Original Research Article

Genetic divergence for grain yield and its components in bread wheat (*Triticum aestivum* L.)

ABSTRACT

The present investigation Comprises 34 advanced breeding lines including checks of bread wheat an experiment was conducted in a complete randomized block design with three replication at the research farm department of genetics and plant breeding, RVSKVV, B.M.College of agriculture, Khandwa during Rabi season (November 2021 to April 2022) for estimation of the multivariate analysis of divergence. The advanced breeding lines were group into seven clusters. Cluster III contained the highest number of advanced breeding lines(12) and the cluster V,VI and VII contained the lowest (1 each).The inter cluster distance in mostly cases were larger than the intra cluster distance which indicated that wider diversity is present among the advanced breeding lines of distant grouped. The highest intra cluster distance was observed in cluster IV revealed maximum genetic divergence among its constituents. The highest inter-cluster distance was found between cluster VI and VII and the lowest was between cluster V and VI. Highest cluster mean exhibited in cluster VII for most of the agro-morphological traits i.e. number of tillers/plant, spike length, spike weight, number of grain/spike followed by cluster II for grain filling period, days to maturity and plant height. On the basis of genetic diversity analysis, maximum percent contribution towards genetic divergence in 34 advanced breeding lines were found in grain filling period, days to maturity, number of grain/spike, days to 50% flowering, biological yield per plant and harvest index. Such differences in the genetic component of traits studied in the manuscript can be applied as a source of variation in other breeding programmes and crossing nurseries for wheat improvement.

Keywords: *Clusters analysis, Genetic divergence, Mahalanobis D^2, Triticum aestivum*

1. INTRODUCTION

Wheat (*Triticum aestivum L.)* is a highly self-pollinated cereal crop belongs to "*Poaceae*" family and genus *Triticum*. It is very popular within farmers due to its easy cultivation, ecologically suitable and wider adaptation in agro-climatic conditions [1,2]. It is most popular cereal crop between the farmers because it is easy to cultivate, ecologically suitable and wider adaptable in agro-climatic conditions. Bread wheat (*Triticum aestivum*) accounts for 95% of all the consumed wheat throughout the world and remaining 5% is made up of durum or hard wheat (*T. Turgidum* sp.) which is mainly used in food production industries. Bread wheat is holding about 17% of crop acreage and feeding about 40% of the world population. It is grown in many areas and environments viz., temperate, irrigated, dry and high rainfall areas and in warm, cold and humid to dry. Wheat is consumed in a variety of ways such as bread, chapatti, porridge, flour, Suji etc [3]. It has high content of niacin and thiamine which are basically concerned in providing the special protein “Gluten”. This protein provides the framework of spongy cellular texture of bread and baked products [4]. Wheat is cultivated on 31.61 million hectares in India, producing 109.52 million tones with a national average yield of 3464 kg/ha in 2020-21 [5]. It is grown on 6.39 million hectares in Madhya Pradesh, with a yield of 20.20 million tonnes and a productivity of 2758 kg/ha. in 2020-21 [6]. It is grown in all the regions of the country and the states, namely, Uttar Pradesh, Punjab, Haryana, Madhya Pradesh, Rajasthan, Bihar, Maharashtra, Gujarat, West Bengal, Uttarakhand and Himachal Pradesh together contribute about 98% to the total wheat production of the country and play an important role of supplying carbohydrate and protein [7,8]. Breeding of wheat through crossing, followed by the desired choice of individuals in segregation generations, depends on the presence of genetic diversity among the parents. Therefore, the first step in wheat crossbreeding program is the choice of the parents and the analysis of the genetic diversity of genotypes is a prerequisite for their efficient exploitation in the plant breeding program. The accurate determination of the genotype is very important during all steps of the breeding program, start from the choice of parents for breeding to obtain new varieties for use in the production of the crop. Estimation of genetic diversity on the basis of genetic distance is useful for wheat breeding as a tool of the parental selection for promoting new genetic recombination to increase the grain yield [9]. The existence of genetic diversity plays a crucial role in formulating a tangible and successful breeding programme. Cluster analysis is an appropriate method for determining family relationship and genetic affinity i.e., to determine the extent of genetic distance of genotypes from each other. Mahalanobis D^2 statistic is a form of generalized distance which was first used to evaluate the genetic diversity between genotypes. Scientists suggested the use of this analysis to estimate genetic diversity in crop improvement programs. Genetic diversity available in the existing germplasm determines the success of any crop improvement programme [10,11]. Therefore, quantitative assessment of genetic diversity present among population usually helps a plant breeder in choosing desirable parents for breeding programme. The higher genetic distance between parents, the higher heterosis in progeny can be achieved. Therefore, keeping in mind the above facts, we investigated the extent of genetic diversity present in a set of 34 bread wheat advanced breeding lines for various traits.

