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Sachin Kumar
Faculty of Agricultural Sciences
and Allied Industries, Rama
University, Kanpur, Uttar
Pradesh, India

Syed Mohd Quatadah
Faculty of Agricultural Sciences
and Allied Industries, Rama
University, Kanpur, Uttar
Pradesh, India

Aneeta Yadav
Faculty of Agricultural Sciences
and Allied Industries, Rama
University, Kanpur, Uttar
Pradesh, India

Nagmi Praween
Department of Genetics and Plant
Breeding, Rajmata Vijayaraje
Scindia Krishi Vishwa Vidyalaya
(RVSKVV), Gwalior-474002,
Madhya Pradesh, India

Jitendra Kumar
Faculty of Agricultural Sciences
and Allied Industries, Rama
University, Kanpur, Uttar
Pradesh, India

Vijay Joseph Silas
Faculty of Agricultural Sciences
and Allied Industries, Rama
University, Kanpur, Uttar
Pradesh, India

Jaza Batool
Faculty of Agricultural Sciences
and Allied Industries, Rama
University, Kanpur, Uttar
Pradesh, India

Aaditya Dubey
Faculty of Agricultural Sciences
and Allied Industries, Rama
University, Kanpur, Uttar
Pradesh, India

Ankur Singh
Faculty of Agricultural Sciences
and Allied Industries, Rama
University, Kanpur, Uttar
Pradesh, India

Corresponding Author:
Syed Mohd Quatadah
Faculty of Agricultural Sciences
and Allied Industries, Rama
University, Kanpur, Uttar
Pradesh, India

Genetic diversity and character association studies for grain yield and its component traits in wheat (*Triticum aestivum* L.) under late soon condition

Sachin Kumar, Syed Mohd Quatadah, Aneeta Yadav, Nagmi Praween, Jitendra Kumar, Vijay Joseph Silas, Jaza Batool, Aaditya Dubey and Ankur Singh

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Abstract

The present investigation entitled “Genetic diversity for yield and quality characters in bread wheat (*Triticum aestivum* L.)” was conducted at research farm of FASAI, Rama University, Kanpur-209217. The experiment was laid out in an Augmented Block Design comprising 50 test entries along with four check varieties. The experimental field was divided into five equal blocks, and the check varieties were randomly allocated within each block.

Observations were recorded on fourteen traits, namely days to 50% flowering, days to 50% maturity, plant height (cm), spike length (cm), number of effective tillers per plant, number of grains per spike, 1000-grain weight (g), grain yield per plant (g), biological yield per plant (g), harvest index (%), protein content (%), sedimentation value (ml), grain zinc content (ppm), and grain iron content (ppm). Among the genotypes evaluated, WG 49 (9.45 g) recorded the highest grain yield per plant, followed by WG 48, WB 02 (check), and WG 47. With respect to quality traits, the genotype WG 36 was found superior for protein content, WG 8 for grain iron content, and WG 12 for grain zinc content. These genotypes also exhibited high to very high mean performance for several yield-contributing traits and may be effectively utilized as donor parents in hybridization program.

Zinc content and sedimentation value exhibited the highest genotypic coefficient of variation and phenotypic coefficient of variation among all the traits studied, indicating substantial genetic variability. High heritability coupled with high genetic advance as per cent of mean was observed for quality traits such as sedimentation value, iron content, and zinc content, as well as yield attributes including number of grains per spike, biological yield per plant, and spike length. Grain yield per plant showed a highly significant and positive correlation with harvest index. Path coefficient analysis further revealed that harvest index, biological yield per plant, and protein content were the major traits contributing directly to grain yield per plant.

Based on Mahalanobis D^2 analysis, all fifty-four wheat genotypes were grouped into six distinct clusters. Cluster VI contained the maximum number of genotypes (21), whereas Cluster IV comprised the minimum number (2). The highest intra-cluster distance was observed in Cluster I, while Cluster VI exhibited the lowest intra-cluster distance. The maximum inter-cluster distance was recorded between Cluster I and Cluster II, whereas the minimum inter-cluster distance was observed between Cluster II and Cluster VI.

