Mainak Barman
Department of Genetics and
Plant Breeding, Bidhan Chandra
Krishi Viswavidyalaya,
Mohanpur, Nadia, West Bengal,
India

Vinay Kumar Choudhary
Department of Plant Breeding
and Genetics, Dr. Rajendra
Prasad Central Agricultural
University, Pusa, Samastipur,
Bihar, India

Satish Kumar Singh
Department of Plant Breeding
and Genetics, Dr. Rajendra
Prasad Central Agricultural
University, Pusa, Samastipur,
Bihar, India

Rabiya Parveen
Department of Plant Breeding
and Genetics, Bihar Agricultural
University, Sabour, Bhagalpur,
Bihar, India

Amitava Roy
Division of Genetics, Indian
Agricultural Research Institute,
Pusa Campus, New Delhi, India

Pulak Debbarma
Division of Genetics, Indian
Agricultural Research Institute,
Pusa Campus, New Delhi, India

Corresponding Author:
Mainak Barman
Department of Genetics and
Plant Breeding, Bidhan Chandra
Krishi Viswavidyalaya,
Mohanpur, Nadia, West Bengal,
India

Cluster analysis in bread wheat (*Tricitum aestivum* L.) genotypes for morpho-physiological traits and grain micronutrient content

Mainak Barman, Vinay Kumar Choudhary, Satish Kumar Singh, Rabiya Parveen, Amitava Roy and Pulak Debbarma

Abstract
Wheat (*Triticum* spp.) is considered as one key staple food crop in numerous places of our globe not only in terms of the area under cultivation but as a source of food also. It covers all the continents of the globe, engaging 17% of the world acreage of crops and feeds almost 40% populations globally. More than 3 billion population worldwide roughly, experiences the malnutrition problems. Malnutrition of micronutrient, predominantly the deficiency in Zinc and Iron worldwide afflicts more than three billion people. Keeping all the above considerations insight, the current evaluation of genetic diversity in bread wheat was performed for morpho-physiological traits and grain micronutrient content. The total 30 bread wheat genotypes under investigation were grouped into nine clusters. Cluster II included eight genotypes which were the highest followed by cluster I, cluster IV and cluster VII containing 6, 6 and 5 genotypes respectively. However, the rest five clusters namely, cluster III, cluster V, cluster VI, cluster VIII and cluster IX were solitary. The utmost inter-cluster distance was noted between the clusters VII and IX and the least inter-cluster distance was noted between the clusters V and VI. Genotypes RAUW-18-15, RAUW-18-21, DBW 16, BHU 25, RAUW-16-4 were recorded genetically most diverse having the highest intra-cluster distance. The highest contribution in manifesting genetic divergence was revealed by grain Fe content, followed by grain Zn content, days to fifty percent flowering, 1000-grain weight, grain yield per plant, number of grains/ ear. This means, it may be rewarding to execute selection for these traits.

Keywords: Bread wheat, clusters, genetic divergence, micronutrient malnutrition, morpho-physiological traits

Introduction

Wheat (*Triticum* spp.) is considered as one key staple food crop in numerous places of our globe not only in terms of the area under cultivation but as a source of food also. Wheat cultivation is distributed geographically in such an abundant manner that it is being reaped in one country or another all around the year. It is a long-day, monocot, C3, self-pollinated plant. It belongs to the tribe Triticeae, under the widely diverse and significance holding "Poaceae" family of the plant kingdom. The total harvest of the crop worldwide in 2017 was about 771 million tons. In India, more than 98 million tons of production was documented in 2017 (FAOSTAT, 2017) [1]. In almost all parts of India, wheat is under cultivation with a contribution of nearly about 30% to the nation's food basket (Kumar *et al.*, 2016) [2]. However, most of the wheat cultivars are micronutrient-deficit, such as Zinc and Iron in prevalence (Cakmak *et al*., 2004) [3]. 'Hidden-hunger' is a massive public health issue affecting all the developing nations striking underprivileged people chiefly (Gani *et al.* 2018)[4]. More than 3 billion population worldwide roughly, experience the malnutrition problems due to lack of micronutrients (White and Broadley, 2009) [5]. Since the Green Revolution, the yields of cereal grains worldwide have been boosted spectacularly, but cereal-based diet falls petite to provide adequate nutrients (Welch and Graham, 2004) [6]. For a balanced diet of human-being, an adequate amount of nutrients from grain is not provided in the developing world by most of the agricultural arrangements (Cakmak *et al*., 2010) [7]. To combat the worldwide malnutrition evil and related health hazards, enrichment of grain nutrient (biofortification), either by agronomic means or by genetic means, is now considered to be the approach with the most proficiency and cost-effectiveness (Peleg *et al*., 2009) [8]. Keeping the above considerations insight, the current investigation was performed with the intention of investigating divergence in Bread Wheat genotypes for yield-attributing traits along with grain zinc and iron content.

