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Genetic variability and characters association in wheat (*Triticum aestivum* L.) genotypes

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Abstract

A research was carried out to measure genetic variability and correlation among selected traits in wheat with the use of forty-three genotypes available at Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture Science and Technology, Allahabad during Rabi, 2015-16 under irrigated condition in augmented block design-2. Analysis of variance revealed significant differences for 14 characters studied among the genotypes and checks vs genotypes. High phenotypic and genotypic coefficients of variation were obtained in seed yield/plant, biological yield and harvest index. High heritability accompanied with high expected genetic advance was reported from flag leaf length, plant height, no. of grains/spike, test weight, biological yield, harvest index and seed yield/plant. Both at phenotypic and genotypic level, traits like grain filling period, no. of tillers/plant, test weight, biological yield and harvest index exhibited strong association with seed yield/plant at desirable direction. Thus, traits showing variability and desirable correlation both at genotypic and phenotypic levels and high heritability coupled with high genetic advance envisage the use of these traits for improvement of grain yield of wheat.

Keywords: PCV, GCV, heritability, genetic advance, correlation

Introduction

Wheat (*Triticum aestivum* L.) is an important staple food crop which occupies second most position after rice in Indian agriculture. During 2013-14, wheat was sown in about 31.19 million ha land with total production of 95.91 million tons in India. In U.P., wheat is grown in about 9.96 million ha land with a total production of 30.25 million tons (Ministry of Agriculture, 2015) [12].

Even though it is favour by most of the people, its yield is at plateau condition for long time period due to cultivation of few dominant cultivars like as HUW234 (Joshi *et al.*, 2007a) [7] since decades. Because of growing population, area under cultivation is reducing consistently. These synergistic effects might be major concerns on the way to achieving desired target of 90 mt wheat production by 2030 (DWR, 2010) [5]. Therefore, collection and characterization of germplasm from different regions of cultivation need specific emphasis for increasing the productivity of wheat under changing climatic scenario.

Grain yield is a complex trait which depends on components traits and their interaction. The study of inheritance of various developmental and productive traits through the estimation of different genetic parameters like components of variances, genotypic and phenotypic coefficients of variability, heritability and genetic advance is helpful for framing the effective breeding programme. The genetic variability, heritability and genetic advance help to formulate selection criteria for evolving high yielding genotypes in wheat. Moreover, correlation study gives degree and direction of traits association between two or more variables. It also provides better understanding of yield components which helps the breeder during selection of desirable genotypes (Robinson *et al.*, 1951 and Johnson *et al.*, 1955) [16, 6]. Several researchers (for *e.g.*, Baranwal *et al.*, 2012; Nukasani *et al.*, 2013 and Tahar *et al.*, 2015) [3, 14, 17] studied genetic variability and characters association in wheat genotypes for different quantitative characters and found effective for selection of desirable genotypes. Hence, the present research work was conducted to measure the genetic variability presence among the wheat genotypes and degree and direction of trait association among the selected characters.

Materials and Methods

The experimental materials comprising of forty-three wheat genotypes (*i.e.*, forty experimental genotypes plus three checks) were grown in a augmented block design-2 in four blocks at Field Experimentation Center, Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture Science and Technology (Deemed-to-be-University),

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Allahabad, India during *Rabi*, 2015-16 under irrigated condition where checks (*viz.*, K 307, NW4035 and WR1451) were replicated four times. Each plot consisted of single row plot of 2 m length with a row spacing of 22.5 cm. seeds were sown continuously in row and maintained 5cm plant to plant distance after thinning. Chemical fertilizers, at the rate of 120:60:40 NPK Kg /ha in the form of Urea, Di-ammonium phosphate (DAP) and Murate of potash (MOP), were applied and other standard agronomical operation and plant protection measures were adapted to raise healthy and uniform crops.

Data were recorded on visual observations of plants on plot basis for traits like days to 50% flowering, days to 50% heading and days to 50% maturity while data for flag leaf length (cm), flag leaf breadth (cm), no. of tillers/plant, plant height (cm), spike length (cm), no. of grains/spike, test weight (g), seed yield/plant (g), biological yield (g) and harvest index (%) were taken from five randomly selected plants from middle of row of each entry in each block. Grain filling period (GFP) was computed by deduction of days to 50% flowering from days to 50% maturity.

The mean values over replications were subject to analysis of variance as suggested by Panse and Sukhatme (1985) [15]. The variability presence in the genotypes was estimated by phenotypic and genotypic variances and coefficient of variations using the procedure suggested by Burton and De Vane (1953) [4]. Heritability in broad sense (h^2_{bs}) was

computed using the formula given by Lush (1949) [10]. The genetic advance (GA) for selection intensity (K) at 5% and genetic advance as percentage of mean (GA as % of mean) was calculated by the formula suggested by Johnson *et al.* (1955) [6] and the correlation coefficient by Al-Jibouri *et al.* (1958) [2].

