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Estimation of genetic variability in recombinant inbred lines of bread wheat (*Triticum aestivum* L.) for yield and yield component traits

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Abstract

The overall objective was to study the extent of genetic variation and association among grain yield and yield related traits. Two hundred ten recombinant inbred lines of bread wheat from the cross of WH542 X WH711, together with their parents were evaluated for two years 2015-16 and 2016-17 using Randomized Block Design with three replications. Thus there was a high magnitude of genotypic variability for all the characters under study among the recombinant inbred lines of bread wheat under both years. The phenotypic coefficients of variation values were higher than genotypic coefficients of variation values. Low values for GCV and PCV and medium to low values of heritability and genetic advance as percent of mean for 100-grain weight, number of spikelets per ear, harvest index, days to heading and days to maturity over the year. Heritability in broad sense and genetic advance was observed in low category for days to heading and days to maturity indicated low chances of selection due to low genetic variability. High values of GCV and medium PCV was observed for grain yield per plant and biological yield. Heritability in broad sense and genetic advance as percent of mean was observed in high category for both the traits over the years. Based on these result, we cannot reach to the final decision. But it can be used as a bench mark for further study. Therefore, it needs additional study over several years and multi locations.

Keywords: Recombinant inbred lines, PCV, GCV, heritability, genetic advance, bread wheat

Introduction

Wheat (*Triticum aestivum* L.) is an important cereal and main food crop for people over the entire world, occupying commanding position in Indian agriculture, which occupies 28 percent area under cereals and contributing 33 percent of the total food grain production in the country (Rangare *et al.* 2010) [14]. Use of varieties with better yield potential and wide range of adaptability is of prime importance for increasing wheat production. Today, the most challenging task for wheat breeders is not only to increase grain yield but also to improve the grain quality for end products to meet the food requirement of ever increasing population. Genetic variability is required to achieve genetic gains in a breeding program. Generating information about the genetic variability, relationships and mechanisms of inheritance of the genetic traits involved is the key task in genetic improvement of any crop plant. The knowledge of heritability helps the plant breeder in predicting the behaviour of the succeeding generation and making desirable selections. Thus, genetic advance is yet another important selection parameter that aids breeder in a selection program. Genetic advance is also of considerable importance because it indicates the magnitude of the expected genetic gain from one cycle of selection (Hamdi *et al.* 1992) [7]. The genetic variation for the trait under selection and a higher heritability are necessary to have response to selection (Falconer *et al.* 1996) [4]. Breeding programs depend on the knowledge of key traits, genetic systems controlling their inheritance, genetic and environmental factors that influence their expression (Kashif *et al.* 2003, Ali *et al.*, 2009, [9, 1]. The study of statistical parameters like mean, variance, heritability and genetic advance is a measure to evaluate genetic potential, variability and stability performance of any genotype for effective selection of particular traits in that genotype. (Ali *et al.* 2009, Firoozian *et al.* 2003) [1, 5]. Risk management is crucial in the investment and financing decisions for farmers in developing countries and in transition economies. Basic risk management in agriculture includes choosing plant varieties against adverse weather events (Roberts 2005) [15]. The plant performance in diverse environments depends on efficiency of developed varieties which should be matched to the production area.

Multi-environment testing is the main tool for understanding varietal responses to the environments, although the process is time-consuming and expensive. The main objectives of this study were to determine genotype by interaction, estimate heritability and genetic advance in recombinant inbred lines, developed from the cross of WH542 X WH711 varieties.

