The Pharma Innovation Journal 2023; 12(3): 5344-5348

www.ThePharmaJournal.com

The Pharma Innovation

ISSN (E): 2277-7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2023; 12(3): 5344-5348

www.thepharmajournal.com
Received: 09-12-2022
Accepted: 13-01-2023

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Studies on genetic divergence (D^2) for yields and its attributing traits in wheat (*Tritium aestivum* L.)

Pradeep Kumar Yadav, RS Sikarwar, Madhurjit Singh Rathore and Sushma Tiwari

Abstract
A field experiment was carried out with 29 diverse advanced breeding lines of bread wheat along with five checks for genetic variability, character association and divergence analysis in randomized Block Design, divided into three replication. Each block had 29 plots of test entries along with 5 checks (*viz*., M.P.4010, GW322, PBW873, GW366 and RVW 4106). The trial was conducted The experimental research work will be carried at KVK farm, College of Agriculture RVSKVV, Gwalior during *Rabi* 2021-2022.The observations were recorded on eleven quantitative traits *viz*., days to 50% heading, days to 50% flowering, Grain filling period, days to maturity, number of tiller, Plant height, Penducle length, flag leaves area, spike length, spike weight, No. of grain/spike, 1000 seed weight, Harvest index, biological yield/plant and grain yield/plant. Results revealed that 29 advanced breeding lines and 5 check varieties of wheat were grouped into nine distinct clusters by using non-hierarchical Tocher method cluster analysis. It indicated the existence of high degree of genetic diversity present in the varieties/lines. Therefore, these varieties/lines may serve as valuable source for selection of diverse parents. Maximum intra-cluster distance was found for cluster-IV followed by cluster-I. The highest inter-cluster distance was observed between cluster III and IV, pursued by cluster VII and VIII, cluster VI and VIII, cluster II and III, cluster II and VII, cluster IV and VII. The lowest inter-cluster distance was observed between cluster III vs. V. Hence, crosses should be made between these widely related genotypes located in intra and inter cluster distances, to get desirable extant of heterotic potential in order to increase the production and productivity of wheat in Madhya Pradesh.

Keywords: wheat (*Triticum aestivum*), genetic diversity (D^2), cluster

Introduction
Wheat (*Triticum aestivum* L.) is the most widely grown crop and an essential component of the global food security mosaic, providing one-fifth of the total calories for the world's population. India is the world's second-largest country, both in terms of area and production, after China. India currently accounts for 13.5 percent of global wheat production. Wheat is cultivated on 31.61 million hectares in India, producing 109.52 million tonnes with a national average yield of 3464 kg/ha in 2020-21 (Anonymous, 2021). 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. (Anonymous, 2021). In terms of both area and production, Uttar Pradesh, Madhya Pradesh, Punjab and Haryana are the most important states. Punjab leads the rank in terms of productivity. Together contribute about 98% to the total wheat production of the country and play an important role of supplying carbohydrate and protein (Tewari *et al*., 2015 and Yadav *et al*., 2021) [18, 19].

Genetic diversity and relationship among genotypes is a prerequisite for any successful breeding Programme. Genetic diversity of plants determines their potential for improved efficiency and hence their use for breeding, which eventually may result in enhanced food production. Evaluation of genetic diversity levels among adapted, elite germplasm can provide predictive estimates of genetic variation among segregating progeny for pure-line cultivar development. Genetic similarity or dissimilarity can be compared by genetic distance between different individuals. Genetic distance can be used to measure the genetic divergence between different sub-species or different varieties of a species. The parents having more genetic distant relationship result into higher heterotic expression in F1 and greater amount of genetic variability in segregating populations (Shekhawat *et al*., 2001) [15]. Jaiswal *et al*., (2010) [6] studied genetic diversity for yield and yield contributing traits in 300 indigenous germplasm of bread wheat. On the basis of dissimilarity coefficient, these genotypes were grouped into 23 clusters.

