

Genetic Evaluation of F₃ Population of Wheat (*Triticum aestivum* L.) for Breeding Strategies

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ABSTRACT

In plant breeding programs development of crop cultivars with superior performance has always been the prime objective. F₃ population (100) of the cross between DBW17 x WH1105 of wheat were characterized on the basis of 11 morphological characters. The genetic variability studies in F₃ generation indicated high mean and wide range for all the traits under evaluation. PCV for all the traits was found higher than GCV. High GCV and moderate PCV were recorded for grain yield per plant, biological yield per plant and number of tillers per plant. Plant height, number of grains per spike, number of spikelets per spike and days to heading exhibited high heritability. GA as 5% means was highest for grain yield per plant followed by biological yield per plant, number of tillers per plant and number of spikelets per spike. Grain yield displayed significant correlations with biological yield per plant, spike length, number of spikelets per spike, spike weight, 100 grain weight, harvest index, number of grains per spike and number of tillers per plant but days to heading and plant height were non-significantly correlated with grain yield per plant. The D² analysis showed 100 F₃ plants including parents in 7 clusters and cluster 5 was potential contributor of 100 grain weight, biological yield per plant and grain yield per plant and this cluster was the most important for selection. Cluster 7 was potential donor of number of grains per spike, number of tillers per plant and also short height plants thus can be used for dwarf trait selection. This suggested better scope for selecting superior transgressive segregants in F₃ population.

Keywords: GCV, Genetic variability, PCV, Wheat.

INTRODUCTION

Wheat (*Triticum aestivum* L. em Thell), a cereal grass of the family Graminae (*Poaceae*) and genus *Triticum*, is the world's largest and most widely cultivated cereal crop. It provides about a fifth of the calories consumed by man

and acts as a staple food in many developing as well as developed countries. The world population is projected to reach 9 billion in 2050. With the growing world population, world wheat demand is estimated to increase by 60 percent in 2050 (Kumar et al., 2017).

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There is a need to increase the productivity of wheat crop by developing high yielding varieties through appropriate breeding program to meet the demand of ever increasing population. The development of elite genotypes depends upon the magnitude of genetic variability and the extent to which desirable characters are heritable. Genetic variability for yield and yield components is essential in the base population for successful crop improvement (Allard, 1960). Study of genetic parameters from segregating population is useful in understanding the genetic consequences of hybridization. The heritability of a character describes the extent to which it is transmitted from one generation to the next generation. The genetic advance is the further estimation of genetic gain resulting from selection pressure in breeding material. High heritability associated with high genetic advance offers the most suitable condition for selection and indicates the presence of additive genes in the trait and further suggests reliable crop improvement through selection of such traits (Ogunniyan and Olakojo, 2014). Degree and direction of relationship between two or more variables lead to estimation of correlation. Correlation studies provide better understanding of yield components which helps the plant breeder during selection (Baranwal et al., 2012). Many workers emphasized the use of Mahalanobis's D^2 statistics for estimating genetic divergence as it permits specific comparison among all the populations before effecting actual crosses (Malav et al., 2016). Hence, the present investigation was conducted to study the extent of the genetic variability, heritability, genetic advance, correlation, D^2 analysis for grain yield and yield contributing traits along with stripe rust resistance in F_3 population of cross DBW17 x WH1105 of wheat.

MATERIALS AND METHODS

Parents and F_3 population of cross DBW17 x WH1105 were sown in 1 row of 2m length. The genotype WH1105 has wide adaptability, excellent biological characteristics and higher

resistance to stripe rust and DBW17 is yellow rust susceptible variety. For selecting superior transgressive segregants F_3 population of the cross DBW17 X WH1105 was evaluated for eleven morphological traits as days to heading, plant height, number of tillers per plant, spike length, spike weight, number of spikelets per spike, number of grains per spike, 100 grain weight, grain yield per plant, biological yield per plant and harvest index as they are found to be the important characters for the yield. The data obtained was subjected to statistical analysis using INDOSTAT and OPSTAT software available online on hau.ac.in. Genotypic and phenotypic coefficients of variation were estimated using formula suggested by Burton (1952) for each character. The broad sense heritability (h^2) was estimated as the ratio of genotypic variance to the total or phenotypic variance as suggested by Burton and Devane (1953). Genetic advance for each character was estimated by using the method suggested by Johnson (1955). Genetic advance as 5% of mean was also estimated following the procedure elaborated by Singh and Chaudhary (2004).