Materials and Methods

The current experiment was carried out in the Wheat Breeding section fields of Dr. Rajendra Prasad Central Agricultural University (DRPCAU), Pusa, Samastipur, Bihar, India during the *Rabi* season of 2019-20. The experimental materials intended for the evaluation consisted of 30 diverse genotypes of bread wheat (*Triticum aestivum* L.) *viz.* DBW 16, DBW 17, HD 2985, RAJ 3763, BHU 25, HD 2824, PBW 648, RAUW-16-4, RAUW-18-9, RAUW-18-12, RAUW-17-9, RAUW-18-15, RAUW-18-11, RAUW-118-4, RAUW-18-13, RAUW-16-11, RAUW-16-9, RAUW-18-7, RAUW-16-5, RAUW-16-7, RAUW-16-9, RAUW-16-10, RAUW-16-15, RAUW-16-17, RAUW-18-18, RAUW-18-21, RAUW-18-25, RAUW-18-26, WB 02, and HD 2967 collected from the department of Plant Breeding and Genetics, DRPCAU. Two varieties *viz.* HD-2967 and WB-02 were employed as checks in the evaluation. The research was carried out with 3 replications in a Randomized Block Design (RBD). Each of the genotypes was nurtured in a plot having five rows of 3-meter length each with 23 centimeter spacing between the rows and 10 centimeter between the plants (within rows) in each of the three replications. Observations were documented for fifteen characters from each replication *viz.* plant height, flag leaf area, no. of tillers/plant, relative water content, canopy temperature, spike length, chlorophyll content, days to fifty percent flowering, thousand-grain weight, no. of grains/ear, harvest index, days to maturity, grain yield/ plant, grain Fe and grain Zn content. Grain zinc and iron contents were estimated at the International Crops Research Institute for the Semi-arid Tropics (ICRISAT), Hyderabad, India, with the help of X-ray Fluorescence Spectrophotometer (XRF). Genetic divergences among 30 bread wheat genotypes were evaluated by performing analysis of the data on fifteen traits through D^2 statistics as suggested by Mahalanobis (1936) [9] and on the basis of Tocher's method, the genotypes were grouped into diverse clusters following Singh and Kumar (2017) [10]. The calculation of average intra-cluster as well as inter-cluster distances were done according to the process of Singh and Chaudhary (1977) [11]. Contribution percentage of individual traits to the total divergence of clusters of different traits was also calculated.

