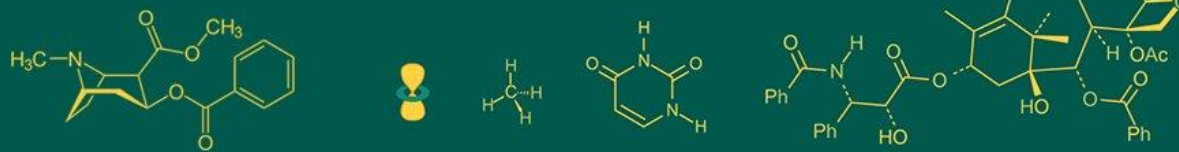


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Genetic variability studies for yield and its component traits in bread wheat (*Triticum aestivum* L.)

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Abstract

Twenty bread wheat genotypes were studied across four environments viz., 15 Nov (E1), 25 Nov (E2), 05 Dec (E3), 15 Dec (E4) during Rabi 2019-20 at Department of Seed Technology, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar and the data were pooled to estimate the genetic variability parameters. The analysis revealed significant differences among the genotypes for all the characters studied in all four sowing seasons indicating sufficient variability existing among genotypes. The estimation of genetic parameters revealed closer affinity of GCV and PCV for the characters days to 50% heading, days to maturity, grain filling period and plant height indicating the scope for the selection for these traits. The characters tillers per meter, tillers per plant, spike length, number of grains per spike, grain weight per spike, grain yield per meter, grain yield per plant, thousand grain weight, biological yield per meter, biological yield per plant and harvest index exhibited larger variation in the values of GCV and PCV showing significant action of environment in the expression of these traits. High heritability with high genetic advance was reported for spike length, number of grains per spike and grain weight per spike indicating predominance of additive gene action with effective selection. Whereas, high heritability with moderate genetic advance were reported for days to 50% heading, grain filling period, plant height, tillers per meter, thousand grain weight and biological yield per plant.

Keywords: Variability, genotypic coefficient of variation, phenotypic coefficient of variation

Introduction

Bread wheat (*Triticum aestivum* L.), one of the crop belonging to *poaceae* family is the most cultivated cereal grain crop around the world and is being cultivated since *pre-historic* times. Wheat is one of the major sources of calories and proteins in many of the developing countries. Wheat is an annual plant, grown in tropical, sub-tropical and temperate climates. In India, three species of wheat are being cultivated; *Triticum aestivum*, *Triticum durum*, and *Triticum dicoccum* (Gupta, 2004) [7]. Bread wheat accounts for around 95% cultivation, *durum* wheat of around 4% and *dicoccum* wheat around 1% respectively (Gupta, 2004) [7]. The major wheat growing states in India are Uttar Pradesh, Punjab, Haryana, Gujarat, Rajasthan, Madhya Pradesh and Bihar. Wheat is consumed in the form of bread, chapattis, biscuits and several other products. Selection of genotypes which are found to be genetically variable in the existing genetic stock is very important process in systematic plant breeding programme has it helps in individual selection, which will be mated to each other to generate further genetic variability. Thus, effectiveness of selection will be very much dependent on nature, extent and magnitude of genetic variability which is present in the material and the extent to which it is heritable. Hence heritability along with genetic advance are important selection parameters. Heritability specifies proportion of total variability due to genetic causes and it is a good index of transmission of characters from parents to their offspring (Falconer 1981) [6]. Genetic advance is the measure of genetic gain under selection and can be defined as difference of mean genotypic value of the selected lines to the mean genotypic value of the parental population. The variability present in any breeding programme can be assessed by simple measures of variability. The genotypic, phenotypic and environmental coefficients of variation are helpful in understanding the existing variability in the populations and along with this for transmissibility of characters, heritability and genetic advance provides the good estimates.

Materials and Methods

The experimental material comprised of 20 diverse wheat genotypes which were grown in Randomized Block Design (RBD) with 3 replications during *rabi* season 2019-2020 in four different date of sowings *viz.*, 15 Nov (E1), 25 Nov (E2), 05 Dec (E3), 15 Dec (E4) with the plot area of 576 m² with the row spacing of 22.5cm between two rows at Department of Seed Technology, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar. The size of each individual plot for the research experiment taken was 1m x 2m, incorporating four individual rows for each genotype for each replication. The recommended agronomic practices were practiced throughout the crop growing period for a good crop stand. The data were recorded for fifteen quantitative characters *viz.* days to 50% heading, days to maturity, grain filling period, plant height, number of effective tillers per meter, number of effective tillers per plant, spike length, number of grains per spike, grain weight per spike, grain yield per meter, grain yield per plant, thousand grain weight, biological yield per meter, biological yield per plant and harvest index. The data were pooled to estimate the genetic variability parameters. The analysis of variance for the Randomized Block Design (RBD) was carried out for every character under each environment on the basis of following model. The formulae used to calculate PCV, GCV and ECV were given by Burton and De vane (1952) [5]. Heritability and Genetic advance as percent of mean was worked out as suggested by Johnson *et al.* (1966) [9].

