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MULTIVARIATE ANALYSIS OF GRAIN YIELD AND ITS RELATED TRAITS IN WHEAT (*TRITICUM AESTIVUM* L.) UNDER SOUTHEASTERN HUMID PLAIN ZONE OF RAJASTHAN INDIA

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ABSTRACT

At present scenario, it is urgent to develop economic, viable, climate and sustainable options of wheat varieties through plant breeding approaches. Therefore, the present study focused on assessing genetic diversity and examining the effects of traits that promote the increase of diversity among the cultivars. The study was conducted in Randomized Complete Block Design (RCBD) with four replications to quantify the multivariate analysis for 12 traits among the Forty-two cultivars of wheat under AICRP on Seed (Crops) at Agriculture University, Kota, Rajasthan during *Rabi* 2023-24. The significant differences and wide range of variation were observed among the tested cultivars for most of the traits. The PCV values for most of traits were closely matched the corresponding GCV value. High H (bs) combined with substantial GAM was observed for the traits such as biological yield per plant, harvest index, and grain yield per plant. In PCA, first four PC with Eigen values >1 contributed 69.56 % total variability among tested cultivars for twelve traits. Five clusters were formed from 42 cultivars studied. Out of 42 cultivars,14 cultivars in cluster IV followed by 12 cultivars in cluster III. Cluster I was solitary with one cultivar. The cluster I (GW- 503) and IV (Raj-4238, Raj-3765, Raj-4037, UP-2338, GW-366, HD-2278, GW-190, Sujata, HD-2967, HD-2781, UP-319, PBW-226, HD-2189 and DBW-16) had the greatest inter cluster distance of 113.42 % showed that the cultivar was more diverged between each pair of clusters. In conclusion, the tested cultivars of wheat exhibited sufficient amount of genetic variability and diversity based on overall appearance and *per se* performance and these cultivars could be employed in hybridization programmes to produce better transgressive segregants, offering a high potential for yield in subsequent generations.

***Keywords*: cultivar, genetic diversity, grain yield, PCA, variability and wheat.

Introduction

The growing global population calls for adequate food to human and animal races. Wheat is a multi-purpose food and feed harvest that is important for the nutritional supply of the world's population (Shewry & Hey, 2015). In world, it is mainly cultivated in Peninsular zone of India, Burma, Pakistan, Thailand, and others Southern Asia countries and this area is known as the fertile crescent. Wheat is sown on 31.83 million hectares area and 113.29 million tonnes production with 35.59 quintals per hectare average productivity during 2023-24 in the country (Anonymous, 2024). However, the national productivity of wheat is lower than the other nations in terms of quantity and quality. The productivity of crop is highly suffered due to climatic factors in the country (Neenu *et al.*, 2025). The global climate change has emerged out as an emerging challenge and consequences includes changes in average annual rainfall, temperature, humidity, pollution, and frequent outbreaks of biotic factors, most of them concurring (Tadesse *et al.*, 2019).

To address this, there is an urgent need to evolve economic, viable and climate resilience cultivars for cultivation. Choices based solely on phenotypic differences often mislead plant breeder as they are influenced by the environment regarding the representation of traits. (Bhandari *et al*., 2017). Morphological traits are considered an important first step in explaining and classifying of germplasm, as breeding programs are primarily based on the magnitude of genetic variability of any crops (Singh *et al*., 2024). The extent of genetic variation within crops plays a critical role in determining characteristics and transmission between germplasm to future generations. (Singh & Upadhyay, 2013). Better genotypes should have high heredity properties of desirable traits associated with high genetic advance (Larik *et al*., 2000). Yield improvement of any crop is dependent on the presence of genetic diversity among the cultivar which is an important factor for hybridization. The improvement in the yield of crops depends on the presence of genetic diversity under the cultivar, a key factor in hybridization. Methodologies useful in diversity studies, including multivariate approaches (PCA & cluster analysis). Multivariate analysis refers to several measurements and statistical methods for each individual. Analysis of two or more variables can be seen more explicitly than multivariate analysis (Hair, 2009). Using multivariate techniques is an important strategy for examining genetic relationships among the genotypes (Ajmal *et al*., 2013). Principal Component Analysis (PCA) eliminates redundancy in data records and results in reliable distribution patterns (Rao,1964). PCA was often used in plant breeding to reduce variable and germplasm grouping (Abebe, 2024). Cluster analysis is used to group similar units to summarize information about relationships between objects and to easily understand and communicate relationships (Peeters & Martinelli,1989). Cluster analysis is a multivariate analysis and it is widely used to describe genetic diversity based on similarities or differences among genotypes (Singh and Rajpoot, 2022). This study focused on finding genetic variability and diversity for the development of economic and stable wheat varieties, as well as possible inclusion criteria, using multivariate analysis.

