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Estimation of variability and genetic parameters for yield and quality traits in spring wheat (*Triticum aestivum* L.)

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Abstract

The present investigation carried out with 19 parents (15 lines and 4 testers) and 60 F₁s evaluated in a RCBD having three replications during *Rabi* 2017-18 to assess the magnitude of genetic variability parameters heritability and genetic advance in spring wheat. Sixteen quantitative different yield and quality traits *viz.*: days to 50%, flowering, days to maturity, plant height, flag leaf area, productive tillers/plant, spike length, spikelets/spike, biological yield/plant, grains per spike, harvest index, 1000 grain weight, gluten content, protein content, ash content, grain yield/plant and phenol colour reaction (grading) included in study. The results corresponding to analysis of variance showed highly significant differences prevail among the genotypes for all the traits. The magnitude of PCV was higher than the (GCV) for all the characters under studied. This indicated that the variability for these traits in the genotypes was not much affected by the environments for the expression of these characters. High heritability coupled with the high genetic advance in % of mean was observed for grain yield/plant, biological yield/plant and ash content this indicated that these traits may be relied upon for selection of the genotypes for improvement in wheat.

Keywords: Variability, PCV, GCV, heritability, genetic advance, spring wheat

Introduction

Wheat (*Triticum aestivum* L.) is the second most universal cereal crop and performed an imperative role in food and nutrition security for this sub-continent. Wheat is the short and extremely erratic winter crop. India has secured the largest second position as producer of wheat around the world. About 20 percent of food calories for the world population are provided by wheat (FAOSTAT, 2015) [17]. It contains carbohydrate 78.10%, protein 14.70%, fat 2.10%, minerals 2.10% and consequential amount of vitamins (thiamine and vitamin-B) and minerals (zinc, iron) (Kumar *et al.*, 2011) [17]. Wheat is also a good source of trace minerals like selenium and magnesium, nutrients essential to good health (Adams *et al.*, 2002) [1]. The two mega environments namely North Western Plain Zone and North Eastern Plain Zone brought forth almost 80% of the total wheat area in the country (Shankarrao *et al.*, 2010).

In the subsequent years, the future of world agriculture has been facing an alarming issue of producing sufficient food to meet its growing demand posed by proliferative population. Recently, India is the second most populous country (1.3 billion) after China (1.41 billion) and expected to surpass that of China in roughly seven years and touching a peak 1.7 billion by 2050 (UNDESA/PD, 2017) [28]. The area under wheat is expected to decline by around 5-6 mha by 2050 due to non-agricultural activities as well as alternate crops and demand for wheat will continue to rise. Therefore, India needs to produce about 140 mt of wheat by 2050 which is more than 46% over the present production level (Vision 2050, 2017) [29]. There is hardly any scope for increment of area under wheat in our country. Therewith, the substantial changes occur in the environment day by day which affected the production of wheat.

To surmount these issues, it is necessary to increase wheat productivity and bridging the existing yield gap which can be achieved by development of improved varieties with superior yield and qualitative traits along with application of improved agronomic techniques. The success of an effective breeding programme will entirely depends upon the existing genetic variability for various economic characters in gene pool and presence of adequate variance plays an important role for productive selection of the potential parents from base population for hybridization programmes (Meles *et al.*, 2017) [21]. Heritability indicates transmissibility of a character in successive generations. High heritability coupled with high genetic advance is good indicated that a specific trait can be improved through selection (Haq *et al.* 2008) [12]. Considering this, experiment was conducted to evaluate the genetic variation present in the

genotypes with respect to yield and quality traits when they are sown timely under irrigated condition.

Materials and Methods

Experimental material and experimental site

A field experiment was implemented with 15 lines and 4 testers to develop 60 F₁s through line x tester design at the Basmati Export Development Foundation, Meerut during Rabi 2016-17. The 19 parents and 60 F₁s were evaluated in a Randomized Complete Block Design with three replications at Technology Park, Sardar Vallabhabhi Patel University of Agriculture and Technology, Meerut (U.P.) during Rabi 2017-18 for their evaluation. Experimental farm located at an elevation of 219.75 meters above mean sea level > 29° 01' N latitude and 77° 45' longitudes, representing the North Western Plain Zone. Parental genotypes were obtained from the core assortment of wheat genotypes maintained by the Department of Genetics and Plant Breeding, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut (U.P.). There were two rows plot of 5 m long with the row to row distance 25 cm and plant to plant distance 10 cm. All the recommended agronomic practices were followed to raise crop for proper expression of material.