Materials and Methods

The current experiment was conducted in the Department of Genetics and Plant Breeding, Chaudhary Charan Singh Haryana Agricultural University, Hisar. Geographically, Hisar is located at latitude of 29.090N, longitude of 75.430E in western Haryana. It has an average elevation of 705ft above sea level. Crop was grown in research area of Wheat Section, Department of Genetics and Plant Breeding, CCS HAU, Hisar, during the Rabi season of 2015-16 and 2016-17. The experiment was carried out in Randomized Block Design (RBD) with three replications and plot was 3 m × 40cm size. The distance between row to row and plant to plant was maintained were 23 cm and 10 cm respectively. Recommended package of practices will be followed to raise the crop. Data will be recorded on the 5 plants/ replication/ genotype. Data were recorded on 11 characters, viz., yield/plant (g), number of tillers/ plant, number of grains/ear, number of spikelets/ear, 100-grain weight (g), Biological yield/plant (g), Harvest index (%), Plant height (cm), Ear length (cm), Days to 50% heading, Days to 75% maturity. The data obtained were subjected to the biometrical analysis that included analysis of variance, heritability, and genetic advance. Genotypic variance (σ^2_g), phenotypic variance (σ^2_p), genotypic coefficient of variation (GCV%), phenotypic coefficient of variation (PCV%), broad sense heritability ($h^2_{(bs)}%$) and genetic advance in percent mean (GAPM) were estimated by the formula suggested by Singh and Chaudhary (1985) [16]. The estimate of GCV and PCV were classified as low, medium and high (Sivasubramanian and Madhavamenon 1973) [17]. The heritability was categorized as suggested by Again, genetic advance was classified by adopting the method of Johnson *et al.* (1955) [8].

Results and Discussion

The results of ANOVA indicated that during the year 2015-16 mean sum of squares due to replications were significant for grain yield per plant, its components and other traits at 1% level of significance except days to heading which was significant at 5% level of significance (Table 1.1). This indicated that significant variation existed among the replications. The mean sum of squares due to genotypes were significant for grain yield per plant, number of tillers per plant, 100-grain weight, number of grains per ear, plant height, ear length, number of spikelets per ear, biological yield, harvest index and days to maturity at 1% level of significance and days to heading at 5% level of significance. This revealed that there was considerable magnitude of genotypic variability for all the characters under study among the recombinant inbred lines of bread wheat.

During the year 2016-17 mean sum of squares due to replications were significant for all the traits at 1% level of significance except days to heading which was significant at 5% level of significance indicating significant differences among the replications. The mean sum of squares due to genotypes were also significant for grain yield per plant, number of tillers per plant, 100-grain weight, number of grains per ear, plant height, ear length, number of spikelets per ear, biological yield, harvest index and days to maturity at

1% level of significance, while for days to heading at 5% level of significance. Thus there was a high magnitude of genotypic variability for all the characters under study among the recombinant inbred lines of bread wheat under both years.

Pooled analysis of variance (ANOVA) for the year 2015-16 and 2016-17

In pooled analysis of variance for both years, the mean sums of squares due to replications within year were significant for all the traits under study at 1% level of significance (Table 1.2). This indicated that there were considerable variations in different replications over the years. The mean sums of squares due to years were significant for all the traits at 1% level of significance. This indicated that significant variations existed over the years. The mean sums of squares due to genotypes were also significant for all the traits at 1% level of significance. This revealed that there was a significant genotypic variation for all the traits over the years. The mean sums of squares due to year × genotype interactions were significant for all the traits. This suggested that different genotypes had different expressions over the different years. Ghallab *et al.* (2016) [6] reported that variations over the years were highly significant for all traits, except heading date and days to maturity in wheat genotypes. Significance of recombinant inbred lines in both the years indicated that these lines were differing significantly for all the traits over the years. Arain *et al.* (2011) [2] revealed highly significant difference for genotypes, environments and genotype × environment (G×E) interaction over the years among bread wheat genotypes indicating grain yield responded differently at different locations over the years. Pour (2015) [12] observed the significant effects of year, replication/year, genotype and genotype × year interaction for all the characters under this study indicating considerable variations for years, replications, genotypes and their interaction among the recombinant inbred lines of wheat.

Genetic parameters

Grain yield per plant

During the year 2015-16 grain yield per plant exhibited mean value of 13.65 ± 0.79 g. The range was from 5.1 g to 22.8 g (Table 1.3). The magnitude of GCV (24.14%) was high, while for PCV (26.15%) was in medium category. The heritability in broad sense (85.26%) and genetic advance as percent of mean (45.93%) were in high category (Table 1.3).

