The Pharma Innovation

Uike AR
Department of Agricultural Botany, Post Graduate Institute, MPKV, Rahuri, Ahmednagar, Maharashtra, India

Dodake SS
Agricultural Research Station, Niphad, Nashik, Maharashtra, India

Shamkuwar SG
Department of Agricultural Botany, Post Graduate Institute, PDKV, Akola, Maharashtra, India

Genetic diversity studies in bread wheat (*Triticum aestivum* L.) under restricted irrigation condition

Uike AR, Dodake SS and Shamkuwar SG

Abstract
Wheat is primarily cultivated in rainfed conditions and production is frequently affected by water and heat stresses. Thus, for sustainable wheat production and food security, we require water efficient wheat varieties. Therefore, the present study was conducted with objectives to estimate the genetic diversity in bread wheat. The experiment was conducted with 54 bread wheat genotypes including three checks in RBD with two replications. On the basis of D^2 values the genotypes were grouped into six clusters. Cluster I was with 49 genotypes, emerged as the largest cluster. The clusters II, III, IV, V and VI were found to be mono genotypic. The maximum inter cluster distance was seen between cluster (IV and VI) followed by cluster (II and V) and cluster (II and VI). Cluster II having high cluster mean for length of peduncle, flag leaf length and number of spikelets spike^{-1}, whereas, cluster IV possesses high cluster mean for number of productive tillers running meter^{-1} and grain yield running meter^{-1}. Thus the genotypes in these clusters might be used in further hybridisation programme for improvement in bread wheat.

Keywords: genetic diversity, D^2 statistics, cluster analysis, restricted irrigation

Introduction
Wheat (*Triticum aestivum* L.) is the world's second most important cereal crop after rice, originated in South-Western Asia. The crop is best suited for temperate climates, but it is also cultivated and consumed in the tropical and sub tropical regions. Wheat cultivation is limited to the winter season in warmer climates because it requires a cool growing season.

India is the world's second largest wheat producer, after China, in terms of both area and production. The world acreages under wheat crop was 217 million hectares with the production of 731 million tonnes (Anonymous, 2019) [1]. On the other hand, in case of India it was cultivated on 30.56 million hectares with the annual production of 109.24 million tones, (Anonymous, 2020) [2]. The largest wheat-growing states in India include Uttar Pradesh, Haryana, Punjab, Rajasthan, Madhya Pradesh, Bihar, Gujarat, Maharashtra and Karnataka.

Genetic diversity, which is the foundation of plant breeding and is formed as a result of inherent genetic variances in plant species, is of great interest to plant breeders. In plant breeding, genetic diversity is vital for exploiting heterosis or generating productive recombinants. In a breeding programme, crop improvement is based on the selection of superior parents that produce superior traits to its progenies.

Wheat is primarily cultivated in rainfed conditions, and production is frequently affected by water and heat stresses. Drought and heat stress at the end of the growing season have a negative impact on wheat grain weight and yield. For sustainable wheat production and food security, the country requires water efficient varieties for such large areas. Therefore, keeping in view these things, the present investigation was undertaken to estimate genetic divergence among the genotypes under restricted irrigation condition by D^2 analysis to select potent parents for further hybridization-selection programme.

Materials and Methods
The experiment was conducted at Agricultural Research Station, Niphad, Dist. Nashik (M.S.) India, with 51 bread wheat genotypes and three standard checks viz., Phule Samadhan, Netravati and Phule Satvik, collected from the office of Wheat specialist, Agricultural Research Station, Niphad. Study was conducted in Randomised Block Design (RBD) with two replications and observations were recorded on 14 morphological traits viz., days to 50 per cent heading, days to maturity, coleoptile length (cm), plant height (cm), number of productive tillers running meter^{-1}, peduncle length (cm), flag leaf length (cm), flag leaf breadth (cm),

Corresponding Author:
Uike AR
Department of Agricultural Botany, Post Graduate Institute, MPKV, Rahuri, Ahmednagar, Maharashtra, India

spike length (cm), number of spikelets spike[-1], number of flowers spike[-1], number of grains spike[-1], 1000 grain weight (g) and grain yield running meter[-1] (g).

