Original Research Article

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

ABSTRACT

The present investigationComprises 34 advanced breeding lines including checks of bread wheat an experiment was conducted in a complete randomized block design with three ~~replication~~replications at the research farm department of genetics and plant breeding, RVSKVV,B.M.College of ~~agriculture~~Agriculture, Khandwa during Rabi season (November 2021 to April 2022) for estimation of the multivariate analysis of divergence. The advanced breeding lines were ~~group~~ groupedinto seven clusters. Cluster III contained the highest number of advanced breeding lines(12) and ~~the cluster~~clusters V,VI, and VII contained the lowest(1 each).The ~~inter cluster~~inter-cluster distance in ~~mostly~~ mostcases ~~were~~ waslarger 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 the 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~~ feedsabout 40% of the ~~world~~ world'spopulation. 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 a high content of niacin and thiamine which are basically concerned ~~in~~ withproviding the special protein "Gluten". This protein provides the framework of the 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~~tons 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 the crossing, followed by the desired choice of individuals in ~~segregation~~ segregatedgenerations, depends on the presence of genetic diversity among the parents. Therefore, the first step in the 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~~ startingfrom the choice of parents for breeding to ~~obtain~~ obtainingnew 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~~program. Cluster analysis is an appropriate method for determining family

~~relationship~~ relationshipsand genetic affinity i.e., to determine the extent of the genetic distance of genotypes from each other. Mahalanobis D^2 statistic is a form of generalized distance ~~which~~ thatwas 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~~ program[10,11]. Therefore, quantitative assessment of genetic diversity present among ~~population~~ populationsusually helps a plant breeder in choosing desirable parents for a breeding ~~programme~~program. The higher the 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~~ checksM.P.4010, GW322, PBW873, GW366 and RVW 4106) atResearch 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 in length with 20 cm spacing and 10cm ~~plant to plant~~plant-to-plant distance. The observations were recorded on fifteen diverse morpho-physiological and ~~yield attributing~~yield-attributing traits. Data was recorded on a whole plot basis for days to 50% heading,days to 50% flowering, grain filling period, days of maturity, number of ~~tiller~~tillers, 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 the 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 the 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~~levels.

Formatted: Highlight

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.

Formatted: Highlight

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~~yield-related traits following Mahalanobis D^2statistics. 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~~ pursuedby cluster I and IV (8 lines), cluster II (3 lines) and the remaining monogenotypic clusters V,VI and VII had one lines's each. ~~Cluster wise~~Cluster-wise distribution of genotypes is summarized in **Table 2** and **Fig 2**&**3**.

