Diversity Analysis Studies in 28th Semi Arid Wheat (*Triticum aestivum* L.) Yield Trial of CIMMYT

Ruchismita Mishra¹, Roshan Parihar^{1*}, AP Agrawal¹, DJ Sharma¹,
NK Chaure² and Dinesh Pandey³

¹Department of Genetics and Plant Breeding, BTC College of Agriculture and
Research Station, Sarkanda, Bilaspur (IGKV, Raipur), Chhattisgarh, India

²Department of Agricultural statistics, BTC College of Agriculture and Research
Station, Sarkanda, Bilaspur (IGKV, Raipur), Chhattisgarh, India

³Department of Agronomy, BTC College of Agriculture and Research Station,
Sarkanda, Bilaspur (IGKV, Raipur), Chhattisgarh, India

***Corresponding Author:** Roshan Parihar, Department of Genetics and Plant
Breeding, BTC College of Agriculture and Research Station, Sarkanda, Bilaspur
(IGKV, Raipur), Chhattisgarh, India.

Received: October 04, 2021

Published: December 10, 2021

© All rights are reserved by **Roshan Parihar.,
et al.**

Abstract

The present study was carried out to access 50 semi arid wheat yield trials of CIMMYT including 1 check (HI-1544). The experiment was laid down in randomized block design during rabi season of 2020-21. The divergence studies revealed that fifty genotypes are clustered into six clusters with maximum genotypes in cluster I viz. forty five and all other five clusters (Cluster II, III, IV, V, VI) were solitary. The highest intra-cluster distance was observed for cluster I. Hence, genotypes belonging to the cluster I may be utilized as parents in future breeding programme with the genotypes belonging to cluster III as the maximum inter-cluster distance was noted between the cluster III and Cluster V. This showed that a hybridization programmes including parents from these clusters would result in a higher frequency of better segregates or desired combinations. Maximum genetic divergence was found for seed yield per plot, followed by biological yield per plot, harvest index and number of seeds per spike.

Keywords: Genetic Divergence; Semi Arid Wheat Yield Trial (SAWYT); Cluster Analysis; CIMMYT; Wheat

Introduction

Wheat (*Triticum aestivum* L.) king of cereals is a true hexaploid crop $2n=6x=42$ and belongs to Poaceae family. It is known for its antiquity as well as its use for human consumption. It is the most commonly grown foodgrain crop in the world and in India it is 2nd largest staple cereal food crop. It is also known as bread wheat. It is grown as an winter wheat during Rabi season in India, Breeders can increase yield per unit area by developing improved genotypes that deliver high grain yields in combination with best management practices. Wheat yields are reduced due to a variety of environmental stresses that impact plant development at different stages. The total wheat cultivated area in India is 31.45 million

ha. Wheat production in India rose from 103.60 million tonnes in 2018-19 to 107.59 million tonnes in 2019-20, rendering it the second most widely grown cereal after paddy [1].

Wheat is an important carbohydrate source as well as its protein level is about 10-13% and also a good source of thiamine and nicotinic acid. Winter temperatures in the ideal wheat climate ranges from 10° to 15°C, with summer temperatures ranging from 21°C to 26°C. However, rise in terminal heat at the time of maturity may be dangerous. Wheat thrives well in regions with an average annual rainfall of 75 cm. Wheat production is limited to 100 cm of annual rainfall.

In a crop improvement programme the evaluation and selection of superior lines from introduced plant materials is the first and most important step in a wheat development programme. The genetic structure of CIMMYT wheat genotypes involves the improvement of traits like high grain yield, disease resistance, tolerance to abiotic stresses (drought and heat), good gluten quality at medium protein content levels, in semi-hard or hard grains. High yielding genotypes with good adaptability and agronomically desirable traits might be reliably exploited for commercial production. Notably, among all the exotic germplasm, CIMMYT materials have played an important role in wheat improvement programmes. The local varieties were rather low yielding, tall and often susceptible to various prevailing diseases, hence exotic varieties were introduced to improve them or for direct use by farmers. Keeping in view the fact of genetic variability in the current study, the exotic germplasm were assessed for yield and its component traits and also heritability of those traits were estimated.

Materials and Methods

The present study was conducted at Research cum Instructional farm at Barrister Thakur Chhedilal College of Agriculture and Research Station, Bilaspur (C.G.) during *rabi* season of 2020-21. Chhattisgarh is located in the East-Central part of the country, between 17°14'N and 24°45' N latitudes and 73°30' E and 84°15' E longitudes, whereas Bilaspur, lies at 21.47° to 23.8° N latitude and 81.14° to 83.15° E longitude with an elevation of 264 meters above the mean sea level.

