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Genetic variability and heritability in bread wheat (*Triticum aestivum* L.) genotypes

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Abstract

Having knowledge of the degree of genetic diversity and heritability, together with the link between agronomically significant traits, is essential for developing an effective plant breeding strategy. During the primary crop growing season of 2018–19, the current study was carried out at Mata Gujri College in Fatehgarh Sahib, Punjab. Three checks and a randomized block design were used to examine sixty different genotypes of wheat as the experimental material. The investigation covered fifteen agronomic traits. For every trait examined, wheat genotypes showed highly significant differences, indicating the potential for enhancing wheat for these qualities. The phenotypic and genotypic coefficients of variation with the highest values were days to booting and number of grains per plant; on the other hand, the days to heading and harvest index showed the lowest values. The genetic advance was largest in the number of grains per plant (18.73) and lowest in the harvest index (-0.1). The heritability value of 83% was highest in the number of grains per plant, while the minimum value was observed in the days to maturity (03%). Therefore, these characteristics might be thought of as appropriate selection factors for the creation of high-yielding wheat cultivars.

Keywords: Genetic variability, flour wheat, genetic advance, PCV, GCV and heritability

Introduction

Bread wheat (*Triticum aestivum*) belongs to family Poaceae. It is an autogamous plant has one of the most complex genome from three genome, designed as A, B and D (AABBDD), were involved in its evolution. It combines the genomes of three diploid ancestral, *Triticum monococcum* (2n = 14, AA), *Aegiolops speltoids* (2n = 14, DD) and Aegiolops species (2n = 14, BB). According to the Directorate of Economics and Statistics, 99.87 million metric tons of wheat would be produced in India in 2017–2018. With 102.19 million tons produced last year, wheat accounted for 15% of all food grains produced in 2018–19. With an anticipated 106.21 million tons this year, wheat production worldwide may have increased by 7.7 million tons, or 1.06%.

In world, it is second important staple food crop, rice being the first. Wheat is grown in 128 counties. Geographically the area spreads from 30◦56’ N latitude, 75◦52’E longitude with an altitude of as high as 247 m from mean sea level (Kaur *et al.* 2017) [6]. It can be grown not only in the tropical and sub-tropical zones but also in the temperate zone.

Genetic variability is a perquisite for the improvement of any crop. With the variation, productivity genotype with high quality attributes acceptable to both procedure and consumers can be developed. The world cultivated area of wheat is 221.55 million hectares with production of 750.44 million tonnes and productivity 3.39 metric tonnes per hectare, (Anonymous, 2018) [1].

How much genetic change results from selecting particular genotypes cannot be determined only by heritability. Therefore, understanding genetic development in conjunction with heritability is crucial. According to Lush (1949) [9] and Johnson *et al*. (1955) [4], genetic advancement is defined as an improvement over the base population in the mean of chosen families. Another way to describe it is as a shift in gene frequency brought on by selection pressure acting in favor of the superior side. Therefore, the goal of this study is to evaluate the relationship between agronomic variables in durum wheat as well as genetic variation, wide sense heritability, and expected genetic advancement.

Methods and Materials

The experimental material for the present investigation comprised 60 accessions of the drawn from wheat genotypes mentioned in Table 1. The current study was carried out in the Experimental Farm of Mata Gujri College in Sri Fatehgarh Sahib, India, during the Rabi season of 2018–19. Sri Fatehgarh Sahib is located at a mean height of 247 meters above mean sea level, between latitudes 30o - 27' and 30o - 46' and between latitudes 76o - 04' and 76o - 38 E. The three distinct seasons of Sri Fatehgarh Sahib's climate are hot and dry summer, monsoon, and chilly winter. The region has a subtropical semi-arid climate.