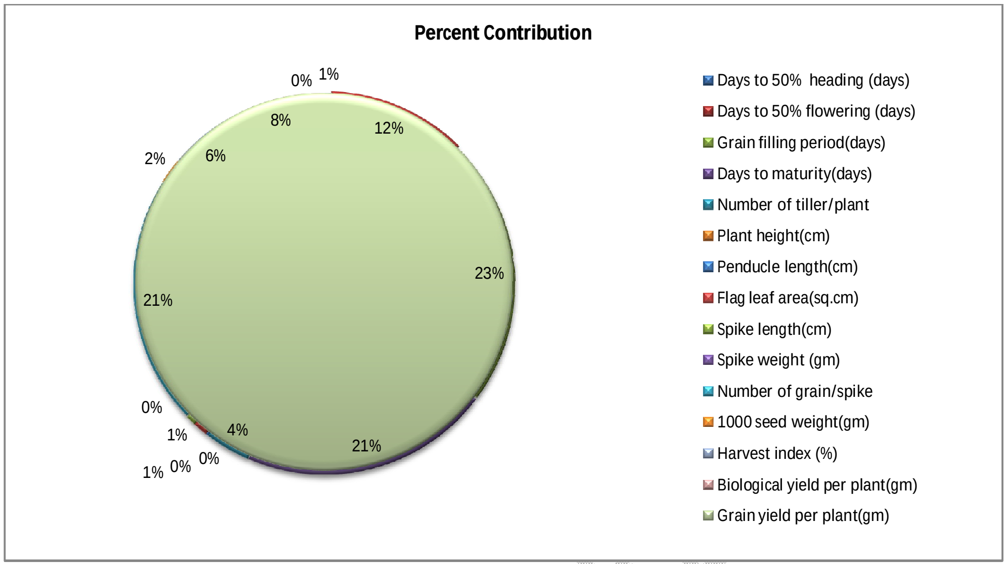

Fig.1 Percent contribution of characters

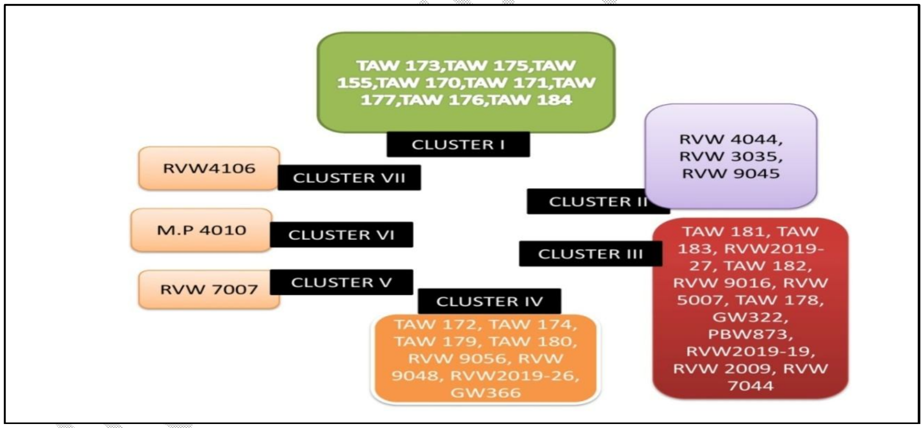

Fig. 2 Clustering pattern of 34 advanced breeding lines of bread wheat on the basis of D^2 statistics

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)

.