Material and Methods

This experiment was conducted during *Rabi* Season 2023-24 under the ICAR-ALL India Coordinate Research Project on Seeds (Crops) at Agricultural University, Kota, Rajasthan. In the experiment, 42 wheat cultivars were sown in randomized block design (RBD0 with four replications. The cultivars were collected from the various institute of the country, and details of the cultivars are shown in Table 1. Each replication had two rows for each cultivar with row length of 4.0 meters. During crop gestation period, all recommended agro-cultural practices and plant protection measures were followed.

The following data were recorded in five randomly selected plants from each cultivar, with each replicate eliminating border and unhealthy plant for twelve traits *viz.* days to 50 % flowering, days to maturity, number of tillers (01m^2 area), plant height (cm), spike length (cm), biological yield per plant (g), number of grains per spike, number of spikelets per spike, number of grains per spikelet, test weight (g), grain yield per plant (g) and harvest index (%) except days to 50 % flowering and days to maturity which were recorded on the plot basis.

The replicated data of each cultivar for each trait were subjected to analysis of variance (ANOVA) according to the method proposed by Panse and Sukhatme (1985). The genotype and phenotypic coefficients of variance were calculated according to the proposed method of Burton and Devane (1953). Heritability in the broad sense was calculated according to the formula proposed by Allard in 1960. The genetic advance as percent mean was categorized into low (<10), moderate (10-20), and high (>20) as per the method suggested by Johnson *et al.* (1955a). Principal component analysis (PCA) computed following Rao (1964) as a linear combination of optimally weighted observed variables, analysed of data by GRAPES (Gopinath, *et al.,* 2020) and k-mean clustering (Mac queen, 1967), one can customize on number of clusters to be formed thus meaning validation of results are possible and grouping of cultivars by OPSTAT (Sheoran *et al.,* 1998).

Results

Analysis of variance and *per se* performance of cultivar

ANOVA indicated the presence of significant differences among the cultivar for all the traits *viz.* days to 50 % flowering, days to maturity, number of tillers, plant height, spike length, biological yield per plant, number of grains per spike, number of spikelets per spike, number of grains per spikelet, test weight, grain yield per plant and harvest index under study indicating the presence of considerable amount of genetic variability in cultivar (Table 2). Therefore, there is a range of choice of potential parents in future breeding programs.

As shown in Table 3, the per se performance of the cultivar showed sufficient genetic variability for the traits examined. The results revealed that days to 50 % flowering varied 47.33 (GW-173) to 66.0 (C-306) with mean value of 56.96 days, days to maturity ranged 114.0 (GW-173) to 141.33 (PBW-215) with the average value of 121.41 days, number of tillers was observed minimum in 236.33 (C-306) to maximum in 355.67(Raj-4037) with mean value of 297.44, plant height 64.0 (GW-503) to 103.33 (C-306) with mean value of 88.77, spike length varied 8.03 (GW-503) to11.83 (Raj-4079) with the average value of 9.36, biological yield per plant from 61.67 (GW-496) to 161.33 (GW-503) with mean value of 103.98, number of grains per spike ranged 35.67 (GW-366)-66.67 (Raj-1482) with the mean value of 48.36, number of spikelets per spike ranged 10.17 (Raj-4037) to 23.67 (GW-273) with the average value of 17.98, number of grains per spikelet was observed lowest in 2.67 (Raj-3765) and higher in 4.33 (PBW-502) with 3.23 mean value, test weight from 29.67 (Sujata) to 41.67 (Raj-4238) with the average value of 34.67, grain yield per plant from 25.33 (Raj-3765) to 51.33 (HD-2781) with the mean value of 40.68 and harvest index varied 31.22 (GW-503) to 58.37 (Raj-4079) with the mean value of 40.28 under studied.

Genetic Variability, Heritability and Genetic advance

The genotypic and phenotypic coefficient of variance (GCV and PCV), heritability, and genetic advance as percent of the mean was studied for traits and the showed considerable variation for investigated traits (Table 4).

The highest values of genotypic and phenotypic coefficients of variation (GCV and PCV) have been observed for biological yield per plant (21.98; 23.37), suggests that this function is determined primarily by additive genes. GCV and PCV moderate values are harvest index (16.15; 18.45), grain yield per plant (14.80; 15.80), number of grains per spike (14.41; 18.70), number of spikelets per spike (10.45; 13.62), number of tillers (10.37; 12.45) and number of grains per spikelet (10.20; 19.39). Days to maturity (4.54; 5.27), days to 50 % flowering (5.72; 6.56), test weight (7.04; 9.53), spike length (7.81; 12.29) and plant height (8.66; 10.40) were recorded lowest value.

Estimates of heritability to be unaffected by the environment show that overall variability indicates the accuracy of selecting better segments in the population due to phenotypic performance, making selection more effective. The highest values of heritability were exhibited in the study for biological yield per plant (88.52), grain yield per plant (87.74), harvest index (76.69), days to 50 % flowering (76.01), days to maturity (74.06), number of tillers (69.39) and plant height (69.33). Heritability moderate value was observed for spike length (40.41), test weight (54.62), number of spikelets per spike (58.87) and number of grains per spike (59.41), and number of grains per spikelet (27.68) was recorded lowest value.

