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Studies on heritability, genetic variability and genetic advance of yield and yield attributing traits in bread wheat (*Triticum aestivum* L.)

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Abstract

Sixty-five genotypes (50 crosses and 15 parents) of wheat were studied for generating scientific information on nature and magnitude of genetic variability for designing suitable breeding programme. The parental lines were grown during Rabi 2016-17 and 50 cross combinations among 10 lines and 5 testers were made and then seeds of 15 parental lines and 50 crosses were obtained. During Rabi 2017-18 the parents and F₁ s were evaluated in a randomized complete block design in three replications at Seed Breeding Farm, Department of Plant breeding and Genetics, College of Agriculture, JNKVV, Jabalpur. The data were recorded on days to 50% flowering, plant height, number of effective tillers per plant, number of spikes per plant, spike length, number of spikelets per spike, spike weight, number of grains per spike, 1000- grain weight, biological yield per plant, grain yield per plant, harvest index, spike density, canopy temperature and chlorophyll content. Maximum phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were observed for grain yield per plant. High heritability was observed for, days to 50% flowering followed by biological yield per plant. Genetic advance was observed maximum for grain yield per plant.

Keywords: Bread wheat, heritability, GCV, PCV, genetic advance

Introduction

Wheat (*Triticum aestivum* L. Em Thell.) is one of the most important cereal crops of the world and provides 20 percent food resources of the world. It is self-pollinated crop of Poaceae family and of the genus *Triticum*. There are 17 different species, out of which only 3 species are mostly cultivated throughout the world viz. *Triticum aestivum* L. (Bread wheat), *Triticum durum* (Macroni wheat), and *Triticum dicoccum* (Emmer wheat). It is widely grown over a wide range of climate from temperate, irrigated to dry, high to low rain fall areas, warm, humid to dry and cold environments. Wide adaptation of wheat has become possible due to its complex nature of the genome, which provides great plasticity to the crop.

Wheat crop was cultivated on 217 million hectares around the globe with the production of 731 million tonnes (Anonymous, 2019) [18] and in India it is around 30.56 million hectares with the production of 109.24 million tonnes (Anonymous, 2020) [19]. It has good nutrition profile with 12.1% protein, 1.8% lipids, 1.8% ash, 2.0% reducing sugars, 6.7% pentosans, 59.2% starch, 70% total carbohydrates and provides 314 Kcal/100 g of food (Lorenz *et al.* 1991) [9]. Wheat provides more nutrition to the human being in comparison to other food crops and hence it is considered as staple food for about 40% of the world's population (Patricia *et al.*, 2019) [13]. It is a challenging task for the breeders to increase the present level of production as the growing population of the country will require much more food. It is not possible to increase the area under production so, increase the productivity by evolving superior varieties and better management of crop production to cope up with increasing demands of food is the only alternative. Thus, breeding approach need to be like, which could integrate the desirable changes either through selection or cross-breeding of superior genotypes. The first basic step for any crossbreeding programme is the assessment of genetic variability among the available genotypes for desirable traits. Information about genetic parameters like heritability and genetic advance among characters under selection is very useful for predicting genetic progress in breeding programme and developing efficient breeding strategies (Falconer and Mackay, 1996) [3]. High genetic advancement as well as high heritability offers the better scope for selection. The various genetic parameters of variability, estimation of heritability and genetic advance were evaluated according to the method suggested by (Johnson *et al.*, 1955) [6].

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The present investigation was conducted with the objectives to determine the genetic variability, heritability and genetic advance for yield and related components.

Materials and Methods

Experimental materials and design

The experimental materials consisted of total 65 genotypes including 50 crosses, 10 female lines (GW 366, HD 2864, MP 1201, GW 273, GW 322, MP 3288, HI 1544, HD 2932, JW-3211 and JW 3173) and 5 testers (PBW 343, DBW 110, PBW 17, MP 3336 and Lok 1) under this study. The pure seeds of these 15 selected genotypes (parents) were grown in crossing blocks to obtain 50 cross combinations during Rabi, 2016-17. During Rabi 2017-18 these 10 lines and 5 testers along with obtained 50 crosses were grown in randomized complete block design with three replications at Seed Breeding Farm, Department of Plant Breeding and Genetics, College of Agriculture, JNKVV, Jabalpur (M.P.) Each plot consists of two rows of 2.5 m length with 20 cm spacing between the rows. The row to row and plant to plant distance was maintained by 20 cm and 10 cm respectively.

Data collection

The observation was recorded on five randomly selected plants from each genotype in each replication on 14 characters which are, days to 50% flowering, plant height (cm), number of effective tillers per plant, number of spikes per plant, number of spikelets per spike, spike weight (g), number of grains per spike, 1000-grain weight (g), biological yield per plant (g), grain yield per plant (g), harvest index (%), spike density (%), canopy temperature and chlorophyll content.

Statistical analysis

The treatment means for all the characters were subjected to compute the analysis of variance on the basis of model proposed by Panse and Sukhatme (1969) [20]. Genotypic coefficient of variability (GCV) and phenotypic coefficient of variability (PCV) were estimated as per the formula given by (Burton, 1952) [1]. Heritability estimates along with genetic advance is normally more powerful than heritability estimates alone in predicting the genetic gain under selection (Burton and Devane 1953) [21]. Genetic advance and Genetic advance as percentage of mean were estimated by the formula suggested by (Johnson *et al.*, 1955) [6]. Genetic advance refers to the improvement in the genetic value of the selected plant over the base population and is the measure of genetic gain under selection.