The following quantitative elements were used to document the observations: Days to heading, days to booting, days to maturity, and days to anthesis quantity of fruitful tillers in each plant, The following measurements are given: plant height (cm), peduncle length (cm), spike length (cm), number of spikelet's per spike, number of grains per spike, number of grains per plant, and weight (g) of 1000 grains. Harvest index (%), biological yield per plant (g), and grain yield per plant (g). According to Burton and de Vane's recommendations, variability for several features was estimated (1953). In a broad sense, heritability was measured as the fraction of genotypic variance to phenotypic variance (Falconer, 1981) [3]. According to Johnson *et al.*'s suggestion, genetic advancement was calculated as a percentage of mean for each character (1955).

Table 1: Description of genotypes used in experiment

S.No.	Genotypes	S.No.	Genotypes
1.	HD 2177	31.	WH 542
2.	HD 2281	32.	HD 2967
3.	HD 1941 (Hira)	33.	PBW 226
4.	PDW 215	34.	PBW 373
5.	PDW 396	35.	HD 2009
6.	WL 410	36.	KSML 3
7.	PDW 299	37.	IWP 72
8.	RAJ 3077	38.	RAJ 2184
9.	DPW 621-50	39.	PBW 560
10.	CPAN 3004(Sangam)	40.	KALYANSONA
11.	PBW 644	41.	CPAN 1676 (Rohini)
12.	PDW 291	42.	WH 1080
13.	WH 291	43.	PBW 343
14.	LAL Bahadur	44.	WH 1021
15.	HD 2329	45.	WL 2265
16).	PBW 34	46.	WH 157
17.	MLKS 11	47.	HD 2287 (Gobind)
18)	WH 283	48.	HD 2204
19.	WH 416	49.	DL 153-2(KUNDAN)
20.	PBW 65	50.	PBW 154
21.	PBW 175	51.	HD 2687 (Shresth)
22.	HD 2270	52.	HD 3043
23.	PBW 590	53.	UP2425
24.	PBW 502	54.	GW120
25.	DBW 90	55.	DWL 5023
26.	RAJ 1972	56.	DWL 17
27.	PDW 314	57.	UP2338
28.	HD 1981	58.	WL 711
29.	PDW 233	59.	WH 1105
30.	PBW 175	60.	RAJ 1482

Results and Discussion

GCV and PCV

The outcome clearly demonstrated that genotypic variance is smaller than phenotypic variance. The yield qualities with the highest PCV and GCV were represented by days to booting (66.41 and 4.87) followed by days to maturity (62.40 and 3.27), no. of grain per plant (17.25 and 15.77), harvest index (13.83 and 0.88), no. of productive tillers per plant (13.76 and 8.25), grain yield (13.31 and 10.36), biological yield (12.37 and 10.77), no. of spikelet's per plant (10.58 and 4.06), spike length (8.99 and 1.72), days to anthesis (8.20 and 2.94), test weight (6.87 and 3.34), peduncle length (6.63 and 3.44), no. of grain per spike (5.92 and 2.84), plant height (4.54 and 2.90) and days to heading (2.83 and 1.93). I.e. Looking through Table 3, one can see that for every trait, PCV was greater than corresponding GCVs, indicating that environmental influences were impacting the traits' expression to some extent. Table 1 summarizes genetic advance as a percent of mean (GAM), genetic advance as GA, and heritability in the broad sense (h2 bs). Kotal *et al.* (2010) [7], Bhoite *et al.* (2008) [2], and Rahman *et al.* (2014) [11] have reported similar outcomes.

Heritability

Highest being for no. of grain per plant (83), followed by biological yield (76), grain yield (63), days to heading (46), plant height (41), no. of productive tillers (36), peduncle length (27), test weight (24), no. of spikelet's per plant and harvest index both have same heritability value (15), days to anthesis (13), days to booting (05), spike length (04) and days to days to maturity (03). A straightforward selection process would be useful in improving these qualities because the high estimate of heritability suggests that most variance is due to genetics and very little is due to environment. Test weight (24) showed a moderate heritability, suggesting that environmental factors have a moderator impact on harvest content than genetic variations. The results are consistent with those of Kaddem (2014) [5] and Kumar *et al.* (2013) [8].