Genetic advance is an important selection parameter that helps to select genotype from diverse populations. The maximum expected genetic advance as a percentage of mean was observed in the biological yield per plant (42,61), followed by the harvest index (29.14), grain yield per plant (28.56), and number of grains per spike (22.88), indicating the presence of the additive gene. Spike length (10.23), days to 50% flowers (10.27), test weight (10.72), number of grains per spikelets (11.06), plant height (14.86), and number of tillers (17.79) were moderately recorded.

Estimating hereditary nature with genetic advance as a percentage of mean is reliable and meaningful for the parameters (Nwangburuka & Denton, 2012). High heritability associated with genetic advance was recorded for biological yield per plant and grain yield per plant. This indicates that the choice of these traits is due to properties that are affected by environmental impacts.

Principal Component Analysis (PCA)

The principal component analysis was performed to identify the most contributing variables of observed total variability (Fig. 1). Of the 12 PCAs, four PCA with Eigen values >1 contributed 69.56% of the total variability among 42 wheat cultivar examined for the twelve traits (Table 5). Number of tillers (0.396) contributed positively in PC1 which account 24.05 % variability of the total variability. In PC2 accounting for 20.56 % of the total variability positive contribute to harvest index % (0.430). The plant height (0.510), days to 50 % flowering (0.330), days to maturity (0.300) and spike length (0.290) contributed positively to the total variation, which is noticed in PC3 that accounts 15.61 % of total variation. PC4 had contributed 9.34 % variation of the total variation. From the entire four PCAs number of tillers, harvest index %, plant height, days to 50 % flowering, days to maturity and spike length significantly contributes to the overall variation and divergence.

K-means clustering pattern and distribution

K-Mean is a wide range of clustering algorithms that help group genotypes into different clusters, and is verified to control the number of clusters formed. The 42 cultivars of wheat were divided into five different clusters according to K-means' clustering algorithm and are shown in Table 6. There are 14 cultivars of cluster IVs, followed by cluster III (12 cultivars), cluster II (9 cultivars), and cluster V (6 cultivars). Cluster I was lonely with diversity.

The cluster mean of cultivars for traits under studied are shown in Table 7. Cluster I was superior for traits viz., days to 50% flowering, days to maturity, biological yield per plant, number of grains per spike, number of spikes per spike, number of grains per spike, number of grains per spike, test weight, and grain yield per plant. Cluster II was the highest plant height. Cluster IV was superior to the number of tillers, and cluster V was for spike length and harvest index.

Diversity from the various geographical origins distributed across all clusters showed no relationship between geographical distribution and genotype diversity. Although extensive phenotypic variability was observed in this study, clustering of genotypes from various sources grouped under many clusters may be attributed to the low genetic distance between them. It should be noted that cluster calculations mean that the advantage of a particular genotype for a particular trait is rebodied and internal or intermediate by another genotype grouped in relation to the same cluster. Aside from the selection of parent from clusters with a high cluster distance for hybridization, we can also imagine choosing parents based on the degree of deviation from the character of interest.

This means that if breeder's intention is to improve the seed yield to plant, then selection should be aimed at parents which are highly divergent for the character of interest. Clusters I and IV, which differ in average values for most characteristics, can be used as parents in hybridization programs to consider their functionality.

Canonical Variate Analysis

It would be desirable to try crossings between parents belonging to clusters removed due to highly heterotic crossings (Venkatesh *et al*., 2017). However, heterosis cannot be used in autogamous crops on a commercial scale. However, crosses in which cluster parents are involved at more distances in clusters will likely provide desirable recombination for advanced generations that can be developed as traditional homozygous varieties. Average inter-cluster D^2 values among the five clusters of forty-two wheat cultivar are presented in Table 8. In this context, we created the distance between clusters taking into account the quantitative properties and the distance between 37.67 (between clusters III and V) and 113.42 (between I and IV). The highest distance between clusters I and IV (113.42) was followed by clusters I and III (98.45) and clusters IV and V (82.17). The maximum distance between clusters indicated that it was far from the type of cluster IV. Similarly, high inter-cluster values between clusters I and IV showed a more different diversity between each cluster couple.

Discussion

Yield is a quantitative trait that together effect on its expression, height, and stability. The selection of economical, viable and climate resilience genotype is utmost requirement under changing scenario of climatic conditions.

Analysis of variance (ANOVA) revealed significant cultivars for studied traits. This indicates that there is a significant amount of genetic variability among the cultivars. Hence, there is a scope for the selection of potential cultivars for the future breeding program. Singh & Upadhyay (2013) and Singh & Rajpoot (2021) were reported similar findings.