Keywords: Wheat (*Triticum aestivum* L.), correlation, D^2 analysis, GCV, PCV, clustering

Introduction

Bread wheat, *Triticum aestivum*, is one of the most important cereal crops of the world and is popularly regarded as the “King of cereals” because of its wide adaptability, high productivity, and major contribution to global food security (Abdellatif and Abouzeid, 2011). It is an allohexaploid species ($2n = 42$) belonging to the family Poaceae and possesses a highly complex genome consisting of A, B, and D genomes (Sears, 1954; Okamoto, 1962). Wheat originated nearly 10,000 years ago during the Neolithic period, with the earliest cultivated forms, einkorn and emmer wheat, believed to have originated in south-eastern Turkey (Heun *et al.*, 1997; Dubcovsky and Dvorak, 2007). Among the cultivated wheat species, bread wheat occupies nearly 90 per cent of the global wheat-growing area due to its superior adaptability and grain quality [19, 16, 9, 5].

Globally, wheat ranks first among cereals in terms of cultivated area and production, occupying almost one-sixth of the world's arable land. India is the second-largest wheat-producing country after China, with major cultivation concentrated in Uttar Pradesh, Punjab, Haryana, and Bihar. During 2020-21, India produced about 109.52 million tonnes of wheat from 31.5 million hectares with an average productivity of 34.76 q ha⁻¹. Wheat grains are nutritionally rich, containing about 65-70 per cent carbohydrates and 11-12 per cent protein, besides essential micronutrients such as iron and zinc. The crop therefore plays a vital role in ensuring nutritional as well as food security.

Grain yield in wheat is a complex quantitative trait controlled by several interacting component characters. Hence, effective selection for yield improvement requires a clear understanding of genetic variability, heritability, and inter-relationship among traits. Estimates of genotypic and phenotypic coefficients of variation, heritability, and genetic advance help in identifying superior genotypes, while correlation and path coefficient analyses provide information on direct and indirect effects of component traits on yield (Dubey and Dixit, 1984). In addition, genetic diversity serves as a basic requirement for crop improvement programmes, as genetically diverse parents are more likely to produce desirable recombinants and heterotic segregants. Assessment of genetic divergence using Mahalanobis' D² statistics, proposed by Mahalanobis (1928) and later applied in plant breeding by Rao (1952), is widely used for grouping genotypes and identifying suitable parents for hybridization [6, 14].

Materials and methods

The present investigation was conducted during Rabi 2025-26 at the Research Farm of the Faculty of Agricultural Sciences and Allied Industries, Rama University. The experimental site is located at 26.4499° N latitude and 80.3319° E longitude with an altitude of about 130 m above mean sea level. The study material consisted of fifty diverse wheat genotypes obtained from Indian Institute of Wheat and Barley Research along with four standard check varieties, namely DBW 187, DBW 222, GW 322, and WB 02. The experiment was laid out in an Augmented Block Design with five blocks, where check varieties were replicated in each block. Sowing was done on 24 November 2025 in six rows of 4 m length with 20 cm row spacing. Observations were recorded from five randomly selected plants of each genotype. Recommended agronomic and plant protection practices were followed throughout the crop season, and border rows were maintained around the experiment to reduce environmental effects and ensure proper crop growth.

Experimental findings

ANOVA for Fourteen Characters of Bread Wheat in Augmented Block Design

The analysis of variance (ANOVA) reveals highly significant genetic variation ($p < 0.01$) among the evaluated wheat lines (Entries) for almost all investigated traits (Table 1), including phenology (days to flowering and maturity), plant architecture (height and spike length), yield components (grains per spike, 1000-grain weight, and overall grain yield), and nutritional quality traits (protein content, sedimentation value, iron, and zinc content). The only exception is Effective tiller, which showed no

statistical significance across any source of variation, indicating that tiller numbers remained uniform or were highly influenced by environmental noise. The massive, highly significant mean squares observed in the Check x entries interaction for iron (369.38) and zinc (863.26) highlight that certain newly developed lines perform drastically differently and likely superior compared to the standard control varieties, making this population highly valuable for biofortification breeding. Furthermore, the significant Blocks effect confirms that field heterogeneity was successfully controlled through blocking, while the remarkably low Error mean squares particularly for iron (0.18) and zinc (0.08) demonstrate that the experiment was conducted with high precision, ensuring that the identified genetic differences are highly reliable for future crop selection.

Mean performance estimates of 14 characters of wheat genotypes:

The mean performance data for the 50 wheat genotypes (WG1 to WG50) and 4 check varieties (C1 to C4) highlights significant phenotypic variation across all 14 evaluated agronomic, yield, and quality traits. Looking closely at crop phenology and architecture, the genotypes showed a wide maturity spectrum, with Days to 50% Maturity (DTM) ranging from a swift 116 days (seen in genotypes like WG26 and WG30) to a prolonged 136 days, averaging out at 125.90 days. Plant height (PHT) averaged 92.49 cm, but reached a maximum of 119.26 cm in WG37, which could indicate a tendency for lodging, while shorter, sturdier lines dipped down to 80.26 cm.

