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Character association and genetic diversity assessment via hierarchical clustering in a diverse panel of improved wheat genotypes

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Abstract

The present study was conducted on fifty-seven diverse wheat genotypes at Wheat and Barley section, Department of Genetics and Plant Breeding, CCS HAU, Hisar to carry out character association and genetic diversity assessment via hierarchical clustering. A total of eleven morphological traits of each genotype was recorded and subjected to statistical analysis. Pearson correlation analysis was done and positive correlation was observed between grain yield and several key traits, including effective tillers per meter, spike length, spikelets per spike, grain per spike, 1000-grain weight, and biological yield per plot. To cluster the 57 wheat genotypes, 2-way clustering dendrogram were constructed and the genotypes were categorized into five clusters, while the traits/variables were classified into three groups. Among the five clusters, cluster I carries minimum one genotype i.e., C-306, while cluster III got maximum nineteen genotypes. Remaining clusters i.e., II, IV and V had thirteen, ten and fourteen genotypes, respectively. As per cluster mean table Cluster V carries superior genotypes performance better in the experiment which was recorded with highest spike length (12.74 cm), spikelet per spike (24.28), grains per spike (64.22), grain yield (1440.43 g/plot) and harvest index (41.71%). More genetically variable genotypes identified in the studies can be used in future crop improvement program along with utilization of superior genotypes as parent in hybridization.

Keywords: Bread wheat, diversity analysis, clustering, correlation analysis

Introduction

Wheat, scientifically known as *Triticum aestivum* L., is a crucial cereal crop on a global scale, serving as a staple food for approximately 40% of the world's population. It not only provides a substantial portion of daily caloric intake but also supplies about 20% of daily dietary protein, surpassing other cereal crops (LACC/IGW, 2018) ^[4]. The ever-increasing global population and the diverse needs of farmers necessitate a call to boost wheat production and productivity to address food security concerns (FAO, 2017) ^[10] (World and Group, 2018) ^[21]. Wheat, like many other crop plants, exhibits a range of quantitative agronomic traits, with yield standing out as one of the most economically significant. The complexity of yield as a quantitative trait arises from its dependence on the intricate interplay of various component traits. Effective selection is the linchpin in crop improvement programs, serving as a cornerstone for achieving breeding goals (Al-Tabbal, 2016) ^[1]. Correlation plays an indispensable role in plant breeding. Genetically correlated traits can be enhanced by directly selecting for any one of these traits. Correlations between traits are influenced by both genetic and environmental factors (Falconer, 1962) ^[9]. Correlation is a measure of the interrelationship between various traits (Sabit *et al.*, 2017) ^[17]. The study on cluster analysis delves into the captivating world of genetic diversity among wheat genotypes, revealing the potential to broaden the genetic basis of wheat by crossing genotypes from different clusters (Balcha *et al.*, 2022) ^[4]. Multivariate analysis techniques are invaluable for dissecting plant traits, providing breeders with the tools to advance genetic improvements in bread wheat genotypes. In light of this context, the present study embarks on a journey to explore the extent of clustering among fifty-seven bread wheat genotypes and identify the key traits associated with grain yield.

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Materials and Methods

The plant material was consisted of biofortified 57 genotypes (table 1) including popular released varieties in Haryana and advanced lines developed in Harvest Plus Yield Trail (HPYT), CIMMYT. The seeds of these genotypes were procured from Wheat & Barley Section, Department of Plant Breeding, CCS Haryana Agricultural University, Hisar to carried out the present study. Field experiment was laid out in Complete Randomized Block Design (CRBD) with a plot size of 3 m² in three replications during *rabi*, 2017. The recommended package of practices was followed for raising crop. All the cultural crop practices were kept constant. The phenotypic observations were recorded on randomly selected plants from each genotype in each replication for days to 50% heading (DH), days to maturity (DM), plant height (PH (cm)) number of effective tillers/meters (ET), spike length (SL (cm)), Number of spikelets per spike (S/S), number of grains per spike (G/S), 1000-grain weight (GW (g)), biological yield per plot (BY/plot (g)), grain yield per plot (GY/plot (g)), harvest index (HI (%)). The data recorded for all the parameters were used for statistical analysis. Pearson correlation analysis was done using KAU-GRAPES. Two-way clustering with heatmap options separate dendrogram were constructed by wards method and PCA calculation was carried out in JMP *version* 17.2.0.

