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Assessment of Genetic Parameters for Spike Traits and Yield Attributes in Bread Wheat Genotypes Following Line × Tester Mating System

BABITA GOLLEN, R. K. YADAVA* AND PAWAN KUMAR

Department of Genetics & Plant Breeding, CCS Haryana Agricultural University
Hisar 125004, India
E-mail : rameshyadava53@yahoo.com
**Correspondence*

Abstract

An investigation was conducted to analyze the genetic parameters for spike and grain yield attributes in the parent lines and F_1 derived through L × T mating system in bread wheat. Twelve Lines viz. $HD2009_M$, R-49, R-6, HT 90, HJP 81, HS-11, HS-17, HS-27, $Rm\text{-}Ts_{13}$, HG-2, DI 717, SG 215 were crossed with six testers, namely WH-711, PBW-502, $Rm\text{-}Ts_{10}$, $Rm\text{-}Ts_{17}$, Rvg and C-591. Significant genotypic differences were observed for all the traits studied indicating considerable amount of variation among genotypes for each trait. It was observed that PCV was higher than the respective GCV and however, it was slightly lower for most of the characters indicating a high magnitude of heritability estimate (broad sense) for most of the characters in general. Further, high variability and genetic advance were observed for tillers per plant and moderate for plant height, spike biomass, peduncle length, weight of grains per spike, number of grains per spike and hundred grain weights indicating the scope of improvement through simple selection for these traits.

Key words : Genetic parameters, Heritability, Genetic advance, Bread wheat, Yield attributes.

Wheat is the most widely grown food grain crop due to its adaptation under wide range of climatic conditions prevailing in the temperate and tropical regions. Wheat grain contributes more calories (20%) and protein to the world diet that any other cereal crops (1). However, still there is an urgent need to increase the productivity level of wheat to reduce the food gap globally resulting from population increase. There is large gap between yield potential of our modern wheat varieties and yield production which indicated that crop yield can be improved through better crop husbandry. Grain yield is a complex trait made up of the interaction between different yield components (number of tillers/plant, 100-grain weight, spike length, numbers of grains per spike and number of spikelet) and environmental effects (2). Because of these complex interactions it is difficult to improve yield through breeding (especially in early generations) if yield is the only factor recorded, suggesting that component traits should also be used as selection criteria for yield improvement. The genetic parameters provide information regarding the presence of genotypic and phenotypic variation and depending upon them the estimate of heritability and extent of improvement that can be brought out for a specific character (3—7). These characters were controlled by additive gene action and expected improvement by direct selection. So, these are important considerations for a breeder so that he can practice his skill and resources for the improvement programme in any crop plant to achieve his objectives of breeding. Thus, genetic parameters like mean squares, phenotypic coefficient of variation, genotypic coefficient of variation, broad sense heritability and genetic advance for spike traits and other yield attributes were estimated in this study.

Methods

Eighteen genetically diverse bread wheat parents (namely $HD2009_M$, R-49, R-6, HT-90, HJP 81, HS-11, HS-17, HS-27, $Rm\text{-}Ts_{13}$, HG-2, DI 717, SG-215, WH-711, PWB 502, $Rm\text{-}Ts_{10}$, $Rm\text{-}Ts_{17}$, C-591 and Rvg) were selected. Out of these, 12 genotypes viz. $HD2009_M$, R-49, R-6, HT 90, HJP 81, HS-11, HS-17, HS-27, $Rm\text{-}Ts_{13}$, HG-2, DI-717, SG-215 were used as

Table 1. Analysis of variance for 12 traits in wheat. DH = Days to heading ; PH = Plant height (cm) ; SL = Spike length (cm) ; PL = Peduncle length (cm) ; SPS = Spikelets per spike ; TPP = Tillers per plant ; SB = Spike biomass (g) ; WGPS = Weight of grains per spike (g) ; NGPS = Number of grains per spike ; HGW = Hundred grain weight (g) ; GSB = Grain - spike biomass ratio ; YPP =Yield per plant (g).