When it comes to the crucial economic traits, Grain Yield Per Plant (GYPP) proved to be highly variable, shifting from a low of 3.09 g up to an impressive maximum of 9.45 g per plant achieved by WG49 substantially outperforming the overall population mean of 6.02 g and the best performing check, C4 (8.41 g). This high yield in WG49 is heavily supported by its strong 1000-grain weight (TW) of 44.09 g and a high Harvest Index (HI) of 57.33%. Another standout line is WG2, which exhibited the absolute highest grain weight (TW) at 59.80 g compared to the mean of 46.36 g.

From a nutritional and quality perspective, Protein Content (PC) hovered at a respectable average of 11.43%, peaking at 14.52% in WG36, which also coincided with the highest sedimentation value (SV) of 59.38 ml, indicating excellent gluten strength for baking. Crucially for biofortification purposes, micronutrient levels showed massive ranges: Iron (Fe) content averaged 40.44 ppm but reached as high as 53.87 ppm in WG8, while Zinc (Zn) content peaked at an impressive 53.79 ppm in WG12 against a population average of 36.01 ppm. Overall, genotypes like WG49 for yield, WG36 for protein quality, and WG8 and WG12 for micronutrient enrichment represent exceptionally high-performing parental lines for targeted wheat improvement programs.

Genetic variability parameters estimate

The evaluation of genetic parameters across fourteen wheat traits revealed substantial inherent variability, with phenotypic variance consistently exceeding genotypic variance a direct indication of environmental influence on trait expression (Table 3). The narrow gap between the Genotypic and Phenotypic Coefficients of Variation (GCV and PCV) across most traits signifies that environmental

noise is relatively minimal, particularly for quality profiles like zinc content (GCV: 24.47%, PCV: 24.48%) and sedimentation value (GCV: 20.86%, PCV: 22.33%). Conversely, effective tillers per plant demonstrated the highest vulnerability to external environments, posting a wide GCV-PCV gap and a low genotypic variance of just 0.05. Broad-sense heritability (h^2) and genetic advance as a percent of mean (GA%M) varied drastically, isolating the traits most governed by additive gene action. Zinc content (99.87% h^2 , 50.37% GA%M) and iron content (99.55% h^2 , 33.15% GA%M) emerged as the premier candidates for successful selection and biofortification breeding, followed closely by highly predictable structural traits like number of grains per spike (96.27% h^2 , 33.01% GA%M) and sedimentation value (87.24% h^2 , 40.14% GA%M). In stark contrast, effective tillers per plant proved poorly suited for direct selection due to an inferior heritability of 24.49% and a minor genetic advance of 7.76%, while highly stable phenological traits like days to 50% maturity expressed high heritability (94.15%) but a low GA%M (10.68%), restricting rapid evolutionary progress through simple selection.

Correlation coefficient analysis estimates

The correlation analysis maps out a web of critical tradeoffs and synergies for breeding, pointing directly to how yield is built. Most importantly, the data establishes that Grain yield per plant is heavily driven by biomass partition, exhibiting a strong and highly significant positive correlation with Harvest index (0.842**) and biological yield per plant (0.676**) (Table 4). These two traits stand out as the major yield-contributing characters in this population, suggesting that selecting for high biomass and efficient grain channeling will directly boost grain yield. However, the analysis also flags a classic breeding dilemma: a sharp, significant negative tradeoff between productivity and grain quality. Grain yield drops significantly as Protein content (-0.334**) and Sedimentation value (-0.321**) go up. This inverse relationship is mirrored by Harvest index, which shares a severe negative correlation with Protein content (-0.419*). On a brighter note for biofortification, the micronutrients and grain quality metrics share powerful synergies. Protein content is almost perfectly tied to Sedimentation value (0.957**) and strongly linked to Zinc content (0.492*), while Iron content shows a highly robust positive partnership with Zinc content (0.485*). The catch for breeders is that Grains per spike acts as a bottleneck; while it helps push up overall Biological yield (0.328*), it drags down Protein (-0.280*), Iron (-0.267*), and Zinc (-0.278*), meaning packing more grains onto a spike tends to dilute grain quality and micronutrient density.