RESULTS AND DISCUSSION

3.1 Determination of Genetic Variations

Pooling information about the genetic variability, relationships and mechanisms of inheritance of different traits is the key task in genetic improvement of any crop plant. In F_3 population ample amount of variability was found for all the traits under study. These traits can be used for selection in further generations. PCV for all the traits was higher than GCV indicating the role of environment in expression of characters. These findings are in corroboration with those reported by earlier reports by Dutamo et al. (2015), Haydar et al. (2020), Kumar et al. (2019), Thakur et al. (2018) and Yadav et al. (2014) who reported that the environmental effect on any trait is indicated by the magnitude of differences between GCV and PCV; large differences reflect a large environmental effect, whereas small differences reveal a high genetic influence. Table 1 revealed that in F_3

population GCV was high for grain yield per plant, biological yield per plant and number of tillers per plant while it was moderate for number of spikelets per spike, spike length, spike weight and number of grains per spike and low for harvest index, plant height, 100 grain weight and days to heading. PCV was found moderate for grain yield per plant, biological yield per plant and number of tillers per plant while it was low for number of spikelets per spike, spike length, spike weight and number of grains per spike, harvest index, plant height, 100 grain weight and days to heading. Basavaraj et al. (2016) reported high PCV and GCV for number of tillers per plant and grain yield per plant whereas moderate PCV and GCV was observed for characters like plant height, number of spikelets per spike and spike length. Narrower difference between the values of GCV and PCV was observed as in the present study indicated that the environmental effect was small for the expression of these characters and these characters are governed by additive gene action. This was also the case for all the traits observed in studies by Baranwal et al. (2012) showing high genotypic coefficient of variation (GCV). These results also supported the findings of Bhardwaj et al. (2014), Dutamo et al. (2015) and Fikre et al. (2015).

3.2 Heritability and Genetic advance

Among all the traits plant height, number of grains per spike and number of spikelets per spike showed high heritability (>80%) while days to heading, harvest index, 100 grain weight, spike weight, biological yield, number of tillers per plant, spike length and grain yield per plant had moderate heritability (60-80%) in this population as shown in Table 1. The high estimate of heritability suggested that heritability is due to additive gene action in early segregating generations and thus it will respond to direct selection. Similar study was done by Rathi et al. (2018) where they reported biological yield and harvest index had high heritability. Grain yield per plant, number of tillers per plant, plant height, 100 grain weight, flag leaf area, flag leaf length, number of spikelets per spike, spike weight, spike

length and number of grains per spike had moderate heritability whereas days to heading had low heritability. Genetic advance accompanying heritability is more helpful in predicting the genetic gain under selection. In F_3 population GA as 5% means was highest for grain yield per plant followed by biological yield per plant, number of tillers per plant, number of spikelets per spike, spike weight, number of grains per spike, spike length, harvest index, plant height, 100 grain weight and days to heading (Table 1). Such results showed significant contribution of additive action in expression of traits making direct selection for such traits more effective. Singh et al. (2012) also reported that genetic advance as percent of mean was high for grain yield, biological yield, spikelets per spike, effective tillers per plant and days to maturity recommending the dominance of additive gene effects in controlling these characters.

