



Genotypes X Traits Biplot for Multivariate Analysis of Yield and Contributing Traits Wheat (*Triticum aestivum* L.) Genotypes

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

Eighty two diverse wheat genotypes have been evaluated in Research area of Wheat and Barley Section, CCS HAU trials at CCSHAU during 2021-22 cropping seasons in augmented design with four established checks replicated five times each. Highest average value recorded for grain yield per plot followed by days to maturity while least value expressed by spike length (cm). Of course lowest error also reported by spike length, whereas extreme large by grain yield per plot. Number of wheat genotypes in non-significant groups had observed 54, 12, 8, 41, 6, 48, 6 genotypes for days to heading, days to maturity, plant height, tillers per meter row length, grains per spike, thousands grains weight, spike length, grain yield per plot respectively. First two principal components explained 51.6% of the total phenotypic variation. Biplot analysis expressed high positive correlation of days to heading with spike length, grains per spike, plant height. Positive association also observed between days to maturity with thousands grains weight, grains per spike and grain filling period, as plant height showed with spike length grain yield per plot, TGW. DWAP1108, GW1348, DWAP1608, HS 628, MACS 5052 observed far from other wheat genotypes. Multivariate hierarchical clustering of genotypes based on Ward's method observed nine different clusters based on important morphological traits. First group consisted of three genotypes (G1, G8, G82) while the last one contained nine genotypes (G70, G81, G74, G76, G77, G78, G73, G80, G75). Only three genotypes G4, G6, G19 placed in third cluster whereas largest cluster of twenty three genotypes was the fifth one.

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1. INTRODUCTION

The wheat crop has ensured the food security and nutritional augmentation of the people and precisely the most widely grown crop in the world [1]. Nearly 60% of all human calories have been supplemented by maize, rice, and wheat as major crops whereas 20% of all calories and protein provided by wheat alone [2]. The better processing and quality characteristics, and be easily transported and stored – it is also the world's most traded crop [3]. Over the years recent breeding programs have been efficiently meeting the demands of a fast-growing population through steady genetic gains. Improvements in wheat have been extremely successful especially since the Green Revolution and much of the progress made was due to the open sharing of Exotic lines, indigenous lines, advance breeding lines and knowledge among wheat scientists [4]. The potential of the genotypes had been assessed by genetic diversity for their judicious in crop improvement program [5]. Estimation of genetic distance, cluster mean values for yield and attributing traits is one of appropriate tools for parental selection in wheat hybridization programs [6]. Genetic divergence analysis plays an important role in assessing the nature of diversity in order to identify the genetically diverse genotypes for their use in plant breeding programmes [7]. The multivariate analysis has been established as a useful tool in identification of degree of divergence between biological populations at genotypic level and also to assess the relative contribution of different components to the total divergence both at inter and intra cluster level [8]. The complete insight into the complex components networks had not provided by univariate statistical analysis and standard deviations for each analyzed variable [9]. Multivariate statistical methods are appropriate tools for the analysis of the complex data matrix. The hierarchical cluster analysis (HCA) used in the current research is a simple way of grouping the set of available data by their similarities according to a set of selected variables. The assessment of phenotypic and genotypic diversity under multivariate clustering analysis aid to identify groups with similar genotypes is important for conserving, evaluating and utilizing genetic resources along with the purpose of protecting a breeders intellectual property rights also.

2. METHODS AND MATERIALS

A diverse set of 82 wheat genotypes have been evaluated in Research area of Wheat and Barley Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar situated at the latitude of 29°10'N, the longitude of 75°46'E and altitude of 215.2 m mean sea length in the semi-tropical region of North Western Plains Zone during 2021-22 cropping seasons. Augmented field design has been laid out with four established checks with five replications each. Checks have been placed after 15 genotypes in a set. Recommended agronomic and cultural practices have been followed to harvest good yield of genotypes. Since the genotypes have been evaluated in augmented designs, the final yields of genotypes calculated after the corrections of variability in the performance of checks in the field trials. Five randomly selected competitive plants for each genotype observed for altogether eight important morphological traits viz DH: Days to heading, DM: Days to Maturity, PH: Plant height(cm), NTP: Tillers per plant row length, NGS: Number of grains per spike, TGW: Thousand grains Weight (gm), SL: Spike length(cm) GY: Grain yield per plot(gm). Descriptive measures of variability viz., range, mean and standard error, Skewness, Kurtosis and CV calculated to measure variation in genotypes. Reputed statistical software SAS version 9.3 was exploited for analysis.