2. MATERIALS AND METHODS

The material for the present investigation comprised of total 34 advanced breeding lines of bread wheat (29 crosses 5 check M.P.4010, GW322, PBW873, GW366 and RVW 4106) at Research Farm, RVSKVV, Department of Genetics and Plant breeding, B.M. College of Agriculture, Khandwa (M.P.). All the 34 advanced breeding lines were grown in randomized complete block design with three replications in *rabi* s34 advanced breeding lines (2021-22) season. Each plot consists of six rows of 6 m length with 20 cm spacing and 10cm plant to plant distance. The observations were recorded on fifteen diverse morpho-physiological and yield attributing traits. Data was recorded on whole plot basis for days to 50% heading ,days to 50% flowering, grain filling period, days of maturity, number of tiller, plant height(cm), penducle length (cm), flag leaves area (m^2), spike length (cm), spike weight (g), number of grain/spike,1000 seed weight (g), harvest index, biological yield per plant (g), grain yield per plant (g) on the basis of five randomly selected plants from each genotype in each replication. Mahalanobis (1936) D^2 statistical analysis was used for estimation of genetic divergence among 34 advanced breeding lines's. The multivariate analysis by means of D^2 statistics is found to be useful in identifying degree of divergence between biological populations at genotypic level and also to assess the relative contribution of different components to the total divergence both at inter and intra cluster level.

3. RESULTS AND DISCUSSION

D^2 statistical analysis was used for estimation of genetic divergence among 34 advanced breeding lines [12]. The clustering of D^2 values was formed by using the Tocher's method as described by [13]. The 34 advanced breeding lines's were grouped into seven clusters.

Table .1: Percent contribution of different characters towards genetic divergence

S.No.	Source	Times Ranked First	Percent Contribution
1	Days to 50% heading (days)	3	0.53 %
2	Days to 50% flowering (days)	67	11.94 %
3	Grain filling period (days)	128	22.82 %
4	Days to maturity (days)	119	21.21 %
5	Number of tiller/plant	22	3.92 %
6	Plant height (cm)	0	0.00 %
7	Penducle length (cm)	1	0.18 %
8	Flag leaf area (cm^2)	7	1.25 %
9	Spike length (cm)	5	0.89 %
10	Spike weight (g)	0	0.00 %
11	Number of grain/spike	119	21.21 %
12	1000 seed weight (g)	12	2.14 %
13	Harvest index (%)	31	5.53 %
14	Biological yield per plant (g)	47	8.38 %
15	Grain yield per plant (g)	0	0.00 %

The percentage contribution towards genetic divergence by all the characters is presented in table 1. The character Grain filling period (22.82%) contributed most toward genetic divergence followed by Number of grain/spike (21.21%), Days of maturity (21.21%), Days of flowering (11.94%), Biological yield/plant (8.38%), Harvest index (5.53%), Number of tillers/plant (3.92%), 1000 seed weight (2.14%), Flag leaf area (1.25%), Spike length (0.89%), Days of 50% heading (0.53%), Penducle length (0.18%) [14] (**Fig.1**).

The study comprised of 34 advanced breeding lines based on 15 morpho-physiological and yield related traits following Mahalanobis D^2 statistics. On the basis of D^2 values, the D^2 34 advanced breeding lines's were grouped into 7 clusters following Tocher Method. The Cluster III polygenotypic had (12 lines) pursed by cluster I and IV (8 lines), cluster II (3 lines) and remaining monogenotypic clusters V, VI and VII had one lines's each. Cluster wise distribution of genotypes is summarized in **Table 2** and **Fig 2** & **3**.

