



ISSN (E): 2277- 7695

ISSN (P): 2349-8242

NAAS Rating: 5.23

TPI 2021; 10(5): 341-345

© 2021 TPI

www.thepharmajournal.com

Received: 02-02-2021

Accepted: 12-03-2021

Amitava Roy

Department of Genetics and Plant Breeding, College of Agriculture, Govind Ballabh Pant University of Agriculture and Technology, Pantnagar, U.S. Nagar, Uttarakhand, India

Anil Kumar

Department of Genetics and Plant Breeding, College of Agriculture, Govind Ballabh Pant University of Agriculture and Technology, Pantnagar, U.S. Nagar, Uttarakhand, India

Anu Singh

Department of Genetics and Plant Breeding, College of Agriculture, Govind Ballabh Pant University of Agriculture and Technology, Pantnagar, U.S. Nagar, Uttarakhand, India

Anusri Mandi

Department of Agronomy, Bidhan Chandra Krishi Viswa Vidyalaya, Mohanpur, West Bengal, India

Mainak Barman

Department of Genetics and Plant Breeding, Bidhan Chandra Krishi Viswa Vidyalaya, Mohanpur, West Bengal, India

Corresponding Author:

Amitava Roy

Department of Genetics and Plant Breeding, College of Agriculture, Govind Ballabh Pant University of Agriculture and Technology, Pantnagar, U.S. Nagar, Uttarakhand, India

Analysis of genetic diversity and correlation studies on grain yield and its component characters in bread wheat (*Triticum aestivum* L. em Thell) genotypes

Amitava Roy, Anil Kumar, Anu Singh, Anusri Mandi and Mainak Barman

Abstract

The present research programme investigates forty-nine genotypes of bread wheat consisting of 33 F₁s obtained by crossing eleven lines with three varieties in a line x tester mating design along with their parents and two well-known checks. The experiment was laid out in a randomized block design with three replications with each row of 1m. Results revealed considerable genetic variability among the genotypes. Traits like grain yield per plant and number of tillers per plant exhibited higher values of PCV with moderate GCV. High heritability with moderate values of genetic advance were recorded for grain weight per spike (17.688%) followed by number of grains per spike (17.392%), biological yield per plant (14.664%), 1000 grain weight (11.996%) indicating involvement of additive gene action in the inheritance of these traits and hence selection along with progeny testing can be employed for improvement of these characters. Correlation studies revealed that number of tillers per plant, harvest index, biological yield per plant have significant positive correlation with the trait grain yield per plant. Therefore, selection for these traits will ultimately aid into increase in overall productivity of the genotypes. It was also observed that days to maturity had a negative association with the yield; hence, early maturing cultivars should be preferred while breeding for the higher yield.

Keywords: Bread wheat, correlation coefficient, GCV, genetic advance, genetic divergence, heritability and PCV

Introduction

Common bread wheat (*triticum aestivum*) is one of the most important grain crops serving as staple food for around 40% of the population throughout the globe (Arya *et al.*, 2017) [13]. India holds second position in terms of overall wheat production after China having highest coverage in terms of area with a record production of 101.20 million tonnes in 2018-19 with an average productivity of 3424 kg/ha (MoA & FW, 2019) [17]. With the ongoing expansion of population in the nation, there will be requirement of more than 140 million tons of wheat grain to be produced by 2050, which is about 40% increase from our present production scenario (Singh *et al.*, 2019) [22]. To achieve this goal there is an urgent need to improve the yield per unit area as the crop acreage cannot be expanded beyond a ceiling. Hence, it is important to increase the genetic potential of the varieties to increase the overall productivity of the crop.