Genetic Divergence Analysis

The genetic divergence analysis classified the fifty-four wheat genotypes into six distinct clusters using D2 statistics, mapping out clear structural boundaries for strategic hybridization. Cluster-VI emerged as the largest group, harboring 21 genotypes, while Cluster-IV proved to be the most highly specialized and exclusive, containing just 2 lines. When looking at the internal consistency of these groups, Cluster-I displayed the highest intra-cluster distance (33.91), marking it as a highly diverse pocket of genetic material. On the flip side, Cluster-VI posted the lowest internal variance (24.97), demonstrating that its 21

constituent genotypes share a highly uniform genetic architecture (Table 5).

To maximize heterosis and unlock superior segregating generations, the inter-cluster distances point exactly to where breeders should look. The most profound genetic divergence was recorded between Cluster-I and Cluster-II (51.60), followed closely by Cluster-IV and Cluster-V (50.37). Crossing parents selected across these specific boundaries creates the highest mathematical probability of producing high-yielding, robust hybrids. Conversely, crossing genotypes between Cluster-II and Cluster-VI would yield minimal evolutionary progress, as they shared the narrowest inter-cluster distance (31.26), indicating close genetic ties (Table 6).

The Yield Specialists (Cluster-II & VI): Cluster-II stands out as the ultimate yield engine, posting the absolute highest mean for Grain yield per plant (7.70 g) and Harvest index (50.14%). Cluster-VI acts as a high-biomass alternative, leading the trial in Biological yield per plant (17.19 g) alongside a very competitive grain yield of 7.18 g.

The Biofortified & Tall Early Lines (Cluster-IV): This small cluster offers an impressive developmental shortcut, holding the lowest means for Days to 50% flowering (74.35 days) and Maturity (116.83 days). It combines this rapid life cycle with the highest Plant height (111.04 cm), an exceptional 1000-grain weight (51.34 g), and the peak mean for Iron content (50.38 ppm) though it suffers from the lowest overall grain yield (4.33 g) (Table 7). The High-Quality Nutrients (Cluster-I): For baking quality and grain enrichment, Cluster-I reigns supreme. It recorded the maximum cluster means for Protein content (12.87%), Sedimentation value (48.07 ml), and Zinc content (42.59 ppm). Ultimately, crossing the nutritional and grain-weight powerhouses of Cluster-I or Cluster-IV with the high-yielding, high-harvest-index lines of Cluster-II offers the most viable path forward to successfully synthesize elite, biofortified wheat varieties.

Discussion

The present study revealed highly significant differences among wheat genotypes for most of the traits studied, indicating the presence of sufficient genetic variability for crop improvement. Similar findings were reported by Sabaghnia *et al.*, (2014), Kumar *et al.*, (2014), Yadav *et al.* (2014) and Hassani *et al.*, (2022) [18, 11, 22, 8]. Low PCV and GCV values for days to 50% flowering and maturity indicated limited variability and greater stability, which agrees with the reports of Kumar *et al.* and Ashfaq *et al.*, Moderate variability was observed for spike length, grains per spike, biological yield, and harvest index, suggesting the possibility of improvement through selection. Higher differences between PCV and GCV for grain yield, harvest index, and effective tillers indicated considerable environmental influence, as also observed by Kalim Ullah *et al.* (2011) and Tabassum *et al.*, (2017) [3, 10, 21].

Zinc content and sedimentation value exhibited high PCV and GCV, indicating greater scope for effective selection. Bread wheat is also considered an important crop for zinc and iron biofortification, as reported by Cakmak *et al.*, High heritability coupled with high genetic advance for traits like zinc content, iron content, grains per spike, spike length, biological yield, and sedimentation value suggested the predominance of additive gene action and effectiveness of direct selection. Similar findings were reported by Ashraf *et*

al., (2014), Majumder *et al.* (2008) and Singh *et al.*, (2022) However, low to moderate heritability and genetic advance for grain yield, harvest index, and protein content indicated greater environmental influence and the need for hybridization followed by selection.

Correlation analysis showed that grain yield per plant had a strong positive association with harvest index and biological yield, indicating their importance in yield improvement. Similar results were reported by Ahmadi *et al.*, (2014), Fellahi *et al.* (2013) and Kumar *et al.*, (2008) Mahalanobis D² analysis grouped 54 genotypes into six clusters, revealing

substantial genetic diversity. Maximum inter-cluster distance between Cluster I and II suggested that hybridization among these clusters may produce superior recombinants. Similar observations were also reported by Yadav *et al.*, (2014), Kumar *et al.*, (2017) and Singh *et al.*, (2022) Overall, the study confirmed the presence of considerable genetic variability and diversity among wheat genotypes, which can be effectively utilized in future breeding programmes for yield and nutritional improvement [4, 15, 20, 2, 7, 12].