The analysis of variance for above characters was performed according to methods given by Panse and Sukhatme (1995) [12]. The characters showing significant differences were subjected to further analysis proposed by Dewey and Lu (1959) [4]. The D^2 statistics of Mahalanobis (1936) [9], as described by Rao (1952) [13], has been used to analyse divergence. The plot averages were used to conduct a covariance analysis for character pairs (Cochran and Cox, 1957) [3].

The generalized distance between two populations was calculated using method suggested by Mahalanobis (1936) [9] as,

$$D^2 = \Sigma\Sigma \lambda i.j.\ di.\ dj$$

Where,

$\lambda i.j$ = Reciprocal matrix to the common dispersion matrix

d i & d j= Difference between the mean values of two populations for i^{th} and j^{th} character respectively

For cluster creation, Tocher's method was used, as described by Rao (1952) [13]. The intra and inter-cluster D and D^2 values were calculated by D^2 analysis.

Results and Discussion

The 51 genotypes of bread wheat along with 3 standard checks were grouped into six clusters by Mahalanobis D^2 statistics, wherein cluster I was with 49 genotypes emerged as the largest cluster. The clusters II, III, IV, V and VI includes one genotype each (Table 1). Earlier workers Singh and Salgotra (2014) [14] grouped 13 wheat genotypes into four clusters, Yadav *et al.* (2014) [15] grouped the 50 genotypes into eight different non-overlapping clusters, Fikre *et al.* (2015) [7] classified 64 genotypes into nine clusters and Getachew *et al.* (2017) [7] grouped 49 genotypes into six clusters.

Although the genotype distribution in distinct clusters was random, it clearly demonstrated a relationship with the characters for which they were studied. It was concluded that genetic and geographic diversity are unrelated. Moll *et al.* (1962) [10] and Lee and Kaltsikes (1973) [8] both reported similar findings.

Cluster I had maximum intra-cluster distance (533.00) and rest of clusters had zero intra-cluster distance as they were monogenic (Table 2). Cluster IV and VI (2908.12) showed maximum inter-cluster distance followed by cluster II and V (2567.85), cluster II and VI (2435.62), cluster III and VI (2360.98) and cluster IV and V (2275.38). These findings indicate that the genotypes classified in these clusters have the maximum divergence, implying that genotypes in one cluster are completely different from genotypes in other cluster.

Cluster means for 14 characters are presented in Table 3. It showed a wide range of variability for maximum characters. Cluster III was early for days to 50 per cent heading and maturity. Also it had observed a short plant height. Cluster IV recorded highest cluster mean for number of productive tillers running meter[-1] and grain yield running meter[-1]. Cluster VI recorded longest spike. Cluster V had observed maximum number of grains spike[-1].

It was observed that number of productive tillers running meter[-1] (37.95) contributed highest for genetic divergence followed by days to maturity (22.85), coleoptile length (8.53). However, the character grain yield running meter[-1] (0.14) and days to 50% heading (0.14) contributed least to genetic divergence (Table 4). Nimbalkar *et al.* (2002) [11] also observed same results for number of productive tillers running meter[-1].

From the results of the inter-cluster distance (Table 2) we can conclude that, there was genetic diversity among the genotypes of different clusters, so that maximum amount of heterosis is expected in cross combinations from the genotypes of the most diverse clusters. Genotypes clumped into the same cluster presumably little diverse from one another. However, a general concept in the theory exists that, "The greater is the divergence between the genotypes, higher will be the heterosis", (Falconer, 1981) [5]. Therefore, it would be feasible to carry out crosses between genotypes from the distant clusters for getting crosses having high heterosis. However, high heterosis is very important in isolating superior segregants subject to additive type of gene action. The genotypes grouped into clusters with maximum inter-cluster distance were clearly genetically more diverse. Hence, it would be economical to include genotypes from those clusters in further hybridization programmes.

Table 1: Distribution of 51 genotypes of bread wheat along with three standard checks into different clusters

Cluster	Number of genotypes	Genotypes
I	49	NIAW 4465, NIAW 4466, NIAW 4467, NIAW 4468, NIAW 4469, NIAW 4470, NIAW 4471, NIAW 4472, NIAW 4473, NIAW 4474, NIAW 4475, NIAW 4476, NIAW 4477, NIAW 4478, NIAW 4479, NIAW 4480, NIAW 4481, NIAW 4499, NIAW 4500, NIAW 4501, NIAW 4502, NIAW 4504, NIAW 4505, NIAW 4506, NIAW 4507, NIAW 4508, NIAW 4509, NIAW 4510, NIAW 4511, NIAW 4512, NIAW 4513, NIAW 4514, NIAW 4515, NIAW 4623, NIAW 4624, NIAW 4625, NIAW 4627, NIAW 4628, NIAW 4629, NIAW 4631, NIAW 4632, NIAW 4634, NIAW 4635, NIAW 4636, NIAW 4638, NIAW 4639, Phule Samadhan, Netravati, Phule Satvik
II	1	NIAW 4637
III	1	NIAW 4633
IV	1	NIAW 4630
V	1	NIAW 4626
VI	1	NIAW 4503