Results and Discussion

All the 30 genotypes (including two checks) in the present evaluation significantly differed concerning the characters studied and displayed marked divergence. On account of D^2 statistics and ward minimum variance, they were grouped into nine clusters (Fig.1). Cluster II included eight genotypes which counted the highest in number among the entire clusters followed by cluster I and cluster IV comprising six genotypes and cluster VII containing five genotypes. However, the rest five clusters namely, Cluster III, cluster V, cluster VI, cluster VIII and cluster IX were solitary (monogenotypic), encompassing single genotypes. Verma *et al.* (2013) [12], Sunilyadav *et al.* (2014) [13], Khan *et al.* (2015) [14], Rajshree and Singh (2018) [15] also documented similar findings based on D^2 statistics. The pattern of clustering indicated that no strict association was there between genetic and geographical diversity as it was revealed that genotypes of diverse geographical origins were stacked in a single group as well as genotypes from same geographical origin were found to be clubbed into same as well as separate cluster(s) also.
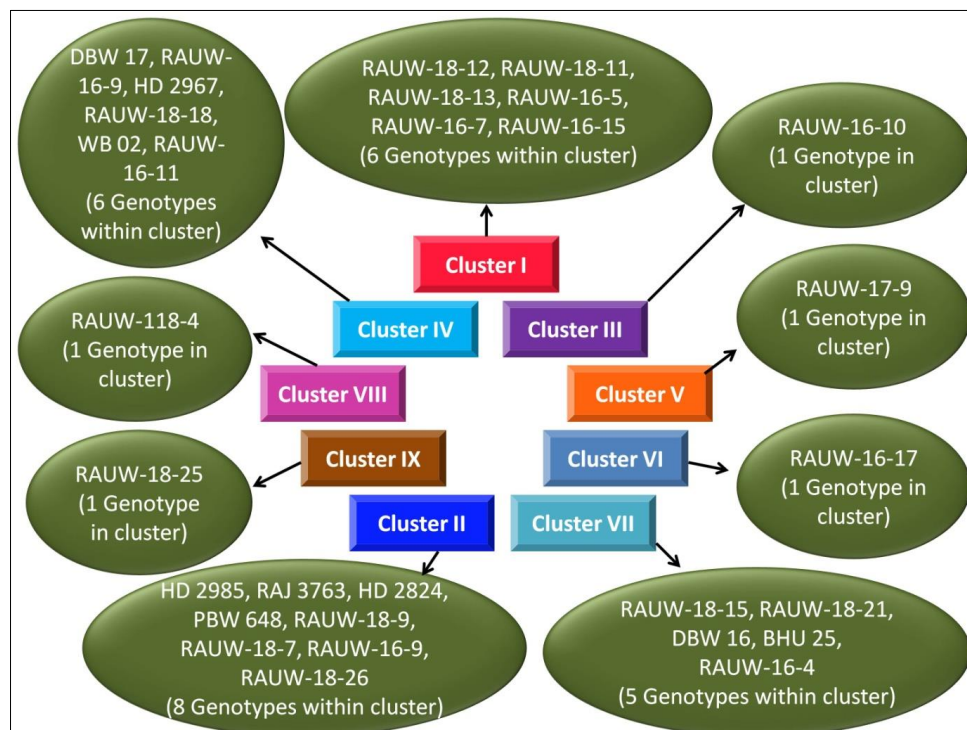

Fig.1 Clustering pattern of 30 genotypes of bread wheat on the basis of D^2 statistics

Cluster VII and cluster IV revealed the highest grain Fe content (47.40) and grain Zn content (34.19) respectively. Highest values for desirable traits like relative water content (91.77), harvest index (61.58), the no. of tillers/ plant (7.48), flag leaf area (36.49), grain yield/ plant (24.60), plant height (100.14), 1000-grain weight (47.88) was demonstrated by Cluster IV. **C**luster III had the uppermost mean values for spike length (11.13) and chlorophyll content (37.20). Cluster IX was recorded with the highest number of grains/ ear (60.54). Cluster VI was found to contain the lowest plant

height. Cluster VIII illustrated the lowest values for days to fifty percent flowering and days to maturity (Table 1). Selection of cluster VI can be done as a donor for dwarfness. Cluster VIII was recorded the most suited to achieve earliness. Cluster IV can be selected for higher grain Zn content along with high grain yield. To achieve higher grain Fe content, cluster VII was recorded as the best option. Earlier workers namely, Rajshree and Singh (2018) [15] and Arya et al. (2017) [16] also reported genotype selection based upon the mean of clusters to attain superior exploitation of genetic potential.

Table 1: Cluster means for fifteen characters in bread wheat

	[1]PH	[2]TP	[3]FLA	[4]DFF	[5]SL	[6]RWC	[7]CT	[8]CC	[9]DM	[10]GPE	[11]TGW	[12]GY	[13]HI	[14]Fe	[15]Zn
Cluster I	91.69	5.36	28.14	77.56	10.47	81.01	23.19	34.49	116.28	54.37	41.42	21.17	52.06	35.39	30.45
Cluster II	93.22	5.79	30.14	82.74	10.65	83.13	23.25	35.54	122.92	54.48	42.79	21.86	53.19	37.25	26.72
Cluster III	97.13	6.73	35.43	76.00	11.13	90.54	21.07	37.20	113.67	58.96	45.33	24.50	61.55	38.61	28.90
Cluster IV	100.14	7.48	36.49	81.83	11.09	91.77	20.74	36.96	121.83	60.16	47.88	24.60	61.58	40.42	34.19
Cluster V	88.53	4.73	25.43	80.67	10.07	77.51	24.29	34.67	121.67	48.45	40.20	19.30	49.55	41.21	20.24
Cluster VI	81.80	4.87	23.13	84.00	10.33	74.34	23.63	32.13	124.67	37.19	37.67	14.10	46.20	37.22	25.10
Cluster VII	90.20	5.47	30.11	80.01	10.28	78.20	23.61	33.40	119.33	49.99	41.44	20.81	52.35	47.40	28.32
Cluster VIII	94.27	5.73	30.13	68.00	10.60	84.42	23.01	36.44	112.33	53.86	43.00	22.50	54.94	38.15	32.50
Cluster IX	94.53	5.93	33.33	74.67	10.93	80.47	22.24	32.67	113.33	60.54	44.67	22.83	56.59	28.70	32.20