During the year 2016-17, the mean value for grain yield per plant was 13.59 ± 0.62 g. The range was from 5.1 g to 22.0 g (Table 1.3). The magnitude of GCV (24.14%) was in high category, while for PCV (25.41%) was in medium category. The heritability in broad sense (90.29%) and genetic advance (47.27%) belonged to high category for this trait. Thus on the basis of both years GCV belonged to high category, PCV in medium, heritability in broad sense and genetic advance in high category. Reported high GCV and PCV estimates for grain yield per plant.

Number of tillers per plant

During the year 2015-16 the number of tillers per plant showed mean value of 9.37 ± 0.82 g. The lowest number of tillers per plant was 4.8 whereas, the highest number of tillers per plant were 14.3. The magnitudes of GCV (16.10%) and of PCV (22.21%) were in medium category. The heritability in broad sense (52.54%) and genetic advance as percent of mean (24.04%) were in medium category.

During the year 2016-17 the lowest number of tillers per plant was 6.3, whereas the highest number of tillers per plant was 15.6 with mean value 10.65 ± 0.43 . The magnitude of GCV (15.01%) was in medium category, while that of PCV (16.61%) was in low category. The heritability in broad sense (81.61%) was observed in high category and genetic advance as percent of mean (27.94%) was medium for this trait. Thus on basis of both years GCV belonged to medium category, while PCV was observed in low to medium category. The heritability in broad sense showed medium to high category, while genetic advance as percent of mean belonged to medium category over the years.

100-grain weight

During the year 2015-16 grain weight showed the mean value of 4.32 ± 0.14 g. The range was observed from 3.07 g to 5.05 g. The magnitudes of GCV (6.16%) and PCV (8.53%) were in low category. The heritability in broad sense (52.14%) belonged to medium category, while genetic advance as percent of mean (9.17%) was in low category.

During the year 2016-17 the mean value for 100-grain weight was of 4.33 ± 0.17 g. The range was observed from 2.82 g to 5.05 g. The magnitude of GCV (5.27%) and PCV (8.60%) belonged to low category. The heritability in broad sense (37.54%) and genetic advance (6.67%) were in low category for this trait. Thus on the basis of both the years GCV, PCV, heritability in broad sense and genetic advance as percent of mean belonged to low category, while heritability in broad sense belonged to low to medium category over the years.

Number of grains per ear

During the year 2015-16 the mean value for number of grains per ear was 53.49 ± 1.8 g. The maximum range was exhibited from 29.80 to 69.40 for this trait. The magnitude of GCV (12.15%) was medium; while for PCV (13.58%) was in low category. The heritability in broad sense (80.13%) and genetic advance as percent of mean (22.41%) belonged to medium category (Table 1.3).

During the year 2016-17 the number of grains per ear exhibited mean value of 53.17 ± 1.83 . The magnitude of GCV (11.83%) was medium while for PCV (13.24%) was in low category. The heritability in broad sense (79.77%) and genetic advance as percent of mean (21.76%) belonged to medium category. The range was observed from 31.7 to 69.3 for this trait. Thus on the basis of both years GCV, heritability in broad sense and genetic advance as percent of mean was in medium category, while PCV belonged to low category for this trait.

Plant height

During the year 2015-16 plant height exhibited mean value of 80.80 ± 0.90 cm. The range was observed from 65.70 cm to 102.6 cm. The magnitude of GCV (6.42%) and PCV (6.71%) were in low category. The heritability in broad sense (91.66%) was in high category while for genetic advance as percent of mean (12.67%) in low category. (Table 1.3).

During the year 2016-17 mean value for plant height was 80.95 ± 1.31 cm with a range of variation of 65.40 cm to 101 cm. The magnitudes of GCV (5.92%) and PCV (6.55%) belonged to low category. The heritability in broad sense (81.84%) belonged to high category while genetic advance as percent of mean (11.05%) belonged to low category for this trait. Thus on the basis of both years GCV, PCV and genetic advance as percent of mean were in low category, while

heritability in broad sense belonged to high category for this trait (Table 1.3).

Ear length

During the year 2015-16 the mean value for spike length was 9.87 ± 0.22 cm with a range of 8.00 cm to 12.5 cm. The magnitude of GCV (5.12%) and PCV (6.42%) were in low category. The heritability in broad sense (63.48%) exhibited medium category, while genetic advance as percent of mean (8.40%) were low. None of the RILs was found better over better parent (12.13 ± 0.68) (Table 1.3).