3.3 Correlation studies

Correlation coefficient analysis tells the association between various plant characters and determines the component characters on which selection can be based for improvement in yield. The extent of correlation between grain yield and its components helps breeder for making selection more effective and efficient as direct selection for yield may not be effective due to contribution from different components and thus correlation increase the efficiency of breeding programs through determining the appropriate selection criteria. Positive correlation between desirable traits are supposed to be favorable and help to breeder in selection whereas, negative correlations hinders the recovery of the combinations in both characters. Grain yield per plant exhibited positive and significant correlation with biological yield per plant, number of tillers per plant, 100 grain weight, spike weight, spike length and harvest index and it was positively and non-significantly correlated with days to heading and plant height. 100 grain weight was having positive and highly significant association with spike length, spike weight, biological yield per plant, harvest index and plant height. However,

number of grains per spike was significantly and positively correlated with grain yield per plant, harvest index, number of spikelets per spike, biological yield per plant, spike length and spike weight (Table 2). Spike length is found to be positive and significantly correlated with the spike weight and plant height. Similar findings were obtained by Azam et al. (2013) while evaluating fourteen F_3 segregating wheat populations and found that grain yield exhibited significant correlations with 1000-grain weight, grain weight per spike, biomass growth rate, vegetative growth rate, grain growth rate and harvest index. Present results confirmed the findings of previous workers Nukasani et al. (2013), Kumari et al. (2017), Sohail et al. (2018) and Farag et al. (2018). Gelalcha and Hanchinal (2013) also presented similar results where grain yield was positively correlated with number of tillers per plant, number of spikelets per spike, number of grains per spike and biological yield per plant. Grain yield was found to be highly correlated with biological yield per plant. Thus, biological yield per plant can be directly selected to increase grain yield. The main contributors to grain yield were biological yield per plant, spike length, number of spikelets per spike, number of grains per spike, spike weight and harvest index.

3.4 Genetic Divergence Analysis

D^2 measures divergence at two levels *i.e.* inter cluster and intra cluster and helps in the selection of genetically divergent parents. A dendrogram was constructed based on Euclidean distance. On the basis of relative magnitude of D^2 value, 100 plants of F_3 population were grouped in seven major clusters in such a way that plants within each cluster had smaller D^2 value than those of between clusters as shown in Fig. 1. Cluster pattern revealed that, cluster 3 was the largest group consisting of 21 plants which was followed by cluster 2, cluster 4, cluster 1, cluster 5, cluster 6 and cluster 7 as shown in Table 3. Cluster 1 and 4 are separated by greatest statistical distance and were identified

as being most divergent (Fig 1) thus they are diverse enough to be selected as parents under breeding program. The maximum difference among the progenies within the same cluster was shown by cluster 7 followed by cluster 5, cluster 3, cluster 4, cluster 2, cluster 6 and cluster 1 (Fig 1). It was evident from the Table 4 that cluster 5 was potential contributor of 100 grain weight, biological yield per plant and grain yield per plant and this cluster is most important for selection. Cluster 7 was potential donor of number of grains per spike, number of tillers per plant and also short height plants thus can be used for dwarf trait selection. This cluster can also be used for selecting early maturing plants. Malav et al. (2016) reported that the cluster VII had the highest mean values for grain yield per plant and 1000 grain weight during analysis of genetic divergence as in the present study. The above results were in collaboration with Ali et al. (2017) by using Mahalanobis D^2 statistic, grouped all the genotypes into 7 clusters and Cluster III had maximum number of genotypes. Khodadadi et al. (2011) revealed that 36 winter wheat genotypes were categorized into seven groups as in this population. The present findings are supported with earlier reports of Fikre et al. (2015), Kalimullah et al. (2012), Dutamo et al. (2015), Priya et al. (2015) and Malav et al. (2016).