The *per se* performance of 42 wheat cultivars were observed more for biological yield per plant, number of spikelets per spike, test weight and grain yield per plant under southeastern Rajasthan. It shows sufficient variation in the cultivars tested. Similar results were made by Bhoite *et al.* (2008) and Singh *et al.* (2015).

High values of GCV and PCV relative to biological yields per plant indicate the possibility of improvements through selection and days to maturity, days to 50% flowering, test weight, spike length and plant height were lower values recorded suggesting that improving of these traits through simple selection may be challenging.

Heritability is estimated without the effect of overall variability. Biological yield per plant, grain yield per plant, harvest index, days to 50% flowering, days to maturity, number of tillers, and plant height showed that there is a high probability of a genotype to be recognized by its phenotypic expression and additive gene action (Chandrababu & Sharma, 1999). Singh *et al.* (2024) showed similar results for wheat. The remaining traits were examined with moderate to low heritability values. This indicates that selection of these traits is ineffective due to the general effects of non-additive genes.

Genetic advance is an important selection parameter that contributes to plant breeders in selection from gene pool. The maximum expected genetic advance as a mean percentage was observed for biological yield per plant, harvest index, grain yield per plant, and number of grains per spike indicating the presence of additive gene.

High heritability coupled with high genetic advance percentage over mean was recorded on biological yield per plant, harvest index and grain yield per plant indicating selection for these traits would be more effective.

Due to the high heredity, these traits have little environmental impact and direct selection of these traits has been shown to be effective in further genetic improvement of plant breeding programs. Similar results were made by Bhoite *et al.* (2008) and Singh *et al.* (2015).

The principal component analysis was performed to identify the most contributing variables of observed total variability. The number of tillers, harvest index, plant height, days to 50% flowering, day to maturity, and spike length contributed significantly to genetic variability and divergence. Research by Singh & Rajpoot (2022) supports the results.

Implementation of genetic divergence studies and time for crop improvement programs prior to initiation of breeding programs to reduce costs (Meena *et al*., 2015). Five cluster were formed from forty-two cultivar of wheat under studied and cluster IV has highest number of 14 cultivars.

The distance between clusters was resolved taking into account the quantitative characteristics and the distances from clusters III and V to I and IV. The maximum value of inter-cluster distance between cluster I and IV indicated that the cultivar was more diverged (Singh & Upadhyay, 2013).

Conclusion

Intrinsic genetic variation in the biological yield per plant, harvest index and grain yield per plant. In PCA, the number of tillers, harvest index, plant height and spike length contributed the total genetic variability. If a selection is exercised, priorities should focus on these characteristics. It has been decided that k-means analysis will organize the genetic diversity available in germplasm. Thus, the cultivar from the clusters I (GW- 503) and IV (Raj-4238, Raj-3765, Raj-4037, UP-2338, GW-366, HD-2278, GW-190, Sujata, HD-2967, HD-2781, UP-319, PBW-226, HD-2189 and DBW-16) were found more divergent. Hence, these cultivars could be used in hybridization programmes for getting desirable transgressive segregants in subsequent generations.

Table 1: Details of forty-two cultivars of wheat used under study.

S. No.	Cultivars	Notification year	Release centre	S. No.	Cultivars	Notification year	Release centre	S. No.	Cultivars	Notification year	Release centre
1	GW 503	1990	SDAU, Vijapur	15	Raj 3077	1989	RARI, Durgapura	29	HD 2781	2002	IARI, New Delhi
2	Lok-1	1982	Lokbharti Gramvidyapith	16	C 306	1978	CCSHAU, Hisar	30	PBW 215	1991	PAU, Ludhiana
3	GW 173	1994	SDAU, Vijapur	17	HW 2004	1997	IARI RS, Wellington	31	UP 319	1974	GBPUA&T, Pantnagar
4	Raj 4238	2016	RARI, Durgapura	18	Raj 3765	1996	RARI, Durgapura	32	HD 2687	1999	IARI, New Delhi
5	PBW 502	2004	PAU, Ludhiana	19	Raj 4037	2014	RARI, Durgapura	33	WH 711	2002	CCSHAU, Hisar
6	GW 496	1990	SDAU, Vijapur	20	UP 2338	1995	GBPUA&T, Pantnagar	34	PBW 373	1997	PAU, Ludhiana
7	WH 147	1980	CCSHAU, Hisar	21	GW 366	2007	SDAU, Vijapur	35	DWR 162	1993	ICAR-IIWBR, Karnal
8	GW 366	2007	SDAU, Vijapur	22	HD 2278	1984	IARI, New Delhi	36	PBW 226	1989	PAU, Ludhiana
9	HI 1544	2008	IARI RS, Indore	23	GW 190	1994	SDAU, Vijapur	37	PBW 154	1988	PAU, Ludhiana
10	Raj 1482	1983	RARI, Durgapura	24	Sujata	1983	IARI RS, Indore	38	HD 2329	1985	IARI, New Delhi
11	PBW 343	1996	PAU, Ludhiana	25	HD 2967	2014	IARI, New Delhi	39	WH 283	1985	CCSHAU, Hisar
12	GW 322	2002	SDAU, Vijapur	26	WH 542	1992	CCSHAU, Hisar	40	HD 2189	1980	IARI, New Delhi
13	Raj 4079	2011	RARI, Durgapura	27	DL 803-3	1995	IARI, New Delhi	41	DBW 16	2006	ICAR-IIWBR, Karnal
14	GW 273	1998	SDAU, Vijapur	28	GW 201	1985	SDAU, Vijapur	42	K 9423	2005	CSAUA&T, Kanpur