During the year 2016-17 spike length exhibited mean value of 9.89 ± 0.22 cm. The range was observed from 8.00 cm to 12.3 cm. The magnitude of GCV (5.40%) and PCV (6.67%) were in low category. The heritability in broad sense (65.68%) belonged to medium category, while genetic advance as percent of mean (9.02%) indicated low category for spike length. Thus on the basis of both years GCV, PCV and genetic advance as percent of mean belonged to low category, while heritability in broad sense indicated medium category for this trait (Table 1.3).

Number of spikelets per ear

During the year 2015-16 the mean value for number of spikelets per ear was 21.23 ± 0.38 . The range was exhibited from 19.00 to 23.50 for this trait. The magnitude of GCV (3.2%) and PCV (4.5%) indicated low category. The heritability in broad sense (50.67%) exhibited medium category, while genetic advance as percent of mean (4.70%) belonged to low category (Table 1.3).

During the year 2016-17 the number of spikelets per ear exhibited mean value of 21.21 ± 0.38 . The range was observed from 17.80 to 23.50 for this trait. The magnitude of GCV (3.10%) and PCV (4.44%) were in low category. The heritability in broad sense (48.99%) and genetic advance as percent of mean (4.48%) belonged to low category. Thus on the basis of both years GCV, PCV and genetic advance as percent of mean belonged to low category, while heritability in broad sense belonged to medium and low over the years.

Biological yield

During the year 2015-16 biological yield exhibited mean value of 35.50 ± 1.74 g. Maximum range was exhibited from 3.90 g to 57.80 g for this trait. The magnitude of GCV (22.58%) was in high category, while for PCV (24.13%) it was in medium category. The heritability in broad sense (87.61%) and genetic advance as percent of mean (43.55%) belonged to high category.

During the year 2016-17 the mean value for biological yield was 35.60 ± 1.34 g. The range was observed from 14.80 g to 57.80g. The magnitude of GCV (22.74%) was in high category while for PCV (23.66%) was in medium category. The heritability in broad sense (92.36%) and genetic advance as percent of mean (45.03%) exhibited high category. Thus on the basis of both years GCV, heritability in broad sense and genetic advance as percent of mean belonged to high category, while PCV was in medium category.

Harvest index

During the year 2015-16 the mean value for harvest index was of $38.53\% \pm 1.36\%$. The range for harvest index was observed from 30.03%- 45.93%. The magnitudes of GCV (9.04%) and PCV (10.93%) were in low category. The heritability in broad sense (68.43%) was in medium category,

while genetic advance as percent of mean (15.41%) was in low category.

During the year 2016-17 harvest index exhibited the mean value of $38.30\% \pm 1.66\%$. The range for this trait was observed from 25.09% - 54.55%. The magnitude of GCV (9.32%) and PCV (11.99%) were low. The magnitude of heritability in broad sense (60.44%) was in medium category, while for genetic advance as percent of mean (14.93%) it was in low category for this trait. Thus on the basis of both years GCV, PCV and genetic advance as percent of mean belonged to low category, while heritability in broad sense indicated medium category.

Days to heading

During the year 2015-16 days to heading showed mean value of 100.28 ± 1.20 days. The range recorded from 93 to 114 days. The magnitudes of GCV (1.27%) and PCV (2.44%) belonged to low category for this trait. The heritability in broad sense (27.29%) and genetic advance as percent of mean (1.37%) belonged to low category.

During the year 2016-17 mean value for days to heading was of 100.29 ± 1.23 days. The range was observed from 93 to 114 days. The magnitudes of GCV (1.09%) and PCV (2.39%) were in low category. The heritability in broad sense (20.89%) and genetic advance as percent of mean (1.03%) were in low category. Thus on the basis of both years GCV, PCV, heritability in broad sense and genetic advance as percent of mean belonged to low category for this trait.