Table 2: Average intra (diagonal) and inter (above diagonal) cluster D and D^2 (in bracket) values of six clusters formed from 51 bread wheat genotypes along with 3 standard checks

Cluster	I	II	III	IV	V	VI
I	23.087 (533.00)	36.294 (1317.25)	37.906 (1436.86)	41.107 (1689.78)	33.648 (1132.18)	41.886 (1754.43)
II		0	23.661 (559.84)	20.653 (426.54)	50.674 (2567.85)	49.352 (2435.62)
III			0	33.494 (1121.84)	43.506 (1892.77)	48.59 (2360.98)
IV				0	47.701 (2275.38)	53.927 (2908.12)
V					0	46.664 (2177.52)
VI						0

Table 3: Mean performance of clusters for 14 characters in 51 bread wheat genotypes along with 3 standard checks

Character / Cluster	Days to 50% heading	Days to maturity	Coleoptile length (cm)	Plant height (cm)	Number of Productive tillers running meter^{-1}	Peduncle length (cm)	Flag leaf length (cm)	Flag leaf breadth (cm)	Spike length (cm)	Number of spikelets spike^{-1}	Number of flowers spike^{-1}	Number of grains spike^{-1}	1000 grain weight (g)	Grain yield running meter^{-1} (g)
I	69.32	111.94	6.42	79.48	56.34	11.39	18.11	1.30	9.99	20.01	57.73	51.78	36.29	57.83
II	66.00	113.00	6.25	73.95	107.45	13.00	21.55	1.30	10.15	24.00	62.20	56.00	33.70	60.42
III	62.00	105.00	6.35	67.90	101.30	10.05	18.90	1.70	8.10	18.20	63.40	58.10	38.10	69.59
IV	74.00	117.00	8.10	73.20	107.95	10.80	16.55	1.30	10.45	22.80	69.10	62.90	32.40	89.59
V	72.00	108.00	9.70	82.00	41.95	7.75	18.20	1.55	10.45	23.00	69.80	63.60	37.80	78.34
VI	70.00	113.50	5.50	74.15	57.30	9.90	17.50	1.25	10.50	22.30	70.70	45.40	32.25	52.50

Table 4: Per cent contribution of 14 characters for divergence in wheat

Sr. No.	Characters	Number of times appeared 1st in ranking	Per cent contribution
1.	Days to 50% heading	2	0.14
2.	Days to maturity	327	22.85
3.	Coleoptile length (cm)	122	8.53
4.	Plant height (cm)	39	2.73
5.	Number of productive tillers running meter^{-1}	543	37.95
6.	Peduncle length (cm)	51	3.56
7.	Flag leaf length (cm)	22	1.54
8.	Flag leaf breadth (cm)	85	5.94
9.	Spike length (cm)	68	4.75
10.	Number of spikelets spike^{-1}	0	0.00
11.	Number of flowers spike^{-1}	7	0.49
12.	Number of grains spike^{-1}	89	6.22
13.	1000 grain weight (g)	74	5.17
14.	Grain yield running meter^{-1} (g)	2	0.14
	Total		100

Conclusion

There is considerable genetic diversity among the genotypes studied. On the basis of inter cluster distances, cluster mean and *per se* performance of genotypes observed in the present study, the genotypes *viz.,* Netravati, Phule Satvik, NIAW-4626, Phule Samadhan, NIAW-4633, NIAW-4637, NIAW-4630, NIAW-4633 and NIAW-4503 were diverse and distinct and can be classified as promising genotypes. These genotypes may be used in future crossing programme to obtain desired segregants in bread wheat. Subsequent crossing between cluster (IV and VI), cluster (II and V) and cluster (II and VI) could result in heterosis in the F_1 generations and a lot of variability in the F_2 generations.

Acknowledgement

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