		Mean squares					
Sources	df	DH	PH (cm)	SL (cm)	PL	SPS	TPP
Replications	2	11.26**	10.57**	0.03	14.98**	4.64**	2.41**
Genotypes	89	103.3**	1720.63**	7.62**	203.62**	5.79**	36.79**
Lines	11	23.83**	1436.06**	10.49**	161.69**	9.32**	8.26**
Testers	5	136.65**	999.59**	8.33**	98.18**	7.82**	1.07
Hybrids	71	97.39**	1722.44**	5.84**	204.09**	4.88**	43.83**
Lines vs testers	1	798.16**	7591.95**	14.09**	973.2**	19.59**	14.82**
Parents vs hybrids	1	535.66**	2456.62**	92.66**	388.62**	7.5**	50.27**
Lines	11	11.33**	1135.43**	6.98**	154.81**	8.5**	31.62**
Testers	5	1256.59**	20145.1**	51.88**	2336.93**	20.95**	371.88**
Lines × Testers	55	9.22**	165.06**	1.42**	20.06**	2.69**	16.47**
Error	178	1.01	3.46	0.11	3.80	0.79	1.39

**Significant at 1%

Table 1. Continued.

		Mean squares					
Sources	df	SB (g)	WGPS (g)	NGPS	HGW (g)	GSB (%)	YPP (g)
Replications	2	0.12**	0.03	13.43**	0.01	3.59	2.94
Genotypes	89	2.68**	1.61**	432.44**	0.92**	54.8**	92.64**
Lines	11	2.95**	1.78**	901.85**	1.46**	43.04**	23.96**
Testers	5	1.92**	1.67**	197.12**	0.74**	179.49**	65.46**
Hybrids	71	2.28**	1.41**	354.84**	0.85**	47.47**	104.51**
Lines vs testers	1	0.39**	0.14**	805.79**	0.27**	1.26	6.08**
Parents vs hybrids	1	33.73**	15.46**	1581.71**	1.17**	135.21**	227.13**
Lines	11	2.78**	1.83**	775.14**	1.52**	35.94**	79.69**
Testers	5	10.07**	6.18**	1172.38**	2.33**	73.39**	669.73**
Lines × Testers	55	1.48**	0.89**	196.46**	0.58**	47.41**	58.09**
Error	178	0.04	0.04	5.12	0.03	5.30	3.94

**Significant at 1%

lines and the remaining six genotypes as testers in hybridization. Seventy two F_1s and eighteen parents were sown in randomized block design (following compact family) with three replications in the field during *rabi* 2008-2009 crop season at Department of Genetics, CCS HAU, Hisar (India). Single row of 2 m length for each genotype was grown in each replication with row to row and plant to plant spacing of 30 and 10 cm, respectively. Recommended practices were followed to raise the crop. At maturity, data were recorded on randomly selected plants from each plot per replication were taken for recording observation on twelve metric traits namely, days to heading, plant height, spike length, peduncle length, spikelets per spike, spike biomass, tillers per plant, weight of grains per spike, number of grains per spike, hundred grain weight and yield per plant while the grain spike biomass ratio (%) was calculated.

Analysis of variance used to test the significance of differences among the genotypes i.e. parents and their hybrids for different characters (8). Different genetic parameters like mean, phenotypic and genotypic coefficients of variation, heritability and genetic advance were calculated (9, 10).

Results

Twelve diverse wheat genotypes exhibited considerable variations for the all characters. Mean squares revealed highly significant differences among Hybrid progenies (F_1) and their parents for all the characters under investigation except for the tillers per plant due to testers and grain-spike biomass ratio due to lines vs testers. Table 1 indicates the presence

Table 2. Genetic parameters for the characters studied in homozygous material (lines and testers), heterozygous (hybrids) and overall. DH = Days to heading ; PH = Plant height (cm) ; SL = Spike length (cm) ; PL = Peduncle length (cm) ; SPS = Spikelets per spike ; TPP = Tillers per plant ; SB = Spike biomass (g) ; WGPS = Weight of grains per spike (g) ; NGPS = Number of grains per spike ; HGW = Hundred grain weight (g) ; GSB = Grain - spike biomass ratio (%) ; YPP = Yield per plant (g).