Results and Discussion

Analysis of variance

The analysis of variance indicated presence of significant genetic variability for most of the characters studied (Table 1). Flag leaf breadth and no. of tillers/plant showed non-significant mean sum of squares due to entries, genotypes while non-significant mean sum of square due to genotypes was found in spike length. ANOVA revealed significant mean sum of square due to genotypes for most of the traits studied reflecting the presence of genetic variability among the genotypes and checks *vs* genotypes for the characters studied which shows sufficient scope for selection of promising genotype from the pre-breeding lines for increasing grain yield of wheat. The presence of large amount of variability might be due to diverse source of material taken as well as environmental influence affecting the phenotypes. Existence of significant variability among the wheat genotypes was also reported by Baranwal *et al.* (2012) [3], Nukasani *et al.* (2013) [14] and Tahar *et al.* (2015) [17].

Table 1: Analysis of variance for 14 different quantitative characters in 43 genotypes of wheat

Characters	Sources of variation					
	Blocks (df=3)	Entries (df=42)	Checks (df=2)	Genotypes (df=39)	Checks <i>vs</i> Genotypes (df=1)	Error (df=6)
Days to 50% flowering	50.63	13.38**	14.58**	12.29**	53.42*	1.14
Days to 50% heading	20.86	11.24**	25.08**	10.05**	30.08**	0.42
Days to 50% maturity	83.19	10.32**	12.25**	6.92**	139.03**	0.36
Flag leaf length	52.73	12.17**	4.91*	10.60**	88.03**	0.79
Flag leaf breadth	0.07	0.06	0.31*	0.05	0.02	0.03
Grain filling period	15.97	6.00**	4.75*	5.82*	15.41**	0.64
No. of tillers/plant	19.04	1.88	6.66*	0.96	27.96**	0.69
Plant height	732.98	242.74**	18.36*	236.77**	924.34**	2.53
Spike length	59.32	3.84**	6.09**	1.63	85.71**	0.45
No. of grains/spike	101.21	63.83**	82.67**	59.03**	213.09**	1.29
Test weight	11.79	40.19**	4.87*	42.59**	17.06**	0.72
Seed yield/plant	41.32	8.29**	9.29*	7.23**	47.45**	0.97
Biological yield	257.07	38.09**	18.28*	31.27**	343.73**	2.32
Harvest index	46.63	158.17**	96.14**	164.22**	46.29**	1.64

*and** significant at 5% and 1%, respectively

Phenotypic and genotypic variations

The estimates of variability parameters for various yield and yield related traits are presented in Table 2. The phenotypic and genotypic variances were ranges from 0.06 – 237.90 and 0.03 – 235.38, respectively (Table 2). Comparatively higher phenotypic variances value of 237.90 for plant height, 163.27 for harvest index, 60.74 for no. of grains/spike, 42.38 for test weight and 30.96 for biological yield were recorded in this study. Similarly, higher genotypic variances values were observed for the same traits demonstrated that genotype could be reflected by phenotype and the effectiveness of selection of genotypes based on phenotypic performance of these traits. The PCV values were ranged from 2.24% for days to 50% maturity to 41.60% for seed yield/plant and GCV values were varied from 2.20% to 38.76% for the same traits (Table 2). High PCV was recorded for no. of tillers/plant, seed yield/plant, biological yield and harvest index while medium PCV was found in traits like flag leaf length, flag leaf breadth, plant height, spike length, no. of grains/spike and test weight.

In addition, high GCV was found in seed yield/plant, biological yield and harvest index whereas medium GCV was reported in traits such as flag leaf length, no. of tillers/plant, plant height, no. of grains/spike and test weight. The selection of genotypes based on these traits would be effective. The differences between PCV and GCV were high for no. of tillers/plant (8.91), flag leaf breadth (4.04) and seed yield/plant (2.84) indicating of more environmental influence for the expression of these traits. PCVs were slightly higher than GCVs for all the characters pointed out the environmental influence on expression of these characters as earlier reported by Baranwal *et al.* (2012) [3]. The present results showed conformity with the finding of Ali *et al.* (2008) [1], Nukasani *et al.* (2013) [14] and Tahar *et al.* (2015) [17].