Table 1: Analysis of variance (ANOVA) for fourteen characters in Bread Wheat

SOV	DF	MEAN SQUARES													
		DF	DFM	TPP	GPS	PHT (cm)	SL (cm)	TW (g)	GYPP (g/plant)	YPP (g/plant)	HI (%)	PC (%)	SV (ml)	Fe content (ppm)	Zn content (ppm)
Blocks	4	1.41	22.27**	0.27	40.72**	73.79**	0.38	7.19**	2.58**	7.14**	66.58**	2.26*	74.80**	14.93**	26.73**
Treat	53	27.47**	42.31**	0.21	58.22**	38.00**	1.07**	13.90**	1.90**	4.26**	49.16**	1.47*	62.16**	33.48**	55.94**
Entries	49	28.18**	33.64**	0.22	50.20**	44.81**	1.07**	12.38**	1.63**	4.73**	41.12**	1.27*	51.22**	22.85**	37.40**
Check	3	22.58**	209.80**	0.07	153.32**	26.96*	1.61**	36.04**	5.10**	3.91*	188.19**	5.15**	215.49**	95.12**	89.74**
Ch x entries	1	7.67	-35.62	0.18	166.25**	-262.58	-0.45	21.86**	5.47**	-17.83	26.11	0.04	138.00**	369.38**	863.26**
Error	12	2.29	2.88	0.16	2.54	5.52	0.17	1.22	0.45	0.91	9.87	0.44	9.13	0.18	0.08

**= significant at 1%, *= significant at 5%

Days to 50% Flowering days (DFF)	Days to 50% Maturity days (DFM)	Effective tiller (TPP)	Grains per spike (GPS)	Plant Height (cm) (PHT)	Spike length (cm) (SL)	1000 grains weight (g) (TW)
Grain yield (g/plant) (GYPP)	Biological yield (g/plant) (BYPP)	Harvest index (%) (HI)	Protein content (%) (PC)	Sedimentation value (ml) (SV)	Iron content (ppm) (Fe)	Zinc content (ppm) (Zn)

Table 2: Mean performance in bread wheat genotypes for fourteen characters.

Characters	Range		Population Mean	CV (%)
	Lowest	Highest		
50% flowering days	72	90	81.84	1.85
50% maturity days	116	136	127.59	1.34
Effective tiller	1.92	4.27	3.03	12.99
Grains per spike	28.81	63.36	49.587	3.08
Plant Height (cm)	80.26	119.26	94.17	2.49
Spike length (cm)	5.77	10.52	8.771	4.62
1000-grains weight (g)	40.64	59.8	46.38	2.43
Grain yield (g/plant)	3.09	9.45	6.5	12.44
Biological yield (g/plant)	10.57	21.05	16.27	5.72
Harvest index (%)	21.59	57.33	39.89	10.73
Protein content (%)	8.97	14.52	11.3	6.04
Sedimentation value (ml)	25.63	58.95	37.88	8.6
Iron content (ppm)	34.24	53.87	38.83	1.17
Zinc content (ppm)	25.99	53.79	33.15	0.99

Table 3: Genetic variability parameters estimation for fourteen characters in bread wheat.

Characters	Phenotypic Variance	Genotypic Variance	PCV (%)	GCV (%)	h ² b. s (%)	GA	GA as % of mean
50% flowering days	31.95	29.66	6.91	6.65	92.83	10.81	13.21
50% maturity days	49.32	46.43	5.50	5.34	94.15	13.62	10.68
Effective tiller	0.22	0.05	15.39	7.61	24.49	0.24	7.76
Grains per spike	68.12	65.58	16.64	16.33	96.27	16.37	33.01
Plant Height (cm)	43.78	38.26	7.03	6.57	87.40	11.91	12.65
Spike length (cm)	1.23	1.06	12.63	11.75	86.46	1.97	22.50
1000-grains weight (g)	16.16	14.94	8.67	8.33	92.47	7.66	16.51
Grain yield (g/plant)	2.02	1.29	22.05	17.62	63.82	1.87	28.99
Biological yield (g/plant)	4.85	3.94	13.54	12.21	81.32	3.69	22.68
Harvest index (%)	50.09	30.45	17.88	13.94	60.79	8.86	22.39
Protein content (%)	1.65	1.21	11.37	9.75	73.55	1.95	17.23
Sedimentation value (ml)	71.59	62.45	22.33	20.86	87.24	15.21	40.14
Iron content (ppm)	39.40	39.22	16.17	16.13	99.55	12.87	33.15
Zinc content (ppm)	65.87	65.79	24.48	24.47	99.87	16.70	50.37

Table 4: Correlation coefficient analysis of fourteen characters of bread wheat.