[1]PH=Plant height, [2]TP= No. of tillers/plant, [3]FLA= Flag leaf area, [4]DFF= Days to fifty percent flowering, [5]SL= Spike length, [6]RWC=Relative water content, [7]CT= Canopy temperature, [8]CC= Chlorophyll content, [9]DM= Days to maturity, [10]GPE= No. of grains/ ear, [11]TGW= Thousand-grain weight, [12]GY= Grain yield/ plant, [13]HI= Harvest index, [14]Fe= Grain Fe and [15]Zn= Grain Zn content

Table 2 depicts that the utmost intra-cluster distance (D^2) was recorded from cluster VII (38.31) indicating that genotypes RAUW-18-15, RAUW-18-21, DBW 16, BHU 25, RAUW-16-4 were genetically most diverse followed by cluster IV (28.84), cluster I (18.92), and cluster II (15.84). Among clusters VII and IX inter-cluster distance was noted as the maximum and put a high degree of genetic diversity on display because of the utmost inter-cluster distance between them and therefore to get recombinants with high-yielding quality, they can be exploited under inter-varietal hybridization programmes. Identical inter-varietal crosses we can attempt between genotypes of cluster VI and IX, VI and VIII, IV and IX, V and IX, VII and VIII. The least inter-cluster distance was noted between the clusters V and VI followed by clusters I and III, I and II, III and VIII. These findings showed that these clusters were divergent to less extent relatively and vigorous offspring (F_1 progenies) would not come out by executing crossing between them. These findings followed Verma et al. (2013) [12], Sunilyadav et al. (2014) [13], Arya et al. (2017) [16], and Rajshree and Singh (2018) [15].

The contributions of characters towards total divergence mainly help to make the decision regarding selection as well as the choice of parents. The uppermost contribution in manifesting genetic divergence was revealed by grain Fe content, followed by days to 50 percent flowering, grain Zn content, grain yield/ plant, thousand-grain weight, no. of grains/ ear (Table 3). This means it may be rewarding to execute selection for these traits. These findings were similar with earlier workers, namely, Arya et al. (2017) [16] for grain yield; Rajshree and Singh (2018) [15] for days to 50 percent flowering and 1000-grain weight.

Table 2: Mean intra and inter-cluster distances (D^2) among nine clusters in bread wheat

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX
Cluster I	18.92	37.45	26.63	81.36	50.69	71.74	107.74	51.98	43.43
Cluster II		15.84	42.38	51.27	30.03	45.02	75.34	114.92	102.62
Cluster III			0.00	46.10	67.40	114.06	96.04	39.06	53.44
Cluster IV				28.84	93.89	132.71	83.36	130.87	148.35
Cluster V					0.00	17.47	50.41	111.30	146.41
Cluster VI						0.00	85.75	165.64	170.82
Cluster VII							38.31	144.24	233.45
Cluster VIII								0.00	64.32
Cluster IX									0.00

Table 3: Contribution percentages of fifteen characters towards genetic divergence in bread wheat

SI. No.	Source	Time ranked First	Contribution %
1	Plant height (cm)	0	0.00
2	No. of tillers/ plant	4	0.92
3	Flag leaf area (cm^2)	2	0.46
4	Days to 50% flowering	88	20.23
5	Spike length (cm)	1	0.23
6	Relative water content (%)	2	0.46
7	Canopy temperature (^{o}C)	0	0.00
8	Chlorophyll content (SPAD)	2	0.46
9	Days to maturity	0	0.00
10	No. of grains per ear	5	1.15
11	1000- grain weight(g)	5	1.15
12	Grain Yield per plant (g)	24	5.52