Crop yield being a complex genetic trait is significantly influenced by various interrelated component traits associated with it and considerably varies according to the prevailing environmental fluctuations. Therefore, direct selection for yield without taking component characters into consideration may produce misleading results with commissioning of a faulty breeding programme. Hence, to increase overall yield our objective must be directed towards increasing the effects of the components with favourable action and minimizing the effects of the undesirable factors. Hence, correlation analysis could be an important tool to decipher the inter relationships between yield and the component traits. Genetic variability and correlation analysis helps us to identify the genetic associations of different plant traits and their association with the overall productivity levels (Haydar *et al.*, 2020) [10].

Genetic variability is the prerequisite for undertaking any successful breeding programme. Therefore, it is very important to have fine knowledge of different variability parameters and their relative significance to improve the overall production level. Information on genetic variability parameters along with heritability and genetic advance provides guidance in

predicting response of a genotype in a breeding programme and leads to the formulation of an efficient breeding programme. Parents with higher genetic distance will be able to produce higher extent of heterosis in the progeny (Joshi and Dhawan, 1966) [12].

Taking into consideration all the previously mentioned aspects the objective of the present research investigation is to evaluate 49 genotypes of wheat in terms of genetic variability, heritability and genetic advance for grain yield and its component characters to identify and isolate the genotypes which are having higher potential for utilization in breeding for improved yield levels.

Materials and Methods

The experimental material of the present research investigation was conducted with 49 genotypes of bread wheat which consisted thirty-three F1s generated by crossing

eleven lines with three varieties to be utilized as a tester in a line x tester mating design. These 33 F1s along with fourteen parents and two standard checks *viz.*, UP 2855 and HD 2967 were then evaluated in rabi 2019-20 at Norman E. Borlaug Crop Research Centre, G.B. Pant University of Agriculture and Technology, Pantnagar in randomized block design with three replications. Details of all the genotypes are given in the Table 1. Each row was one meter in length and the plants were spaced at 20 cm between row to row and 10 cm between plant to plant. Recommended cultural practices were provided accordingly to the plants. Observations were recorded on thirteen characters *viz.*, days to 75% heading, days to maturity, number of productive tillers per plant, plant height, peduncle length, spike length, number of spikelets per spike, number of grains per spike, grain weight per spike, 1000 grain weight, biological yield per plant, grain yield per plant and harvest index.

Table 1: Lines, Testers and Checks utilized for the study

SL. No.	Lines	Testers	Checks
1.	QBP 12-11	HD 3237	UP 2855
2.	SOKOLL	PBW 725	HD 2967
3.	WH 1182	HI 1621	
4.	QLD 75		
5.	PRL/2*PASTOR*2//FH6-1-7/3/KINGBIRD#1//...		
6.	QLD 65		
7.	NW 6036		
8.	K 1402		
9.	VORB/4/D67.2/PARANA 66.270		
10	HPBW 01		
11.	NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR/5/...		

Statistical analysis

Data recorded on the various characters were analyzed utilizing analysis of variance carried out by Randomized Block Design to test the significance of differences among all the genotypes. Significance of difference among the genotypes (treatment means) was tested by 'F' test at 5% level.

The genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and environmental coefficient of variation (ECV) were calculated according to the formula suggested by Burton and Devane (1953) [5].

$$\text{Genotypic coefficient of variation} = \frac{\sqrt{\sigma_G^2}}{\bar{x}} \times 100$$

$$\text{Phenotypic coefficient of variation} = \frac{\sqrt{\sigma_P^2}}{\bar{x}} \times 100$$

$$\text{Environmental coefficient of variation} = \frac{\sqrt{\sigma_e^2}}{\bar{x}} \times 100$$

Heritability in broad sense was estimated according to the formula suggested by Falconer et al. (1996) [7] as follows.

$$h^2_b = \frac{\sigma_G^2}{\sigma_P^2} \times 100$$

Genetic advance in terms of percent of mean for each character was calculated according to Johnson *et al.* (1955) [11].

$$\text{GAM} = \frac{\text{G.A.}}{x_i}$$

Analysis of correlation coefficient was carried out according to Al-Jibouri *et al.* (1958) [1].

