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Study of Genetic Variability Parameters in Different Segregating Generations of Bread Wheat (*Triticum aestivum* L.)

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Abstract The aim of this study was to estimate the extent of genetic variability for grain yield, its component traits in F_4 and F_5 population of the cross MP3299 × NIL PBW343. High and moderate Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV) were observed for all the characters except for spike length and plant height. High heritability and genetic advance were recorded for all the characters except thousand grain weight and number of spikelets per spike. This suggested better scope for selecting superior trangressive segregants in this population. Present investigation suggests that selection in F_4 and F_5 population of MP3299 × NIL PBW343 will be effective in selecting superior plants for yield parameters evolving high yielding genotype in wheat.

Keywords Variability, Coefficient of variation, Heritability, Genetic advance.

Introduction

Wheat (*Triticum* spp.) is a cereal grain, belong to the Poaceae, the largest family within the monocotyledonous plants and a crop of global significance, grown in diversified environments. In India, wheat is the second most important crop after rice occupying 30.64 million hectares with a production of 94.70 million tones and the average productivity is 31.40 kg h^{-1} [1]. Yield is a quantitative trait controlled by many genes and is greatly influenced by the environment. Variation in yield from year to year due to unpredictable weather and biotic stresses can have major economic impact. To increase the genetic yield potential, there is need to exploit the existing genetic variability and maximum utilization of the desirable characters in wheat for developing high yielding varieties that can be adjusting and highly productive under changing climatic scenario [2]. It is important that variability for economic traits must exist in the working population for profitable exploitation following recombination breeding and selection. The Importance of genetic diversity for selecting plants for recombination breeding in an autogamous crop such as wheat to recover trangressive segregants has also been repeatedly emphasized [3]. Variability in wheat is as such expected to be immense as it is an allohexaploid ($2n = 42$) with 3 distinct but genetically related (homoeologous) genomes A, B, and D each with 7 chromosomes and a large genome, 16 million kilo bases per haploid, which came together during the course of evolution [4]. High magnitude of variability in a population provides the opportunity for selection to evolve a variety having desirable characters [5].

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Therefore, it is necessary to estimate and study the genetic variation and mode of inheritance in different yield parameters to initiate productive wheat breeding programs. Study of genetic parameters from segregating population is useful in understanding the genetic consequences of hybridization. The heritability of a character describes the extent to which it is transmitted from one generation to the next. The genetic advance is the further estimation of expected gain resulting from selection pressure in breeding material. High heritability associated with high genetic advance for different yield components have a better scope for selecting high yielding genotypes [6]. Considering all the facts described above the present investigation was undertaken to estimate genetic variability in the advanced segregating generations obtained from the cross MP3299 × NIL PBW343.

Materials and Methods

The present study was conducted during *rabi* 2014-2015 in the experimental area of Dr Sanjay Rajaram Wheat Laboratory, All India Coordinated Wheat Improvement Project (AICWIP), Main Agricultural Research Station (MARS), University of Agricultural Sciences, Dharwad. The experimental material comprised of the F_4 and F_5 population of cross MP3299 × NIL PBW343. F_4 and F_5 seeds along with parents MP3299, NIL PBW343 and four checks viz. NI 5439, UAS347, HD 2888 and NIAW 1415 were sown by following augmented design in two rows of one meter length, keeping plant to plant distance of 20 cm and row to row distance of 23 cm. The recommended package of practices was followed to raise a good crop stand. Data was recorded on five randomly selected plants in each progeny row line of F_4 and F_5 segregating population for grain yield and its attributing traits viz., plant height (cm), number of tillers per plant, number of spikelets per spike, number of grains per spike, spike length (cm), thousand grain weight, grain yield per plant (g) and coefficient of infection for leaf rust.

Statistical analysis

Statistical analysis was done on the observation recorded on each individual plant in F_4 and F_5 generation using the statistical package WINDOSTAT 9.2.(a) General mean (X) = Sum of observations of selected plants in each genotype/Number of plants selected (b) Range = the minimum and maximum values for each trait within a genotype.

Estimation of genetic parameters

The analysis of variances for different characters were measured [7]. Genotypic and phenotypic variance and coefficients of variances were computed based on the expected mean sum of squares from the ANOVA table as follows: The treatment mean sum of squares due to genotypes is made up of environmental variance along with 'r' times the genetic variance.

$$\sigma^2 g = \frac{M_t - M_e}{r}$$

$$\sigma^2 p = \frac{M_t - M_e}{r} + M_e \text{ or } \sigma^2 g + \sigma^2 e$$

Where, Mt = Mean sum of squares due to treatments, Me = Mean sum of squares due to error, r = Number of replications, $\sigma^2 g$ = Genotypic variance, $\sigma^2 p$ = Phenotypic variance, $\sigma^2 e$ = Environmental variance.