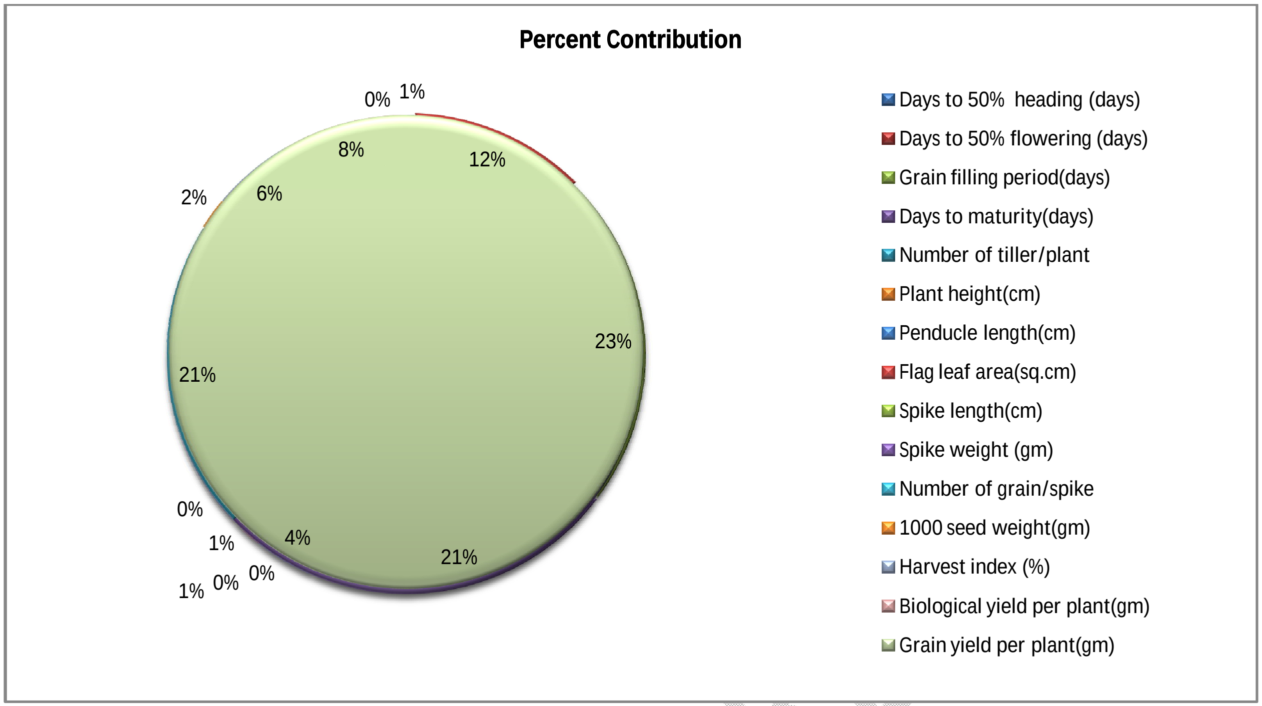

Fig.1 Percent contribution of characters

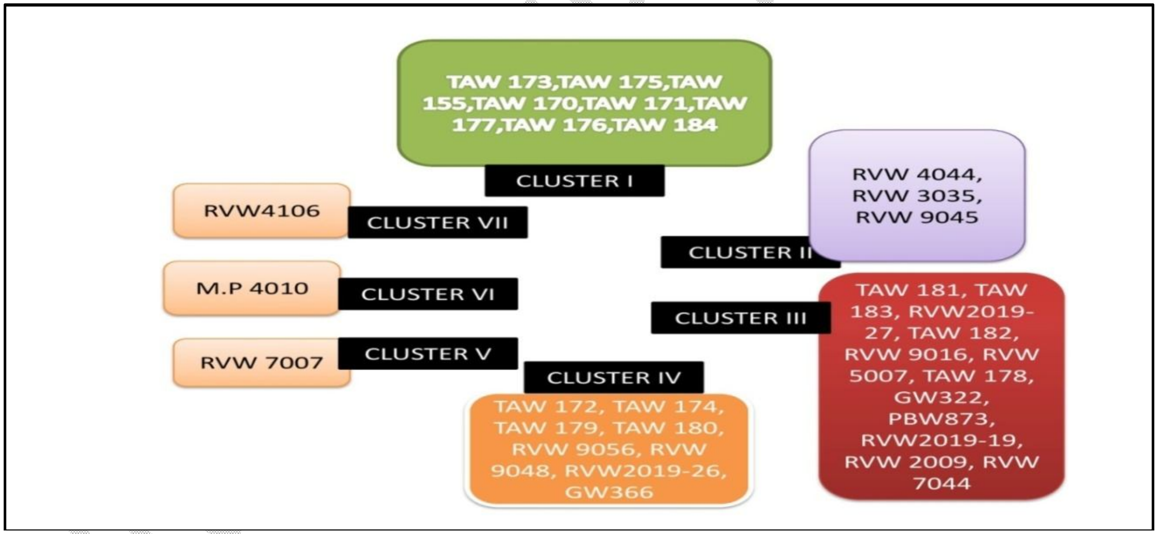

Fig. 2 Clustering pattern of 34 advanced breeding lines of bread wheat on the basis of D^2 statistics

Table 2. Distribution pattern of 32 genotypes under different clusters

S. No.	Cluster No.	NO. of Genotypes	Name of Genotypes
1.	I	8	TAW 173,TAW 175,TAW 155,TAW 170,TAW 171,TAW 177,TAW 176,TAW 184