Results and Discussion

The analysis of variance revealed significant differences among the genotypes for all the characters studied in all four sowing seasons indicating sufficient variability existing among genotypes (Table 1). Similar results were been reported by Sabaghnia *et al.* (2014) [16], Arya *et al.* (2017) [1] and Bharadwaj (2018) [3]. The magnitude of PCV was comparatively higher than GCV suggesting significant influence of environment on the phenotypic expression of these traits. Similar findings were reported by Kotal *et al.* (2010) [10].

The GCV and PCV showed low to moderate variability among all the characters studied across environments (Table 2). The characters days to 50% heading (7.27 and 7.60%), days to maturity (1.28 and 1.98%), grain filling period (7.05 and 7.94%), plant height (8.12 and 8.77%), number of effective tillers per meter (5.98 and 7.11%), number of effective tillers per plant (5.76 and 7.33%), biological yield per meter (6.85 and 8.96%), biological yield per plant (6.93 and 8.86%) and harvest index (6.65 and 9.60%) showed low estimates of GCV and PCV, respectively indicating low variability for these traits. Similar results were been reported by Bhushan *et al.* (2013) [4], Hazra *et al.* (2019) [8]. The traits spike length (10.84 and 11.69%), number of grains per spike (14.35 and 15.56%) and grain weight per spike (12.90 and 15.72%) showed moderate estimates of GCV and PCV, respectively indicating average chances for selection for these characters. Similar findings were reported by Arya *et al.* (2017) [1]. The characters grain yield per meter (7.13 and 11.05%), grain yield per plant (6.79 and 10.68%) and thousand grain weight (7.99 and 10.26%) showed low GCV and moderate PCV, respectively. Similar results were reported by Mishra *et al.* (2019) [11].

The characters tillers per meter, tillers per plant, spike length, number of grains per spike, grain weight per spike, grain yield per meter, grain yield per plant, thousand grain weight, biological yield per meter, biological yield per plant and harvest index exhibited larger variation in the values of GCV and PCV showing significant action of environment in the expression of these traits. Similar findings were reported by Kotal *et al.* (2010) [10] while for the characters days to 50% heading, days to maturity, grain filling period and plant height GCV and PCV were in close affinity indicating the scope for the selection for these traits. These results were in line with Hazra *et al.* (2019) [8] and Rani *et al.* (2018) [14].

The estimates of broad sense heritability ranged from 40.43% (grain yield per plant) to 91.40% (days to 50% heading). High heritability estimates were observed for days to 50% heading (91.40%), grain filling period (78.88%), plant height (85.66%), number of effective tillers per meter (70.69%), number of effective tillers per plant (61.71%), spike length (86.09%), number of grains per spike (85.11%), grain weight per spike (67.37%), thousand grain weight (60.56%) and biological yield per plant (61.20%) indicated variation for these characters were solely due to genetic control, less influenced by environment and selection would be effective. Similar results were obtained for the characters days to heading, plant height, spike length, thousand grain weight and Rajshree *et al.* (2018) [15] for tillers per plant and number of grains per spike. Moderate estimates of heritability were observed for days to maturity (41.52%), grain yield per meter (41.60%), grain yield per plant (40.43%), biological yield per meter (58.48%) and harvest index (48.02%) indicates variation seen were partly due to genetic control and more influence of environment. These results were in line with Mishra *et al.* (2019) [11] for grain yield and days to maturity.

The GAM values ranged from 1.70% (days to maturity) to 27.28% (number of grains per spike). For the characters like spike length (20.73%), number of grains per spike (27.28%) and grain weight per spike (21.82%) GAM was recorded high. Rani *et al.* (2018) [14] also reported high genetic advance as percent of mean for number of grains per spike and grain weight per spike. The characters days to 50% heading (14.31%), grain filling period (12.90%), plant height (15.48%), number of effective tillers per meter (10.35%), thousand grain weight (12.80%), biological yield per meter (10.79%) and biological yield per plant (11.71%) the GAM were moderate. Mishra *et al.* (2019) [11] and Yadav *et al.* (2011) [18] too reported moderate GAM for thousand grain weight and Rani *et al.* (2018) [14] for biological yield per plant. Low estimates of GAM were recorded for days to maturity (1.70%), number of effective tillers per plant (9.32%), grain yield per meter (9.47%), grain yield per plant (8.90%) and harvest index (9.50%). Mishra *et al.* (2019) [11] and Yadav *et al.* (2011) [18] also reported low genetic advance as percent mean for days to maturity and harvest index respectively.

The estimates of heritability and genetic advance alone will not yield good estimates for selection, hence for selection to be effective, heritability and genetic advance as percent of mean should be considered together. High heritability with high genetic advance were reported for spike length, number of grains per spike and grain weight per spike exhibited predominance of additive gene action with less environmental influence and effective selection. Similar

findings were reported by Rajshree *et al.* (2018) [15] for spike length and number of grains per spike, whereas high heritability with moderate genetic advance were reported for days to 50% heading, grain filling period, plant height, tillers per meter, thousand grain weight and biological yield per plant indicating predominance of both additive and non-additive gene action hence mass selection can be used for the improvement of these traits. Similar results were obtained by Naik *et al.* (2015) [12] for days to heading and thousand grain weight and Hazra *et al.* (2019) [8] for plant height and biological yield per plant, while high heritability

with low genetic advance for tillers per plant was observed which indicated predominance of non-additive gene action and selection will not be effective but heterosis breeding can be adopted. Moderate heritability with moderate genetic advance was observed for biological yield per meter showed less scope for direct selection but delayed selection might be effective and moderate heritability with low genetic advance for days to maturity, grain yield per meter, grain yield per plant and harvest index indicates high macro environmental influence in the expression of these traits.