The genetic diversity of genotypes is not always based on factors such as geographical diversity, place of release and ploidy level etc. Hence characterization of genotypes should be based on statistical procedures. Different statistical methods have been developed to assess the genetic diversity such as D2-statistics and hierarchical ecludean cluster analysis. These methods determine the genetic divergence using the similarity or dissimilarity based on aggregate effect of different economic important traits. Some appropriate methods, cluster analysis, PCA and factor analysis, for genetic diversity dentification, parental selection, tracing the pathway to evolution of crops, centre of origin and diversity, and study interaction between the environment are currently available (Carves *et al*., 1987; Mohammadi and Prasanna, 2003) [3, 12]. Precise information on nature and degree of genetic divergence helps the plant breeder in selecting the genetically diverse parents for the purposeful hybridization (Arunachalam, 1981) [1]. Genetic improvement of yield especially in self-pollinated crops depends on nature and amount of genetic diversity (Joshi and Dhawan, 1966) [7].

One of the important approaches to wheat breeding is hybridization and subsequent selection. Parents' choice is the first step in plant breeding program through hybridization. In order to obtain transgressive segregants, genetic distance between parents is necessary (Joshi *et al*., 2004) [8]. Higher heterosis in progeny can be observed with higher genetic distance between parents (Joshi and Dhawan, 1966) [7]. Estimation of genetic distance is one of appropriate tools for parental selection in wheat hybridization programs. One of the important approaches to wheat breeding is hybridization and subsequent selection. Parents' choice is the first step in plant breeding program through hybridization. In order to obtain transgressive segregants, genetic distance between parents is necessary (Joshi *et al*., 2004) [8]. Higher heterosis in progeny can be observed with higher genetic distance between parents (Joshi and Dhawan, 1966) [7]. Estimation of genetic distance is one of appropriate tools for parental selection in wheat hybridization programs.

Method and Materials

The present investigation was carried out during Rabi 2021-22 at crop research farm of Rajmata Vijyaraje Scindhia Krishi Vishwa Vidhyalaya, Gwalior (M.P.) using Randomized Block Design with three replications to work. These lines were taken from the germplasm maintained, in the Genetics and Plant breeding department of the university. Each genotype was sown in two lines of 6.0 m long with 2.5 m wide plot and 5 cm plant to plant distance. The experimental material consists of 29 advanced breeding lines of bread wheat including 5 checks namely M.P.4010, GW322, PBW873, GW366, RVW 4106. The experiment was laid out in randomized complete block design (RBD) with three replications. Each entry was planted in 6 meter long six rows plot. The rows were spaced 20 cm apart. All the recommended package of practices for wheat was followed to raise a healthy crop. All the morho-agronomic and physiological observations on most of the characters were recorded on single plant basis except for days to 50% heading, flowering, and maturity. Five representative plants from each plot were randomly selected and tagged for recording the observations on single plant basis. Average data from selected plants in respect of different characters were used for statistical analysis. The observations were recorded for the sixteen morpho-agronomic traits *viz*., days to 50% heading, days to 50% flowering, grain filling period, days of maturity, number of tiller, plant height, penducle length, flag leaves area, spike length, spike weight, number of grain/spike, 1000 seed weight, harvest index, biological yield per plant, grain yield per plant. The statistical analysis for genetic divergence was done using Mahalanobis-D2 statistics (Mahalanobis, 1936) [11] and clustering of genotypes was done using Tocher method (Rao 1952) [14].

Results and Discussion

The percentage contribution towards genetic divergence by all the characters is presented in table 1.the character 1000 seed weight (30.12%) contributed most toward genetic divergence followed by Days of maturity (17.83%), Biological yield per plant (17.65%), Days of flowering (12.30%), Number of grain/spike (11.94%), Plant height (4.10%), Harvest index (2.14%), Grain yield per plant (1.25%), Spike weight (1.07%), Days of 50% heading (0.71%), Flag leaves area (0.36%), Number of tillers (0.36%), (7.13%), Penducle length (0.18%). The remaining characters did not show contribution towards genetic divergence. The contribution of number of spikelet per spike has also been observed by Dobariya *et al*., (2006) [4] and biological yield per plant by Arya *et al*., (2017) [2]. The Contribution of various characters towards the expression of genetic divergence should be taken into account as a criterion for choosing parents for crossing Programme for the improvement in such characters (fig.1).