2.	II	3	RVW 4044, RVW 3035, RVW 9045
3.	III	12	TAW 181, TAW 183, RVW2019-27, TAW 182, RVW 9016, RVW 5007, TAW 178, GW322, PBW873, RVW2019-19, RVW 2009, RVW 7044
4.	IV	8	TAW 172, TAW 174, TAW 179, TAW 180, RVW 9056, RVW 9048, RVW2019-26, GW366
5.	V	1	RVW 7007
6.	VI	1	M.P 4010(Check)
7.	VII	1	RVW4106(Check)

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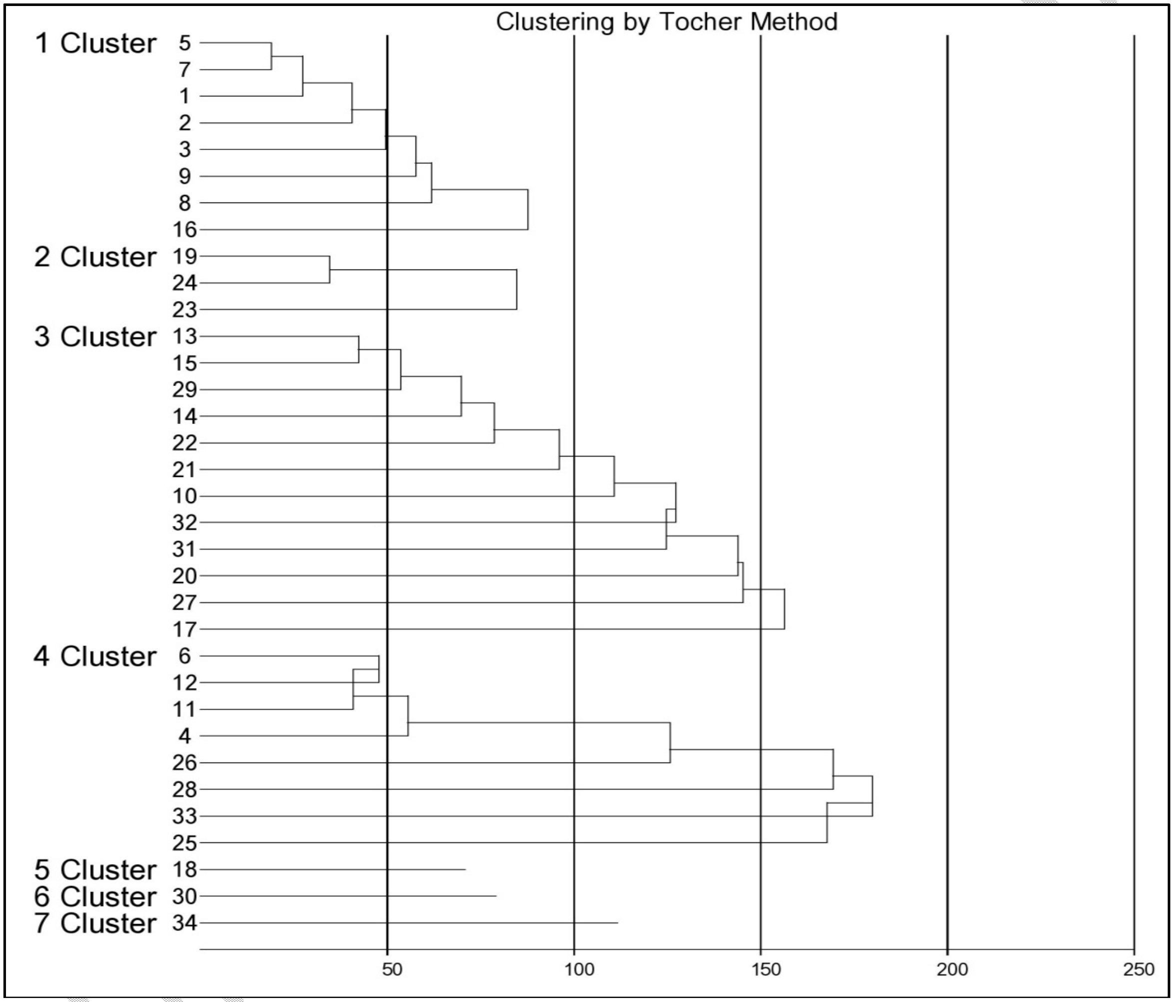