Days to maturity

During the year 2015-16 the number of days to maturity possessed mean value of 141.98 ± 1.53 days. The range was observed from 130 to 151 days. The magnitudes of GCV (1.62%), PCV (2.48%), heritability in broad sense (42.67%) and genetic advance as percent of mean (2.18%) indicated low category.

During the year 2016-17 the mean value for number days to maturity was of 142.00 ± 1.54 days. The range was observed from 126 to 151 days. The magnitudes of GCV (1.61%), PCV (2.47%), heritability in broad sense (42.23%) and genetic advance as percent of mean (2.15%) belonged to low category for this trait. Thus on the basis of both years GCV, PCV, heritability in broad sense and genetic advance as percent of mean were in low category.

Although the genotypic coefficient of variation revealed the extent of genetic variability present in the genotypes for

various traits, it does not provide full scope to assess the variation that is heritable. The genotypic coefficient of variation along with heritability estimates provide reliable estimates of the magnitude of genetic advance to be expected through phenotypic selection (Burton, 1952) [3]. The magnitude of heritability permits greater effectiveness of selection by separating out the environmental influence from the total variability and to indicate accuracy with which a genotype can be identified phenotypically. In present study, estimation of genetic parameters, mean, range, GCV, PCV, heritability and predicted genetic advance as percent of mean were obtained for all the traits (Table 1.3). The value of range observed in recombinant inbred lines was high for almost all the traits under study. Mean values showed consistent performance for all the traits under study over the years. Low values for GCV and PCV and medium to low values of heritability and genetic advance as percent of mean were observed for 100-grain weight, ear length, number of spikelets per ear and harvest index over the years. This indicated low to medium scope of selection for these traits. The low genetic variability for these traits in the present set of material may be due to limited variability in parents for these traits because there were non-significant differences in the mean values of parents for these traits. Kifle *et al.* (2016) [10] reported that number of spikelets per spike, days to heading, test weight, harvest index, grain filling period and days to maturity exhibited low genotypic and phenotypic coefficients of variation along with medium heritability and genetic advance in bread wheat genotypes. Days to heading and maturity also indicated low chances of selection due to low genetic variability on the basis of GCV and PCV values, heritability and genetic advance as percent of mean. This is due to the fact that the parents, namely WH542 and WH711 were had low variability for these traits. Yaqoob (2016) [18] had also observed lower GCV, PCV, heritability and genetic advance in days to heading, days to maturity for yield and yield related traits in wheat. High values of GCV and medium PCV coupled with high values of heritability and genetic advance as percent of mean were observed for grain yield per plant and biological yield in both years. Thus indicated a high scope of selection for these traits in the recombinant inbred lines. Kumar *et al.* (2017) [11] recorded high values of GCV, PCV, estimates of heritability and genetic advance for grain yield per plant and biological yield per plant in quantitative characters of bread wheat over two generations.

Table 1.1: Mean sum of squares for various traits in recombinant inbred lines of bread wheat for the years 2015-16 and 2016-17

Source of variation	Year	Degree of freedom	Characters										
			Grain yield/plant	Number of tillers/plant	100-grain weight	Number of grains/ear	Plant height	Ear length	Number of spikelets/ear	Biological Yield	Harvest Index	Days to heading	Days to Maturity
Replication	2015-16	2	9.66**	24.53**	3.01**	123.46**	52.76**	0.67**	6.28**	17.65**	41.02**	2.49*	15.26**
	2016-17	2	4.52**	29.54**	2.89**	114.30**	50.28**	0.54**	6.29**	11.94**	20.32**	2.09*	17.10**
Genotypes	2015-16	211	34.48**	8.89**	0.27**	137.34**	83.36**	0.91**	1.84**	201.96**	42.03**	9.30*	22.98**
	2016-17	211	33.47**	8.25**	0.24**	128.76**	74.23**	1.00**	1.75**	202.13**	46.62**	8.16*	22.83**
Error	2015-16	422	1.87	2.05	0.06	10.48	2.45	0.14	0.45	9.09	5.60	4.37	7.10
	2016-17	422	1.87	0.57	0.08	10.03	5.11	0.14	0.45	5.41	8.34	4.55	7.15

