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Assessment of Genetic Variability to Emphasizes the Yield and its Components in Bread Wheat (*Triticum aestivum* L.)

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ABSTRACT: An experiment was conducted to find out the extent genetic variability for yield and its contributing characters in 40 bread wheat genotypes to contribute a significant work in order to wheat improvement programme. Research work has been conducted at SVPUAT, Meerut, (U.P.) in Randomized Block Design with 3 replications. Analysis of variance revealed substantial amount of variability among the genotypes for all the characters under study. The estimates of GCV in all the traits studied were lower than those of the PCV. Most of the characters displayed high heredity. High genetic advance coupled with high heritability (as % mean) were recorded for gluten content, grain yield per plant, biological yield per plant, harvest index and number of productive tillers per plants, showing that heritability might be to additive gene effects and direct selection for these traits may be successful. Thus these are traits which may be used for an effective breeding (hybridization) programme in order to improve yield in bread wheat.

Keywords: GCV and PCV, Heritability, Variability, Genetic advance.

INTRODUCTION

Wheat is world's leading cereal crop, cultivated near about 217 million hectares with a production of 731 million tonnes of grain with 3424 kg/ha productivity (2020-21). Among the three main cereals, wheat, maize, and rice the wheat is a staple crop that is essential globally and contributes significantly to daily protein and calorie consumption (Kizilgeci *et al*., 2021; Iqbal *et al*., 2021). India wheat production has touched the landmark figure of 108.75 million tonnes (3rd AE, 2021) from 31.76 million hectares (13.43% of global area) registering an all-time highest crop productivity of 3424 kg/ha (Annual report 2020-21, IIWBR, Karnal). After China, India is the world's second-largest producer of wheat (Kumar *et al.,* 2019). It is primarily grown on the plains of India, as opposed to the mountainous regions of North India, the Nilgiris, and the Palani hills in South India, where it is grown in the hills. Wheat production is affected by several environmental factors responsible for yield losses over world including India. According to reports, drought and heat stress brought on by climate change have decreased wheat productivity and production by 5.5% over the past three decades (Daryanto *et al.,* 2016). To fulfill the anticipated demand for wheat, it is necessary to create wheat cultivars with increased yield potential and biotic and abiotic stress resistance. One of the main factors limiting wheat yield and production is drought stress. According to Daryanto *et al.* (2016), 40% reduction in moisture availability in wheat might result in a yield loss of 21% on average. This requirement can be satisfied by creating high yielding cultivars with improved biotic and abiotic stress resistance. The complex polygenic trait of grain yield is highly influenced by genetic, physico-morphological, ecological, and pathological factors. A cultivar's and genotype's hereditary potential is reliant on stability and productivity. Genetically related to yield contributing features such as yield components (productive tillers, number of grains, 1000 grain weight, etc.), there genetic type and magnitude of association are accountable for realisation of yield potential impacted by altering seraphic, agroclimatic condition. Thus, it is essential to accumulate information on these aspects to resolve and quantify their mode of contribution to grain yield. Existence of large genetic variability is a prime pre-requisite for any breeding programme aimed at developing new varieties with high yield potential and yield stability. If a trait's heritability is high, it should be very simple to improve that trait. Heritability provides an index of the transmissibility to quantify the genetic link of a trait in the population. Genetic advance estimates provide insight into an experiment's mean performance improvement of the chosen clusters over the base populations. Breeding programme not getting proper flow due to lack of information of variable genotypes and traits regarding grain yield. Superior people can be chosen through selection due to genetic variance. Lack of genetic variation, loss of genetic diversity in better cultivars, substantial environmental variance encountered during phenotyping, and other variables have all made it difficult to breed wheat populations to tolerate dryness. Stalling yields and wheat's great susceptibility to environmental stress are both effects of genetic variety loss. (Keneni*et al*., 2012; Voss-Fels*et al*., 2015).This aspect need an extensive research, as most of the quality constituents of wheat are having contrary relationship with yield. The present study aim to vanquish all these constraints and to help the breeders by providing the information about variability present in wheat in particular genotypes for yield and its contributing traits so researcher can utilize this for wheat improvement.