Table 1: List of all the 57 wheat genotypes under experiment

Sr. no.	Genotypes	Sr. no.	Genotypes	Sr. no.	Genotypes
1	C306	20	HPYT 423	39	QBPB 1409
2	DPW 621-50	21	HPYT 424	40	RWP 2014-22
3	GW322	22	HPYT 425	41	RWP 2014-27
4	HPPAU 3	23	HPYT 426	42	SLPWB 6
5	HPPAU 4	24	HPYT 428	43	SLPWB 8
6	HPPAU 5	25	HPYT 429	44	SLPWB 10
7	HPPAU 6	26	HPYT 430	45	VG 2014-1
8	HPPAU 7	27	HPYT 431	46	VG 2014-2
9	HPPAU 9	28	HPYT 432	47	VG 2014-7
10	HPPAU 11	29	HPYT 433	48	WH 1025
11	HPPAU 12	30	HPYT 435	49	WH 1061
12	HPPAU 15	31	HPYT 436	50	WH 1063
13	HPYT 403	32	HPYT 445	51	WH 1080
14	HPYT 412	33	HPYT 446	52	WH 1097
15	HPYT 414	34	HPYT 449	53	WH 1105
16	HPYT 415	35	K0307	54	WH1127
17	HPYT 416	36	MACS6222	55	WH 1129
18	HPYT 419	37	NIAW1994	56	WH 1136
19	HPYT 420	38	P13020	57	WH 1179

Results and Discussion

The current study was carried out to assess the genetic variability present in the panel of 57 biofortified genotypes. The mean squares from the ANOVA for the yield contributing traits presented in Table 2, revealed that the mean sum of squares due to genotypes were highly significant ($P \leq 0.01$) for all the characters namely, days to 50% heading, days to maturity, plant height (cm), number of effective tillers/meter, ear length (cm), number of spikelet/ear, number of grains/ear, grain yield/plot (g), 1000-grain weight (g), biological yield/plot (g) and harvest index (%), indicating the presence of adequate genetic variability for all the characters. Hence, the data was subjected to further statistical analysis for correlation analysis and multivariate hierarchical clustering using ward method based on the yield contributing traits. Many early workers, including Drikvand *et al.*, 2013 [8], Bhutto *et al.* 2016 [6], Khan *et al.*, 2017 [12] and Antim *et al.*, 2022 [2] reported high variability for different traits in wheat. The presence of appreciable differences among genotypes for most of the characters studied makes the possibility to carry out further breeding and genetic analysis.

Correlation analysis

Grain yield is a genetically complex trait and is influenced by several component characters, so it is very difficult to improve yield by directly selecting for seed yield per plant. It was felt that it would be of great help in selecting the desirable genotypes for yield if there is certain association of seed yield with certain easily measurable plant characters. The component traits related to grain yield were analyzed using Pearson's correlation analysis to uncover any potential relationships between them. The matrices show the values of the Pearson's correlation coefficient (R) with the direction and strength of correlation between all important variables, with the positive values in blue and negative in red. Grain yield shows positive and significant correlation with plant height (0.16), effective tillers per meter (0.25), spike length (0.26), spikelets per spike (0.25), grain per spike (0.25), 1000-grain weight (0.36) biological yield per plot (0.77) and harvest index (0.55), while negative correlation with days to maturity (-0.23). Similarly, the association of grain yield with either one or more than one trait has also been reported Suleiman *et al.*, (2014) [19], Wahidy *et al.*, (2016) [20], Desheva, (2016) [7], Phougat *et al.*, (2017) [15] and Arya *et al.*, (2017) [3]. Grain yield showing negative association with days to maturity as at terminal heat stress

Table 2: Analysis of variance (ANOVA) of the morphological traits recorded during the study