		DH	PH	SL	PL	SPS	TPP
GCV	Homozygous	6.200	20.69	14.24	19.68	6.880	13.17
	Hybrids	5.840	19.71	9.870	18.78	4.760	33.16
	Overall	6.060	19.95	11.47	19.06	5.230	30.88
PCV	Homozygous	6.330	20.76	15.06	19.80	8.070	16.56
	Hybrids	5.920	19.77	9.980	19.41	5.840	34.79
	Overall	6.150	20.01	11.73	19.59	6.340	32.66
h^2 (broad sense)	Homozygous	0.960	0.993	0.893	0.988	0.727	0.635
	Hybrids	0.970	0.990	0.980	0.940	0.660	0.910
	Overall	0.970	0.990	0.960	0.950	0.680	0.890
Genetic Advancement 5%	Homozygous	11.72	48.38	3.490	16.29	2.950	2.220
	Hybrids	11.52	49.17	2.830	16.25	1.980	7.380
	Overall	11.85	49.14	3.190	16.35	2.190	6.690
Genetic Advancement 1%	Homozygous	15.02	61.99	4.480	20.88	3.770	2.840
	Hybrids	14.76	63.01	3.620	20.83	2.530	9.460
	Overall	15.19	62.97	4.090	20.96	2.810	8.580
Gen Adv as % of Mean 5%	Homozygous	12.52	42.48	27.71	40.29	12.08	21.62
	Hybrids	11.86	40.49	20.08	37.42	7.980	65.11
	Overall	12.29	40.98	23.13	38.18	8.870	60.17
Gen Adv as % of Mean 1%	Homozygous	16.04	54.44	35.52	51.64	15.49	27.71
	Hybrids	15.19	51.89	25.74	47.96	10.22	83.44
	Overall	15.75	52.51	29.64	48.93	11.37	77.11

Table 2. Continued.

		SB	WGPS	NGPS	HGW	GSB (%)	YPP
GCV	Homozygous	19.44	20.17	21.91	17.79	6.280	16.62
	Hybrids	15.61	15.93	14.40	14.29	4.930	25.85
	Overall	17.48	17.58	16.18	15.01	5.270	24.85
PCV	Homozygous	19.96	20.79	22.15	18.19	7.230	17.91
	Hybrids	16.06	16.54	14.71	15.07	5.670	27.54
	Overall	17.92	18.16	16.47	15.70	6.060	26.45
h^2 (broad sense)	Homozygous	0.949	0.941	0.978	0.958	0.753	0.860
	Hybrids	0.940	0.930	0.960	0.890	0.760	0.880
	Overall	0.950	0.940	0.970	0.910	0.760	0.880
Genetic Advancement 5%	Homozygous	1.820	1.470	30.77	1.250	8.810	6.370
	Hybrids	1.730	1.340	21.79	1.020	6.770	11.16
	Overall	1.880	1.450	24.16	1.070	7.280	10.52
Genetic Advancement 1%	Homozygous	2.330	1.880	39.43	1.610	11.29	8.16
	Hybrids	2.220	1.720	27.92	1.310	8.680	14.31
	Overall	2.410	1.850	30.96	1.370	9.330	13.49
Gen Adv as % of Mean 5%	Homozygous	39.01	40.29	44.64	35.88	11.23	31.77
	Hybrids	31.24	31.61	29.06	27.91	8.830	49.97
	Overall	35.15	35.06	32.75	29.57	9.450	48.09
Gen Adv as % of Mean 1%	Homozygous	49.99	51.64	57.21	45.98	14.39	40.73
	Hybrids	40.04	40.51	37.24	35.77	11.31	64.05
	Overall	45.04	44.93	41.97	37.89	12.11	61.63

of considerable amount of genetic variability for these traits. These findings are in confirmation of earlier reports (11, 12). The genetic parameters were worked out separately for the characters studied considering the break up of the material as homozygous material (lines and testers), heterozygous (F_1 crosses) and overall for both together.