Heritability (broad sense) and expected genetic advance

In the present study, the range of heritability in broad sense was from 23.61 to 98.99%. Eleven characters like as harvest

index (98.99%) followed by plant height (98.94%), test weight (98.36%), no. of grains/spike (97.87%), etc. showed higher estimates of heritability (Table 2). High heritability estimates for these traits indicating that these traits are more likely to be controlled by additive genetic component. Nukasani *et al.* (2013) [14] reported high heritability for the traits such as no. of tillers, test weight, plant height, spike length, grain yield, no. of grains/spike. Wani *et al.* (2007) [18] suggested the additive genetic control in the inheritance of characters with high heritability.

The expected genetic advance and genetic advance as % of mean by selecting top 5% (high yielder) of wheat genotypes was 0.23 for flag leaf breadth to 31.44 plant height and 4.35 for days to maturity to 74.81 for harvest index, respectively (Table 2). Estimated of genetic advance and genetic advance as percentage of mean, respectively were high for harvest index (26.06 & 74.81%) and plant height (31.44 & 29.47%) whereas no. of grains/spike (15.71 & 35.97%), test weight (13.19 & 31.36%) and biological yield (10.60 & 55.22%).

Lowest genetic advance was found in flag leaf breadth (0.23%) and genetic advance as percentage of mean was observed in days to 50% maturity (4.35%). The results of present study were also supported by the finding of Baranwal *et al.* (2012) [3], Nukasani *et al.* (2013) [14] and Tahar *et al.* (2015) [17].

Jonson *et al.* (1995) and Panse & Sukhatme (1985) [15] suggested high estimates of heritability and genetic advance as per cent of mean should be taken into consideration for selection for base improvement. In this study, flag leaf length, plant height, no. of grains/spike, test weight, biological yield, harvest index and seed yield/plant exhibited higher heritability coupled with higher expected genetic advance, which in fact indicates the presence of additive gene effect suggesting effectiveness of selection for the improvement of traits. Heritability alone provides no indication of the amount of genetic improvement that would result from selection of the individual genotypes.

Table 2: Estimate of mean and genetic variability components of various characters for 43 wheat genotypes

Characters	Vp	Vg	PCV	GCV	h ² (bs)	GA	GA as % of mean
Days to 50% flowering	12.33	11.19	4.58	4.42	90.76	6.57	8.56
Days to 50% heading	10.42	10.01	4.50	4.45	96.00	6.39	8.90
Days to 50% maturity	6.37	6.01	2.24	2.20	94.33	4.90	4.35
Flag leaf length (cm)	11.41	10.61	12.39	11.46	92.96	6.47	23.73
Flag leaf breadth (cm)	0.06	0.03	12.22	8.19	46.24	0.23	11.64
Grain filling period (days)	6.34	5.70	6.94	6.70	89.92	4.66	12.86
No. of tillers/plant	0.90	0.21	20.95	12.04	23.61	0.46	10.19
Plant height (cm)	237.90	235.38	14.46	13.83	98.94	31.44	29.47
Spike length (cm)	1.56	1.11	10.47	9.86	71.45	1.84	15.41
No. of grains/spike	60.74	59.45	17.84	16.98	97.87	15.71	35.97
Test weight (g)	42.38	41.68	15.48	15.35	98.36	13.19	31.36
Seed yield/plant (g)	7.34	6.37	41.60	38.76	86.83	4.85	74.40
Biological yield (g)	30.96	28.64	28.98	27.87	92.50	10.60	55.22
Harvest index (%)	163.27	161.62	36.68	36.50	98.99	26.06	74.81

Vp = Phenotypic variance; Vg = genotypic variance; PCV = Phenotypic coefficient of variation (%); GCV = Genotypic coefficient of variation (%); h²(bs) = Heritability in broad sense (%); GA = Genetic advance (%)

Phenotypic and genotypic correlations

The phenotypic and genotypic correlation coefficients for different quantitative characters are presented in Table 3. In present study, higher genotypic correlation coefficients were observed than phenotypic values reflecting that strong inherent association is reduced at phenotypic level due to significant environmental effects as earlier reported by Mahesh *et al.* (2013) [11].

The phenotypic correlations coefficient was highly significant and positive for seed yield/plant with test weight (0.32*), biological yield (0.64**) and harvest index (0.63**). Grain filling period (0.12) and no. of tillers/plant exhibited non-significant but positive association with seed yield/plant. At genotypic level, strong positive association was reported between seed yield/plant and grain filling period, no. of tillers/plant, test weight, biological yield and harvest index envisages the use of these traits for yield improvement supported by earlier findings of Khan *et al.* (2010) [8], Khokar *et al.* (2010) [9] and Baranwal *et al.* (2012) [3].