*, **: significant at 5% and 1% level of significance, respectively

Table 1.2: Pooled mean sum of squares of various traits in recombinant inbred lines of bread wheat for the years 2015-16 and 2016-17

Source of Variation	Degree of freedom	Characters										
		Grain yield/plant	Number of tillers/plant	100-grain weight	Number of grains/ear	Plant height	Ear length	Number of spikelets/ear	Biological Yield	Harvest index	Days to heading	Days to Maturity
Replications / year	4	2.47**	2.84**	9.50**	23.78**	1.35**	14.04**	0.258**	33.23**	22.55**	7.06**	4.52**
Years	1	2.50**	298.43**	623.10**	8.95**	3.77**	9.64**	33.59**	1076.29**	30.35**	18.62**	209.88**
Genotypes	211	3351.9**	3312.3**	3067.9**	3155.9**	3187.3**	3170.6**	3123.75**	3198.93**	2799.99**	3004.82**	3083.5**
Years X Genotypes	211	7221.3**	7107.4**	7762.1**	7914.5**	7717.5**	7829.1**	7394.6**	7820.5**	7941.4**	8055.3**	7896.3**
Error	844	3.28	2.97	4.34	4.68	3.80	4.30	5.77	4.63	3.65	4.24	5.39

*, **: significant at 5% and 1% level of significance, respectively

Table 1.3: Mean, range, genotypic coefficient of variance, phenotypic coefficient of variance, heritability in broad sense and genetic advance as percent of mean in RILs of bread wheat for the years 2015-16 and 2016-17

Characters	Year	Mean \pm S.E(m)	Range	Genotypic coefficient of variance	Phenotypic coefficient of variance	Heritability	Genetic advance (% of mean)
Yield per plant	2015-16	13.65 \pm 0.79	5.1-22.8	24.14	26.15	85.26	45.93
	2016-17	13.59 \pm 0.62	5.1-22.0	24.14	25.41	90.29	47.27
Number of tillers per plant	2015-16	9.37 \pm 0.82	4.8-14.3	16.10	22.21	52.54	24.04
	2016-17	10.66 \pm 0.43	6.3-15.6	15.01	16.61	81.61	27.94
100-grain weight	2015-16	4.32 \pm 0.14	3.07-5.05	6.16	8.53	52.14	9.17
	2016-17	4.33 \pm 0.17	2.82-5.05	5.27	8.60	37.54	6.65
Number of grains per ear	2015-16	53.49 \pm 1.87	29.8-69.4	12.15	13.58	80.13	22.41
	2016-17	53.17 \pm 1.83	31.7-69.3	11.83	13.24	79.77	21.76
Plant height	2015-16	80.80 \pm 0.90	65.70-102.6	6.42	6.71	91.66	12.67
	2016-17	80.95 \pm 1.31	65.4-101	5.92	6.55	81.84	11.05
Ear length	2015-16	9.87 \pm 0.22	8-12.5	5.12	6.42	63.48	8.40
	2016-17	9.89 \pm 0.22	8-12.3	5.40	6.67	65.68	9.02
Number of spikelets per ear	2015-16	21.23 \pm 0.38	19-23.5	3.20	4.50	50.67	4.70
	2016-17	21.21 \pm 0.38	17.8-23.5	3.10	4.44	48.99	4.48
Biological yield	2015-16	35.50 \pm 1.74	13.9-57.8	22.58	24.13	87.61	43.55
	2016-17	35.60 \pm 1.34	14.8-57.8	22.74	23.66	92.36	45.03
Harvest index	2015-16	38.53 \pm 1.36	30.03-45.93	9.04	10.93	68.43	15.41
	2016-17	38.30 \pm 1.66	25.09-54.55	9.32	11.99	60.44	14.93
Days to heading	2015-16	100.28 \pm 1.20	93-114	1.27	2.44	27.29	1.37
	2016-17	100.29 \pm 1.23	93-114	1.09	2.39	20.89	1.03
Days to maturity	2015-16	141.98 \pm 1.53	130-151	1.62	2.48	42.67	2.18
	2016-17	142.00 \pm 1.54	6-151	1.61	2.47	42.23	2.15

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