Table 1: Percent contribution of different characters towards genetic divergence

S. No.	Source	Times Ranked First	Percent Contribution
1.	Days to 50% heading	4	0.71%
2.	Days to 50% flowering	69	12.30%
3.	Grain filling period	0	0.00%
4.	Days of maturity	100	17.83%
5.	Number of tiller/plant	2	0.36%
6.	Plant height	23	4.10%
7.	Penducle length	1	0.18%
8.	Flag leaves area	2	0.36%
9.	Spike length	0	0.00%
10.	Spike weight	6	1.07%
11.	Number of grain/spike	67	11.94%
12.	1000 seed weight	169	30.12%
13.	Harvest index	12	2.14%
14.	Biological yield/plant	99	17.65%
15.	Grain yield/plant	7	1.25%

Table 2: Distribution pattern of 32 genotypes under different clusters

S. No.	Cluster No.	No. of Genotypes	Name of Genotypes
1.	I	22	TAW171, TAW172, TAW173, TAW174, TAW175, TAW176, TAW177, TAW179, TAW181, TAW182, TAW183, 7007, 4044, 2009, 9016, 5007, 9045, 9056, 9048, RVW2019-19, RVW2019-26, RVW2019-27, GW322(Cheak)
2.	II	1	TAW183
3.	III	1	TAW155
4.	IV	6	TAW170, PBW873 (Check), TAW180, TAW184, GW366 (Check), 7044
5.	V	1	TAW178
6.	VI	1	RVW4106 (Check)
7.	VII	1	3035
8.	VIII	1	M.P.4010 (Check)

Cluster information

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^2values, the $D^2$34 advanced breeding lines were grouped into 8 clusters following Tocher Method. The Cluster 1 polygenotypic had (22 advanced breeding lines) pursed by cluster IV (6 advanced breeding lines), and remaining monogenotypic clusters 2, 3, 5, 6, 7 and 8 had only one genotypes respectively. Cluster wise distribution of genotypes is summarized in table 3 and fig 1. The pattern of distribution of genotypes in different cluster exhibited that geographical diversity was not related to genetic diversity as genotypes of same geographical region were grouped into different clusters and vice-versa (Kumar *et al.* 2009) [10].

Table 3: Intra and Inter-Cluster Distances

Cluster	I	II	III	IV	V	VI	VII	VIII
I	14.77	17.43	17.87	20.58	17.86	19.88	16.79	21.66
II		0.00	24.44	14.88	18.84	21.55	24.27	17.44
III			0.00	25.14	13.02	15.21	15.70	24.90
IV				14.78	20.61	22.84	24.19	18.87
V					0.00	17.85	22.39	20.92
VI						0.00	15.61	24.66
VII							0.00	25.05
VIII								0.00