The yield components exhibited varying levels of association themselves. At phenotypic levels, the flag leaf length also showed significant positive association with test weight and plant height. Days to 50% flowering exhibited strong relationship with days to 50% heading and days to 50% maturity. Significant positive correlation was observed between grain filling period and no. of tillers/plant; spike length and days to 50% flowering, heading and maturity. Significant but negative relations were exhibited by days to 50% flowering and heading with grain filling period; plant height with no. of tillers/plant; spike length with harvest index. At genotypic level, days to 50% flowering demonstrated strong positive association with days to 50% heading, days to 50% maturity, spike length. Also, days to 50% heading showed strong relation with days to 50% maturity and spike length; days to 50% maturity with spike length; no. of tillers/plant with biological yield. Varying trends of association among yield components were also reported by Ali *et al.* (2008) [1] and Mohibullah *et al.* (2011) [13].

Table 3: Phenotypic (r_p) and genotypic (r_g) correlation coefficient for 14 characters in 43 wheat genotypes

Characters	Correlations	Days to 50% flowering	Days to 50% heading	Days to 50% maturity	Flag leaf length	Flag leaf breadth	Grain filling period	No. of tillers /plant	Plant height	Spike length	No. of grains /spike	Test weight	Biological yield	Harvest index	Seed yield /plant
Days to 50% flowering	r_p	1.00	0.88**	0.77**	0.09	0.08	-0.61**	-0.18	0.04	0.55**	0.24	-0.22	-0.16	-0.19	-0.24
	r_g	1.00	0.93	0.89	0.13	0.19	-0.68	-0.26	0.05	0.65	0.24	-0.20	-0.18	-0.22	-0.28
Days to 50% heading	r_p		1.00	0.71**	0.06	0.13	-0.48**	-0.24	0.17	0.64**	0.24	-0.17	-0.08	-0.25	-0.23
	r_g		1.00	0.74	0.05	0.03	-0.54	-0.50	0.17	0.77	0.25	-0.17	-0.07	-0.27	-0.30
Days to 50% maturity	r_p			1.00	0.02	0.17	0.00	0.01	0.17	0.62**	0.13	-0.12	-0.12	-0.24	-0.23
	r_g			1.00	-0.01	0.24	-0.04	-0.05	0.17	0.82	0.14	-0.14	-0.13	-0.24	-0.29
Flag leaf length	r_p				1.00	0.13	-0.20	-0.26	0.44**	0.24	0.15	0.33*	0.02	-0.06	-0.01
	r_g				1.00	0.19	-0.26	-0.29	0.44	0.29	0.16	0.36	-0.01	-0.07	0.02
Flag leaf breadth	r_p					1.00	0.00	-0.13	0.07	0.14	0.20	-0.14	-0.30	-0.21	-0.43**
	r_g					1.00	0.14	-0.76	0.12	0.35	0.29	-0.26	-0.44	-0.35	-0.76
Grain filling period	r_p						1.00	0.44**	0.05	-0.20	-0.15	0.05	0.08	0.03	0.12
	r_g						1.00	1.28	0.05	-0.15	-0.15	0.07	0.04	0.02	0.12
No. of tillers /plant	r_p							1.00	-0.52**	-0.33*	-0.10	-0.14	0.13	0.09	0.25
	r_g							1.00	-0.98	-1.06	-0.33	-0.42	0.72	0.32	0.25
Plant height	r_p								1.00	0.38*	-0.02	0.20	0.14	-0.19	-0.07
	r_g								1.00	0.42	-0.02	0.21	0.15	-0.20	-0.06
Spike length	r_p									1.00	0.14	0.07	0.03	-0.34*	-0.27
	r_g									1.00	0.16	0.12	0.15	-0.40	-0.31
No. of grains /spike	r_p										1.00	-0.18	-0.32*	0.07	-0.18
	r_g										1.00	-0.18	-0.33	0.08	-0.18
Test weight	r_p											1.00	0.19	0.29	0.32*
	r_g											1.00	0.20	0.30	0.33
Biological yield	r_p												1.00	-0.13	0.64**
	r_g												1.00	-0.15	0.77
Harvest index	r_p													1.00	0.63**
	r_g													1.00	0.68
Seed yield /plant	r_p														1.00
	r_g														1.00

*and** significant at 5% and 1%, respectively

Conclusion

Seed yield enhancement through selection will be effective when sufficient variability among pre-breeding lines exist. Improvement of seed yield of wheat could be achieved when selection of genotypes is done by paying attention to the traits like grain filling period, no. of tillers/plant, test weight, biological yield, harvest index and seed yield/plant which have high variability, heritability, genetic advance. These traits also have strong positive correlations with seed yield/plant.

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