Results and Discussion

Analysis of variance revealed that mean sum of squares for all the characters were highly significant ($P \leq 0.05$). Mean sum of square was observed highest for biological yield per plant (376.385) followed by number of grains per spike (86.169), grain yield per plant (81.302), plant height (43.88), 1000 grain weight (20.243), days to maturity (16.42), number of tillers per plant (13.332) harvest index (12.152), days to 75% heading (10.19), peduncle length (9.068), number of spikelets per spike (1.493), spike length (0.818) and grain weight per spike (0.119). Analysis of variance revealed that there was significant variability existing among all the genotypes for all the characters studied. Therefore, there is a good scope for improvement of the genotypes for the characters. These results are found in accordance with the experimental findings of Cheema *et al.* (2006) [6], Bhushan *et al.* (2013) [15] and Nizamani *et al.* (2020) [19].

Components of genetic variability

Genetic variability with respect to different characters measured in terms of range, general mean and coefficients of variation along with heritability and genetic advance is presented in table 2.

Estimates of phenotypic coefficients of variation were found higher than the estimates of genotypic coefficients of variation for all the characters under study. This reflected the considerable influence of environmental variation in inheritance of these traits. Traits like grain yield per plant (15.806%) followed by number of tillers per plant (15.162%),

biological yield per plant (11.832%), number of grains per spike (11.046%) and grain weight per spike (10.196%) exhibited moderate estimates of phenotypic coefficients of variation, whereas, remaining all the other traits had low estimates of PCV. Likewise, moderate values for genotypic coefficients of variation were recorded for grain yield per plant (13.368%), followed by number of tillers per plant

(11.563%), while rest of the traits registered low values of GCV. The results observed are in agreement with earlier findings of Yashpal *et al.* (2005) [25], Sidharthan *et al.* (2007) [23], Nukasani *et al.* (2013) [20], Fikre *et al.* (2015) [9], Zerga *et al.* (2016) [26], Arya *et al.* (2017) [3], and Kumar *et al.* (2019) [22].

Table 2: Analysis of variance for different characters in wheat

Source Of variation	d. f.	Days to 75% heading	Days to maturity	Number of tillers per plant	Plant height (cm)	Peduncle length (cm)	Spike length (cm)	Number of spikelets per spike
Replication	2	12.660	20.959	25.309	257.035	12.586	2.432	10.877
Treatment	48	10.192**	16.418**	13.332**	43.888**	9.068**	0.818**	1.493**
Error	96	2.910	5.834	2.579	18.238	5.124	0.296	0.823

Source of variation	d. f.	Number of grains per spike	Grain weight per spike	Thousand grain weight (g)	Biological yield per plant (g)	Grain yield per plant (g)	Harvest Index (%)
Replication	2	43.257	0.002	0.223	1,032.037	170.477	5.255
Treatment	48	86.169**	0.119**	20.243**	376.385**	81.302**	12.152**
Error	96	8.029	0.007	1.122	68.052	9.524	1.898

