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Estimation of genetic variability parameters for various qualitative and quantitative traits in bread wheat (*Triticum aestivum* L. EM. Thell)

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Abstract

The present investigation was carried out during Rabi 2017-2018 at Norman E. Borlaug Crop Research Centre, G.B. Pant University of Agriculture and Technology, Pantnagar, Uttarakhand. The experimental material comprised of 17 parental genotypes (14 lines, 3 testers) and 42 F_1 hybrids, obtained after crossing them in a line × tester fashion with the objective to study genetic variability parameters for various qualitative and quantitative traits. The experiment was carried out in Randomized Block Design (RBD) with three replications and observations were recorded on various qualitative and quantitative characters. In general, PCV was higher than GCV for all the characters studied. GCV was higher than ECV for most of the characters. The magnitude of PCV and GCV was highest for phenol color reaction followed by number of effective tillers per plant and number of grains per spike. High heritability was observed for grain yield per plant, grain weight per spike and biological yield per plant. High genetic advance as percent of mean was found for phenol color reaction, number of effective tillers per plant and number of grains per spike. High heritability with high genetic advance is helpful for improvement through mass selection by fixing additive gene action, while high heritability with low genetic advance showed the preponderance of non-additive gene action due to high influence of environment.

Keywords: Wheat, genetic variability, heritability, yield and quality

Introduction

Wheat (*Triticum aestivum* L.em. Thell), an allohexaploid (2n=6x=42), belongs to the family Poaceae (Graminae). It is one of the premier and important cereal crop of worldwide importance and is being grown under a wide range of climatic conditions. Wheat offers, 55% of the carbohydrates and 20% of the food calories fed on globally (Breiman and Graur, 1995) [5]. It is the staple food and is cultivated in almost all parts of India and contributing about 36% of the country's total food grain production. The major objective of plant breeder is to create and exploit the maximum extent of genetic variability and variation is the basis of plant breeding. Therefore, the success of any improvement programme will depend on the magnitude and range of variability in the existing genetic stocks (Basavaraja *et al*., 2013) [4]. Genetic variability is a measure of tendency of individual genotypes in a population to vary from one another. The variability of the characters describes how much traits tend to vary in response to environment and genetic influences. The effectiveness of selection depends on the magnitude of heritability for the traits being selected. Heritability gives information about genetic variation and is useful for predicting the response to selection in the succeeding generation. Genetic advance is a measure of genetic gain under selection. Heritability estimates along with genetic advance are helpful in predicting the gain under selection than heritability alone (Chaudhary *et al*., 2004) [6]. Heritability estimates helps in selecting superior genotypes from the diverse genetic populations. However, it is not necessary that a character showing high heritability will also show high genetic advance (Johnson *et al.* 1955) [14]. Therefore, considering all these points, present investigation was under taken with the view to estimate out genetic variability and heritability for various qualitative and quantitative traits.

Materials and Methods

The present investigation was conducted during *Rabi* season 2017-2018 at the Norman E. Borlaug Crop Research Centre, G.B. Pant University of Agriculture and Technology, Pantnagar, Uttarakhand.

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The experimental materials of present study comprised of 42 F_1 hybrids, and seventeen parents (14 lines and 3 testers) and two checks. Line × Tester system of mating was used to get F_1s by crossing fourteen lines with three testers and two popular released varieties were used as checks. The experimental materials were planted in Randomized Block Design (RBD) with three replications. Each plot consisted of 2 rows of 1 m length with a row to row distance of 20 cm and plant to plant distance was maintained at 10 cm by dibbling.

Results and Discussion

Observations were recorded on the basis of the whole plot for days to 75% heading and days to physiological maturity whereas, for the rest of the characters *viz.*, plant height (cm), spike length (cm), number of effective tillers per plant, peduncle length (cm), number of spikelets per spike, number of grains per spike, grains weight per spike (g), 1000 grain weight (g), biological yield per plant (g), grain yield per plant (g), harvest index (%), hectolitre weight (Kg/hl) and phenol colour reaction observations were recorded on five randomly selected plants from each plot. The data obtained for different traits were analyzed using standard statistical analysis.

The phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), environmental coefficient of variation (ECV), heritability and genetic advance for different characters are given in Table 1. The values of phenotypic coefficient of variation were higher than genotypic coefficient of variation for all the characters studied. The GCV was greater than ECV for most of the characters except for peduncle length, spike length, number of spikelets per spike and biological yield per plant indicating the predominance of heritable variation. Phenol colour reaction (32.023%) showed highest phenotypic coefficient of variation followed by number of effective tillers per plant (19.310%), number of grains per spike (15.249%), grains weight per spike (15.239%), harvest index (11.482%), biological yield per plant (11.138%), 1000 grain weight (10.752%), grain yield per plant (10.026%), peduncle length (7.592%), plant height (6.404%), spike length (6.185%), number of spikelets per spike (5.242%), days to 75% heading (3.288%), days to maturity (2.243%) and hectoliter weight (1.066%).