Phenotypic coefficient of variance (PCV)

Genotypic and phenotypic coefficient of variation was calculated using the method suggested [8].

$$PCV = \frac{\sqrt{Vp}}{\bar{X}} \times 100$$

Where, Vp = Phenotypic variance, $\bar{X}$ = General mean of the character, Low =1–10%, Moderate = 10—20%, High = More than 20%.

Genotypic coefficient of variance (GCV)

GCV was calculated by the following formula.

Table 1. Analysis of variance in F_4 generation of the cross MP3299 × NIL PBW 343.

	DF	DFF	PH (cm)	PTT	SL (cm)	SPP	GPP	TGW	GYP
Treatments	110	148.51*	87.40	71.08*	8.98*	8.56**	108.80*	201.76*	138.34*
Checks	4	277.10**	44.44	30.60	1.58	9.85**	7.10	50.92	2.74
Checks+ Var vs Var	106	143.66*	89.02*	73.32*	9.26*	8.51**	112.63*	208.09*	143.46*
Block	1	8.10	19.03	2.50	0.03	1.60	0.09	3.53	13.45
Entries	110	150.47*	87.23	71.36*	8.98*	8.54**	109.31*	203.14*	139.06*
Varieties	105	146.68*	77.59*	70.23*	6.95*	8.34**	113.71*	201.49*	138.78*
Checks vs Varieties	1	41.76	1269.64**	160.61*	252.48**	25.078**	56.42	861.89*	713.51**
Error	4	17.10	15.54	9.50	3.08	0.35	17.10	47.38	23.75

$$GCV = \frac{\sqrt{Vg}}{\overline{X}} \times 100$$

Where, Vg = Genotypic variance, $\overline{X}$ = General mean of the character, Low = 1—10%, Moderate = 10—20%, High = More than 20%.

Heritability

Heritability in broad sense was estimated by following formula and expressed in percentage: Heritability (h^2_{bs}) = ($\sigma^2 g / \sigma^2 p$) × 100, Where, $\sigma^2 g$ = Genotypic variance $\sigma^2 p$= Phenotypic variance. The heritability estimates were categorized [9] as given below: Low=1–30%, Moderate = 30–60%, High = More than 60%.

Genetic advance

The extent of genetic advance to be expected from selecting five per cent of the superior progeny was calculated using the following formula: $GA = 1\sigma_p h^2$ (bs) Where, i = Intensity of selection, σp = Phenotypic standard deviation, h^2 (bs) = Heritability in broad sense. The genetic advance estimates were categorized [10] as given below: Low = 1—10%, Moderate = 10—20%, High = More than 20%.

Genetic advance as percentage over mean (GAM)

GAM = (GA / $\overline{X}$) × 100, Where, $\overline{X}$ = General mean of the character. Genetic advance is categorized based on reports (10) as follows: Low = 1–10%, Moderate = 10–20%, High = More than 20%.

Table 2. Estimates of components of variability in F_4 population.

Characters	Mean	Range Min	Max	PCV	GCV	h^2 % (BS)	GA	GAM (%)
DFF	60.00	45.00	80.0	19.13	17.89	87.47	21.04	34.48
PG (cm)	77.18	41.0	88.3	13.49	11.96	78.61	13.80	21.85
PTT	11.61	2	36	58.98	53.88	83.45	13.91	101.39
SL (cm)	10.21	3.2	16.9	24.28	22.54	86.21	4.51	43.12
SPP	20.13	12	26	13.84	13.52	95.45	5.45	27.22
GPP	57.49	15	75	21.64	19.82	83.38	17.79	37.40
TGW	26.91	3.03	56.25	29.16	26.70	83.84	23.67	50.37
GYP	13.16	14.2	16.2	48.92	44.22	81.68	19.16	82.33
CI	31.25	0	90	67.37	66.43	97.22	37.96	134.92

Table 3. Analysis of variance for yield and its contributing traits in F_5 generation.