3. RESULTS AND DISCUSSION

3.1 Diversity Measures

Descriptive measures of variability viz mean, range, standard error, and coefficient of variation for traits have been presented in Table 1. Highest average value recorded for grain yield followed by days to maturity while least value expressed by spike length. Of course lowest error also reported by spike length, whereas extreme large by grain yield [10]. The near normal variability expressed by grain yield via Kurtosis value followed by thousand's grains weight. Positive skewness expressed by traits namely days to maturity, grain yield, plant height and negative for days to heading & grains per spike traits. Largest confidence interval observed for grain yield per plot and least by spike length for this set of wheat genotypes.

Days to heading of genotypes expressed variation from 88.8 to 101.3 while days taken to maturity showed 126 to 147 values (Fig. 1). Plant height showed divergence observed from 89 to 126 whereas tillers per plant row length registered change from 39 to 179. Values of grains per spike ranged from 24 to 79 and Marginal variation from 22 to 56 exhibited by TGW, while spike length reflected 6.4 to maximum 14.1 (Fig. 2). Grain yield per plot expressed variation from 197 to 1070 only among the genotypes [11]. Evaluated genotypes have been ranked for individual traits as larger rank defines the maximum value of respective trait (Table 2). Number of genotypes in non-significant group had registered 54, 12 8, 41, 6, 48, 6 for days to heading, days to maturity, plant height, tillers per meter, grains per spike, thousands grains weight, spike length, grain yield per plot respectively (Table 2).

3.2 Principal Components

First two components explained 51.6% of the total phenotypic variation among the 82 wheat genotypes (Table 3). The first principal component (PC-1) accounted for 29.6% of the total variation. The variations in grains/ spike, tiller per meter row length, plant height, days to

heading were important for first component. Significant Second Principal component (PC-2) contributed 21.9% to the total variation. Six variables namely thousands grain weight, spike length, days to maturity, grains yield per plot was to contribute more to PC-2. Out of the Traits which have been studied, 03 contributed most to the first two principal components (Table 3) and these considered most desirable to summarize phenotypic variation among the genotypes [12].

3.3 Association Analysis by Biplots

The interaction between genotypes and traits had been felicitated by biplot analysis and appropriate of this analyse to narrowing down the major contributing traits to the variability had been very appreciated. The first two components explained 51.6% of the total variation in genotypes (Fig. 2). In the biplot, vectors of traits showing acute angles are positively correlated whereas those showing obtuse or straight angles are negatively correlated and those with right angles have no correlation [2]. The long length of the vector corresponding to traits or genotypes pointed for large or extreme values. Selection among such genotypes may be performed either for further trials or for their use as parents in breeding programme aiming towards development of high yielding genotypes.