Observation Recorded

Observations were recorded from five randomly selected plants in each plot for days to 50%, flowering, days to maturity, plant height (cm), flag leaf area (cm²), productive tillers per plant, spike length (cm), spikelets per spike, biological yield per plant (g), grains per spike, harvest index (%), 1000 grain weight (g), gluten content (%), protein content (%), ash content (%), grain yield per plant (g) and phenol colour reaction (grading).

Statistical analysis

Statistical analysis was done on the mean values of 5 competitive plants per treatment in each of three replications for 15 characters aside from phenol colour reaction (grading based). The statistical software (SPSS version 16) was used to work out analysis of variance and genotypic & phenotypic coefficient of variation, heritability, genetic advance and the statistical methods adopted were as follows. Analysis of variance was carried out for each of the characters studied as per Panse and Sukhatme (1967) [22]. For computation of genotypic and phenotypic coefficient of variations (GCV & PCV) according to Burton and de Vane (1953) [5]; for heritability in broad sense Hanson (1963) [11] and genetic advance and the genetic advance in per cent of mean Johnson *et al.* (1955) [14] were followed.

Results and Discussion

The analyses of variance revealed that there was a highly significant variation present within the genotypes for all the traits under study (Table 1). Therefore, the ample scope for further selection of different yield and quality traits for the

wheat improvement and also indicated that the genotypes selected for research were quite variable and constant levels of variability are present among them. The present findings corroborate the earlier reports of Arya *et al.*, (2017), Kumar *et al.*, (2018), Imran *et al.*, (2018) [3, 18, 13] in wheat.

The values of genotypic and phenotypic coefficient of variation, heritability, genetic advance and genetic advance as percent of mean (5%) were given in Table 2. The categorization of the genotypic and phenotypic variability is difficult because both of them do not have any clear limits and. Therefore, both are unsuitable for comparison between genotypes and traits. To overcome this concern, the genotypic and phenotypic coefficients of variation can be effectively utilized (Dinesh and Kerkhi, 2015) [16]. The relative values obtained for genotypic and phenotypic coefficient of variation which indicates presence of the variation. The values recorded for genotypic coefficient of variation (GCV) was lower than the phenotypic coefficient of variation (PCV) for all the characters under observation indicating. The magnitude of genotypic coefficient of variation was lower than phenotypic coefficient of variation for all the characters studied indicating ample of variability not only due to genotype but also environmental interaction in the expression of the characters. Aside from that, both phenotypic and genotypic coefficients of variation were found to be in close agreement with each other. The findings were in agreement with previous study in wheat Gupta *et al.* (2009) and Shankarrao *et al.* (2010). A wide range of phenotypic coefficient of variation (2.97–12.04%) and genotypic coefficient of variation (2.97–11.97%) was observed for the traits studied (Table 2). As per Sivasubramanian and Madhavamenon (1973) [26], PCV and GCV were classified as high (>25%), medium (10–25%) and low (<10%). The presence of moderate PCV and GCV were observed for grain yield per plant (12.09% & 11.97%), ash content (11.56% & 11.16%) and biological yield per plant (10.32% & 10.26%). Hence, it is considered to have moderate amount of variability and hence could be improved through selection in later generations. These findings are in general agreement with the results of Fikre *et al.* (2015), Wahidy *et al.* (2016) and Imran *et al.* (2018) [9, 30, 13]. The low PCV and GCV were recorded for productive tiller per plant (7.89% & 7.60%), spike length (6.53% & 6.24%), plant height (5.15% & 5.12%), harvest index (5.16% & 5.07%), gluten content (5.81% & 4.87%), flag leaf area (4.65% & 4.34%), protein content (5.08% & 4.26%), days to 50% flowering (4.30% & 4.20%), grains per spike (4.15% & 4.09%), days to maturity (3.80% & 3.66%), spikelets per spike (3.54% & 3.20%) and 1000 grain weight (2.97% & 2.63%) that elucidate the presence of narrow genetic base for such traits. The present findings are in agreement with those of Patel and Monpara (2007), Kumar *et al.* (2013) and Imran *et al.* (2018) [23, 4, 13]. Hence, hybridization can be used to widen the genetic base, followed by pedigree selection in the advanced generations for improvement for these traits.