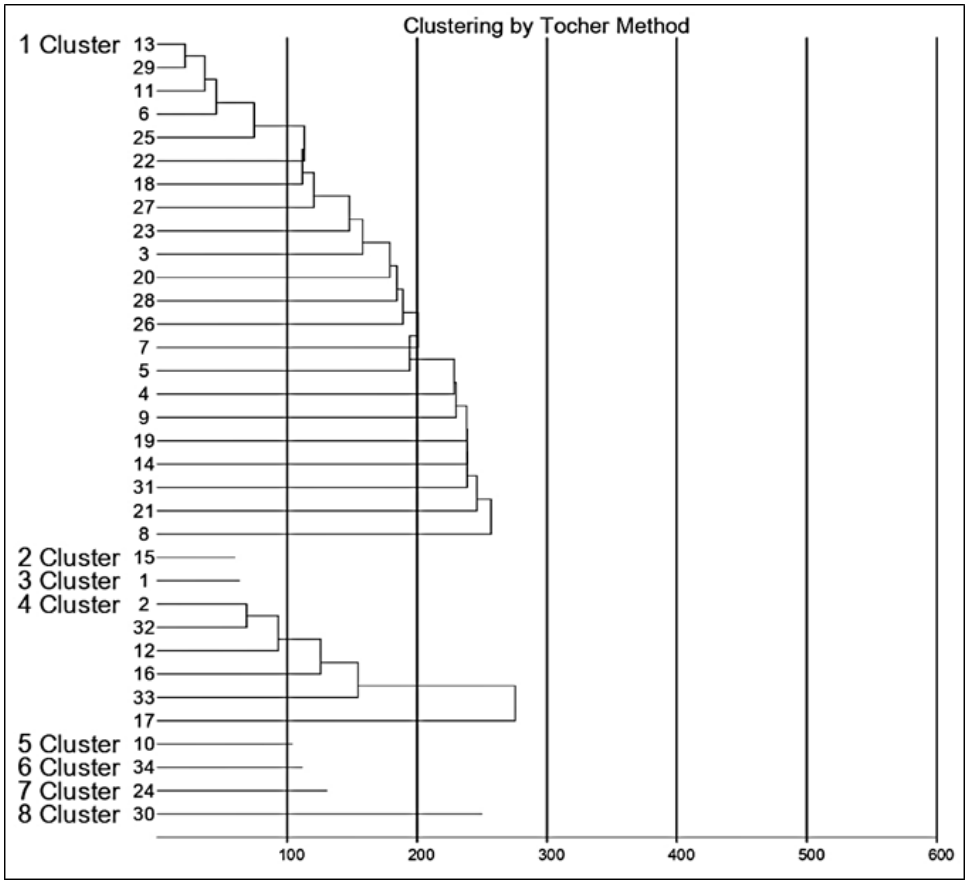

Fig 1: Clustering of Genotypes by Tocher Method

Intra and Inter-Cluster Distances

The average intra and inter cluster D^2 values estimated as per the procedure given by Singh and Choudhary (1977) [17]. Cluster number IV showed maximum intra cluster D^2 value (D^2=14.78) chased by cluster number I (D^2=14.71). While, other cluster were mono-genotypic with no intra cluster divergence. Intra cluster D^2 values ranges from 0.00 (cluster II, III, V, VI, VII and VII) to IV (cluster IV).

Inter-cluster distance is the main criterion for selection of genotypes using D2 analysis (Khare *et al.*, 2015) [9]. The genotypes belonging to those clusters having maximum inter-cluster distance are genetically more divergent and hybridization between these genotypes of different clusters is likely to produce wide variability with desirable individuals (Singh *et al.*, 2006) [16]. The VIII cluster highest inter cluster divergence was observed between 34 advanced breeding lines, of cluster I and VIII (D^2=21.66), pursued by cluster II and III (D^2=24.44), cluster III and IV (D^2=25.14), cluster IV and VII (D^2=24.19), cluster V and VII (D^2=22.39), cluster VI and VIII (D^2=24.66), cluster VII and VIII (D^2=25.05), Cluster I vs. IV (D^2=20.58), cluster I vs. VI (D^2=19.88), cluster Ivs. III (D^2=17.87), Cluster I vs. V (D^2=17.86) Cluster I vs. II (D^2=17.43), Cluster I vs. VII(D^2=16.79), Cluster II vs. VII(D^2=24.27), Cluster II vs. VI(D^2=21.55), Cluster II vs. V(D^2=18.84), Cluster II vs. VIII(D^2=17.44), Cluster II vs. IV(D^2=14.88), Cluster III vs. VIII(D^2=24.90), Cluster III vs. VII(D^2=15.70), Cluster III vs. VI(D^2=15.21), Cluster IV vs. VI(D^2=22.84), Cluster IV vs. V(D^2=20.61), Cluster IV vs. VIII(D^2=18.87), Cluster V vs. VIII (D^2=20.92), Cluster V vs. VI(D^2=17.85), Cluster VI vs. VII(D^2=15.61), here least inter cluster divergence was observed between advanced breeding lines of cluster III vs. V (D^2=13.02). The inter cluster distance in mostly case were larger than the intra cluster which indicated that wider diversity is present among the advanced breeding lines of distant group. (Table 4) suggested a closer relationship between these two clusters and low degree of

genetic diversity among the genotypes. Presence of substantial genetic diversity among the parental material screened in the present study indicated that this material may serve a good source for selecting the diverse parents for hybridization Programme. In order to increase the possibility of isolating good transgressive segregants in the segregating generations it would be logical to attempt crosses between the diverse genotypes belonging to clusters separated by large inter-cluster distances. (Rathore *et al*., 2022) [13].