Table 2: Analysis of variances (ANOVA) for twelve traits under study in wheat.

S. No.	S.V.	d. f.	C-1	C-2	C-3	C-4	C-5	C-6	C-7	C-8	C-9	C-10	C-11	C-12
1	Replication	3	7.84	12.39	1273.75	68.48	0.76	67.17	45.02	2.51	0.03	0.10	12.10	2.19
2	Cultivar	41	35.22**	101.62**	3273.55**	203.49**	2.39**	1635.37**	178.92**	13.05**	0.61**	23.23**	113.80**	139.88**
3	Error	123	3.35	10.62	419.68	26.15	0.79	67.76	33.19	2.47	0.28	5.04	5.06	12.87

*and ** represent 5% and 1% level of significant, respectively

Trait details: C-1: Days to 50 (%) flowering, C-2: Days to maturity, C-3: Number of tillers in one-meter^2 area, C-4: Plant height (cm), C-5: Spike length(cm), C-6: Biological yield per plant(g), C-7: Number of grains per spike,C-8:Number of spikelet's per spike,C-9:Number of grain per spikelet,C-10: Test weight (g),C-11: Grain yield per plant (g) and C-12: Harvest index(%).

Table 3: Mean value of forty-two cultivars of wheat on grain yield per plant and its contributing traits under Southern eastern humid plain of Rajasthan.