*, ** significant at 5% and 1% probability levels, respectively

Table 3: Variability parameters with respect to different characters in wheat

Sl. No.	Character	GM	Range (Min.-Max.)	CD5%	CD1%	CV%	PCV	GCV	ECV	h_{bs}^2 (%)	GA	GA (% of mean)
1	Days to 75% heading	88.027	84.667-91.333	2.765	3.66	1.938	2.624	1.77	1.937	45.481	2.164	2.459
2	Days to maturity	127.837	123.33-132.33	3.915	5.183	1.889	2.394	1.469	1.89	37.684	2.375	1.858
3	Number of tillers per plant	16.374	12.783-22.33	2.603	3.446	9.807	15.162	11.563	9.807	58.158	2.974	18.165
4	Plant height (cm)	90.045	83.733-101.9	6.922	9.164	4.743	5.748	3.247	4.743	31.916	3.403	3.779
5	Peduncle Length (cm)	33.663	29.675-37.167	3.669	4.857	6.724	7.538	3.406	6.725	20.423	1.068	3.171
6	Spike length (cm)	11.356	9.767-12.408	0.881	1.167	4.788	6.036	3.675	4.786	37.071	0.523	4.609
7	Number of spikelets/spike	21.628	20.22-23.26	1.47	1.946	4.193	4.729	2.186	4.193	21.364	0.45	2.081
8	No. of grains/spike	52.849	43.933-65.917	4.593	6.080	5.362	11.046	9.657	5.363	76.437	9.192	17.392
9	Grain weight/ spike (g)	2.064	1.655-2.61	0.136	0.179	4.051	10.196	9.357	4.05	84.215	0.365	17.688
10	1000 grain weight (g)	39.977	35.043-44.65	1.717	2.273	2.65	6.849	6.315	2.651	85.028	4.796	11.996
11	Biological yield/plant (g)	110.468	90.16-130.633	13.370	17.701	7.468	11.832	9.177	7.469	60.164	16.199	14.664
12	Grin yield per plant (g)	36.592	27.8-47.72	5.002	6.622	8.434	15.806	13.368	8.434	71.527	8.522	23.289
13	Harvest Index (%)	33.039	30.28-38.55	2.233	2.957	4.17	6.979	5.596	4.17	64.29	3.054	9.242

Estimation of heritability and genetic advance

Heritability provides information regarding the transmission of traits from parents to progeny. Higher estimates of heritability in conjunction with higher genetic advance values provide a useful criterion for selection (Johnson *et al.*, 1955) [11]. In our investigation high heritability with moderate values of genetic advance were recorded for grain weight per spike (17.688%) followed by number of grains per spike (17.392%), biological yield per plant (14.664%), 1000 grain weight (11.996%) and moderate heritability with moderate genetic advance was observed for tillers per plant (18.165%). It is a reflection of significant predominance of additive gene action involved in the inheritance of the trait. Therefore, selection along with progeny testing may be beneficial in the breeding programme for the improvement of these traits. While, traits like spike length, plant height, peduncle length, days to 75% heading, number of spikelets per spike and days to maturity had low heritability with low GA which indicated presence of non-additive gene action and influence of environment in the inheritance of these traits. Therefore these traits are not useful for selection and further utilization in breeding programme. The results presented are in a close confirmation with earlier observations of Yashpal *et al.* (2005) [25], Kumar *et al.* (2014) [14], Naik *et al.* (2015) [18], Fikre *et al.* (2015) [9] and Bhanu *et al.* (2018) [4].

Analysis of correlation coefficient

Analysis of correlation coefficient revealed that number of tillers per plant, harvest index, biological yield per plant possessed significant positive correlation with the trait grain yield per plant. Therefore, selection for these traits will ultimately aid into increase in overall productivity of the genotypes. It was also observed that days to maturity had a negative association with the yield; hence, early maturing cultivars should be preferred while breeding for the higher yield.

Among other traits plant height showed significant positive correlation with days to 75% heading and days to maturity while, showing negative correlation with number of tillers per plant thus indirectly hampering the yield levels. Number of spikelets per spike was observed having a positive correlation with biological yield and grain yield per plant and grain weight per spike had a significant positive correlation with harvest index. Harvest index had a strong positive correlation with number of tillers per plant, 1000 grain weight and number of tillers plant with grain yield.