Fig. 3 Clustering of Genotypes by Tocher Method

Table 3. Intra and Inter-Cluster Distances

Cluster	I	II	III	IV	V	VI	VII
I	**8.43**	19.80	14.28	16.39	17.92	18.54	12.31

II		**9.81**	20.14	14.70	12.20	17.27	16.71
III			**11.86**	15.24	17.68	14.72	19.96
IV				**12.87**	16.44	15.83	18.89
V					**0.00**	11.78	14.88
VI						**0.00**	20.75
VII							**0.00**

The average intra and inter cluster D^2 values estimated as per the procedure given [15]. Cluster number IV showed maximum intra cluster value (D^2=12.87) [16] followed by cluster number III (D^2=11.86) and cluster number I value (D^2=9.81) while, other cluster were mono-genotypic with no intra cluster divergence. Intra cluster D^2 values ranges from 0.00 (cluster V, VI, and VII) to 12.87 (cluster IV).

From the inter cluster D^2 values among the VII cluster highest inter cluster divergence was observed between 34 advanced breeding lines's of cluster VI and VII (D^2=20.75), pursued by cluster II and III (D^2=20.14), cluster III and VII (D^2=19.96), cluster I and II (D^2=19.80), cluster IV and VII (D^2=18.89), cluster V and VII (D^2=14.88), least inter cluster divergence was observed between Cluster I and VI (D^2=11.78).The inter cluster distance in mostly case were larger than the intra cluster which indicated that wider diversity is present among the lines of distant group (**Table 3**) indicating close relationship between these clusters and would not provide good results. The maximum distance between clusters, indicating that the genotypes included in these clusters showed broad spectrum of genetic diversity and may be used in hybridization programme for wheat improvement programme [17]. In order to increase the probability of isolating good recombinants in the segregating generations would be useful to crossing between the diverse genotypes belonging to clusters separated by large inter cluster distances. Hence, diversified wheat genotypes may be chosen from cluster II and cluster III which could result in beneficial segregants as a result of genetic recombination. This result is in conformity with the findings of [18,19].