The clustering pattern could be utilized in selecting the parents and deciding the cross combinations which may generate the highest possible variability for various traits. The genotypes with high values of any cluster can be used in hybridization programme for further selection and improvement. Based on the maximum genetic distance, it is advisable to attempt crossing the plants from cluster 1 and cluster 4, which may lead to the generation of broad spectrum of favorable genetic variability for yield improvement in bread wheat and intercrossing of plants would be useful for inducing variability in respective characters and their rational improvement for increasing the grain yield in bread wheat.

Table 1: Estimates of genotypic and phenotypic coefficient of variance, heritability and genetic advance for grain yield and component characters in F₃ population of cross DBW17 x WH1105 in wheat

Character	Mean	Range	PCV	GCV	Heritability (%)	GA as 5% mean
Days to heading	90.61	88.00-95.00	2.65	2.39	81.00	4.44
Plant height	96.53	85.00-106.50	6.09	5.81	91.00	11.40
No of tillers/ plant	9.22	5.00-13.00	22.26	18.44	68.00	31.48
Spike length(cm.)	10.68	8.20-14.00	14.28	11.62	66.00	19.51
Spike weight (g)	3.03	2.02-4.00	14.01	12.14	75.00	21.68
No of spikelet/spike	19.74	15.00-25.00	14.45	13.11	82.00	24.49
No. of grains/spike	57.73	48.00-72.00	12.24	11.33	86.00	21.62
100 grain wt. (g)	3.96	3.56-4.50	5.64	5.03	79.00	9.25
Biological yield/plant (g)	27.45	13.47-42.28	25.86	21.43	69.00	36.59
Grain yield/plant (g)	10.82	5.86-18.52	28.36	22.86	65.00	37.95
Harvest index (%)	39.29	35.00-45.80	7.43	6.70	80.00	12.34

Table 2: Phenotypic Correlation coefficients among various traits of F₃ population of cross DBW17 x WH1105

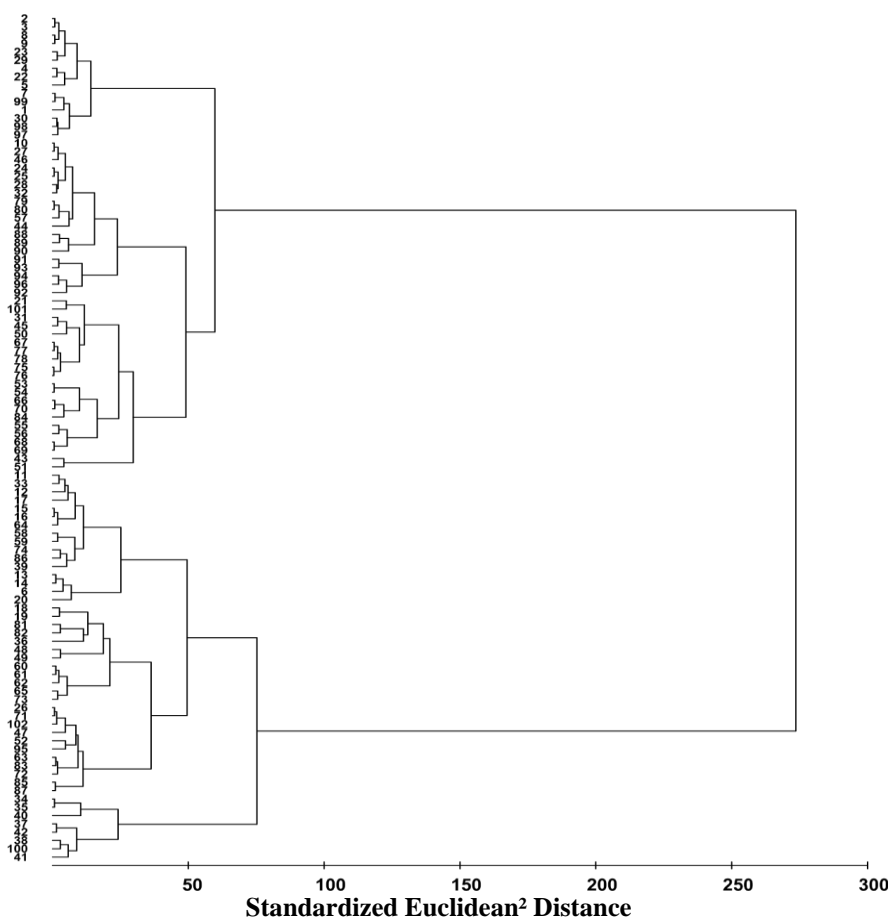
Characters	Days to Heading	Plant height (cm)	No of tillers/ plant	Spike length (cm)	Spike weight (g)	No of spikelet/ spike	No. of grains/ spike	100 grain wt. (g)	Biological yield/plant (g)	Grain yield/plant (g)	Harvest index (%)
Days to heading											
Plant height (cm)	-0.033										
No of tillers/ plant	0.064	-0.108									
Spike length (cm)	0.038	0.242*	0.100								
Spike weight (g)	0.151	0.169	0.001	0.560**							
No of spikelet/ spike	0.175	0.065	0.287**	0.545**	0.541**						
No. of grains/spike	-0.086	0.018	0.093	0.277**	0.253*	0.363**					
100 grain wt. (g)	0.237*	0.267**	0.141	0.433**	0.421**	0.014	0.178				
Biological yield/plant (g)	0.035	0.009	0.189	0.601**	0.412**	0.431**	0.363**	0.401**			
Grain yield/plant (g)	0.068	0.015	0.248*	0.665**	0.462**	0.508**	0.422**	0.445**	0.961**		
Harvest index (%)	0.103	0.102	0.242*	0.415**	0.330**	0.459**	0.373**	0.279**	0.184	0.438**	