Results and Discussion

Genetic Variability

The estimates of Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) along with grand mean for all the 14 traits presented in (Table 1). The magnitude of PCV was greater than GCV for all the characters indicating vital role of environmental interaction in the expression of the characters. The findings were in agreement with previous study in wheat by (Imran *et al.*, 2018) [5], (Saini *et al.*, 2017) [14]. Highest GCV was observed for grain yield per plant (17.75%) followed by biological yield (13.10%), number of spikes per plant (12.91%), 1000-grain weight (12.85%) and spike weight (12.75%). Maximum PCV were observed in grain yield per plant (18.09%)

followed by spike weight (14.06%), number of spikes per plant (13.61%) and biological yield (13.31%) Similar results were also reported by (Yadav *et al.* 2014) [17] and (Kumar *et al.* 2013) [8]. The PCV values for most characters were closer than the corresponding GCV values showing little environment effect on the expression of these characters. Similar results were also observed by (Mohammed *et al.* 2011) [11]. The least difference between PCV and GCV was noticed for number of spikelets per spike, number of grains per spike and grain yield per plant indicating these characters are less influence by environment on the expression of these Characters. Moderate estimate of GCV and PCV were noticed for number of effective tillers per plant (12.60%, 13.55%), plant height (11.97%, 12.31%), number of grains per spike (11.94%, 12.40%) and days to 50% flowering (10.17%, 10.20%). Chlorophyll Content (7.56%, 8.10%) harvest Index (7.49%, 8.09%), canopy temperature (7.34%, 7.46%) and number of spikelets per spike (6.82%, 7.55%) showed low values of GCV and PCV. This suggested low variability for such characters among genotypes.

Heritability

The proportion of variability inherited from parents to offspring is manifested by heritability (Lush, 1949) [10]. In this concern, high heritability was observed for days to 50% flowering (0.99) followed by biological yield per plant (0.97), canopy temperature (0.97), 1000-grain weight (0.96), grain yield per plant (0.96) and plant height (0.95) whereas moderate for number of effective tillers per plant (0.87), chlorophyll content (0.87), harvest index (0.86) number of spikelets per spike (0.82) and spike weight (0.82). Similar results were also reported by (Soumitra *et al.*, 2016) [16]. This shows the presence of additive gene effect and selection may be made for the improvement of these characters. Whereas low heritability for spike density (0.61) exhibited that the characters were highly influenced by environmental effect and genetic improvement through selection will be difficult due to effect of environment.

Genetic advance

Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability alone however, it is necessary that a character showing high heritability will also exhibit high genetic advance (Johnson *et al.* 1955) [6]. Therefore, estimation of heritability along with genetic advance is more useful to understand the type of gene action involved in the expression of various polygenic characters. In the present study high genetic advance as percentage of mean (at 5% selection intensity) was recorded for grain yield (35.86%) followed by 1000-grain weight (25.94%), biological yield per plant (26.56%), number of spikes per plant spike (23.70%) Whereas, moderate value was observed for canopy temperature (14.89%), chlorophyll content (14.56%), harvest index (14.27%) and this indicates substantial contribution of additive gene action in the expression of the characters. Hence, direct selection for such characters would be more effective. Similar findings were reported by (Khokhar *et al.*, 2011) [22]. The traits for number of spikelets per spike (12.70%) and spike density (8.57) exhibited low heritability with low genetic advance which indicated that the characters highly influenced by environment and selection might not be effective (Hossain *et al.*, 2021) [4].

Table 1: Estimate of general mean, phenotypic coefficient of variation and genotypic coefficient of variation, heritability, genetic advance and genetic advance in percent of mean for 14 characters in wheat

S. No.	Characters	General Mean	GCV	PCV	h ² (Broad Sense)	GA	GA % of mean
1	Days to 50% flowering	70.29	10.17	10.20	0.99	14.67	20.87
2	Plant Height	78.27	11.97	12.31	0.95	18.76	23.97
3	No. of effective tillers per plant	10.15	12.60	13.55	0.87	2.45	24.14
4	No. of spike per plant	9.27	12.91	13.61	0.90	2.34	25.25
5	No. of spikelets per spike	19.40	6.82	7.55	0.82	2.46	12.70
6	Spike Weight	2.86	12.75	14.06	0.82	0.68	23.82
7	No. of grains per spike	45.93	11.94	12.40	0.93	10.88	23.70
8	1000 Grain Weight	41.47	12.85	13.12	0.96	10.76	25.94
9	Biological yield per plant	43.81	13.10	13.31	0.97	11.63	26.56
10	Grain yield per plant	15.06	17.75	18.09	0.96	5.40	35.86
11	Harvest Index	34.38	7.49	8.09	0.86	4.89	14.27
12	Spike Density	1.83	5.34	6.87	0.61	0.16	8.57
13	Canopy Temperature	24.49	7.34	7.46	0.97	3.65	14.89
14	Chlorophyll Content	46.76	7.56	8.10	0.87	6.81	14.56

*GCV-Genotypic coefficient of variation, PCV- Phenotypic coefficient of variation, h² (Broad Sense)-Heritability broad sense (%), GA- Genetic Advance 5%, GA % of mean- Genetic advance as % of Mean 5%

Conclusion

The present study illustrated the existence of wide range of variations for most of the traits among genotypes. Higher GCV and PCV were observed among genotypes with six having high broad sense heritability and maximum genetic advance as percentage of mean like, grain yield per plant, biological yield per plant, number of spikes per plant, 1000 grain weight, number of effective tillers per plant and number of grains per spike. Thus, these traits can be used as selection indices in wheat to bring about the improvement in yield.

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