Cluster Mean Values

The cluster means for each of the 15 characters are presented in (**Table 4**).From the data it can be seen that considerable differences existed for the traits under studied. The data indicated that Cluster number V showed highest cluster mean for Grain yield per plant (99) and least in cluster VII (75.67). Cluster number V showed highest cluster mean for Biological yield per plant (220.67) and least in cluster III (183.56).Cluster number III showed highest cluster mean for Harvest index (49.56) and least in cluster VII (41.14).Cluster number IV showed highest cluster mean for 1000 seed weight (44.14) and least in cluster VII (38.23).Cluster number VII showed highest cluster mean for Number of grain/spike (65.53) and least in cluster VI (40.13).Cluster number VII showed highest cluster mean for Spike weight (3.63) and least in cluster VI (2.66).Cluster number VII showed highest cluster mean for Spike length (10.73) and least in cluster V (7.87).Cluster number IV showed highest cluster mean for Flag leaves area (45.27) and least in cluster V (40.33).Cluster number I showed highest cluster mean for Penducle length (14.22) and least in cluster II (11.87).Cluster number VII showed highest cluster mean for Plant height (81.52) and least in cluster II (77.30).Cluster number VII showed highest cluster mean for Number of tillers (6.67) and least in cluster VI (4.27).Cluster number II showed highest cluster mean for days of maturity (137.78) and least in cluster VI (130.33).Cluster number II showed highest cluster mean for grain filling period (45.33) and least in cluster VI (35). Cluster number VI showed highest cluster mean for days to 50% flowering (95.33) and least in cluster V (91.67). Cluster number VI showed highest cluster mean for days to 50% heading (84.33) and least in cluster VIII (80.67). These are expected to exhibit high heterosis and also likely to produce new recombinants with desired characters. Similar result was also in conformity to the results of [20]. Therefore, these genotypes could be exploited for their direct release as a variety after testing under different environments. Moreover, these genotypes can also be used as parents in hybridization programmes to develop high-yielding wheat varieties.

CONCLUSION

Based on the present investigation, it can be concluded that sufficient diversity existed among the 34 advanced breeding lines including checks. The characters grain yield per plant, number of grain/spike days of maturity, days of flowering, biological yield per plant and harvest index were observed to major contributor to diversity among the genotypes. Hybridization between the genotypes in Cluster I and VI and cluster VI and VII which recorded wide diversity between them and they could result in recombinants with better yielding ability.

Table.4: Cluster Means for different characters

Cluster	I	II	III	IV	V	VI	VII
Days to 50% heading	81.58	81.44	81.00	81.96	80.67*	84.33**	83.67
Days to 50% flowering	92.58	92.44	92.00	92.96	91.67*	95.33**	94.67
Grain filling period	38.83	45.33**	40.94	44.37	40.33	35.00*	36.00
Days of maturity	131.42	137.78**	132.94	137.33	132.00	130.33*	130.67
Number of tiller	6.54	5.50	5.71	5.54	5.53	4.27*	6.67**
Plant height	77.88	81.52**	80.50	79.45	80.23	80.50	77.30*
Penduce length	14.22**	11.87*	13.08	13.34	12.03	13.87	12.27
Flag leaves area	43.17	44.29	41.01	45.27**	40.33*	40.83	41.73
Spike length	10.46	9.20	9.16	8.53	7.87*	8.07	10.73**
Spike weight	3.34	3.03	3.18	3.23	3.21	2.66*	3.63**
Number of grain/spike	64.91	50.72	54.99	53.11	49.03	40.13*	65.53**
1000 seed weight	39.77	39.85	41.38	44.14**	42.02	42.43	38.23*
Harvest index	42.76	46.17	49.56**	45.85	44.98	43.77	41.14*
Biological yield per plant	190.71	188.44	183.56*	187.63	220.67**	207.00	184.00
Grain yield per plant	81.13	87.11	90.67	85.71	99.00**	90.67	75.67*

For minimum value (*) and maximum (**)

REFERENCES

1. Nirala Tanisha, Jha AK, Verma Badal, Yadav Pushpendra Singh, Anjna Mahendra, Bhalse Lakhan. Bio efficacy of Pinoxaden on Weed Flora and Yield of Wheat (Triticum aestivum L.). Biological Forum – An International Journal. 2022;14(4):558-561.
2. Patel Raghav, Jha AK, Verma Badal, Kumbhare Rahul, Singh Richa. Bio-efficacy of Pinoxaden as Post-emergence Herbicide against Weeds in Wheat Crop. Pollution research. 2023;42(1):115-117.
3. Verma B, Bhan M, Jha AK, Khatoon S, Raghuwanshi M, Bhayal L, Sahu MP, Patel Rajendra and Singh Vikash. Weeds of direct-seeded rice influenced by herbicide mixture. Pharma Innovation. 2022; 11(2), 1080-1082.