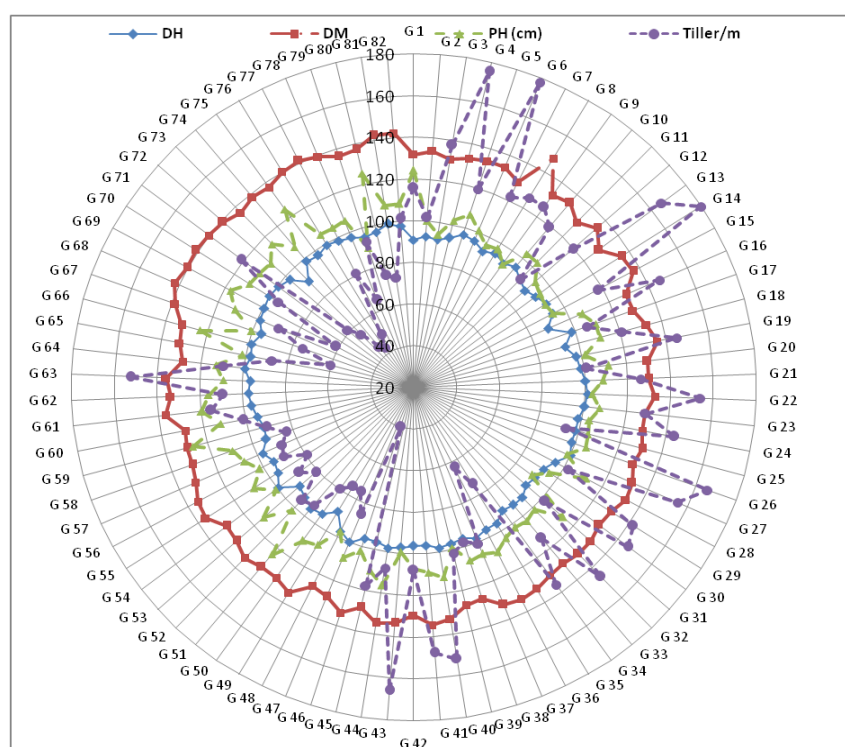


Fig. 1. Divergence of traits for evaluated wheat genotypes

Table 1. Descriptive measures of wheat genotypes

Measures	Days to Heading	Days to Maturity	Plant Height (cm)	Tiller/m	Grain/spike	TGW (g)	Spike length	Grain Yield (g/plot)
Mean	95.78	133.35	106.53	106.95	48.89	34.53	10.28	579.35
Standard Error	0.333	0.479	0.905	3.704	1.450	0.661	0.196	16.919
Median	96.05	132.85	107.03	101.88	49.80	35.15	10.40	560.00
Mode	96.05	128.85	111.40	119.75	32.05	30.90	10.65	640.00
Standard Deviation	3.016	4.342	8.198	33.540	13.128	5.987	1.779	153.205
Sample Variance	9.094	18.852	67.210	1124.949	172.339	35.849	3.164	23471.633
Kurtosis	-0.707	0.539	0.190	-0.513	-0.720	0.941	-0.270	1.271
Skewness	-0.361	0.873	0.363	0.216	-0.091	0.349	0.152	0.621
Range	12.50	21.50	37.50	140.00	55.25	34.25	7.75	872.50
Minimum	88.80	126.35	89.40	39.75	24.05	21.90	6.40	197.50
Maximum	101.30	147.85	126.90	179.75	79.30	56.15	14.15	1070.00
Confidence Level (95.0%)	0.663	0.954	1.801	7.370	2.884	1.316	0.391	33.663

Table 2. Ranking and grouping of evaluated wheat genotypes

Genotypes	DH	Rk	G	DM	Rk	G	PH (cm)	Rk	G	Tiller/m	Rk	G	Gr/ sp	Rk	G	TGW(g)	Rk	G	Sp. lgth	Rk	G	Gr Yld	Rk	G
HI 8805	90.8	77	0	131.85	47	0	124.15	4	1	115.75	32	1	41.05	57	0	45.65	2	1	7.15	78	0	1070	1	1
PBW 822	92.8	66	0	133.85	30	0	100.15	67	0	101.75	42	1	45.05	53	0	35.65	38	0	11.15	18	1	600	36	0
PBW 821	91.8	72	0	130.85	53	0	94.15	76	0	137.75	18	1	40.05	59	0	32.65	51	0	11.15	18	1	460	63	0