Table 1: Analysis of variance for quantitative characters of wheat evaluated across four environments

Sl. No.	Source of variation df	Genotypes 19	Environments 3	GxE 57	E+(GxE) 60	E(linear) 1	GxE (linear) 19	Pooled deviation 40	Pooled error 152
1	Days to 50% heading	69.44**	108.57**	1.59*	6.94**	325.71**	1.83*	1.40	1.05
2	Days to maturity	9.39**	482.48**	2.46*	26.46**	1447.45**	2.43	2.35*	1.51
3	Grain filling period	45.97**	144.38**	2.88*	9.96**	433.15**	3.14*	2.62	1.80
4	Plant height	214.89**	140.75**	8.64*	15.25**	422.25**	9.95	7.59	6.06
5	Number of effective tillers per meter	172.39**	730.73**	16.17	51.90	2192.18**	33.10	7.34	47.41
6	Number of effective tillers per plant	0.05**	0.28**	0.01	0.02*	0.85**	0.01	0.00	0.01
7	Spike length	4.35**	4.02**	0.17*	0.36**	12.05**	0.18	0.15	0.12
8	Number of grains per spike	173.07**	231.55**	7.25*	18.46**	694.64**	11.99**	4.63	5.07
9	Grain weight per spike	0.32**	1.88**	0.04*	0.13**	5.63**	0.06**	0.02	0.02
10	Grain yield/meter	3563.68**	66248.27**	926.04*	4192.15**	198744.80**	1501.55**	606.37	622.93
11	Grain yield/plant	0.95**	17.63**	0.26*	1.13**	52.89**	0.40**	0.18	0.18
12	Thousand grain weight	65.92**	387.75**	9.23*	28.15**	1163.26**	17.64**	4.77	6.30
13	Biological yield per meter	24730.95**	56220.80**	3727.47	6352.13	168662.41**	4837.90	3013.57	5625.75
14	Biological yield per plant	7.02**	21.87**	0.96	2.01	65.61**	1.16	0.82	1.60
15	Harvest index	25.96**	323.37**	5.53	21.42**	970.11**	8.22	3.97	7.11

* Significant at 5 percent probability level, when tested against pooled error ** Significant at 1 percent probability level, when tested against pooled error

Table 2: Estimation of variability parameter in wheat evaluated across four environments

Sl. No.	Characters	GCV (%)	PCV (%)	h ² (%)	GAM (%)
1	Days to 50% heading	7.27	7.60	91.40	14.31
2	Days to maturity	1.28	1.98	41.52	1.70
3	Grain filling period	7.05	7.94	78.88	12.90
4	Plant height (cm)	8.12	8.77	85.66	15.48
5	Number of effective tillers per meter	5.98	7.11	70.69	10.35
6	Number of effective tillers per plant	5.76	7.33	61.71	9.32
7	Spike length (cm)	10.84	11.69	86.09	20.73
8	Number of grains per spike	14.35	15.56	85.11	27.28
9	Grain weight per spike (g)	12.90	15.72	67.37	21.82
10	Grain yield per meter (g)	7.13	11.05	41.60	9.47
11	Grain yield per plant (g)	6.79	10.68	40.43	8.90
12	Thousand grain weight (g)	7.99	10.26	60.56	12.80
13	Biological yield per meter (g)	6.85	8.96	58.48	10.79
14	Biological yield per plant (g)	6.93	8.86	61.20	11.17
15	Harvest index (%)	6.65	9.60	48.02	9.50

Conclusion

The analysis revealed significant differences among the genotypes for all the characters studied in all four sowing seasons indicating sufficient variability existing among genotypes. The mean performance of twenty genotypes across environments indicates the grain yield was seen higher when planted in normal dates of sowing recommended for wheat. Under late sown conditions there is a reduction in the grain yield. Estimation of genetic parameters revealed closer affinity of GCV and PCV for the characters days to 50% heading, days to maturity, grain filling period and plant height indicating the scope for the selection for these traits. The characters tillers per meter, tillers per plant, spike length, number of grains per spike, grain weight per spike, grain yield per meter, grain yield per

plant, thousand grain weight, biological yield per meter, biological yield per plant and harvest index exhibited larger variation in the values of GCV and PCV showing significant action of environment in the expression of these traits. High heritability with high genetic advance was reported for spike length, number of grains per spike and grain weight per spike indicating predominance of additive gene action with effective selection. Whereas high heritability with moderate genetic advance were reported for days to 50% heading, grain filling period, plant height, tillers per meter, thousand grain weight and biological yield per plant.

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