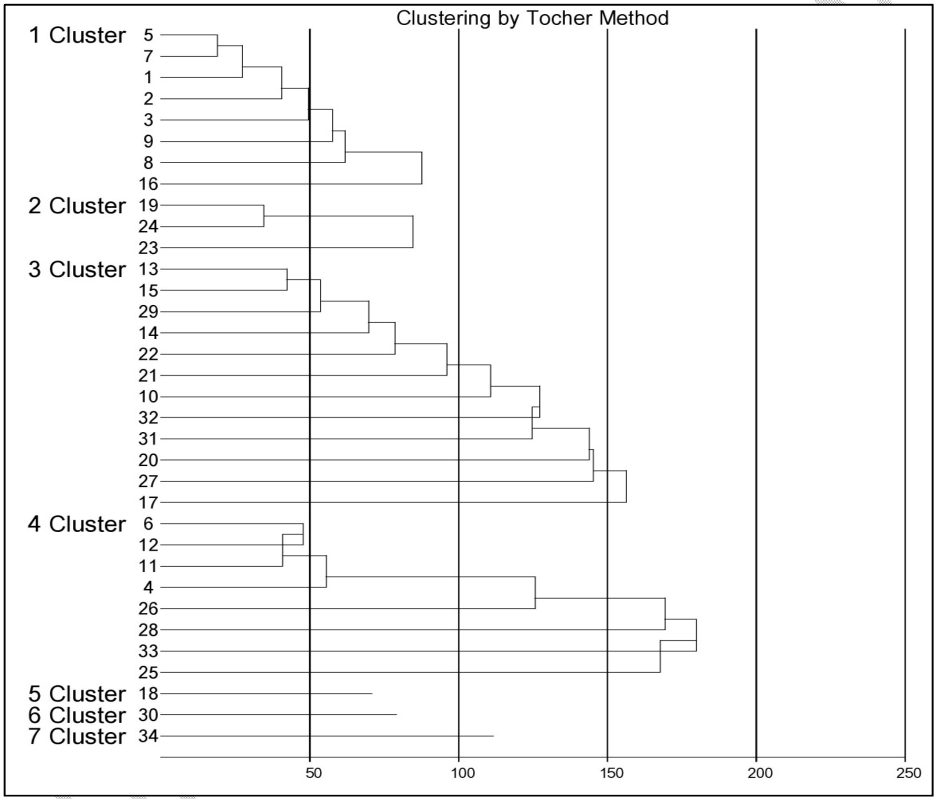

Fig. 3Clustering of Genotypes by Tocher Method

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~~inter-cluster D^2 values among the VII~~cluster~~ clustershighest 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~~inter-cluster divergence was observed between Cluster I and VI (D^2=11.78).The ~~inter cluster~~inter-cluster distance in ~~mostly~~ mostcase ~~were~~ waslarger than the ~~intra cluster~~intra-cluster which indicated that wider diversity is present among the lines of the distant group(**Table 3**) indicating a close relationship between these clusters and would not provide good results. The maximum distance between clusters~~,indicating~~ indicatesthat the genotypes included in these clusters showeda broad spectrum of genetic diversity and may be used in a hybridization ~~programme~~program for wheat improvement~~programme~~program [17]. In order to increase the probability of isolating good recombinants in the segregating generations would be useful to ~~crossing~~ crossbetween the diverse genotypes belonging to clusters separated by large ~~inter cluster~~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~~study. The data indicated that Cluster number V showed the highest cluster mean for Grain yield per plant (99) and the least in cluster VII (75.67). Cluster number V showed the highest cluster ~~mean ~~meansfor ~~Biological~~biological yield per plant (220.67) and the least in cluster III (183.56).Cluster number III showed the highest cluster mean for the Harvest index (49.56) and the least in cluster VII (41.14).Cluster number IV showed the highest cluster mean for 1000 seed weight (44.14) and the least in cluster VII (38.23).Cluster number VII showed the highest cluster mean for the Number of grain/~~spike~~spikes(65.53) and the least in cluster VI (40.13).Cluster number VII showed the highest cluster mean for Spike weight (3.63) and the least in cluster VI (2.66).Cluster number VII showed the highest cluster mean for Spike length (10.73) and the least in cluster V (7.87).Cluster number IV showed the highest cluster mean for the Flag leaves the area (45.27) and the least in cluster V (40.33).Cluster number I showed the highest cluster mean for Penducle length (14.22) ~~and~~and the least in cluster II (11.87).Cluster number VII showed the highest cluster mean for Plant height (81.52) and the least in cluster II (77.30).Cluster number VII showed the highest cluster mean for the Number of tillers (6.67) and the least in cluster VI (4.27).Cluster number II showed the highest cluster mean for days of maturity (137.78) and the least in cluster VI (130.33).Cluster number II showed the highest cluster mean for the grain filling period (45.33) and the least in cluster VI (35). Cluster number VI showed the highest cluster mean for days to 50% flowering (95.33) and the least in cluster V (91.67). Cluster number VI showed the highest cluster mean for days to 50% heading (84.33) and the least in cluster VIII (80.67). These are expected to exhibit high heterosis and are also likely to produce new recombinants with desired characters. ~~Similar ~~A similarresult was also in conformity ~~to ~~withthe 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 ~~programsto develop high-yielding wheat varieties.

The candidate manuscript does not have a robust scientific discussion, I suggest the authors incorporate the suggested paragraphs, in this way it would improve the scientific quality of the manuscript:

G~~enetic~~enetic divergence refers to the variation in genetic composition among individuals within a population or among populations of the same species. In bread wheat (*Triticum aestivum* L.), genetic divergence plays a crucial role in determining the variability of grain yield and its components, such as the number of spikes per plant, spike length, grain weight, and number of grains per spike. Understanding the genetic divergence in these traits can help breeders develop new varieties of bread wheat with improved yield potential.

Formatted: Font: Italic

Several factors can influence genetic divergence in grain yield and its components in bread wheat, including agro-environmental factors such as temperature [21], rainfall [22, 23, 24], soil fertility [25, 26, 27], and management practices [28, 29, 30]. Studies have shown that environmental factors can interact with the genetic makeup of bread wheat to influence grain yield and its components. For example, drought stress can reduce grain yield by affecting the number of spikes per plant and the number of grains per spike [31, 32, 33]., while high temperatures can reduce grain weight and spike length [34, 35].

To investigate the genetic divergence for grain yield and its components in bread wheat, several studies have employed molecular markers to identify genetic variations among different wheat genotypes. These studies have identified several quantitative trait loci (QTLs) associated with grain yield and its components, indicating the complex genetic basis of these traits. Moreover, studies have shown that genetic divergence can vary depending on the wheat genotypes and the environment in which they are grown.