S. No.	Cultivars	C-1	C-2	C-3	C-4	C-5	C-6	C-7	C-8	C-9	C-10	C-11	C-12
1	GW-503	52.67	118.67	241.67	64.00	8.03	161.33	64.67	19.33	4.00	37.00	50.33	31.22
2	Lok-1	51.33	118.67	257.00	86.00	9.83	118.67	42.67	17.00	3.33	36.67	41.67	35.09
3	GW-173	47.33	114.00	292.67	93.33	9.77	76.67	52.00	21.00	3.67	40.00	32.33	42.15
4	Raj-4238	53.67	122.00	350.67	70.67	9.00	104.33	43.00	17.00	3.33	41.67	47.33	45.44
5	PBW-502	61.33	128.67	257.33	73.33	10.10	92.67	61.67	21.33	4.33	37.00	32.67	35.31
6	GW-496	54.00	115.67	310.00	88.67	11.13	61.67	55.00	17.67	3.67	34.67	35.67	57.96
7	WH-147	52.67	119.33	258.00	84.00	8.83	102.33	56.00	19.00	3.33	35.33	42.00	41.03
8	GW-366	55.00	117.33	286.33	92.67	8.33	67.00	35.67	16.33	3.33	36.33	31.33	46.78
9	HI-1544	55.33	122.33	258.67	96.67	9.33	78.00	45.67	17.00	4.00	33.33	42.67	54.71
10	Raj-1482	52.67	120.00	286.00	88.67	9.23	93.67	66.67	17.67	4.00	34.00	32.67	34.86
11	PBW-343	58.67	127.33	286.33	91.33	9.77	102.00	50.00	20.00	3.67	34.67	32.00	31.35
12	GW-322	54.00	117.67	257.33	98.33	10.17	87.33	58.33	21.33	3.33	30.67	34.67	39.74
13	Raj-4079	55.00	117.33	271.33	85.67	11.83	75.00	53.33	19.00	3.33	35.33	43.67	58.37
14	GW-273	54.00	124.67	280.00	93.33	11.33	122.33	66.67	23.67	3.67	32.00	44.00	35.99
15	Raj-3077	60.67	118.67	285.33	83.33	9.33	75.33	44.67	19.33	3.00	32.33	30.00	39.82
16	C-306	66.00	127.33	236.33	103.33	9.00	105.33	44.00	16.67	3.00	33.00	40.33	38.29
17	HW-2004	64.00	125.67	255.33	102.67	10.67	138.00	50.67	19.67	2.67	31.67	44.00	31.87
18	Raj-3765	56.00	118.67	355.33	86.67	8.33	77.33	37.33	15.00	2.67	33.33	25.33	32.76
19	Raj-4037	59.33	118.00	355.67	82.67	10.33	80.67	44.67	10.17	2.67	36.67	34.67	42.99
20	UP-2338	58.67	114.00	335.67	86.67	8.33	98.67	43.67	16.33	3.00	38.67	36.67	37.16
21	GW-366	57.33	120.67	340.00	90.67	8.83	141.67	42.67	17.67	2.67	36.67	47.33	33.55
22	HD-2278	58.00	116.00	345.00	83.33	8.93	146.67	44.00	19.67	3.33	33.33	47.33	32.29
23	GW-190	57.33	116.33	334.67	95.67	8.57	95.00	42.67	17.00	3.00	32.00	42.33	44.55
24	Sujata	57.67	121.33	330.00	102.67	8.33	103.67	39.33	16.67	2.67	29.67	41.67	40.25
25	HD-2967	59.00	132.00	340.67	83.67	8.93	93.00	39.33	17.33	3.00	33.00	44.33	47.78
26	WH-542	58.00	119.00	310.00	88.67	9.33	98.00	43.00	16.33	2.67	35.67	50.00	51.06
27	DL-803-3	57.33	118.67	296.67	94.00	8.43	98.00	42.00	17.00	2.67	31.33	44.33	45.26
28	GW-201	57.33	121.33	310.00	93.67	8.73	134.00	59.00	19.33	3.33	41.33	50.00	37.32
29	HD-2781	59.00	122.67	343.33	82.67	9.70	138.33	57.67	19.33	4.00	38.00	51.33	37.11
30	PBW-215	61.33	141.33	258.67	98.00	8.87	136.67	46.67	18.00	3.00	38.67	47.33	34.64
31	UP-319	58.67	137.67	316.67	96.67	9.00	129.00	44.00	17.00	3.00	31.33	45.67	35.45
32	HD-2687	57.67	116.67	282.00	78.33	8.07	118.67	41.33	16.67	2.67	33.67	42.67	35.96
33	WH-711	57.67	122.67	287.33	82.00	8.30	127.33	49.33	17.67	3.00	34.33	42.67	34.02
34	PBW-373	54.00	116.67	285.33	87.67	10.67	116.00	47.67	19.00	3.33	33.33	41.33	36.82
35	DWR-162	53.67	115.67	302.00	92.00	9.60	83.67	45.00	17.67	3.67	32.00	38.67	46.54
36	PBW-226	55.67	122.67	317.33	89.33	9.33	108.67	49.67	18.00	2.67	36.33	44.00	40.74
37	PBW-154	60.33	127.33	296.67	79.33	9.47	87.33	48.00	18.67	3.00	33.00	35.33	41.34
38	HD-2329	58.00	119.67	276.67	94.00	9.80	89.33	46.00	16.33	3.00	34.00	40.33	46.72
39	WH-283	58.67	121.00	274.00	93.33	9.83	110.00	47.67	18.33	3.00	33.33	42.00	38.67
40	HD-2189	56.33	118.00	316.33	92.67	8.70	103.00	42.00	17.33	3.33	33.00	38.00	36.90
41	DBW-16	57.67	120.00	320.33	87.00	9.67	95.33	46.00	18.33	3.00	34.33	41.67	43.72

42	K-9423	59.33	126.00	291.67	91.00	9.17	95.33	51.67	17.33	3.67	33.67	36.33	38.08
Mean		56.96	121.41	297.44	88.77	9.36	103.98	48.36	17.98	3.23	34.67	40.68	40.28
Range		**47.33-66.00**	**114.00-141.33**	**236.33-355.67**	**64.00-103.33**	**8.03-11.83**	**61.67-161.33**	**35.67-66.67**	**10.17-23.67**	**2.67-4.33**	**29.67-41.67**	**25.33-51.33**	**31.22-58.37**
CD		**2.97**	**5.29**	**33.28**	**8.31**	**1.44**	**13.37**	**9.36**	**2.55**	**0.87**	**3.65**	**3.65**	**5.83**
CV		**3.21**	**2.68**	**6.89**	**5.76**	**9.49**	**7.92**	**11.91**	**8.73**	**16.49**	**6.42**	**5.53**	**8.91**

Traits details: C-1: Days to 50 (%) flowering, C-2: Days to maturity, C-3: Number of tillers in one-meter^2 area, C-4: Plant height (cm), C-5: Spike length(cm), C-6: Biological yield per plant(g), C-7: Number of grains per spike,C-8:Number of spikelet's per spike,C-9:Number of grain per spikelet,C-10: Test weight (g),C-11: Grain yield per plant (g) and C-12: Harvest index(%).

Table 4: Estimation of variance components for the twelve traits under study.