Table 2: Estimates of genetic parameters for fifteen morphological traits in Bread wheat

Characters	Heritability (%)	Coefficient of Variations	
		Genotypic	Phenotypic
Days to anthesis	13	8.20	2.94
Days to maturity	03	62.40	3.27
Days to booting	05	66.41	4.87
Days to heading	46	2.83	1.93
Number of productive tillers per plant	36	13.76	8.25
Plant height (cm)	41	4.54	2.90
Peduncle length (cm)	27	6.63	3.44
Spike length (cm)	04	8.99	1.72
Number of spikelet's per spike	15	10.58	4.06
Number of grains per spike	40	5.92	2.84
Number of grains per plant	83	17.25	15.77
1000 grains weight (g)	24	6.87	3.34
Biological yield per plant (g)	76	12.37	10.77
Harvest index (%)	15	13.83	0.88

Conclusion

Significant genetic variation has been generated for the most of the traits studied. Days of booting high in GCV, Number of grains per plant both high in PCV and heritability.

References

1. Anonymous. World Agricultural production united states department of Agriculture (USDA), Foreign

Agricultural Service; c2018. Available at https://apps.fas.usda.gov/accesed on 31 January, 2018.

2. Bhoite KD, Rasel PM, Gadekar DA. Genetic variability, heritability and genetic advance in durum wheat. Wheat (*Triticum durum* L.). Journal of Maharashtra Agricultural University. 2008;33(1):102-103.
3. Falconer DS. Introduction to Quantitative Genetics, Second edition. Longman, New York; c1981.
4. Johnson HW, Robinson HF, Comstock RE. Genotypic and phenotypic correlations and their implication in selection. Agronomy Journal. 1955;47:477-483.
5. Kaddem WL, Marker S, Lavanya GR. Investigation of genetic variability and correlation analysis of wheat (*Triticum aestivum* L.) genotypes for grain yield and its Component traits. European academic research. 2014;2(5):314-321.
6. Kaur RA, Dey T, Sharma BC, Rai GK, Wani SH, Lone JA. Genetic Variability and Correlation Studies in Winter Wheat (*Triticum aestivum* L.) Germplasm for Morphological and Biochemical Characters. International Journal of Pure and Applied Bioscience. 2017;5(1):82-91.
7. Kotal BD, Das A, Choudhury BK. Genetic variability and association of characters in wheat (*Triticum aestivum* L.). Asian Journal of Crop Science. 2010;2(3):155-160.
8. Kumar R, Gaurav SS, Bhushan B, Pal R. Study of genetic parameters and genetic divergence for yield and yield components of bread wheat (*Triticum aestivum* L.) Journal of Wheat Research. 2013;5(2):39-42.
9. Lush JL. Heritability of quantitative characters in farm animals. Diversity Using Morphological Characters and Microsatallite Markers. World Journal of Agriculture Science. 1949;4:538-544.
10. Mahmood Q, Lei WD, Qureshi AS, Khan MR, Hayat Y, Jilani G, *et al*. Heterosis, correlation and path analysis of morphological and biochemical characters in wheat (*Triticum aestivum* L. Emp. Thell). Agricultural Journal. 2006;1(3):180-185.
11. Rahman MS, Hossain MS, Islam MS, Shoma JF, Ali L. Genetic variability, correlation and path analysis for some quantitative traits in wheat. Eco-friendly Agriculture Journal. 2014;7(12):158-162.
12. Rahman MS, Hossain MS, Islam MS, Shoma JF, Ali L. Genetic variability correlation and path analysis for some quantitative traits in wheat. Eco-friendly Agricultural Journal. 2014a;7(12):158-162.
13. Singh B, Upadhya PK. Genetic divergence analysis in wheat (*Triticum aestivum* L.) International Journal of Plant Science. 2013b;8(2):297-299.