The influence of agro-environmental factors on genetic divergence in grain yield and its components in bread wheat has been extensively studied. For example, studies have shown that soil fertility can influence genetic divergence in grain yield and its components by affecting the expression of QTLs associated with these traits. Similarly, studies have shown that the interaction between temperature and genetic makeup can influence grain yield and its components in bread wheat. For instance, some wheat genotypes may perform better under high-temperature conditions than others, indicating the role of genetic divergence in determining the response of wheat to environmental stress.

In conclusion, genetic divergence plays a crucial role in determining the variability of grain yield and its components in bread wheat. Agro-environmental factors such as temperature, rainfall, soil fertility, and management practices can influence genetic divergence in these traits, highlighting the need for breeding programs that account for the interaction between genetic makeup and environmental factors. Therefore, future research should focus on understanding the genetic basis of grain yield and its components in bread wheat and the interaction between genetic makeup and agro-environmental factors to develop new varieties of wheat with improved yield potential.

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/spikedays of maturity, days of flowering, biological yield per plant, and harvest index were observed to be major ~~contributor~~ contributorsto diversity among the genotypes. Hybridization between the genotypes in Cluster I and VI and ~~cluster~~ clustersVI 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~~% 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~~tillers	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*
Penducle 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**~~**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

I suggest adding recent references which address the issue in question, suggested citations are for genuine scientific reasons that emphasize the current topic of study in context.

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.

21. Olivares B, Guevara E, Oliveros Y, López, L. Aplicación del índice de confort térmico como estimador del estrés calórico en la producción pecuaria de la Mesa de Guanipa, estado Anzoátegui. Revista Zootecnia Tropical. 2013; 31 (3): 209-223.https://n9.cl/ovcu9
22. Casana S, Olivares B. Evolution and trend of surface temperature and windspeed (1994 - 2014) at the Parque Nacional Doñana, Spain. Rev. Fac. Agron. (LUZ). 2020; 37(1):1-25. https://n9.cl/c815e
23. Cortez A., Rodríguez M.F., Rey J.C., Ovalles F., González W., Parra R., Olivares B, Marquina, J. Temporaryspacevariabilityofprecipitation inGuaricostate, Venezuela. Rev. Fac. Agron. (LUZ). 2016; 33 (3): 292-310.https://n9.cl/m5q2x5
24. Rodríguez, M.F., Cortez, A., Olivares, B., Rey, J.C, Parra, R., Lobo, D. Time-space analisys of rainfall in state of Anzoategui and surrounding. Agronomía Tropical. 2013;63 (1-2): 57-65. https://n9.cl/14iow
25. Olivares, B.O.; Rey, J.C.; Perichi, G.; Lobo, D. Relationship of Microbial Activity with Soil Properties in Banana Plantations in Venezuela. Sustainability. 2022; 14, 13531. https://doi.org/10.3390/su142013531
26. Olivares, B., Paredes, F., Rey, J., Lobo, D., Galvis-Causil, S. The relationship between the normalized difference vegetation index, rainfall, and potential evapotranspiration in a banana plantation of Venezuela. SAINS TANAH - Journal of Soil Science and Agroclimatology, 2021; 18(1), 58-64. http://dx.doi.org/10.20961/stjssa.v18i1.50379
27. Olivares, B., López, M. Normalized Difference Vegetation Index (NDVI) applied to the agricultural indigenous territory of Kashaama, Venezuela. UNED Research Journal. 2019. 11(;): 112-121. https://doi.org/10.22458/urj.v11i2.2299
28. Olivares, B., López-Beltrán, M., Lobo-Luján, D. Cambios de usos de suelo y vegetación en la comunidad agraria Kashaama, Anzoátegui, Venezuela: 2001-2013. Revista Geográfica De América Central. 2019;2(63):269-291. https://doi.org/10.15359/rgac.63-2.10
29. Olivares, B., Hernández, R; Coelho, R., Molina, JC., Pereira, Y. Analysis of climate types: Main strategies for sustainable decisions in agricultural areas of Carabobo, Venezuela. ScientiaAgropecuaria, 2018; 9(3): 359 – 369. DOI: 10.17268/sci.agropecu.2018.03.07
30. Olivares, B.; Hernandez, R.; Arias, A; Molina, JC., Pereira, Y. Eco-territorialadaptabilityoftomatocrops for sustainableagriculturalproduction in Carabobo, Venezuela. Idesia, 2020; 38(2):95-102. http://dx.doi.org/10.4067/S0718-34292020000200095
31. Olivares, B., Cortez, A., Parra, R., Lobo, D., Rodríguez, M.F y Rey, J.C. Evaluation of agricultural vulnerability to drought weather in different locations of Venezuela. Rev. Fac. Agron. (LUZ) 2017; 34 (1): 103-129. https://n9.cl/d827w
32. Olivares, B., Cortez, A., Rodríguez, M., Parra, R., Lobo, D. y Rey, J.C. Análisis temporal de la sequía meteorológica en localidades semiáridas de Venezuela. UGCiencia,2016;22 (1):11-24. https://doi.org/10.18634/ugcj.22v.1i.481
33. Olivares, B., Zingaretti, ML. Análisis de la sequía meteorológica en cuatro localidades agrícolas de Venezuela mediante la combinación de métodos multivariados. UNED ResearchJournal. 2018; 10 (1):181-192. http://dx.doi.org/10.22458/urj.v10i1.2026
34. Olivares, B., Hernández, R. Ecoterritorial sectorization for the sustainable agricultural production of potato (*Solanum tuberosum* L.) in Carabobo, Venezuela. Agricultural Science and Technology. 2019; 20(2): 339-354. https://doi.org/10.21930/rcta.vol20_num2_art:1462
35. Olivares, B. Hernández, R; Arias, A; Molina, JC., Pereira, Y. Zonificación agroclimática del cultivo de maíz para la sostenibilidad de la producción agrícola en Carabobo, Venezuela. RevistaUniversitaria de Geografía. 2018; 27 (2): 139-159. https://n9.cl/l2m83