Spike length showed a positive correlation with peduncle length while having strong negative correlation with biological yield per plant and tillers per plant. Similarly, spikelets per spike had a positive correlation with days to 75% heading, days to maturity, plant height, number of grains per spike and peduncle length. Biological yield per plant was

observed with a strong positive correlation with number of spikelets per spike, harvest index and grain yield, whereas, number grains per spike was positively correlated with days to 75% heading and peduncle length. 1000 grain weight possessed a positive correlation with plant height and grain weight per spike had a significant positive association with harvest index. Lastly, peduncle length was observed with

strong positive correlation with plant height, spike length and number of grains per spike. The findings from present research investigation are in accordance with the previous observations of Majumdar *et al.* (2008) [16], Fellahi *et al.* (2013) [8], Nukasani *et al.* (2013) [20], Zerga *et al.* (2016) [26] Bhanu *et al.* (2018) [4], Sohail *et al.* (2018) [24] and Rajput, R.S. (2019) [21]

Table 4: Genotypic Correlations Matrix

	Days to 75% heading	Days to maturity	Number of tillers per plant	Plant height	Spike length	Number spikelets per spike	Biological yield per plant	Number of grains per spike	1000 Grain weight	Grain yield per plant	Grain weight per spike	Harvest index	Peduncle length
Days to 75% heading													
Days to maturity	0.727**												
Number of tillers per plant	-0.125 ^{NS}	-0.229**											
Plant height	0.359**	0.321**	-0.301**										
Spike length	-0.154 ^{NS}	-0.139 ^{NS}	-0.251**	-0.162*									
Number of spikelets per spike	0.966**	0.641**	0.117 ^{NS}	0.558**	-0.025 ^{NS}								
Biological yield per plant	-0.044 ^{NS}	-0.128 ^{NS}	0.946**	-0.125 ^{NS}	-0.217**	0.179*							
Number of grains per spike	0.182*	0.083 ^{NS}	-0.384**	0.019 ^{NS}	0.131 ^{NS}	0.311**	-0.368**						
1000 grain weight	0.085 ^{NS}	-0.042 ^{NS}	-0.120 ^{NS}	0.228**	0.124 ^{NS}	-0.135 ^{NS}	-0.006 ^{NS}	0.034 ^{NS}					
Grain yield per plant	-0.046 ^{NS}	-0.193*	0.861**	-0.160 ^{NS}	-0.089 ^{NS}	0.098 ^{NS}	0.910**	-0.274**	0.006 ^{NS}				
Grain weight per spike	0.027 ^{NS}	0.091 ^{NS}	-0.073 ^{NS}	-0.041 ^{NS}	-0.084 ^{NS}	-0.026 ^{NS}	-0.099 ^{NS}	0.037 ^{NS}	0.005 ^{NS}	0.047 ^{NS}			
Harvest index	0.051 ^{NS}	-0.176*	0.478**	-0.248**	0.136 ^{NS}	0.057 ^{NS}	0.536**	-0.049 ^{NS}	0.025 ^{NS}	0.842**	0.223**		
Peduncle length	-0.562**	-0.369**	-0.460**	0.833**	0.306**	0.176*	-0.370**	0.307**	0.159 ^{NS}	-0.286**	-0.095 ^{NS}	-0.169*	