Source of variation (SV)	DF	Mean sum of squares										
		DH	DM	PH	ET	EL	S/S	G/S	GW	GY	BY	HI
Replication	2	17.38	4.32	318.3	153.29	1.4	29.44	925.45	20.73	8,716.333	46,782.129	0.970
Genotypes	56	19.01**	6.29**	100.834**	400.33**	2.27**	6.21**	132.38**	24.93**	89,176.410**	373,329.617**	33.105**
Error	112	1.31	0.58	10.09	156.72	0.76	1.4	49.53	13.66	10,831.262	50,864.414	2.971

DF- Days to 50% heading

DM- Days to maturity

PH- Plant height (cm)

ET- Effective tillers per meter

SL- Spike length (cm)

S/S- Number of spikelets per spike

G/S- Number of grains per spike

GY- Grain yield per plot (gm/plot)

GW- 1000 grains weight (gm)

BY- Biological yield per plot (gm/plot)

HI- Harvest index (%)

Table 3: Mean of 57 wheat genotypes arranged in clusters with use of hierarchical clustering by Ward method

Cluster	Count	DH	DM	PH (cm)	ET	SL (cm)	S/S	G/S	GW (g)	GY/plot (g)	BY/plot (g)	HI (%)
1	1	93.67	139.33	121.40	94.00	8.90	20.92	55.59	35.41	753.33	3546.67	21.25
2	13	96.49	136.05	104.88	103.44	12.42	23.55	55.42	38.16	1118.59	2848.82	39.36
3	19	93.25	134.37	107.58	106.32	12.06	21.88	52.97	40.91	1270.19	3179.37	39.98
4	10	97.40	136.87	105.00	116.70	11.89	23.29	58.98	42.43	1355.43	3325.33	40.79
5	14	94.24	134.71	111.71	107.48	12.74	24.28	64.22	41.16	1440.43	3463.43	41.71

DF- Days to 50% heading

DM- Days to maturity

PH- Plant height (cm)

ET- Effective tillers per meter

SL- Spike length (cm)

S/S- Number of spikelets per spike

G/S- Number of grains per spike

GY- Grain yield per plot (gm/plot)

GW- 1000 grains weight (gm)

BY- Biological yield per plot (gm/plot)

HI- Harvest index (%)