The different genetic parameters like mean, genotypic (GCV) and phenotypic coefficients of variations (PCV), heritability (broad sense) and expected genetic advance as per cent of mean are represented in Table 2. The genotypic coefficient of variation were slightly lower in magnitude to that of the respective phenotypic coefficient of variation indicating negligible influence of the environment on the characters studied in present investigation and further confirmed by the high heritability (bs) for most of the characters except spikelets per spike (0.68) and grain-spike biomass ratio (0.76) where the estimates of the heritability (bs) were considered as moderate in comparison to other traits for which the heritability (bs) estimates were in the range of 0.88 for yield per plant to 0.99 for plant height on an overall basis considering all the genotypes involved in this study.

The genetic advance in terms of percent mean at 1% selection intensity has been indicated as moderate and were high for tillers per plant (77.11%) moderate for plant height (52.51%), peduncle length (48.93%), spike biomass (45.04%), weight of grains per spike (44.93%), number of grains per spike (41.97%), hundred grain weight (37.89%) whereas the value of genetic advance for yield per plant has been exhibited to the extent of 61.63% in the present investigation on the basis of considering all the genotypes together.

Table 2 further reveals that lines and testers had higher magnitude of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for the characters studied excepting tillers per plant and the yield per plant in comparison with that of the crosses. However, the heritability estimates were quite close in homozygous and heterozygous material excepting the tillers per plant where it has been moderate for the homozygous genotypes taken up for the present study.

Discussion

The genetic parameters provide information regarding the presence of genotypic and phenotypic variation and depending upon them the estimate of heritability and extent of improvement that can be brought out for a specific character. So these are important considerations for a breeder so that he can practice his skill and resources for the improvement programme in any crop plant to achieve his objectives of breeding. From the present investigation, it has been exhibited that PCV is higher than the respective GCV and however, it is slightly lower for most of the characters thus indicating a high magnitude of heritability estimate in broad sense for most of the characters in general. The extent of GCV has been reported more than 20% for the characters viz. tillers per plant and grain yield/plant. The former is one of the components for grain yield/ plant and thus reveal that there is some scope for improvement of tillers per plant by simple selection. However, for days to heading and spikelets per spike, there is not much scope and as indicated by the prevalence of GCV just around 5—6% for these two traits.

Heritability estimates provide the information about index of transmissibility of the quantitative characters of economic importance and are essential for an effective crop breeding strategy. The magnitude of heritability also helps in predicting the behavior of succeeding generations by devising the appropriate selection criteria and assessing the level of genetic improvement (13). Similarly, genetic advance gives clear picture and precise view of segregating generations for possible selection. Higher estimates of heritability coupled with better genetic advance confirm the scope of selection in developing new genotypes with desirable characteristics. It was found that high heritability estimates along with greater values of genetic advance for number of spikes per plant, number of grains per spike, 100 grain weight, grain yield and plant height (3, 14, 15). However, it was reported low to high estimates of heritability and genetic advance for these traits except plant height (16) and phenotypic and genotypic variance, heritability genetic advance (GA) and correlation coefficients for yield and yield components in eight genotypes of wheat under rainfed conditions (17). High heritability estimates coupled with increasingly high GA were observed for plant height and tillers per plant, biological yield, spike length and yield per hectare (18).

The estimate of heritability in the present investigation in general have been quite high for most of the traits, however, the moderate estimate of heritability (bs) have been recorded for spikelets per spike. The high estimates of the broad sense heritability as observed in the present investigation may be ascribed to the optimum expression of the genotype for the trait under the given environment created to raise the experiment. Because of manifestation of favorable environment, the expression of the character due to its genetic constitution has not been materially different to its phenotypic expression and hence acquired the value close to each other in present study. These results are in agreement with the finding of (3, 18—20), who have recorded moderate to very high estimates for broad sense heritability for all the morphological characters in wheat.

Further, the genetic advance expressed as per cent of mean has been as high as 77.1% for tillers per plant, the major component and followed by the other spike traits namely spike biomass, weight of grains per spike, number of grains per spike and hundred grain weight for which the values have been ranging from 37.89 to 45.04. Moreover, the yield by itself reflected the genetic advance in terms of percent mean as high as 61.63%. High heritability with high genetic advance indicates predominance of additive gene effects and therefore, these characters can be better exploited through simple selection. Similar results were found (20) for yield per plant and productive tillers per plant in bread wheat (6, 21).

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