Table 3: Distribution of F₃ population including parents in different clusters

	Plant Number	Number of plants
Cluster1	1, 2, 3, 4, 5, 7, 8, 9, 22, 23, 29, 30, 97, 98, 99	15
Cluster2	10, 24, 25, 27, 28, 32, 44, 46, 57, 79, 80, 88, 89, 90, 91, 92, 93, 94, 96	19
Cluster3	DBW17, 21, 31, 43, 45, 50, 51, 53, 54, 55, 56, 66, 67, 68, 69, 70, 75, 76, 77, 78, 84	21
Cluster4	6, 11, 12, 13, 14, 15, 16, 17, 20, 33, 39, 58, 59, 64, 74, 86	16
Cluster5	18, 19, 36, 48, 49, 60, 61, 62, 65, 73, 81, 82	12
Cluster6	WH1105, 26, 47, 52, 63, 71, 72, 95, 83, 85, 87	11
Cluster7	34, 35, 37, 38, 40, 41, 42, 100	8

Table 4: Cluster means of different traits of F₃ population of cross DBW17 x WH1105

	Days to Heading	Plant height (cm)	No. of tillers per plant	Spike length (cm)	Spike weight (g)	No. of spikelets per spike	No. of grains per spike	100 grain weight (g)	Biological yield/plant (g)	Grain yield/plant (g)	Harvest Index (%)
Cluster 1	90.53	89.47	9.13	8.81	2.60	16.60	51.87	3.82	21.56	7.97	36.86
Cluster 2	92.63	96.80	8.95	10.01	3.22	19.84	56.16	3.96	24.44	9.36	38.45
Cluster 3	88.85	100.55	8.83	10.20	2.77	18.09	53.60	3.84	22.02	8.48	38.80
Cluster 4	93.06	96.36	9.56	12.48	3.35	22.75	62.19	4.12	34.01	14.50	42.60
Cluster 5	89.92	100.58	9.58	11.50	3.22	20.83	60.08	4.30	35.74	13.86	38.86
Cluster 6	88.67	98.84	6.93	12.02	3.23	20.02	61.11	3.98	28.94	11.85	41.13
Cluster 7	88.50	88.75	10.38	10.38	2.86	21.25	67.13	3.71	32.57	12.50	38.75