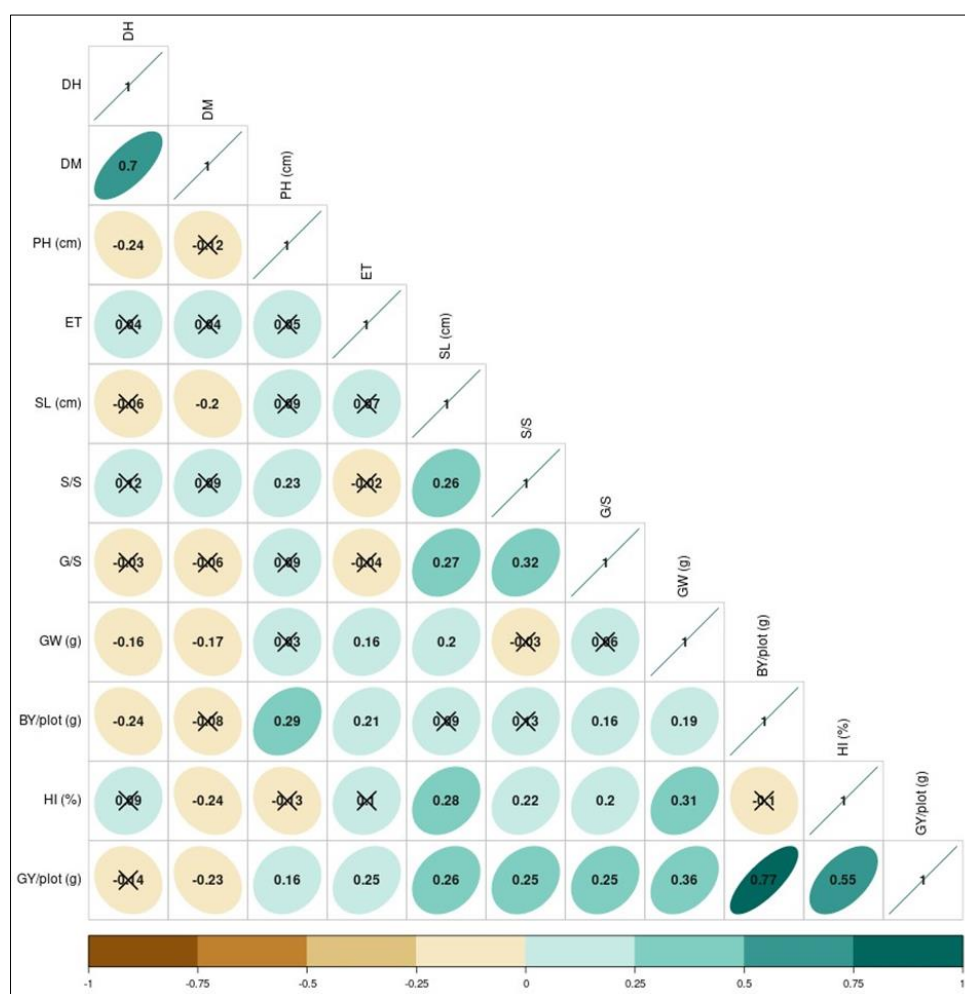


Fig 1: Pearson correlation coefficient among morphological traits recorded on wheat genotypes cause negative impact on yield, so selection for early maturing genotype is useful for crop production (Kumar *et. al.*, 2023) ^[13]

Cluster analysis: To cluster the 57 wheat genotypes based on mean values of morphological traits, using 2-way clustering and heatmap options, dendrogram were constructed by wards method in JMP *ver.* 7.2.0. Using a robust co-clustering algorithm, the genotypes were categorized into five clusters (Figure 2), while the traits/variables were classified into three groups. The results were then visualized as a co-cluster heatmap. Genotypes showing high similarity were grouped in a row cluster, while traits with strong associations were placed in a column cluster. Among the five clusters, cluster I

carries minimum one genotype i.e., C-306, while cluster III got maximum nineteen genotype as shown in dendrogram (Fig. 2.). Remaining clusters i.e., II, IV and V had thirteen, ten and fourteen genotypes, respectively. Cluster mean (table 3) depicted that cluster I had maximum days to maturity (139 days), plant height (121.40 cm) and biological weight (3546.67 g/plot), while lowest effective tillers per meter (94), spike length (8.9 cm), spikelet per spike (20.92), 1000-grain weight (35.41), grain yield (753.33 g/plot) and harvest index (21.25%).