Source	DF	DFF	PH (cm)	PTT	SL (cm)	SPP	GPP	TGW	GYP
Treatments	18	143.0*	88.2	37.9**	4.2*	13.9**	148.6*	152.4*	174.6*
Checks	4	280.7**	44.4	22.3*	7.6*	9.6**	12.6	174.6	2.0
Checks+ Var vs Var	14	103.3*	100.7*	42.4**	3.2	15.9**	187.5**	146.0	224.0*
Block	1	52.9	19.0	1.6	0.08	6.4**	48.3	50.4	3.18
Entries	18	141.5*	93.2*	42.3**	4.3*	13.7**	149.7*	150.0	179.1*
Varieties	13	97.4*	92.2*	30.8*	1.9*	10.7**	142.7*	147.9	186.6*
Checks vs Varieties	1	158.6*	302.6*	272.0**	21.9**	69.1**	788.8**	78.7	790.2**
Error	4	16.1	15.5	1.8	0.74	0.15	14.1	101.4	21.5

Results and Discussion

The analysis of variance revealed highly significant difference among genotypes for all except for plant height which recorded non significant differences (Tables 1 and 2). The significant difference among genotypes for the traits implies the presence of substantial variation among genotypes in both the segregating populations which is central to the study of both quantitative and qualitative traits and gives an opportunity to plant breeders for improvement of these characters through breeding. The genetic variability parameters studied in F_4 and F_5 generation are presented in (Tables 3 and 4).

Range of variation

One of the ways in which variability is assessed through a simple approach of examining the range of variation. The genetic variability in F_4 and F_5 generation indicated higher mean and wider range for all the traits under evaluation. For most of the characters such as number of tillers per plant, thousand grain weights and grain yield per plant higher range of variation was observed in the present study as compared to [11] who had reported low range of variation.

Genetic variability

High PCV (phenotypic coefficient of variation) and GCV (genotypic coefficient of variation) was recorded for number of productive tillers, grain yield per plant and coefficient of infection for leaf rust. High PCV and moderate GCV for thousand grain weight was recorded and Moderate PCV and low GCV for spike length and plant height, Low GCV indicated that there is less variability and the difficulty of manipulating these traits through plant breeding. Very narrow dif-

Table 4. Estimates of components of variability in F_5 population.

Characters	Mean	Range		PCV	GCV	h^2 % (BS)	GA	GAM (%)
		Min	Max					
DFF	62.7	48	77	12.77	11.05	74.84	12.35	19.69
PH (cm)	67.8	47.5	85.0	11.51	9.93	75.45	11.96	17.65
PTT	17.4	9	28	25.01	23.76	90.26	8.10	46.50
SL (cm)	10.40	8	13	11.62	8.17	49.42	1.23	11.83
SPP	20.60	13	24	12.24	12.10	97.65	5.08	24.63
GPP	56.40	45	87	16.82	15.44	84.30	16.48	29.21
TGW	40.30	18.70	55.64	26.70	12.32	21.30	4.98	11.71
GYP	23.20	5.37	53.34	43.41	39.29	81.92	18.41	73.26
CI	7.9	0	70	193.43	187.85	94.31	29.52	375.80

ference between the values of GCV and PCV indicated that the effect was small for the expression of these characters and these are governed by additive gene action. This is in accordance with the findings of Subhashchandra et al. [12]. Similar reports of high PCV and GCV in wheat for different quantitative traits has been reported by Abinasa et al. [13] in early segregating generations. Whereas, others traits like days to 50% flowering and spikelets per spike recorded moderate PCV and GCV. These results are in consonance with reports of other workers in wheat earlier [14, 15].

Heritability and genetic advance

The high estimates of heritability and genetic advance (as percentage of mean) was observed in the present study for grain yield per plant and yield related traits like days to 50% flowering, number of tiller per plant, plant height, grains per spike and coefficient of infection for leaf rust, whereas number of spikelets per spike and thousand grain weight have moderate heritability and moderate genetic advance over mean. This suggested most likely that heritability is due to the additive genetic effects and selection could be effective in early segregating generations for these traits and the possibility of improveing wheat grain yield through direct selection for grain yield related traits. These findings were similar to reports earlier [15, 16]. Thus, it is evident from the present finding that substantial genetic variability was envisaged for yield and its component traits in the both the population of cross MP3299 × NIL PBW 343. It also exhibited high heritability coupled with high genetic advance as percent of mean for grain yield per plant, plant height, number of tillers per plant and grains per spike. Therefore, these traits should be taken into account while selecting superior and desirable plants for further improvement of yield parameters in evolving high yielding genotype in wheat.

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