The experimental material consists of 50 CIMMYT semi arid wheat yield trials (SAWYT) including one check (HI-1544). The crop was sown in a Randomized Block Design (RBD) with two replications. Each entry had a plot size of 1.20 m x 6 m with 20 cm row to row spacing and 6 cm plant to plant spacing for a total plot size of 7.2 m². During the growing season, five irrigations were applied at critical stages: crown root initiation stage (CRI), late tillering, late jointing stage, flowering and milking stage.

D2 statistics was calculated for fifty wheat genotypes [2]. This is one of the potential method for determining genetic divergence. Rao [3] recommended that this method can be used to determine genetic divergence in plant breeding. The varieties were grouped into a no. of clusters as per standard procedure given in Tocher method.

$$D^2 = \lambda I_j \cdot \Delta_i \cdot \delta_j$$

Where,

λI_j = Reciprocal matrix to the common dispersion matrix.

Δ_i = Difference between the mean values of the two populations for i^{th} character

δ_j = Difference between the mean values of the two populations for j^{th} character.

The parameter D^2 was estimated as D^2 [3]

$$D^2 = \sum \sum \delta_{ij}$$

$d_i \cdot d_j$ = Sample estimate of X_{ij}

Where,

δ_{ij} = Sample estimates of X_{ij}

d_i = Sample estimates of δ_i

d_j = Sample estimates of δ_j

Result and discussion

In the present study, all the 50 genotypes of wheat were grouped into six clusters (Table 1) (Figure 2). It reveals considerable amount of genetic diversity exists in the material. Results of cluster analysis revealed that the cluster I was the largest which consist of (45 genotypes) while clusters II, III, IV, V and VI each has single genotype only (Table 3). The wheat genotypes were found to be genetically diverse based on the clustering pattern. Present results confirms the findings of the previous workers Santosh., *et al.* (2019), Singh *et al.* [4], Zaman., *et al.* [5] and Ferdous., *et al.* [6].

Intra and inter cluster distance (D2 value)

The intra and inter-cluster distances were determined to assess the genetic relationship among the individuals within a cluster and between members of different clusters (Table 1) (Figure 1). The maximum inter cluster distance was found between cluster III and V (162.81) revealed a genetically distant relationship between these two clusters and a high degree of genetic diversity followed by cluster II and V (149.28), cluster IV and V (145.41), cluster V and VI (136.95), cluster IV and VI (110.75), cluster III and IV (94.42), cluster I and VI (77.32), cluster I and V (73.09), cluster II and VI (70.86), cluster I and IV (70.41), cluster I and II (65.23), cluster I and III (65.05), cluster II and III (56.67), cluster III and VI (33.20) while the minimum inter-cluster distance was observed between clusters II and IV (20.50) which revealed a closer relationship between these two clusters as well as a low degree of genetic diversity among genotypes.

The highest average intra-cluster distance was exhibited by cluster I (39.10) implying that genotypes in cluster-I were more diverse than genotypes in other clusters. The use of divergent genotypes from the above cluster would result in a broad spectrum of variability for the quantitative traits being studied, allowing for further selection and improvement. Present results confirm the findings of previous worker Tsegaye., *et al.* [7].

Cluster mean analysis

Cluster means were determined for all the traits which showed significant differences among the clusters (Table 2). The mean performances of the clusters were used to identify genetically diverse and superior genotypes out of the 50 genotypes studied. The re-

sults of analysis revealed that days to 50 percent flowering showed maximum mean (77.00) in cluster number V followed by cluster VI (75.50), cluster III (74.50), cluster I (72.42) and lowest mean for this character was observed in cluster II and cluster IV (70.50).

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6
Cluster 1	39.1	65.23	65.05	70.41	73.09	77.32
Cluster 2		0	56.67	20.5	149.28	70.86
Cluster 3			0	94.42	162.81	33.2
Cluster 4				0	145.41	110.75
Cluster 5					0	136.95
Cluster 6						0

Table 1: Intra and Inter - Cluster Distances.

Figure 1: Diagrammatic representation of intra and inter - cluster distances using Tocher method.

The days to maturity was observed maximum in cluster III (116.00) followed by cluster V (114.50), cluster I (112.88), cluster VI (112.50), cluster II (111.00) and lowest mean for this character was observed in cluster IV (109.50).

The plant height was observed maximum in cluster III (90.56) followed by cluster I (84.12), cluster II (80.38), cluster VI (79.38), cluster IV (78.70) and lowest mean for this character was observed in cluster V (76.38).