Table 1: Analysis of variance for different characters in spring wheat

Source of variation	DF	Days to 50% Flowering	Days To maturity	Plant height	Flag leaf area	Productive tillers/ plant	Spike length	Spikelets/ spike	Biological yield/plant
Replication	2	1.33	0.62	0.12	1.61	0.01	0.04	0.01	0.50
Treatments	78	39.17**	71.47**	59.60**	9.08**	1.78**	1.19**	1.29**	85.55**
Error	156	0.65	1.77	0.27	0.42	0.04	0.04	0.09	0.33

Source of variation	DF	Grains/ spike	Harvest index	1000 grain weight	Gluten content	Protein content	Ash content	Grain yield/plant
Replication	2	0.21	0.28	0.05	0.07	0.002	0.06	0.07
Treatments	78	14.01**	3.81**	0.61**	0.96**	0.102**	19.04**	12.70**
Error	156	0.15	0.33	0.08	0.12	0.002	0.07	0.15

*, ** Significant at 5% and 1% probability level respectively

Table 2: Estimates of mean, range, phenotypic (PCV) and genotypic (GCV) coefficient of variation, heritability in broad sense (h^2b) and genetic advance for 15 characters in spring wheat

Characters	Mean	Range	PCV (%)	GCV (%)	Heritability (%) (Broad sense)	Genetic advance	Genetic advance (% of mean)
Days to 50% flowering	85.36	79.33-93.00	4.30	4.20	95.22	7.20	8.44
Days to maturity	131.56	121.67-140.33	3.80	3.66	92.91	9.57	7.28
Plant height	86.90	78.30-96.33	5.15	5.12	98.65	9.10	10.47
Flag leaf area	39.13	32.94-43.03	4.65	4.34	87.39	3.27	8.36
Productive tillers/ plant	9.99	8.53-12.07	7.89	7.60	92.78	1.51	15.08
Spike length	9.96	8.60-11.67	6.53	6.24	91.38	1.22	12.29
Spikelets/ spike	19.79	18.03-21.60	3.54	3.20	81.45	1.18	5.95
Biological yield/ plant	51.97	40.50-68.97	10.32	10.26	98.85	10.92	21.01
Grains/ spike	52.60	47.87-57.93	4.15	4.09	96.86	4.36	8.29
Harvest index	40.35	35.95-44.19	5.16	5.07	96.60	4.14	10.27
1000 grain weight	41.01	38.85-43.97	2.97	2.63	78.10	1.96	4.78
Gluten content	8.65	7.40-9.62	5.81	4.87	70.19	0.73	8.40
Protein content	12.42	11.11-13.75	5.08	4.26	70.25	0.91	7.35
Ash content	1.63	1.30-2.08	11.56	11.16	93.13	0.36	22.18
Grain yield/plant	21.01	15.58-27.05	12.04	11.97	96.76	5.15	24.51

Heritability decides the resemblance of progeny with their parents (Falconer, 1981) [6]. Heritability in broad sense quantifies the proportion of phenotypic variance that is due to genotype, *i.e.*, heritable. The estimates of heritability in broad sense were arbitrarily categorized according to Johnson *et al.* (1955) [14] in three major groups, namely, high heritability (> 60%), moderate generally (30% - 60%) and low heritability (< 30%). High estimates of broad sense heritability was observed for all traits under study *viz*: grain yield per plant (96.76%), biological yield per plant (98.85%), plant height (98.65%), grains per spike (69.86%), harvest index (96.60%), days to 50% flowering (95.22), ash content (93.13%), days to maturity (92.91%), productive tillers per plant (92.78%), spike length (91.38%), flag leaf area (87.39%), spikelets per spike (81.45%), 1000 grain weight (78.10%), protein content (70.25%) and gluten content (70.19%) as discussed by Fellahi *et al.* (2013), Tabussum *et al.* (2017) and Adhikari *et al.* (2018) [8, 27, 2]. This is an indication that any genotype can be differentiating by its phenotype correctly. Hence, there is a predominance of additive genetic variation in the expression of these characters and the effectiveness of selection in the early segregating generations for improving these traits. The estimates of heritability are more advantageous when expressed in terms of genetic advance. High heritability correlated with the high genetic advance in per cent of mean was observed for the characters like grain yield per plant, biological yield per plant and ash content. The corroborative findings were also reported by Sabit *et al.* (2017) and Tabussum *et al.* (2017) [24, 27]. High heritability coupled with the moderate genetic advance in per cent of mean was exhibited by characters namely plant height, harvest index, productive tillers per plant and spike length. Similar conclusions were also reported by previous researchers

namely Bhushan *et al.* (2013) and Kumar *et al.* (2018) [4, 19]. Therefore, these characters show additive genetic variation and improvement through direct selection could be possible for these characters.

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