence it is most important to learn about genetic development coupled with heritability. Genetic progress is an improvement over the base population in the mean of selected families (Lush 1949 and Johnson *et al.*, 1955). It is also expressed as the change in gene frequency on the exercise of selection pressure towards the superior side. The present study is therefore, aimed at assessing genetic variation, broad sense heritability and expected genetic advance as well as relationship among agronomic traits in

durum wheat.

Materials and Methods

The experimental material for the present investigation comprised 80 accessions of the drawn from wheat gene pool maintained at University mentioned in Table 1. The accessions were raised and followed recommended packages and practices during Rabi season, 2018-19. The experiment was laid out in a Augmented Block Design with three checks. Each experimental plot was 2.5 m long and 2.4 m wide, with twelve rows 20 cm apart, giving a gross plot area of 6 m² and net plot area of 5 m². Adjacent blocks were 1 m apart. Sowing was done by hand drilling and covered lightly with soil. The seed rate was 150 kg ha⁻¹. All other agronomic practices are done as recommended for wheat production in the area.

The characters studied and techniques adopted to record the observations are given below:

1. Days to 50% flowering:
2. Days to maturity:
3. Plant height (cm):
4. Spike length (cm)
5. Number of productive tillers per plant:
6. Number of grains per spike:
7. Grain weight per spike:
8. Thousand-grain weight (g):
9. Grain yield/plant (g):
10. Biological yield per plant (g)
11. Harvest index (%)

Variability for different characters was estimated as suggested by Burton and de Vane (1953). Heritability in broad sense was calculated as the ratio of genotypic variance to the phenotypic variance and expressed as percentage (Falconer, 1981). Genetic advance as per cent of mean for each character was worked out as suggested by Johnson *et al.*,

(1955).

$$GCV\% = \frac{\sqrt{\text{genotypic variance}}}{\text{mean of trait}} \times 100$$

$$PCV\% = \frac{\sqrt{\text{phenotypic variance}}}{\text{mean of trait}} \times 100$$

$$h^2_B = \frac{\text{genotypic variance}}{\text{phenotypic variance}} \times 100$$

$$GAM = k \times h^2 \frac{\sqrt{\text{phenotypic variance}}}{\text{mean of trait}} \times 100$$

Where,

K= selection intensity (5% = 2.06),

h^2_B = broad- sense heritability

Results and Discussion

Analysis of variance revealed highly significant differences for all characters under study among the 80 genotypes at 5% level of significance, indicating the presence of sufficient variability among genotypes.

Genetic Variability

Genotypic coefficient of variation (GCV) ranged from 2.599 to 24.41. Higher magnitude of GCV was recorded for harvest index (24.41), followed by biological yield per plant (20.426), peduncle length (18.07), days to maturity (13.46), plant height (10.4), days to 50% flowering (9.97), thousand grain weight (8.55), grain yield per plant (8.37), number of tillers per pant (6.90), flag leaf area (6.17), spike length (2.59) showed lowest GCV values.

A wide range of phenotypic coefficient of variation (PCV) was observed and ranged from 25.43 to 2.79. High magnitude of phenotypic coefficient of variation (PCV) was recorded for harvest index (25.43) followed

biological yield per plant (20.97), peduncle length (18.33), number of tillers per pant (16.71), days to maturity (16.49), plant height (11.2), days to 50% flowering (10.47), thousand grain weight (10.12), grain yield per plant (9.77), flag leaf area (6.40), and spike length (2.79) showed lowest PCV values. Estimates of genotypic variance, phenotypic variance, genotypic coefficient of variation (GCV), phenotypic of variation (PCV), heritability in broad sense (h^2 bs), genetic advance (GA) and genetic advance as percent of mean (GAM) are summarized in Table 1. These were also reported by Yousaf Ali *et al.*, (2008), Zecevic *et al.*, (2010) and Kalimullah *et al.*, (2012).

Heritability

The estimates of genotypic coefficient of variation (GCV) reflect the total amount of genotypic variability present in material. However, the proportion of this genotypic variability which is transmitted from parents to progeny is reflected by heritability. Lush (1949) gave the concept of broad sense heritability. It determines the efficiency with which we can utilize the genotypic variability in a breeding programme. The genotypic variance and its components are influenced by the gene frequencies. Because the frequencies of genes differ from one population to another, estimates of heritability also vary from one population to another for a given character. Burton (1952) suggested the genetic variation along with heritability estimates would give a better idea about the expected efficiency of selection thus a character possessing high GCV along the high heritability will be valuable in selection programme.