PBW 752	93.8	58	0	132.85	38	0	102.15	56	0	175.75	3	1	36.05	65	0	31.65	56	0	11.15	18	1	800	6	1
UP 3043	96.8	36	1	133.85	30	0	107.15	39	0	119.75	27	1	44.05	54	0	35.65	38	0	12.15	12	1	760	9	0
HI 8808	95.8	47	1	133.85	30	0	101.15	64	0	177.75	2	1	33.05	67	0	33.65	48	0	13.15	8	1	640	25	0
GW 1348	92.8	66	0	129.85	59	0	96.15	73	0	121.75	24	1	32.05	69	0	43.65	3	1	7.15	78	0	740	10	0
WH 1270	94.8	53	1	147.85	1	1	97.15	71	0	125.75	22	1	43.05	55	0	38.65	19	0	7.15	78	0	890	4	1
VL 3020	92.8	66	0	132.85	38	0	92.15	80	0	125.75	22	1	49.05	45	0	39.65	16	0	8.15	69	0	660	20	0
VL 3021	94.8	53	1	134.85	24	0	103.15	53	0	119.75	27	1	31.05	73	0	37.65	23	0	11.15	18	1	640	25	0
DBW 302	91.8	72	0	129.85	59	0	103.15	53	0	91.75	54	1	38.05	63	0	39.65	16	0	9.15	59	0	700	14	0
GW 509	89.8	80	0	134.85	24	0	96.15	73	0	119.75	27	1	32.05	69	0	41.65	10	0	9.15	59	0	630	30	0
MACS 5052	91.8	72	0	128.85	69	0	94.15	76	0	165.75	5	1	32.05	69	0	28.65	69	0	9.15	59	0	630	30	0
DDK 1056	93.8	58	0	135.85	20	0	93.15	79	0	179.75	1	1	24.05	79	0	32.65	51	0	8.15	69	0	490	60	0
DDK 1057	93.8	58	0	136.85	16	0	94.15	76	0	117.75	30	1	24.05	79	0	27.65	72	0	8.15	69	0	390	77	0
DBW 328	88.8	82	0	128.85	69	0	106.15	44	0	145.75	14	1	33.05	67	0	37.65	23	0	9.65	51	0	780	7	0
HD 3334	98.3	17	1	128.85	69	0	110.4	21	0	106	39	1	40.05	59	0	35.9	35	0	10.65	30	1	727.5	11	0
MP 1358	93.3	61	0	132.85	38	0	110.4	21	0	121	26	1	24.05	79	0	35.9	35	0	7.15	78	0	607.5	34	0
DBW 332	97.3	30	1	135.85	20	0	101.4	61	0	145	15	1	30.05	77	0	31.9	54	0	10.65	30	1	907.5	3	1