Phenol colour reaction showed highest genotypic coefficient of variation (29.777%) followed by number of effective tillers per plant (16.592%), number of grains per spike (13.126%), grain weight per spike (12.723%), 1000 grain weight (10.158%), grain yield per plant (7.445%), harvest index (7.001%), biological yield per plant (4.80%), plant height (4.173%), peduncle length (3.424%), days to 75% heading (2.969%), number of spikelets per spike (2.593%), spike length (2.534%), days to maturity (1.965%) and hectoliter weight (0.668%). The environmental coefficient of variation (ECV) for biological yield per plant (6.338%) was observed highest followed by harvest index (4.481%) and peduncle length (4.168%). The lowest environmental coefficient of variation was observed for days to 75% heading (0.278%).

Highest phenotypic coefficient of variation and genotypic coefficient of variation was recorded for characters as phenol colour reaction, number of grains per spike, grain weight per spike, harvest index, number of effective tillers per plant, biological yield per plant, 1000 grain weight and grain yield per plant. These results are in accordance with the earlier findings of Makwana *et al.* (2009), Khan *et al.* (2015), Fikre *et al.* (2015) and Arya *et al.* (2017) [20, 18, 8, 3]. High coefficient of variability indicated that there is a scope of selection for improvement of these traits. Low values indicated the need for creation of variability either by hybridization or mutation followed by selection.

The proportion of genetic variability which is transmitted from parents to offspring is reflected by heritability. In present investigation, highest estimates of heritability were obtained for grain yield per plant (91.12%) followed by grain weight per spike (90.74%) and biological yield per plant (90.52%). The genetic advance as per cent of mean was found to be highest for number of grains per spike (12.644) followed by 1000 grain weight (8.644) and plant height (5.15). These results are in accordance with the earlier findings of Ajmal *et al*. (2009), Kumar *et al*. (2014) and Khan *et al.* (2015) [1, 19, 18].

Conclusion

The present investigation revealed the presence of wide range of genetic variability for almost all the traits studied. High heritability estimates were observed for most the characters studied. High heritability indicates the scope of genetic improvement of these characters through mass selection by fixing additive gene action, whereas high heritability with low genetic advance indicates non-additive gene action. The high genetic advance observed for number of grains per spike followed by 1000 grain weight and plant height, showed the presence of additive gene action for these traits. Hence, selection would be helpful for improving these traits in further breeding programmes.

Table 1: Analysis of variances for different characters

S. No.	Characters	Replication	Mean Squares Sources of variation	
			Treatment	Error
		2	60	120
1	Days to 75% heading	2.05	24.549**	1.754
2	Days to maturity	4.297	22.159**	2.033
3	Number of effective tillers per plant	0.527	23.084**	2.439
4	Peduncle length (cm)	6.876	9.845**	5.577
5	Plant height (cm)	26.594	64.102**	19.952
6	Spike length (cm)	0.503	0.682*	0.425
7	Number of spikelets per spike	3.684	1.652**	0.837
8	Number of grains per spike	415.076	170.31**	17.781
9	Grain weight per spike (g)	0.605	0.317**	0.401
10	1000 grain weight (g)	3.345	61.55**	2.372
11	Biological yield per plant (g)	3.752	156.445*	94.94
12	Grain yield per plant (g)	3.127	31.868**	6.508
13	Harvest index	14.396	39.018**	14.248
14	Hectolitre weight (kg/hl)	0.168	1.162**	0.397
15	Phenol colour reaction	0.398	6.138**	0.304

* significant at 5% probability level

** significant at 1% probability level

Table 2: Coefficient of variance, heritability and genetic advance for various characters in wheat

S. No.	Characters	Range	PCV	GCV	ECV	Heritability (%)	Genetic advance	GA as % mean
1	Days to 75% heading	85 – 97	3.288	2.969	0.319	81.515	5.042	5.522
2	Days to maturity	126 – 137	2.243	1.965	0.278	76.742	4.674	3.546
3	Number of effective tillers/plant	11 - 21.75	19.31	16.59	2.718	85.88	4.643	29.369
4	Peduncle length (cm)	31.79 - 39.05	7.592	3.424	4.168	78.19	1.108	3.18
5	Plant height (cm)	82.05 - 102.8	6.404	4.173	2.231	86.94	5.15	5.602
6	Spike length (cm)	10.3 - 12.9	6.185	2.534	3.651	16.783	0.247	2.138
7	Number of spikelets per spike	18.33 - 21.56	5.242	2.593	2.649	24.466	0.531	2.642
8	Number of grains per spike	41.32 - 67.93	15.249	13.126	2.123	74.093	12.644	23.275
9	Grain weight per spike (g)	1.63 - 2.97	15.239	12.723	2.516	90.74	0.523	21.882
10	1000 grain weight (g)	33.6 - 52.72	10.752	10.158	0.594	87.99	8.644	19.771
11	Biological yield per plant (g)	72.53 - 112.73	11.138	4.8	6.338	90.52	3.96	4.262
12	Grain yield per plant (g)	29.93 - 45.77	10.026	7.445	2.581	91.12	4.422	11.388
13	Harvest index (%)	33.28 - 49.74	11.482	7.001	4.481	85.87	3.694	8.993
14	Hectolitre weight (Kg/hl)	74.5 - 77.14	1.066	0.668	0.398	29.216	0.653	0.862
15	Phenol colour reaction	2.00 - 7.66	32.023	29.777	2.246	86.462	2.671	57.037

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