Cluster Mean Values

Cluster means were calculated for all the physiological and agronomic characters which exhibited considerable differences among the clusters. The mean performance of the clusters (Table 5) was used to select genetically diverse and agronomically superior genotypes out of 34 genotypes studied. The cluster means for each of the 15 characters are presented in (Table 5). From the data it can be seen that considerable differences existed for the traits under studied. The data indicated that Cluster number VII showed highest cluster mean for Grain yield per plant (88.67) and least in cluster IV (48.33). Cluster number VII showed highest cluster mean for Biological yield per plant (232.67) and least in cluster IV (137.28). Cluster number VIII showed highest cluster mean for Harvest index (45.46) and least in cluster IV (35.67). Cluster number I showed highest cluster mean for 1000 seed weight (42.57) and least in cluster VI (31.67). Cluster number VII showed highest cluster mean for Number of grain/spike (84.27) and least in cluster II (48.13). Cluster number V showed highest cluster mean for Spike weight (3.83) and least in cluster IV (2.01). Cluster number V showed highest cluster mean for Spike length (11.73) and least in cluster VIII (10.13). Cluster number VII showed highest cluster mean for Flag leaves area (49.67) and least in cluster III (37.30). Cluster number V showed highest cluster mean for Penducle length (18.37) and least in cluster VII (12.73). Cluster number IV showed highest cluster mean for Plant height (93.68) and least in cluster VIII (76.05). Cluster number III showed highest cluster mean for Number of tillers (9.97) and least in cluster VII (8.27). Cluster number III showed highest cluster mean for days of maturity (127.67) and least in cluster VIII (124). Cluster number III and VIII showed highest cluster mean for grain filling period (31.67) and least in cluster VI and VII (27.67). Cluster number VII showed highest cluster mean for days to 50% flowering (99.67) and least in cluster VIII (92.33). Cluster number VII showed highest cluster mean for days to 50% heading (89.67) and least in cluster VIII (82.33).

In conclusion, the most important trait that causing maximum genetic divergence was 1000 seed weight and it was responsible for differentiating the genotypes studied.

Table 4: Cluster Means for different characters

Cluster	I	II	III	IV	V	VI	VII	VIII
Days to 50% heading	86.23	87.67	86.00	86.00	85.67	87.00	89.67	82.33
Days to 50% flowering	96.23	97.67	96.00	96.00	95.67	97.00	99.67	92.33
Grain filling period	29.41	27.33	31.67	29.00	29.00	27.67	27.67	31.67
Days of maturity	125.64	125.00	127.67	125.00	124.67	124.67	127.33	124.00
Number of tiller/plants	9.62	9.70	9.97	9.24	9.77	9.30	8.27	8.57
Plant height	91.10	86.87	86.27	93.68	87.20	86.60	89.13	76.05
Penducle length	16.08	17.70	13.70	16.12	18.37	17.70	12.73	15.69
Flag leaves area	43.92	43.60	37.30	45.16	42.13	42.20	49.67	47.03
Spike length	11.65	11.13	11.37	10.58	11.73	11.28	11.47	10.13
Spike weight	3.34	2.53	3.47	2.01	3.83	3.33	3.50	2.23
Number of grain/spike	66.24	48.13	73.23	55.80	55.92	68.55	84.27	50.77
1000 seed weight	42.57	40.77	40.40	38.06	42.63	31.67	35.93	38.50
Harvest index	38.91	36.77	41.53	35.67	36.13	36.40	38.07	45.46
Biological yield per plant	206.21	176.67	185.33	137.28	174.67	227.33	232.67	144.00
Grain yield per plant	79.24	65.00	77.00	48.33	63.33	82.67	88.67	65.33

The highest inter-cluster distance was found between clusters-III and IV (25.14) suggesting that crossing between the members of these two clusters will lead to development of wide range of genetic variability and breeder will have greater chances to get desired segregants while the lowest inter-cluster distance observed between cluster-III & V (13.02) indicates that the genotypes in these two clusters were relatively close to each other, exhibiting poor range of genetic variability. Cluster-VII exhibited highest cluster means for the characters days of 50% heading, days of 50% flowering, grain filling period, number of tillers per plants, penduncle length, flag leaves areas, number of grains per spike, biological yield per plant, grain yield per plant and cluster-VII was marked by highest cluster means for the traits days of 50% heading, days of 50% flowering, penduncle length, number of grains per spike, biological yield per plant, grain yield per plant value in wheat could also be used in hybridization programmes for physiological traits. Hence, crossing between genotypes belonging to these clusters may result in high heterosis, which could be exploited in crop improvement by plant breeder to get desired transgressive segregants. Inter and intra-cluster distance provide index of genetic diversity between and within clusters. It would be desirable to choose the donor from different clusters. Larger the distance between the clusters better the chances of getting transgressive segregants. These findings suggest that the experimental material had sufficient genetic diversity for yield contributing traits. Diversity in these characters may be exploited through hybridization for the development of superior individuals for yield traits.