Genotypes	DH	Rk	G	DM	Rk	G	PH (cm)	Rk	G	Tiller/m	Rk	G	Gr/ sp	Rk	G	TGW(g)	Rk	G	Sp. lgth	Rk	G	Gr Yld	Rk	G
VL 3022	98.3	17	1	129.85	59	0	111.4	17	0	101	46	1	38.05	63	0	29.9	64	0	11.15	18	1	547.5	44	0
HPW 373	100.3	3	1	129.85	59	0	108.4	31	0	126	21	1	43.05	55	0	27.9	70	0	11.65	14	1	457.5	64	0
HPW 360	101.3	1	1	132.85	38	0	103.4	51	0	154	8	1	54.05	31	1	24.9	78	0	9.65	51	0	347.5	79	0
HPW 368	100.3	3	1	128.85	69	0	107.4	37	0	129	20	1	51.05	39	1	29.9	64	0	10.65	30	1	507.5	57	0
UP 2903	98.3	17	1	128.85	69	0	103.4	51	0	144	16	1	29.05	78	0	25.9	75	0	10.65	30	1	637.5	28	0
UP 2938	98.3	17	1	130.85	53	0	104.4	49	0	94	51	1	31.05	73	0	27.9	70	0	11.65	14	1	507.5	57	0
UP 2944	98.3	17	1	128.85	69	0	105.4	46	0	166	4	1	31.05	73	0	23.9	80	0	10.15	43	1	407.5	75	0
VL-GEHUN-2015	100.3	3	1	131.85	47	0	98.4	70	0	155	7	1	24.05	79	0	25.9	75	0	10.15	43	1	617.5	32	0
GW 1346	95.3	50	1	132.85	38	0	111.4	17	0	102	40	1	32.05	69	0	36.9	28	0	8.15	69	0	537.5	48	0
GW 499	92.3	69	0	129.85	59	0	95.4	75	0	142	17	1	35.05	66	0	28.9	67	0	10.65	30	1	507.5	57	0
GW 1339	91.3	75	0	128.85	69	0	89.4	82	0	146	12	1	39.05	61	0	32.9	50	0	8.65	67	0	727.5	11	0
CG 1023	90.3	79	0	130.85	53	0	113.4	13	0	102	40	1	39.05	61	0	35.9	35	0	9.65	51	0	767.5	8	0
CG 1029	93.3	61	0	130.85	53	0	101.4	61	0	146	12	1	31.05	73	0	36.9	28	0	7.65	76	0	457.5	64	0
RAJ 3765	93.05	65	0	129.35	67	0	103.15	53	0	113.75	34	1	53.55	33	1	30.4	62	0	10.4	41	1	695	15	0
RAJ 4238	92.05	71	0	130.35	58	0	102.15	56	0	135.75	19	1	40.55	58	0	35.4	40	0	9.4	56	0	425	73	0
DBW 88	96.05	40	1	132.35	43	0	104.15	50	0	73.75	71	0	59.55	19	1	32.4	53	0	9.4	56	0	635	29	0
DBW 173	96.05	40	1	133.35	35	0	108.15	34	0	62.75	74	0	59.55	19	1	33.4	49	0	9.9	49	0	587	37	0
DBW 168	98.05	22	1	132.35	43	0	106.15	44	0	100.75	47	1	61.55	14	1	34.4	43	0	8.4	68	0	695	15	0
DDW 47	96.05	40	1	126.35	81	0	107.15	39	0	97.75	48	1	53.55	33	1	26.4	73	0	7.4	77	0	565	39	0
DDW 48	97.05	33	1	127.35	80	0	99.15	68	0	101.75	42	1	53.55	33	1	29.4	66	0	6.4	82	0	535	50	0
DBW 221	98.05	22	1	132.35	43	0	112.15	15	0	151.75	10	1	68.55	6	1	26.4	73	0	10.4	41	1	645	24	0
DBW 107	96.05	40	1	134.35	28	0	109.15	28	0	147.75	11	1	65.55	8	1	30.4	62	0	10.9	27	1	445	67	0
DBW 252	96.05	40	1	129.35	67	0	107.15	39	0	107.75	37	1	49.55	42	0	36.4	30	0	11.4	17	1	445	67	0
DBW 110	97.05	33	1	133.35	35	0	99.15	68	0	165.75	5	1	55.55	26	1	34.4	43	0	11.9	13	1	565	39	0
HD 3293	98.05	22	1	134.35	28	0	116.15	9	0	107.75	37	1	55.55	26	1	36.4	30	0	10.9	27	1	655	21	0
K 1317	96.05	40	1	128.35	78	0	110.15	24	0	117.75	30	1	62.55	13	1	34.4	43	0	10.9	27	1	865	5	1
HD 2932	96.05	40	1	133.35	35	0	102.15	56	0	39.75	82	0	57.55	22	1	35.4	40	0	9.9	49	0	545	46	0
DBW 296	100.05	6	1	128.35	78	0	108.15	34	0	85.75	61	1	53.55	33	1	41.4	11	0	9.4	56	0	435	71	0
DBW 327	97.05	33	1	126.35	81	0	97.15	71	0	75.75	67	0	48.55	46	0	40.4	13	0	8.9	66	0	655	21	0
HI 1636	89.3	81	0	134.6	26	0	107.9	36	0	75.25	68	0	61.3	15	1	37.9	21	0	13.65	2	1	510	55	0
HI 8823	94.3	55	0	131.6	49	0	109.9	25	0	79.25	65	0	54.3	30	1	37.9	21	0	9.65	51	0	520	52	0
HI 8802	95.3	50	1	131.6	49	0	123.9	5	1	93.25	52	1	79.3	1	1	28.9	67	0	9.65	51	0	610	33	0
HI 1634	93.3	61	0	133.6	33	0	101.9	59	0	95.25	49	1	51.3	38	1	30.9	57	0	13.65	2	1	510	55	0
HI 1617	91.3	75	0	130.6	57	0	113.9	12	0	81.25	63	0	53.3	37	1	30.9	57	0	11.15	18	1	540	47	0
HI 1633	99.3	11	1	129.6	64	0	100.9	65	0	87.25	58	1	66.3	7	1	31.9	54	0	11.65	14	1	440	69	0
HD 3086	95.3	50	1	135.6	22	0	108.9	29	0	79.25	65	0	61.3	15	1	30.9	57	0	10.65	30	1	560	41	0
KRL 283	94.3	55	0	134.6	26	0	101.9	59	0	89.25	56	1	57.3	23	1	30.9	57	0	10.15	43	1	560	41	0