S. No.	**Traits**	**Coefficient of variance**		**Heritability in broad sense (h^2_{bs}) (%)**	**Genetic advance (GA)**	**GA as (%) of mean**
		Genotypic	**Phenotypic**			
1	Days to 50 (%) flowering	5.72	6.56	76.01	5.85	10.27
2	Days to maturity	4.54	5.27	74.06	9.74	8.06
3	Number of tillers in 1 square meter area	10.37	12.45	69.39	52.93	17.79
4	Plant height at maturity (cm)	8.66	10.40	69.33	13.19	14.86
5	Spike length(cm)	7.81	12.29	40.41	0.96	10.23
6	Biological yield per plant(g)	21.98	23.37	88.52	44.30	42.61
7	Number of grains per spike	14.41	18.70	59.41	11.07	22.88
8	Number of spikelets per spike	10.45	13.62	58.87	2.97	16.51
9	Number of grains per spikelet	10.20	19.39	27.68	0.36	11.06
10	Test weight(g)	7.04	9.53	54.62	3.75	10.72
11	Grain yield per plant(g)	14.80	15.80	87.74	11.62	28.56
12	Harvest index (%)	16.15	18.45	76.69	11.74	29.14

Table 5: Eigen value, variance (%) and cumulative variance (%) for corresponding twelve traits of forty-two cultivar of wheat

Variables	**PC1**	**PC2**	**PC3**	**PC4**	**PC5**	**PC6**	**PC7**	**PC8**	**PC9**	**PC10**	**PC11**	**PC12**
Days to 50 (%) flowering	0.19	-0.34	**0.33**	-0.01	**0.44**	0.19	0.27	0.15	-0.15	**0.62**	-0.04	0.00
Days to maturity	-0.05	-0.37	**0.30**	-0.09	**0.54**	-0.09	-0.22	-0.37	0.21	-0.47	0.12	0.02
Number of tillers in 1 square meter area	**0.31**	0.00	-0.36	-0.09	0.01	**0.69**	-0.30	-0.43	-0.07	0.10	0.09	0.03
Plant height (cm)	0.16	-0.01	**0.51**	-0.15	-0.33	-0.15	-0.69	0.04	-0.26	0.17	0.01	0.02
Spike length(cm)	-0.24	0.27	**0.29**	-0.39	0.11	**0.53**	0.02	**0.37**	0.00	-0.30	-0.35	-0.04
Biological yield per plant(g)	-0.18	-0.56	-0.14	-0.08	-0.26	0.07	0.04	0.09	-0.14	-0.10	-0.22	**0.69**
Number of grains per spike	-0.52	0.03	0.03	0.00	0.04	0.16	0.02	0.05	-0.43	0.01	**0.72**	0.02
Number of spikelets per spike	-0.47	-0.04	0.18	0.03	-0.23	0.16	-0.09	-0.18	**0.69**	**0.39**	0.05	0.02
Number of grains per spikelet	-0.46	0.18	-0.06	0.12	0.20	-0.13	-0.09	-0.46	-0.39	0.19	-0.52	-0.04
Test weight(g)	-0.15	-0.03	-0.50	-0.15	**0.40**	-0.17	-0.50	**0.45**	0.15	0.19	0.00	0.01
Grain yield per plant(g)	-0.09	-0.38	-0.18	-0.66	-0.22	-0.14	0.16	-0.13	-0.08	0.05	-0.03	-0.52
Harvest index (%)	0.13	**0.43**	0.03	-0.58	0.13	-0.25	0.17	-0.23	0.07	0.16	0.16	**0.50**
Eigen value	**2.89**	**2.47**	**1.87**	**1.12**	**0.96**	**0.68**	**0.58**	**0.51**	**0.36**	**0.33**	**0.23**	**0.01**
Percentage of variance	**24.05**	**20.56**	**15.61**	**9.34**	**7.98**	**5.69**	**4.81**	**4.25**	**2.98**	**2.73**	**1.92**	**0.09**
Cumulative percentage of variance	**24.05**	**44.62**	**60.23**	**69.57**	**77.54**	**83.23**	**88.04**	**92.29**	**95.27**	**98.00**	**99.92**	**100.00**

Table 6: Clustering pattern of forty-two cultivars of wheat formed by k-mean (Tocher's method)

Clusters	**I**	**II**	**III**	**IV**	**V**
No. of Members	**1**	**9**	**12**	**14**	**6**
Cultivars	GW-503	Lok-1, GW 273, HW 2004, GW 201, PBW 215, HD-2687, WH 711, PBW 373 and WH 283	GW 173, GW 496, GW 366, Raj 1482, PBW 343, Raj 3077, WH 542, DL 803-3, DWR 162, PBW 154, HD 2329 and K 9423	Raj-42.38, Raj-3765, Raj-4037, UP-2338, GW-366, HD-2278, GW-190, Sujata, HD-2967, HD-2781, UP-319, PBW-226, HD-2189 and DBW-16	PBW-502, WH-147, HI-1544, GW-322, Raj-4079 and C-306

Table 7: Cluster mean for twelve traits in forty-two wheat cultivars (Tocher's method)