Characters	DFE	DTM (50%)	TPP	GPS	PHT (cm)	SL (cm)	TW (g)	BYPP (g/plant)	HI (%)	PC (%)	SV (ml)	Fe (ppm)	Ze (ppm)	gypp (g/plant)
DFE	1	0.726**	-0.086	0.261	0.155	0.203	-0.143	0.107	-0.148	-0.111	-0.036	-0.386**	-0.218	-0.057
DTM (50%)		1	-0.011	0.100	0.118	0.119	-0.217	0.217	-0.166	0.097	0.185	-0.200	0.017	-0.007
TPP			1	0.041	-0.029	-0.213	0.222	0.444**	-0.022	-0.103	-0.101	0.216	-0.023	0.210
GPS				1	-0.315*	0.136	-0.199	0.328*	0.056	-0.280*	-0.215	-0.267*	-0.278*	0.212
PHT (cm)					1	0.005	0.083	-0.177	-0.080	0.053	0.019	0.230	-0.006	-0.167
SL (cm)						1	-0.018	-0.138	-0.222	-0.028	0.012	-0.094	-0.425**	-0.242
TW (g)							1	0.046	-0.036	0.003	-0.058	0.040	0.088	-0.004
BYPP (g/plant)								1	0.179	-0.047	0.012	0.100	0.094	0.676**
HI (%)									1	-0.419**	-0.440**	-0.242	-0.246	0.842**
PC (%)										1	0.957**	0.203	0.492**	-0.334*
SV (ml)											1	0.211	0.503**	-0.321*
Fe (ppm)												1	0.485**	-0.129
Zn (ppm)													1	-0.126

*, ** = Significant at 5% and 1% probability levels respectively

Table 5: Grouping of genotypes into different clusters.

Clusters	No. of Germplasm	Genotypes
I	9	WG28, GW 2021-1026, WG 12, WG 20, WG 9, WG 44, WG 26, WG8, WG 22
II	7	WG 40, WG 34, WG 25, WG 39, WG 29, WG 36, WG 35
III	7	WG23, WG 4, WG38, WG17, WG 3, WG6, WG5
IV	2	WG 37, WG 30
V	8	WG 33, WB 02 (c), WG 45, WG 49, WG 11, WG 10, WG 7, WG 2
VI	21	WG 21, WG 1, WG 32, WG 31, WG 43, DBW 187 ©, WG 13, WG 42, WG 15, DBW 222, WG 46, WG 19, GW 322 (C), WG 14, WG 41, WG 16, WG 27, WG 29, WG 18, WG 48, WG 47

Table 6: Estimates of average Intra- and Inter-cluster distance for six clusters in bread wheat.

Clusters	C1	C2	C3	C4	C5	C6
C1	33.91	51.60	43.47	43.67	46.24	39.16
C2		28.71	37.29	44.09	43.81	31.26
C3			25.09	46.03	37.12	34.14
C4				27.80	50.37	39.00
C5					30.90	36.83
C6						24.97

Table 7: Cluster Mean value of fourteen characters of wheat genotypes

Clusters	DFE	DFM	TPP	GPS	PHT (cm)	SL (cm)	TW (g)	GYPP (g/plant)	BYPP (g/plant)	HI (%)	PC (%)	SV (ml)	Fe (ppm)	Zn (ppm)
C1	83.79	132.51	2.89	44.12	95.69	8.56	47.01	4.92	15.31	32.21	12.87	48.07	42.99	42.59
C2	78.74	123.92	3.00	46.17	92.59	8.21	47.26	7.70	15.41	50.14	11.07	35.67	38.55	31.33
C3	85.56	131.45	2.99	53.72	93.05	9.05	45.60	6.00	16.32	36.65	11.08	37.57	37.04	31.77
C4	74.35	116.83	3.30	35.31	111.04	7.72	51.34	4.33	12.54	34.91	11.00	33.66	50.38	41.46
C5	75.79	120.23	2.98	48.78	88.49	8.90	48.63	5.71	15.99	35.63	11.99	42.79	42.66	38.30
C6	83.42	131.73	2.88	46.11	96.31	8.90	47.31	7.18	17.19	41.95	10.96	36.81	43.38	37.68

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