Table 5: Phenotypic Correlation Matrix

	Days to 75% heading	Days to maturity	Number of tillers per plant	Plant height	Spike length	Number spikelets per spike	Biological yield per plant	Number of grains per spike	1000 Grain weight	Grain yield per plant	Grain weight per spike	Harvest index	Peduncle length
Days to 75% heading													
Days to maturity	0.754**												
Number of tillers per plant	0.048 ^{NS}	0.026 ^{NS}											
Plant height	0.034 ^{NS}	0.069 ^{NS}	-0.094 ^{NS}										
Spike length	-0.193*	-0.123 ^{NS}	-0.095 ^{NS}	0.157 ^{NS}									
Number of spikelets per spike	0.255**	0.184*	0.052 ^{NS}	0.192*	0.134 ^{NS}								
Biological yield per plant	0.035 ^{NS}	-0.025 ^{NS}	0.877**	-0.033 ^{NS}	-0.061 ^{NS}	0.000 ^{NS}							
Number of grains per spike	0.047 ^{NS}	-0.008 ^{NS}	-0.256**	-0.003 ^{NS}	0.115 ^{NS}	0.353**	-0.263**						
1000 grain weight	0.124 ^{NS}	0.040 ^{NS}	-0.056 ^{NS}	0.117 ^{NS}	0.049 ^{NS}	-0.078 ^{NS}	-0.001 ^{NS}	0.025 ^{NS}					
Grain yield per plant	0.051 ^{NS}	-0.033 ^{NS}	0.827**	-0.048 ^{NS}	0.001 ^{NS}	0.014 ^{NS}	0.910**	-0.213**	0.017 ^{NS}				
Grain weight per spike	0.022 ^{NS}	0.026 ^{NS}	-0.073 ^{NS}	-0.016 ^{NS}	-0.012 ^{NS}	0.012 ^{NS}	-0.073 ^{NS}	0.027 ^{NS}	0.019 ^{NS}	0.047 ^{NS}			
Harvest index	0.109 ^{NS}	-0.012 ^{NS}	0.350**	-0.074 ^{NS}	0.063 ^{NS}	-0.001 ^{NS}	0.377**	-0.052 ^{NS}	0.041 ^{NS}	0.693**	0.180*		
Peduncle length	-0.153 ^{NS}	-0.098 ^{NS}	-0.108 ^{NS}	0.308**	0.119 ^{NS}	-0.042 ^{NS}	-0.056 ^{NS}	0.082 ^{NS}	0.096 ^{NS}	-0.058 ^{NS}	-0.042 ^{NS}	-0.025 ^{NS}	

Conclusion

Our investigation revealed that genotypes possessed considerable genetic variability for different characters under

study which makes them suitable for utilization in different breeding programmes. Traits like number of grains per spike, biological yield per plant and 1000 grain weight showed high

heritability with moderate values of GA which indicates that selection with progeny testing should be rewarding in the breeding for improvement of these traits. Similarly, traits which were observed with strong positive correlation with the overall yield viz., tillers per plant, harvest index (%) and biological yield per plant should also be given preference while breeding for the higher yield through indirect selection for higher yield.