13	Harvest index (%)	0	0.00
14	Grain Fe content	220	50.57
15	Grain Zn content	82	18.85

Conclusion

To conclude we can say that the study can aid in finding suitable parents for further breeding program in order to achieve higher grain yield and superior micronutrient content-rich bread wheat genotypes. Cluster II included 8 genotypes which was the highest number among the entire clusters. The utmost inter-cluster distance was noted between the clusters VII and IX which put a high degree of genetic diversity on display because of the maximum inter-cluster distance between them and therefore to get recombinants with high-yielding quality, both can be exploited under inter-varietal hybridization programmes. Identical inter-varietal crosses we can attempt between the genotypes of clusters VI and IX, VI and VIII, IV and IX, V and IX, VII and VIII. The least inter-cluster distance was noted between the clusters V and VI followed by the clusters I and III, I and II, III and VIII. These findings proved that these clusters were less divergent relatively and therefore offspring (F_1 progenies) made by executing crossing between them would be less vigorous. Genotypes RAUW-18-15, RAUW-18-21, DBW 16, BHU 25, RAUW-16-4 were recorded genetically diverse having the highest intra-cluster distance and also superiority for the grain Fe content. In manifesting genetic divergence, the highest contribution was revealed by grain Fe content, followed by grain Zn content, days to fifty percent flowering, grain yield per plant, thousand-grain weight, no. of grains/ ear. This means it may be rewarding to execute selection for these traits.

Acknowledgement

Reference

1. FAO Stat. Statistics Data: the Food and Agriculture Organization of the United Nations. Official website 2017 [Weblink http://www.fao.org/faostat/ en/#data]. (Visited on 10th March, 2021).
2. Kumar A, Joshi G, Jaiswal JP *et al*. Path analysis for yield and yield contributing traits in wheat (*Triticum aestivum L. em. Thell*) germplasm. Progressive Research – An International Journal 2016;11(V):2986-2989.
3. Cakmak I, Torun A, Millet E. *Triticum dicoccoides*: An important genetic resource for increasing zinc and iron concentration in modern cultivated wheat. Soil Science and Plant Nutrition 2004;50(2):1047–1054.
4. Gani G, Beenish, Bashir O, Bhat TA, Naseer B, Qadri T, Jan N. Hidden hunger and its prevention by food processing: A review. International Journal of Unani and Integrative Medicine 2018;2(3):01-10
5. White PJ, Broadley MR. Biofortification of crops with seven mineral elements often lacking in human diets– iron, zinc, copper, calcium, magnesium, selenium and iodine. New Phytologist 2009;182(1):49-84.
6. Welch RM, Graham RD. Breeding for micronutrients in staple food crops from a human nutrition perspective. Journal of Experimental Botany 2004;55(396):353-364.
7. Cakmak I, Pfeiffer WH, McClafferty B. Biofortification of durum wheat with zinc and iron. Cereal chemistry 2010;87(1):10-20.
8. Peleg Z, Cakmak I, Ozturk L *et al*. Quantitative trait loci conferring grain mineral nutrient concentrations in durum wheat× wild emmer wheat RIL population. Theoretical and Applied Genetics 2009;119(2):353-369.
9. Mahalanobis PC. On the generalised distance in statistics. Proceedings of National Institution of Science, India 1936;2:49-55.
10. Singh G, Kumar R. Genetic Diversity for yield and yield traits in wheat. Journal of Pharmacognosy and Phytochemistry 2017;6(5):2062-2066.
11. Singh RK, Chaudhary BD. The order effects in double-cross hybrids. Crop Improvement 1977;4:213.
12. Verma PN, Singh BN, Yadav RK. Genetic variability and divergence analysis of yield and its contributing traits in wheat *(T. aestivum* L.) International Journal of Agricultural Sciences 2013;3(2):395-399.
13. Sunilyadav K, Singh AK, Baghel SS, Mahesh J. Assessment of Genetic variability and Diversity for Yield and its Contributing Traits among CIMMYT Based Wheat Germplasm. Journal of Wheat Research 2014;6(1):154-159.
14. Khan MK, Pandey A, Thomas G, *et al*. Genetic diversity and population structure of wheat in India and Turkey. Oxford Journals Science and Mathematics AOB PLANTS 2015;10(2):1093.
15. Rajshree, Singh SK. Assessment of genetic diversity in promising bread wheat (*Triticum aesti*vum L.) genotypes. International Journal of Current Microbiology and Applied Sciences 2018;7(3):2319-7706.
16. Arya V, Singh J, Kumar L, Kumar R and Kumar P. Genetic variability and diversity analysis for yield and its components in wheat (*Triticum aestivum* L.). Indian Journal of Agricultural Research 2017;51(2):128-134.