WARD'S MINIMUM VARIANCE DENDROGRAM**Fig. 1: Dendrogram showing clustering pattern of F₃ population**

REFERENCES

- Ali, T., Singh, M. K., Bharadwaj, D. N., & Singh, L. (2017). Analysis of genetic divergence in wheat (*Triticum aestivum* L.). *Environment & Ecology*, 35(3B), 2081-2083.
- Allard, R. W. (1960). Principles of plant breeding. *John Wiley and sons, NewYork*: 185.
- Azam, S. M., Mohammad, F., Ahmad, I., Khalil, I. H., Jadoon, S. A., & Nasim, A. (2013). Divergence in F₃ segregating bread wheat populations. *International Journal of Basic and Applied Sciences*, 13(3), 94- 99.
- Baranwal, D. K., Mishra, V. K., Vishwakarma, M. K., Yadav, P. S., & Arun, B. (2012). Studies on genetic variability, correlation and path analysis for yield and yield contributing traits in wheat (*T. aestivum* L. em Thell.). *Plant Archives*, 12(1), 99-104.
- Basavaraja, S., Naik, V. R., Biradar, S. S., Desai, S. A., & Veerasha, B. A. (2016). Genetic Variability Parameters for Yield and Rust Resistance in F₅ populations of Bread Wheat. *Environment & Ecology*, 34(4C), 1958-1961.
- Bhardwaj, S. (2014). Genetic analysis and molecular characterization of wheat (*Triticum aestivum* L) genotypes under Chhattisgarh plains. (Doctoral dissertation, Indira Gandhi Krishi Vishwavidyalaya, Raipur).
- Burton, G. W. (1952). Quantitative inheritance in grasses. *Proceedings of 6th International Grassland Congress*, 1(2), 227-285.
- Burton, G. W., & Devane, E. H. (1953). Estimating heritability in tall Fescue (*Festuca arundinacea*) from replicated clonal material. *Journal of Agronomy*, 45, 478-481.
- Dutamo, D., Alamerew, S., Eticha, F., & Assefa, E. (2015). Genetic variability in bread wheat (*Triticum aestivum* L.) germplasm for yield and yield component traits. *Journal of Biology, Agriculture and Healthcare*, 5(13), 39-46.
- Farag, S. A., Ismail, S. K. A., & Sawsan, A. (2018). Estimating phenotypic and genotypic path coefficient, an application on wheat (*Triticum aestivum* L.) Genotypes. *International Journal of Current Microbiology and Applied Sciences*, 7(2), 2494-2505.
- Fikre, G., Alamerew, S., & Tadesse, Z. (2015). Genetic Variability Studies in Bread Wheat (*Triticum aestivum* L.) Genotypes at Kulumsa Agricultural Research Center, South East Ethiopia. *Journal of Biology, Agriculture and Healthcare*, 5(7), 89-98.
- Gelalcha, S., & Hanchinal, R. R. (2013). Correlation and path analysis in yield and yield components in spring bread wheat (*Triticum aestivum* L.) genotypes under irrigated condition in Southern India. *African Journal of Agricultural Research*, 8(24), 3186-3192.
- Haydar, F. M. A., Ahamed, M. S., Siddique, A. B., Uddin, G. M., Biswas, K. L., & Alam, M. F. (2020). Estimation of genetic variability, heritability and correlation for some quantitative traits in wheat (*Triticum aestivum* L.). *Journal of Bio-Science*, 28, 81-86.
- Johnson, H. W., Robinson, H. F., & Comstock, R. E. (1955). Estimates of genetic and environmental variability in soybean. *Agronomy Journal*, 47, 314-318.
- Kalimullah, S., Khan, J., Irfaq, M., & Rahman, H. U. (2012). Genetic variability, correlation and diversity studies in bread wheat (*Triticum aestivum* L.) germplasm. *Journal of Animal and Plant Sciences*, 22(2), 330- 333.
- Khodadadi, M., Fotokian, M. H., & Miransari, M. (2011). Genetic diversity of wheat (*Triticum aestivum* L.) genotypes based on cluster and principal component analyses for breeding strategies. *Australian Journal of Crop Science*, 5(1), 17.