The number of tillers per plant was observed maximum in cluster V (3.60), followed by cluster VI (3.40), cluster I (2.92), cluster II (2.80), cluster III (2.70) and lowest mean for this character was observed in cluster IV (1.70).

The peduncle length was observed maximum in cluster IV (37.28), followed by cluster VI (35.90), cluster II (35.23), cluster I

(34.34), cluster III (34.23) and lowest mean for this character was observed in cluster V (31.53).

The spike length was observed maximum in cluster V (9.95), followed by cluster VI (9.87), cluster III (9.03), cluster I (8.43), cluster II (7.92) and lowest mean for this character was observed in cluster IV (6.96).

The number of spikelets per spike was observed maximum in cluster IV (19.20), followed by cluster VI (18.70), cluster V (17.20), cluster I (16.92), cluster II (16.40) and lowest mean for this character was observed in cluster III (15.50).

The number of seeds per spike was observed maximum in cluster VI (62.70), followed by cluster III (58.40), cluster II (44.50), cluster I (42.43), cluster IV (39.50) and lowest mean for this character was observed in cluster V (34.40).

The 1000 seed weight was observed maximum in cluster I (45.79), followed by cluster II (45.17), cluster III (44.85), cluster V (43.70), cluster VI (43.15) and lowest mean for this character was observed in cluster IV (42.65).

The biological yield per plot was observed maximum in cluster V (5.75), followed by cluster IV (5.10), cluster I (4.87), cluster II (4.65) and lowest mean for this character was observed in cluster III and VI (3.90).

The seed yield per plot was observed maximum in cluster V (2845.0), followed by cluster I (2150.8), cluster VI (1680.00), cluster IV (1675.0), cluster III (1545.0) and lowest mean for this character was observed in cluster II (1470.0).

The harvest index was observed maximum in cluster V (49.46), followed by I (44.35), cluster VI (43.06), cluster III (39.66), cluster IV (32.84) and lowest mean for this character was observed in cluster II (31.49).

Similar findings were obtained by Gurjar and Marker [8] for plant height, days to 50% flowering, tillers per plant, spike length, seeds per spike, biological yield per plot, thousand seed weight and harvest index; (Santosh., *et al.* 2019) for plant height, spikelets per spike, peduncle length, spike length, seeds per spike, biological yield per plot, seed yield per plot, number of tillers per plant, and 1000 grain weight. The identified genotypes superior in the above clusters may be used in multiple crossing programmes to recover transgressive segregants with high genetic yield potential. Evaluation of genetic diversity aids in the selection of most effective genotypes. The grouping of genotypes indicated that they may be utilised as donors in various hybridization programmes to enhance yield in the future.

Cluster Nos.	DF	DM	PH	NTPP	PL	SL	NSPPS	NSEPS	TSW	BYPP	SYPP	HI
Cluster 1	72.42	112.88	84.12	2.92	34.34	8.43	16.92	42.43	45.79	4.87	2150.88	44.35
Cluster 2	70.5	111	80.38	2.8	35.23	7.92	16.4	44.5	45.17	4.65	1470	31.49
Cluster 3	74.5	116	90.56	2.7	34.23	9.03	15.5	58.4	44.85	3.9	1545	39.66
Cluster 4	70.5	109.5	78.7	1.7	37.28	6.96	19.2	39.5	42.65	5.1	1675	32.84
Cluster 5	77	114.5	76.38	3.6	31.53	9.95	17.2	34.4	43.7	5.75	2845	49.46
Cluster 6	75.5	112.5	79.38	3.4	35.9	9.87	18.7	62.7	43.15	3.9	1680	43.06

Table 2: Cluster means by Tocher’s method.

Abbreviations: DF: Days to Flowering; DM: Days to Maturity; PH: Plant Height (cm); NTPP: No. of Tillers Per Plant, PL: Peduncle Length (cm); SL: Spike Length (cm); NSPPS +: No. of Spikelets Per Spike, NSEPS: No. of Seeds Per Spike, TSW: Thousand Seed Weight (g); BYPP: Biological Yield Per Plot (g); SYPP: Seed Yield Per Plot (g); HI: Harvest Index (%).