MATERIAL AND METHODS

The present experiment was carried out during Rabi 2019-20 at Technology Park of SVPUAT, Meerut-250110 (U.P.) using 40 indigenous genotypes of wheat (*Triticum aestivum* L).The experiment was laid out in Randomized Block Design with 3 replication. All the recommended agronomic practices were followed to raise a good crop of wheat with keeping row to row spacing 20 cm. Observations were recorded on yield and yield attributing characters. All the observations were taken from each plot, on randomly five selected plants from each genotype. The data were recorded for the following characters: 1. Days of 50% flowering, 2. Days to maturity, 3. Plant height (cm), 4. Number of productive tillers/plant, 5. Spike length (cm), 6. Total number of spikelet's/spike, 7. Number of grains/ spike, 8. Biological yield / plant (g), 9. Grain yield / plant (g), 10. Harvest index (%), 11. 1000 seed weight (g), 12. Gluten content (%). For statistical analysis, the genotype mean values from each replication were used. The procedures used to analyse the RBD were those that Panse and Sukhatme specified (1985).Heritability in broad sense h^2 was computed as a ratio of genotypic variance to phenotypic variance by applying the method of Allard, (1960). According to Johnson, *et al.,* (1955) recommendation, the projected genetic advance under selection for the various traits was estimated.

RESULT AND DISCUSSION

Analysis of variance. The analysis of variance revealed significant differences for all the 12 characters studied in 40 wheat genotypes Table 1 and it revealed that mean sum of squares due to genotypes were highly significant for all the characters under study *viz.,* days of 50% flowering (21.45),days to maturity (114.84), plant height in cm (120.82), number of productive tillers per plant (1.04), spike length in cm (1.24), total number of spikelets per spike (4.68), number of grains per spike (23.67), 1000 seed weight in gram (8.90), gluten content in % (14.84), biological yield per plant in gram (79.10), harvest index in % (67.92), grain yield per plant in gram (14.17), . The results of the present study are in accordance with the Paul *et al.* (2006); Singh and Sharma (2007); Yousaf *et al.* (2008); Kalimullah *et al.,* (2012); Ashish *et al.,* (2020); Prasad *et al.* (2021) who had also reported the high variability in wheat for different traits.

Table 1: Analysis of variance.

Source of variation	DF	1	2	3	4	5	6	7	8	9	10	11	12
Replication	2	0.81	1.02	1.16	0.00	0.19	0.17	2.35	0.24	0.09	0.43	0.56	0.07
Treatment	39	21.45**	114.84**	120.82**	1.04**	1.24**	4.68**	23.67**	8.90**	14.84**	79.10**	67.92**	14.17**
Error	78	1.53	4.91	4.37	0.02	0.08	0.22	1.98	0.49	0.05	0.46	0.84	0.07

*, ** significant at 5% and 1% level, respectively

1.Days of 50% flowering;
2. days to maturity
3.Plant heigth cm;
4. No. of productive tillers /plants
5.Spike Length cm
6. Total no. of spikelets/ spikes
7.No. of Grains / spikes
8.1000 Seeds weight
9.Gluten content %
10. Biological yield / plant gm
11.Harvest index %
12.Grain yield / plant gm

Genetic variability, Heritability and Genetic Advance. The study of genetic variability including mean, genotypic and phenotypic coefficient of variation, heritability and genetic advance presented in Table 2.

Phenotypic and genotypic coefficient of variation. In the present study both phenotypic and genotypic coefficient of variation was found to be high for gluten content % (P 27.84, G 27.69) and grain yield per plant (P 21.12, G 20.97,). Similar observation were also reported by Kalimullah *et al.* (2012); Ranjana *et al.* (2013); Dutamo *et al.* (2015); Arya *et al.* (2017); Kumar *et al.* (2019); Prasad *et al.* (2021); Mohan, *et al.* (2022). Moderate PCV and GCV were observed in number of productive tiller per plant (P 10.89, G 10.60), biological yield per plant (P 17.70, G 17.55), harvest index (P 13.55, G 13.30). Low PCV and GCV were found for Days to 50% flowering (P 3.11, G 2.80), days to maturity (P 4.96, G 4.66), plant height (P 6.94, G 6.58), spike length (P 7.10, G 6.49), total number of spikelets per spike(P 7.29, G 6.80), number of grains per spike (P 5.85, G 5.19), 1000 seed weight (P 4.69, G 4.33).

Heritability: High heritability observed in days to 50 % flowering (81.26), days to maturity (88.17), plant height (89.89), number of productive tiller per plant (94.75), spike length (83.59), total number of spikelet per spike (87.03), biological yield per plant (98.26), grin yield per plant (98.57), harvest index (96.40), 1000 seed weight (85.10), gluten content (98.92) . It is in confirmation with the results of earlier workers Kumar *et al*.,(2003); Saktipada *et al.* (2008); Ajmal *et al.* (2009); Kumar *et al.,* (2012), Kumar *et al.,* (2013); Fellahin *et al.,* (2013); Bhushan *et al.* (2013); Desheva and Kyosev *et al.* (2015); Dutamo *et al.* (2015); Fikre *et al.,* (2015); Arya *et al.* (2017); Ashish *et al.* (2020); Prasad *et al.* (2021); Mohan *et al.* (2022). Moderate heritability was observed in number of grains per spikes (78.51) which is according to the previous report by Desheva and Kyosev *et al.* (2015).