Formatted: Spanish (Spain, International Sort)

Formatted: Spanish (Spain, International Sort)

Field Code Changed

Formatted: No underline, Spanish (Spain, International Sort)

Formatted: No underline, Spanish (Spain, International Sort)

Formatted: Font: (Default) Arial, 10 pt, No underline, Font color: Text 1

Formatted: No underline, Spanish (Spain, International Sort)

Formatted: Font: (Default) Arial, 10 pt, No underline, Font color: Text 1

Formatted: No underline, English (United States)

Formatted: No underline, English (United States)

Formatted: No underline, Spanish (Spain, International Sort)

Formatted: No underline, Spanish (Spain, International Sort)

Formatted: No underline, English (United States)

Field Code Changed

Formatted: Hyperlink, Font: (Default) +Body, 11 pt, No underline, Font color: Auto, English (United States)

Formatted: No underline, Spanish (Spain, International Sort)

Formatted: No underline, Portuguese (Brazil)

Field Code Changed

Formatted: Hyperlink, Font: (Default) +Body, 11 pt, No underline, Font color: Auto, Portuguese (Brazil)

Formatted: No underline, English (United States)

Formatted: No underline, English (United States)

Formatted ... [1]

Formatted ... [2]

Formatted: Spanish (Spain, International Sort)

Formatted ... [3]

Formatted ... [4]

Formatted ... [5]

Field Code Changed

Formatted ... [6]

Formatted ... [7]

Formatted ... [8]

Formatted: Indent: Left: 0.25"

Page 13: [1] Formatted	Autor

No underline, Spanish (Spain, International Sort)

Page 13: [2] Formatted	Autor

No underline, Spanish (Spain, International Sort)

Page 13: [3] Formatted	Autor

No underline, English (United States)

Page 13: [4] Formatted	Autor

Font: Italic, No underline, English (United States)

Page 13: [5] Formatted	Autor

No underline, English (United States)

Page 13: [6] Formatted	Autor

Hyperlink, Font: (Default) +Body, 11 pt, No underline, Font color: Auto, English (United States)

Page 13: [7] Formatted	Autor

No underline, Spanish (Spain, International Sort)

Page 13: [8] Formatted	Autor

Font: (Default) Arial, 10 pt, Font color: Text 1