Cluster Nos.	Number of genotypes	Name of genotypes
Cluster I	45	28 th SAWYT 306, 325, 341, 332, 345, 343, 308, 335, 334, 326, 348, 338, 342, 317, 305, 328, 313, 321, 336, 310, 307, 314, 315, 333, 323, 327, 312, 302, 311, 318, 330, 349, 309, 319, 304, 322, 329, 303, 337, 324, 350, 331, 344, 320 and, LOCAL CHECK (HI-1544)
Cluster II	1	28 th SAWYT 339
Cluster III	1	28 th SAWYT 346
Cluster IV	1	28 th SAWYT 340
Cluster VI	1	28 th SAWYT 347

Table 3: Distribution pattern of 50 genotypes under different clusters.

Figure 2: Dendrogram representing clustering pattern in Tocher method.

Percent contribution of characters towards genetic divergence

The selection and choice of parents mainly depends upon the contribution of characters towards divergence. The most important trait causing maximum genetic divergence was seed yield per plot (28.5%) and it was responsible for creating diversity in the studied gene pool. It was followed by biological yield per plot (12.32%),

harvest index (10.2%), number of seeds per spike (9.55%), thousand seed weight (8.22%), number of tillers per plant (7.7%), number of spikelets per spike (6%), plant height (5%), spike length (4.5%), days to maturity (3.0%), peduncle length (3.0%) and the least divergence was shown by days to flowering (2%). This finding is in agreement with the report Jaiswal, *et al.* [9] and Singh, *et al.* [4].

Figure 3

Sl. No.	Source	Contribution %	Times ranked 1 st
	Seed yield per plot (g)	28.5	351
	Biological yield per plot (kg)	12.32	152
	Harvest index (%)	10.2	126
	Number of seeds per spike	9.55	118
	1000 seed weight (g)	8.22	101
	Number of tillers per plant	7.7	95
	Number of spikelets per spike	6	74
	Plant height (cm)	5	62
	Spike length (cm)	4.5	55
	Days to maturity	3	37
	Peduncle length (cm)	3	37
	Days to flowering	2	25

Table 4: Percent contribution of different characters towards genetic divergence.

Conclusion

Cluster analysis revealed the division into six clusters, indicating that wheat genotypes are quite diverse. The most important trait causing maximum genetic divergence was seed yield per plot, followed by biological yield per plot, harvest index, number of seeds per spike, thousand seed weight, number of tillers per plant, number of spikelets per spike, plant height, spike length, days to maturity and peduncle length and the least divergence was shown by days to 50% flowering. The highest intra-cluster distance was observed for cluster I. Hence, genotypes belonging to cluster I may be utilized as parents in future breeding programmes with the genotype belonging to cluster III, as the maximum inter-cluster distance was observed between cluster III and Cluster V. This showed that a hybridization programme including parents from these clusters would result in a higher frequency of better segregates or desired combinations, which would be important for the production of valuable genetic stocks.

Bibliography

1. Anonymous. "Agriculture statistics at a glance" (2020).
2. Mahalanobis PC. "On the generalized distance in statistics". *Proceedings of the National Academy of Sciences, India* 2.1 (1939): 49-55.
3. Rao CR. "Advanced statistical methods in biometrical research". 1st Edition. John Wiley and Sons, New work. (1952): 390.
4. Singh G., *et al.* "Genetic diversity analysis for various morphological and quality traits in bread wheat (*Triticum aestivum* L.)". *Journal of Applied and Natural Science* 10.1 (2018): 24-29.
5. Zaman MA., *et al.* "Divergence analysis of drought tolerant genotypes of wheat (*Triticum aestivum* L.)". *Bangladesh Journal of Agricultural Research* 39.3 (2014): 385-396.
6. Ferdous M., *et al.* "Genetic divergence and genetic gain in bread wheat through selection practices". *Journal of Bangladesh Agricultural University* 9.1 (2011): 1-4.
7. Tsegaye D., *et al.* "Analysis of genetic diversity in some durum wheat (*Triticum durum* Desf.) genotypes grown in Ethiopia". *African Journal of Biotechnology* 11.40 (2012): 9606-9611.
8. Gurjar D and Marker S. "Evaluation of genetic divergence in wheat (*Triticum aestivum* L.) germplasm". *Electronic Journal of Plant Breeding* 9.1 (2018): 361-367.
9. Jaiswal S., *et al.* "Genetic diversity analysis in bread wheat (*Triticum aestivum* L.em.Thell.) for yield and physiological traits". *International Journal of Current Microbiology and Applied Sciences* 8.2 (2019): 3059-3068.

Assets from publication with us

- Prompt Acknowledgement after receiving the article
- Thorough Double blinded peer review
- Rapid Publication
- Issue of Publication Certificate
- High visibility of your Published work

Website: www.actascientific.com/

Submit Article: www.actascientific.com/submission.php

Email us: editor@actascientific.com

Contact us: +91 9182824667