References

- AL-Jibouri HA, Miller PA, Robinson HF. Genotypic and environmental variation and correlation in upland cotton cross of interspecies origin. *Agron, J* 1958;50:633-636.
- Allard RW. Principles of Plant Breeding. John Wiley & Sons. New York, 1999, 485.
- Arya VK, Singh J, Kumar L, Kumar R, Kumar P, Chand P. Genetic variability and diversity analysis for yield and its components in wheat (*Triticum aestivum* L.). *Indian Journal of Agricultural Research* 2017;51(2):128-134.
- Bhanu AN, Arun B, Mishra V. Genetic variability, heritability and correlation study of physiological and yield traits in relation to heat tolerance in wheat (*Triticum aestivum* L.). *Biomedical Journal of Scientific & Technical Research* 2018;2(1):2112-2116.
- Burton GW, Devane DE. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agronomy Journal* 1953;45(10):478-481.
- Cheema NM, Mian MA, Ihsan M, Rabbani G, Mahmood A. Studies on variability and some genetic parameters in spring wheat. *Pak. J. Agric. Sci* 2006;43(1, 2):32-35.
- Falconer DS. Introduction to Quantitative Genetics. Pearson Education India 1996.
- Fellahi Z, Hannachi A, Guendouz A, Bouzerzour H, Boutekrabt A. Genetic variability, heritability and association studies in bread wheat (*Triticum aestivum* L.) genotypes. *Electronic Journal of Plant Breeding* 2013;4(2):1161-1166.
- Fikre G, Alamerew S, Tadesse Z. Genetic variability studies in bread wheat (*Triticum aestivum* L.) genotypes at Kulumsa Agricultural Research Center, South East Ethiopia. *Journal of Biology, Agriculture and Healthcare* 2015;5(7):89-98.
- Haydar FMA, Ahamed MS, Siddique AB, Uddin GM, Biswas KL, Alam MF. Estimation of genetic variability, heritability and correlation for some quantitative traits in wheat (*Triticum aestivum* L.). *Journal of Bio-Science* 2020;28:81-86.
- Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans. *Agronomy Journal* 1955;47(7):314-318.
- Joshi AB, Dhawan NL. Genetic improvement in yield with special reference to self-fertilizing crops. In *Indian Journal of Genetics and Plant Breeding Indian Agriculture Res Inst, New Delhi Delhi-110012, India: Indian Soc Genet Plant Breed* 1966, 101.
- Kour A, Kumar B, Singh B. Genetic evaluation of yield and yield attributing traits in rice (*Oryza sativa* L.) using line x tester analysis. *Electronic Journal of Plant Breeding* 2019;10(1):39-46.
- Kumar N, Makkar S, Kumar V. Studies on heritability and genetic advance estimates in timely sown bread wheat (*Triticum aestivum* L.). *Bioscience Discovery* 2014;5(1):64-69.
- Kumar R, Gaurav SS, Bhushan B, Pal R. Study of genetic parameters and genetic divergence for yield and yield components of bread wheat (*Triticum aestivum* L.). *Journal of Wheat Research* 2013;5(2):39-42.
- Majumdar DAN, Shamsuddin AKM, Kabir MA, Hassan L. Genetic variability, correlated response and path analysis of yield and yield contributing traits of spring wheat. *Journal of the Bangladesh Agricultural University* 2008;6(2):227-234.
- MoA and FW 2020. https://eands.dacnet.nic.in/Advance_Estimate/3rd_Adv_Estimates.2019-20_Eng.pdf [Accessed: 2020-09-14].
- Naik VR, Biradar SS, Yadawad A, Desai SA, Veerasha BA. Study of genetic variability parameters in bread wheat (*Triticum aestivum* L.) genotypes. *Res. J. Agric. Sci.* 2015;6(1):123-125.
- Nizamani MM, Nizamani FG, Rind RA, Khokhar AA, Mehmood A, Nizamani M. Heritability and genetic variability estimates in F3 populations of bread wheat (*Triticum aestivum* L.). *Pure and Applied Biology (PAB)*, 2020;9(1):352-368.
- Nukasani V, Potdukhe NR, Bharad S, Deshmukh S, Shinde SM. Genetic variability, correlation and path analysis in wheat. *Journal of Wheat Research*, 2013;5(2):48-51.
- Rajput RS. Path analysis and genetic parameters for grain yield in bread wheat (*Triticum aestivum* L.). *Annual Research & Review in Biology* 2019, 1-8.
- Ramadas S, Kumar TMK, Singh GP. Wheat production in india: Trends and prospects. In: Shah F, Khan Z, Iqbal A, Turan M, Olgun M, edited. *Recent Advances in Grain Crops Research. London: Intech Open Limited.* 2019, 1-16. doi: 10.5772/intechopen.86341
- Sidharthan B, Malik SK. Variability studies in wheat. *Int. J. Agric. Sci* 2007;3(1):142-144.
- Sohail A, Rahman H, Ullah F, Shah SM, Burni T, Ali S. Evaluation of F4 bread wheat (*Triticum aestivum* L.) genotypes for genetic variability, heritability, genetic advance and correlation studies. *Journal of Plant Breeding and Genetics*, 2018;6(1):01-07.
- Yashpal P, Mridula B, Prasad SVS. Morphological variability and genetic diversity in relation to grain yield and its component traits in wheat. *National Journal of Plant Improvement*, 2005;7(2):69-72.
- Zerga K, Mekbib F, Dessalegn T. Genetic variability, heritability and genetic advance in bread wheat (*Triticum aestivum* L.) genotypes at Gurage zone, Ethiopia. *International Journal of Microbiology and Biotechnology* 2016;1(1):1-9.