Cluster	C-1	C-2	C-3	C-4	C-5	C-6	C-7	C-8	C-9	C-10	C-11	C-12
I	52.67	118.67	241.67	64	8.03	161.33	64.67	19.33	4	37	50.33	31.22
II	57.333	123.187	276.629	90.556	9.589	124.63	50.187	18.816	3.111	35	43.963	35.598
III	56.25	119.945	293.362	89.75	9.447	85.667	48.307	17.944	3.335	34.306	36.583	43.493
IV	57.453	121.429	335.834	87.931	8.999	108.239	44.001	16.916	3.024	34.857	41.976	39.335
V	57.388	122.11	256.498	90.222	9.877	90.11	53.167	19.055	3.553	34.11	39.335	44.575

Traits details: C-1: Days to 50 percent flowering, C-2: Days to maturity, C-3: Number of tillers in one-meter^2 area, C-4: Plant height (cm), C-5: Spike length(cm), C-6: Biological yield per plant(g), C-7: Number of grains per spike, C-8: Number of spikelets per spike, C-9: Number of grains per spikelet, C-10: Test weight (g), C-11: Grain yield per plant (g) and C-12: Harvest index (%).

Table 8: Inter-cluster D^2 values for five clusters in forty-two cultivars of wheat

Cluster	I	II	III	IV	V
I	-	59.944	98.456	113.419	80.358
II		-	43.956	62.000	41.354
III			-	48.856	37.666
IV				-	82.177
V					-

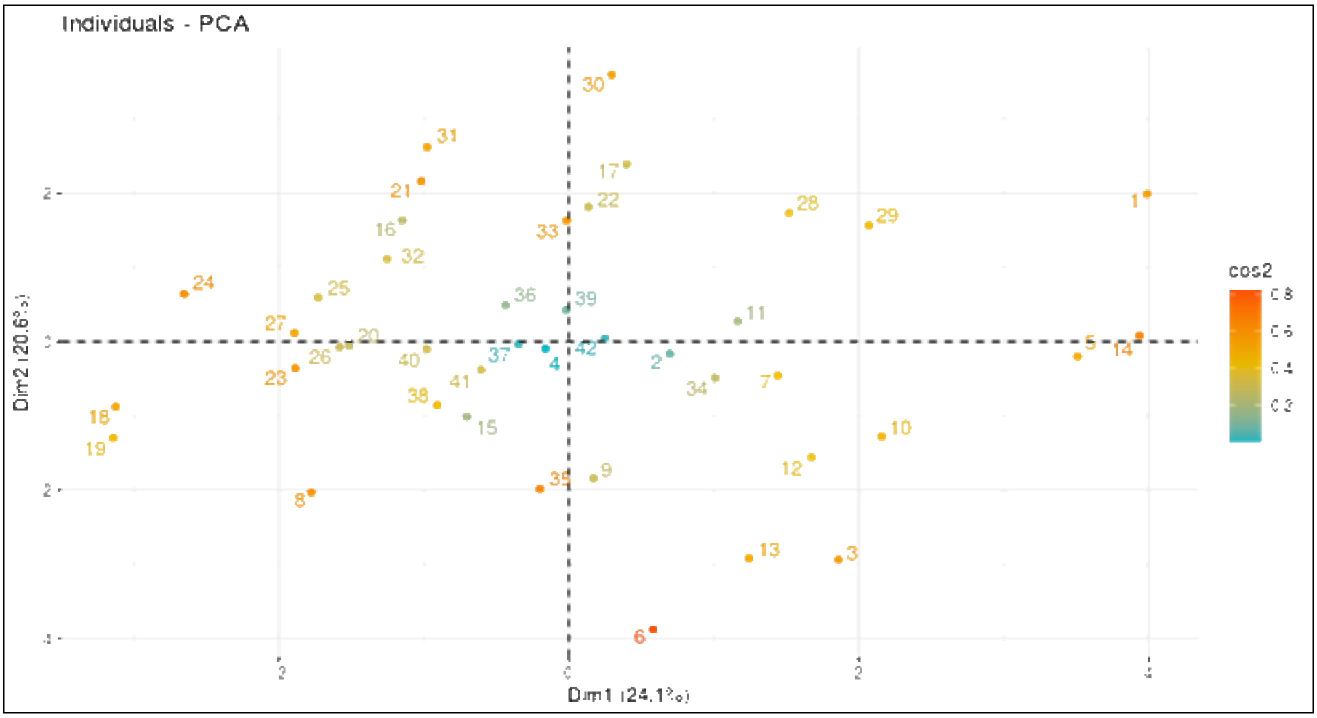

Fig. 1: Distribution of cultivar across PC1, PC 2

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Bhuri Singh and Khajan Singh: Investigation, Experiments, Data observation.

Bhuri Singh, Khajan Singh, Sanjay Kumar Sharma, Rajesh Kumar and Vivechana Rajpoot: Planning Experimentation, Analysis, Writing and Reviewing.

Conflict of interest

The authors do not explain conflicts of interest.

AI tool usage declaration

The authors here explain that AI, related tools, and image generation were not used during manuscript writing or editing.

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