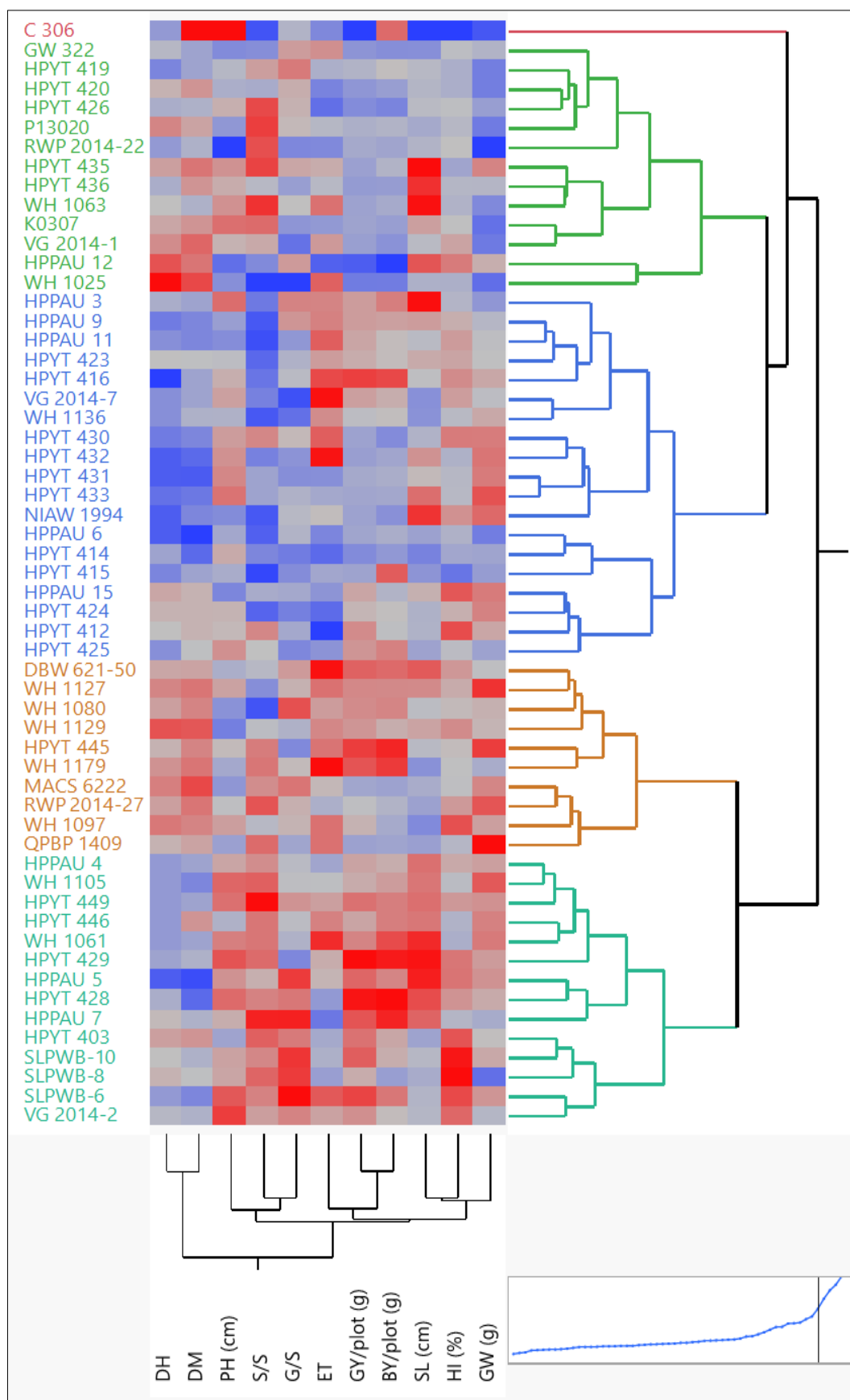


Fig 2: Two-way hierarchical cluster of fifty-seven wheat genotypes

Among all the cluster means, cluster II had minimum plant height (104.88 cm) and biological weight (2848.82 g/plot). Cluster III had lowest days to 50% heading (93.25 days), days to maturity (134.37 days) and grain per spike (52.97 grains).

Cluster IV took maximum days to 50% heading (97.40 days) with highest effective tillers (116.70) and 1000-grain weight (42.43 g). Cluster V was recorded with highest spike length (12.74 cm), spikelet per spike (24.28), grains per spike

(64.22), grain yield (1440.43 g/plot) and harvest index (41.71%), which carries superior genotypes as per performance in the experiment. Findings of earlier workers, namely, Arya *et al.* (2017)^[3], Rajshree and Singh (2018)^[16] and Barman *et al.*, 2021^[5] were also cluster the different diverse genotypes and concluded that most diverse clusters can be used for selection of parent for crop improvement hybridizing program. Selection of genotypes from cluster having higher mean of target trait may be rewarding towards the crop improvement (Barman *et al.*, 2021)^[5].

Conclusion

The present study draws the conclusion that a collection of 57 wheat genotypes exhibits substantial genetic variability, making them suitable candidates for inclusion in a wheat improvement program. Notably, a positive correlation was observed between grain yield and several key traits, including effective tillers per meter, spike length, spikelets per spike, grain per spike, 1000-grain weight, and biological yield per plot. This correlation underscores the significance of targeting these specific traits in a breeding program to enhance wheat grain yield. Additionally, the cluster analysis has identified Cluster V as harboring superior genotypes, providing valuable options for integration into wheat improvement initiatives.

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