The heritability (%) in broad sense for eleven characters studied, which range from (97.12%) to (17.04%).peduncle length (97.12), biological yield per plant (94.83),

flag leaf area (92.87), harvest index (92.11), days to 50% flowering (90.56), and spike length (86.79), showed high heritability. Moderate heritability was recorded for plant height (86.35) grain yield per plant (73.51), and thousand grain weight (71.30), whereas days to maturity (66.63), and tillers per pant (17.04), showed lowest heritability. Result are in conformity with the findings of Satyavart

(2002) for spike length, Nawracaa *et al.*, (2004) for plant height, number of grains per spike and number of spikelets per spike, Wahid Abdul and Karim Shahla (2014) also reported high heritability plant height and Kumar Naveen *et al.*, (2013) revealed that characters exhibited high heritability for test weight

Table.1 Description of genotypes used in experiment

S.No.	Genotypes
1	DDK-1051
2	HW-3631
3	HD-3043
4	HTW-6
5	BRW-3723
6	HUW-699
7	HI-8765
8	HI-8708 (d)
9	HS-626
10	MACS-3949 (d)
11	WH-1127
12	DBW-110
13	TL-3007
14	HI-8737 (d)
15	PBW-756
16	NIAW-1994
17	HI-8751
18	PDW-344
19	DBW-105
20	HI-8777 (d)
21	HS-627
22	DBW-129
23	WH-1216
24	K-1006
25	GJW-463
26	HI-8759
27	AKAW-3717
28	K-1317
29	DBW-39
30	HI-1612
31	DWAP-1530
32	HIKK-09
33	KBRL-82-2
34	PBW-725
35	HD-3171
36	TL-3006
37	COH-1105

38	DHTW-60
39	HTW-11
40	HW-5207
41	KBRL-79-2
42	UASD-DT-6
43	AKAW-4901
44	CG-1013
45	DBW-187
46	DBW-88
47	HI-1620
48	MACS-5044
49	DBW-246
50	KRL-283
51	MP-3382
52	PWD-752
53	UAS-334
54	UAS-357
55	WH-1080
56	AKAW-4927
57	DBW-173
58	DBW-93
59	DBW-179
60	FLW-10
61	FLW-22
62	HIKK-05
63	HTW-9
64	PBW-703
65	PWD-757
66	DBW-71
67	HD-1609
68	HD-3086
69	FLW-16
70	HIKK-06
71	WH-1310
72	GRU-2010-18/7
73	HD-3237
74	DBW-220
75	PBW-760
76	UAS-459
77	WH-730
78	DBW-107
79	DWAP-1531
80	HD-2967 (CH.)
81	HI-8713 (CH.)
82	SONALIKA (CH.)

Table.2 Estimates of genetic parameters for eleven agro-morphological traits in wheat

Traits	Heritability (%)	Coefficient of Variations		Genetic Advance	Genetic Advance as % means	Block (adj) (MSS)
		Genotypic	Phenotypic			
DFE	90.563	9.971	10.478	11.161	19.548	6.3
FLA	92.874	6.17	6.402	8.904	12.249	32.58*
PH	86.352	10.408	11.2	4.231	19.924	117.9*
DM	66.636	13.461	16.49	2.354	22.636	0.75
TP	17.041	6.901	16.718	0.074	5.869	0.52
SL	86.799	2.599	2.79	5.944	4.988	5.20
PL	97.121	18.071	18.337	20.097	36.687	7.24?*
BYP	94.813	20.426	20.978	12.943	40.972	98.07*
GYP	73.51	8.379	9.773	6.539	14.799	21.62
TW	71.301	8.55	10.126	3.213	14.872	6.87
HI	92.11	24.41	25.434	6.768	48.26	42.33

Genetic advance as percent of mean

Heritability alone does not provide any indication of how much genetic change will come from choosing individual genotypes. Hence it is most important to learn about genetic development coupled with heritability. Genetic progress is an improvement over the base population in the mean of selected families (Lush 1949 and Johnson *et al.*, 1955). It is also expressed as the change in gene frequency on the exercise of selection pressure towards the superior side.

A character with high heritability cannot automatically offer substantial genetic advancement. Johnson *et al.*, (1955) suggested that heritability and genetic advancement would prove more useful when computed together, predicting the resulting effect of selection on phenotypic expression. Maximum genetic improvement was reported for peduncle length (20.09), biological yield per plant (40.97) and flowering days to 50 percent (11.16). However, for harvest index (48.26), biological yield per plant (40.97) and

peduncle length (36.68) a high estimate of genetic progress as a percent of the mean was reported similar observation were reported by Kalimullah *et al.*, (2012) and Vamshikrishna Nukasani *et al.*, (2013) reported high heritability coupled with high genetic advance for traits grain weight per spike and grains per spike.

According to Paul K *et al.*, (2006) high heritability along with high genetic advance was observed for grains weight per spike, grain per spike length, plant height and productive tillers.

In conclusion the studies on variability, heritability and genetic advance showed that biological yield per plant, peduncle length, days to 50% flowering, flag leaf area, days to maturity, followed by grain yield per plant, 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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