4. Bhushan B, Bharti S, Ojha A, Pandey M, Singh S, Singh B. Genetic variability, correlation coefficient and path analysis of some quantitative traits in bread wheat. Journal Wheat Research. 2013;5(1):24-29.
5. Anonymous. 2021. Annual Report 2021-2022, Department of Agriculture and Cooperation, Ministry of Agriculture, Government of Madhya Pradesh.
6. ICAR-IIWBR, 2021. Director's Report of AICRP on Wheat and Barley Improvement Project 2020-21. Ed: G. P. Singh, ICAR-Indian Institute of Wheat and Barley Research, Karnal, India. p.87.
7. Jaiswal SP, Singh A, Gahatyari NC. Genetic diversity analysis in bread wheat (*Triticum aestivum* L. EM Thell.) For yield and physiological traits. *Int. J Curr. Microbiol. App. Sci*. 2019; 8(2): 3059-3068.
8. Verma B, Bhan M, Jha AK, Singh V, Patel R, Sahu MP and Kumar V. Weed management in direct-seeded rice through herbicidal mixtures under diverse agroecosystems. AMA, Agricultural Mechanization in Asia, Africa and Latin America. 2022; 53(4): 7299-7306.
9. Poudel A, Thapa DB, Sapkota M. Assessment of genetic diversity of bread wheat (*Triticum aestivum* L.) genotypes through cluster and principal component analysis. Int. J. Exp. Res. Rev. 2017;11:1-9.
10. Harlan. Genetic resources in wild relatives of crop. Crop Sci. 1976;16:329-333.
11. Moose SP, Rita HM. Molecular plant breeding as the foundation for 21st century crop improvement. Plant Physiol. 2008;147:969-977.
12. Mahalanobis PC. On the generalized distance in statistics, proceeding of the national institute of sciences of India. 1936;2(1):49-55.
13. Rao CR. Advanced Statistical Methods in Biometrical Research, Wiley and Sons, New York, 1952.
14. Yadav PK, Tiwari S, Kushwah A, Tripathi MK, Gupta N, Tomar RS, Kandalkar VS. Morpho-physiological characterization of bread wheat genotypes and their molecular validation for rustresistance genes Sr2, Sr31 and Lr24. Proc. Indian Natl. Sci. Acad. 2021;87: 534-545.
15. Singh RK and Chaudhary BD. 1977. Biometrical methods in quantitative genetic analysis . Kalyani Publishers, Ludhiana, New Delhi.
16. Dobariya KL, Ribadia KH, Padhar PR, Ponkia HP. Analysis of genetic divergence in some synthetic lines of bread wheat (*Triticum aestivum* L.). Advances in Plant Sciences. 2006;19(1):221-225.
17. Chapla JN, Dobariya KL, Khanpara MD, Jivani LL, Kachhadia VH. Genetic divergence in bread wheat (*Triticum aestivum* L.). J of Plant Improvement. 2008;10(2):97-102.
18. Elahi T, Pandey S, Shukla RS. Agro-morphological diversity in promising wheat genotypes grown under restricted irrigated condition. Electronic Journal of Plant Breeding. 2021;12(3):643-651.
19. Mishra V, Chand P. Assessing genetic diversity for yield and quality traits in germplasm lines of bread wheat (*Triticum aestivum* L.). Int. J Curr. Microbiol. App. Sci. 2018;7(2):2281-2285.

20. Rajneesh K, Madakemohekar AH, Sravani M, Swetha M, Kamboj A, Thakur G, et al. Genetic evaluation of different genotypes of wheat (*Triticum aestivum* L.) in normal sowing condition in Punjab. Electronic Journal of Plant Breeding. 2019;10(3):970-979.