References

1. Arunachalam VA. Genetic distances in plant breeding. Indian J Genet. 1981;4:226-236.
2. 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 J Agric. Res. 2017;51(2):128-134.

3. Carves BF, Smith EL, England HO. Regression and cluster analysis of environmental responses of hybrid and pure line winter wheat cultivars. Crop Sci. 1987;27:659-664.
4. 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.
5. ICAR-IIWBR. Director's Report of AICRP on Wheat and Barley Improvement Project 2020-21. Ed: Singh GP, ICAR-Indian Institute of Wheat and Barley Research, Karnal, India; c2021. p. 87.
6. Jaiswal JP, Arya M, Kumar A, Swati, Rawat RS. Assessing genetic diversity for yield and quality traits in indigenous bread wheat germplasm. Electronic J of Plant Breeding. 2010;1(4):370-378.
7. Joshi AB, Dhawan NL. Genetic improvement of yield with special reference to self-fertilizing crops. Ind J Genet and Plant Breed. 1966;26:101-113.
8. Joshi BK, Mudwari A, Bhatta MR, Ferrara GO. Genetic diversity in Nepalese wheat cultivars based on agro-morphological traits and coefficients of parentage. Nep Agric Res J. 2004;5:7-17.
9. Khare M, Rangare NR, Singh RP. Evaluation of genetic diversity in Mexican wheat (*Triticum aestivum* L.) genotypes for quantitative and qualitative traits. International Journal of Plant Protection. 2015;8(1):77-80.
10. Kumar B, Lal GM, Ruchi, Upadhyay A. Genetic variability, Diversity and association of quantitative traits with grain yield in bread wheat (*Triticum aestivum* L.). Asian Journal of Agricultural Sciences. 2009;1(1):4-6.
11. Mahalanobis PC. On the generalized distance in statistics. Proc. Nat. Inst. Sci. India. 1936;2:49-55.
12. Mohammdi SA, Prasanna BH. Analysis of genetic diversity in crop plant salient statistical tools and considerations, Crop Sci. 2003;43(4):1235-1248.
13. Rathore MS, Tiwari S, Tripathi MK, Gupta Neha, Yadav S, Singh S, *et al*. Genetic diversity analysis of groundnut germplasm lines in respect to early and late leaf spot diseases and biochemical traits Legume Research-An International Journal, 2022, (1). 10.18805/LR-4833
14. Rao CR. Advanced statistical method in biometric research. John Wiley and Sons Inc. New York, USA; c1952.
15. Shekhawat US, Vijay P, Singhania DL. Genetic divergence in barley (*Hordeum vulgare* L.) Indian J Agric. Res. 2001;35(2):121-123.
16. Singh SK, Singh BN, Singh PK, Sharma CL. Genetic divergence of exotic germplasm lines in wheat (*T. aestivum* L.). Indian J Plant Genet. Resources. 2006;19(2):218-220.
17. Singh RK, Chaudhary BD. Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi; c1977. p. 252.
18. Tewari R, Jaiswal JP, Gangwar RP, Singh PK. Genetic diversity analysis in exotic germplasm accessions of wheat (*Triticum aestivum* L.) by cluster analysis. Electronic Journal of Plant Breeding. 2015;6(4):1111-1117.
19. Yadav PK, Tiwari S, Kushwah A, Tripathi MK, Gupta N, Tomar RS, *et al*. Morpho-physiological characterization of bread wheat genotypes and their molecular validation for rust resistance genes Sr2, Sr31 and Lr24. Proc. Indian Natl. Sci. Acad. 2021;87:534-545. https://doi.org/10.1007/s43538-021-00049-y41.