- Kumar, G. A., Hanchinal, R. R., Desai, S., & Biradar, S. (2017). Identification of superior recombinant lines for yield and leaf rust resistance in the cross between DWR 162 X NIL PBW 343 in bread wheat (*Triticum aestivum* L.). *International Journal of Pure Applied Biosciences*, 5(4), 1800-1807.
- Kumar, D., Kumar, A., Srivastava, R., & Kumar, A. (2019). Studies on variability, heritability And genetic advance in some quantitative characters in bread wheat (*Triticum Aestivum* L.). *Journal of Pharmacognosy and Phytochemistry*, 8(4), 402-404.
- Kumari, M., Kumar, M., Singh, V., Kumar, V., & Rathi, M. (2017). Trait association and morphological diversity in wheat (*Triticum aestivum* L.) genotypes. *Electronic Journal of Plant Breeding*, 8(2), 534-540.
- Malav, A. K., Monpara, B., Indu, S., & Raghuwanshi, S. (2016). Analysis of genetic divergence for yield contributing traits in breadwheat (*Triticum aestivum* L.) genotypes. *The Bioscan*, 11(3), 1865-1869.
- Nukasani, V., Potdukhe, N. R., Bharad, S., Deshmukh, S., & Shinde, S. M. (2013). Genetic variability, correlation and path analysis in wheat. *Journal of Wheat Research*, 5(2), 48-51.
- Ogunniyan, D. J., & Olakojo, S. A. (2014). Genetic variation, heritability, genetic advance and agronomic character association of yellow elite inbred lines of maize (*Zea mays* L.). *Nigerian Journal of Genetics*, 28(2), 24-28.
- Priya, B., Diyali, S., Mukherjee, S., & Srinivasarao, M. (2015). Genetic diversity based on cluster and principal component analysis in wheat and triticale genotypes. *Research on Crops*, 16(4), 712-718.
- Rathi, M., Kumar, M., Singh, V., Gupta, V., & Anu (2019). Trait Associations, path analysis and genetic diversity in bread wheat (*Triticum aestivum* L.) genotypes. *Green Farming*, 10(5), 533-538.
- Singh, R. K., & Chaudhary, B. D. (2004). *Biometrical Methods in Quantitative Genetic Analysis*, Kalyani Publishers, New Delhi, India: 318.
- Singh, A. K., Singh, S. B., Singh, A. P., & Sharma, A. K. (2012). Genetic variability, character association and path analysis for seed yield and its component characters in wheat (*Triticum aestivum* L.) under rainfed environment. *Indian Journal of Agricultural Research*, 46(1), 48-53.
- Sohail, A., Rahman, H., Ullah, F., Shah, S. M., Burni, T., & Ali, S. (2018). Evaluation of F₄ bread wheat (*Triticum aestivum* L.) genotypes for genetic variability, heritability, genetic advance and correlation studies. *Journal of Plant Breeding and Genetics*, 6(1), 1-7.
- Thakur, P., Upadhyay, P., Rashmi, K., Prasad, R., Chandra, K., Madhukar, K., & Prasad, L. C. (2018). Study of genetic variability, path analysis and diversity of selected germplasm lines of wheat (*Triticum aestivum* L.) under very late sown condition. *International Journal of Bio-resource and Stress Management*, 9(2), 203-208.
- Yadav, S. K., Singh, A. K., Baghel, S. S., Jarman, M., & Singh, A. K. (2014). Assessment of genetic variability and diversity for yield and its contributing traits among CIMMYT based wheat germplasm. *Journal of Wheat Research*, 6(2), 154-159.