Genetic Advance. High genetic advance were observed for number of productive tiller per plant (21.26), biological yield (35.83), grin yield per plant (42.88), harvest index (26.90), gluten content (56.73). These results were confirmed by earlier findings of Kumar *et al.* (2003); Saktipada *et al.* (2008); Ajmal *et al.* (2009); Kumar *et al.* (2012); Kumar *et al.* (2013); Bhushan *et al.* (2013); Desheva and Kyosev *et al.* (2015); Fikre *et al.* (2015); Arya *et al.* (2017); Ashish *et al.* (2020). Moderate genetic advance was observed in total number of spikelets per spike (13.06), plant height (12.85), spike length (12.22) which is according to the previous report by Kumar *et al.* (2012); Fikre *et al.* (2015). Low genetic advance was observed in number of grain per spikes (9.47), days to maturity (9.01), 1000 seeds weight (8.22) and days of 50% flowering (5.20) which is according to the previous report by Saktipada *et al.* (2008).

High Heritability observed with High Genetic Advance for number of productive tiller per plant (94.75, 21.26), biological yield (98.26, 35.83), grin yield per plant (98.57, 42.88), harvest index (96.40, 26.90), gluten content (98.92, 56.73).

Table 2: Analysis of Genetic Variability.

Genotypes	Mean	Heritability (%)	GA	GA% mean	GCV (%)	PCV (%)
Days of 50% flowering	91.99	81.26	4.78	5.20	2.80	3.11
days to maturity	129.99	88.17	11.71	9.01	4.66	4.96
Plant height cm.	94.70	89.89	12.17	12.85	6.58	6.94
No. of productive tillers /plants	5.51	94.75	1.17	21.26	10.60	10.89
Spike Length cm.	9.59	83.59	1.17	12.22	6.49	7.10
Total no. of spikelets/ spikes	17.92	87.03	2.34	13.06	6.80	7.29
No. of Grains / spikes	51.84	78.51	4.91	9.47	5.19	5.85
1000 Seeds weight	38.70	85.10	3.18	8.22	4.33	4.69
Gluten content %	8.02	98.92	4.55	56.73	27.69	27.84
Biological yield / plant gm.	29.18	98.26	10.45	35.83	17.55	17.70
Harvest index %	35.55	96.40	9.56	26.90	13.30	13.55
Grain yield / plant gm.	10.34	98.57	4.43	42.88	20.97	21.12

Table 3: List of promising genotypes for each traits.

Traits	Genotypes
1. Days of 50% flowering	HD-2664, NW-307,HD-3045
2. Days to maturity	HD-3045, HD-3076, NW-305
3. Plant height (cm)	WCW-98-4, PBW-550,HD-2864
4. Number of productive tillers/plant	DBW-621-50, HD-3086, NW-307
5. Spike length (cm)	WB-1, NW-115,HD-3086
6. Total number of spikelet's/spike	WB-1, NW-115, HD-3086
7. Number of grains/ spike	PBW-62-50, HD-3086,NW-115
8. Biological yield / plant (g)	NW-306, NW-307
9. Grain yield / plant (g)	HD-3086, NW-104, PBW-226, WB-1
10. Harvest index (%)	HD-3086, PBW-226, NW-104
11. 1000 seed weight (g)	HD-3086, WB-1, PBW-5903
12. Gluten content (%)	HD-2664, HD-3045, PBW-343

Hence direct selection of genotypes can be done through these characters for further improvement of genotypes of wheat. Such finding were earlier reported by Ajmal *et al.* (2009); Kumar *et al.* (2012); Bhushan *et al.* (2013); Dutamo *et al.* (2015); Arya *et al.* (2017); Kumar *et al.* (2019); Ashish *et al.* (2020); Mangroliya *et al.* (2020); Prasad *et al.,* (2021); Mohan *et al*. (2022).

CONCLUSION

It is established that there was sufficiently wide variation in the experimental material because the current analysis found significant differences for all the features under examination. High heritability coupled with high genetic advance observed for gluten content, grain yield per plant, biological yield per plant, harvest index, number of productive tillers per plants. Hence, direct selection of genotypes can be done through these characters for further improvement of genotypes of wheat. The estimates of PCV and GCV were high for characters *viz.,* gluten content, and grain yield per plant. Moderate PCV and moderate GCV were observed for biological yield per plant, harvest index, number of productive tillers per plants. Variability analysis revealed that important agronomic characters namely gluten content, grain yield per plant, biological yield per plant, 1000 seed weight, number of productive tillers per plants and plant height. The study provides the opportunity to identify the promising genotypes which can be used in direct selection for further utilization in breeding (hybridization) programme.

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Conflict of interest. None.

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