Genotypes	DH	Rk	G	DM	Rk	G	PH (cm)	Rk	G	Tiller/m	Rk	G	Gr/ sp	Rk	G	TGW(g)	Rk	G	Sp. lgth	Rk	G	Gr Yld	Rk	G
WH 730	97.3	30	1	131.6	49	0	106.9	42	0	87.25	58	1	49.3	43	0	30.9	57	0	10.65	30	1	560	41	0
GW-2010-288	93.3	61	0	129.6	64	0	109.9	25	0	83.25	62	1	70.3	4	1	34.9	42	0	13.65	2	1	520	52	0
GW-2014-596	92.3	69	0	129.6	64	0	126.9	1	1	91.25	55	1	56.3	24	1	33.9	46	0	10.65	30	1	420	74	0
HS 628	94.3	55	0	128.6	76	0	111.9	16	0	101.25	44	1	64.3	10	1	21.9	82	0	13.65	2	1	360	78	0
DBW 222	96.3	38	1	136.6	17	0	119.9	7	1	115.25	33	1	50.3	40	1	25.9	75	0	13.65	2	1	680	17	0
BRW 3806	97.3	30	1	133.6	33	0	115.9	10	0	109.25	35	1	49.3	43	0	33.9	46	0	14.15	1	1	580	38	0
KHTW 1	96.3	38	1	135.6	22	0	108.9	29	0	152.25	9	1	60.3	18	1	24.9	78	0	10.65	30	1	430	72	0
DWAP 1608	99.3	11	1	128.6	76	0	112.9	14	0	109.25	35	1	71.3	3	1	22.9	81	0	13.65	2	1	640	25	0
DWAP 1925	97.55	25	1	131.35	52	0	101.4	61	0	87.25	58	1	63.05	11	1	36.15	32	0	12.65	10	1	607.5	34	0
DBW 278	98.55	13	1	132.35	43	0	123.4	6	1	60.25	77	0	65.05	9	1	40.15	14	0	12.65	10	1	337.5	80	0
GW 477	95.55	48	1	138.35	12	1	100.4	66	0	75.25	68	0	46.05	50	0	38.15	20	0	10.15	43	1	197.5	82	0
WH 1252	98.55	13	1	142.35	2	1	111.4	17	0	89.25	56	1	69.05	5	1	36.15	32	0	13.15	8	1	477.5	61	0
RWP-2019-41	99.55	7	1	140.35	7	1	117.4	8	1	61.25	75	0	61.05	17	1	37.15	25	0	11.15	18	1	397.5	76	0
RWP-2019-38	100.55	2	1	141.35	5	1	111.4	17	0	95.25	49	1	55.05	28	1	41.15	12	0	11.15	18	1	647.5	23	0
RWP-2019-32	99.55	7	1	140.35	7	1	110.4	21	0	121.25	25	1	54.05	31	1	36.15	32	0	10.65	30	1	447.5	66	0
WSM 138	97.55	25	1	139.35	10	1	109.4	27	0	61.25	75	0	73.05	2	1	37.15	25	0	9.15	59	0	277.5	81	0
AKAW 4842	90.55	78	0	136.35	18	0	115.4	11	0	55.25	78	0	46.05	50	0	37.15	25	0	8.15	69	0	537.5	48	0
LBP-2017-2	98.55	13	1	138.35	12	1	107.4	37	0	45.25	80	0	48.05	47	0	40.15	14	0	8.15	69	0	667.5	18	0
DWAP 1108	97.55	25	1	137.35	14	0	124.4	3	1	43.25	81	0	59.05	21	1	56.15	1	1	10.65	30	1	517.5	54	0
RWP-2018-32	99.55	7	1	140.35	7	1	105.4	46	0	49.25	79	0	56.05	25	1	43.15	4	1	9.15	59	0	477.5	61	0
(MP) JW 3465	98.55	13	1	141.35	5	1	105.4	46	0	81.25	63	0	47.05	49	0	42.15	7	0	10.15	43	1	547.5	44	0
PBW 723(PBW 343 UNNAT)	97.55	25	1	139.35	10	1	106.4	43	0	65.25	73	0	50.05	41	1	42.15	7	0	10.15	43	1	527.5	51	0
PBW 771	95.55	48	1	136.35	18	0	90.4	81	0	93.25	52	1	46.05	50	0	42.15	7	0	11.15	18	1	667.5	18	0
MACS 4058	96.55	37	1	137.35	14	0	125.4	2	1	75.25	68	0	48.05	47	0	43.15	4	1	8.15	69	0	437.5	70	0
HUW 838	99.55	7	1	142.35	2	1	108.4	31	0	73.25	72	0	63.05	11	1	43.15	4	1	9.15	59	0	727.5	11	0
JKW 261	97.55	25	1	142.35	2	1	108.4	31	0	101.25	44	1	55.05	28	1	39.15	18	0	9.15	59	0	1027.5	2	1
CD at 5%	6.942			9.733			10.080			97.205			29.698			13.816			4.018			272.723		

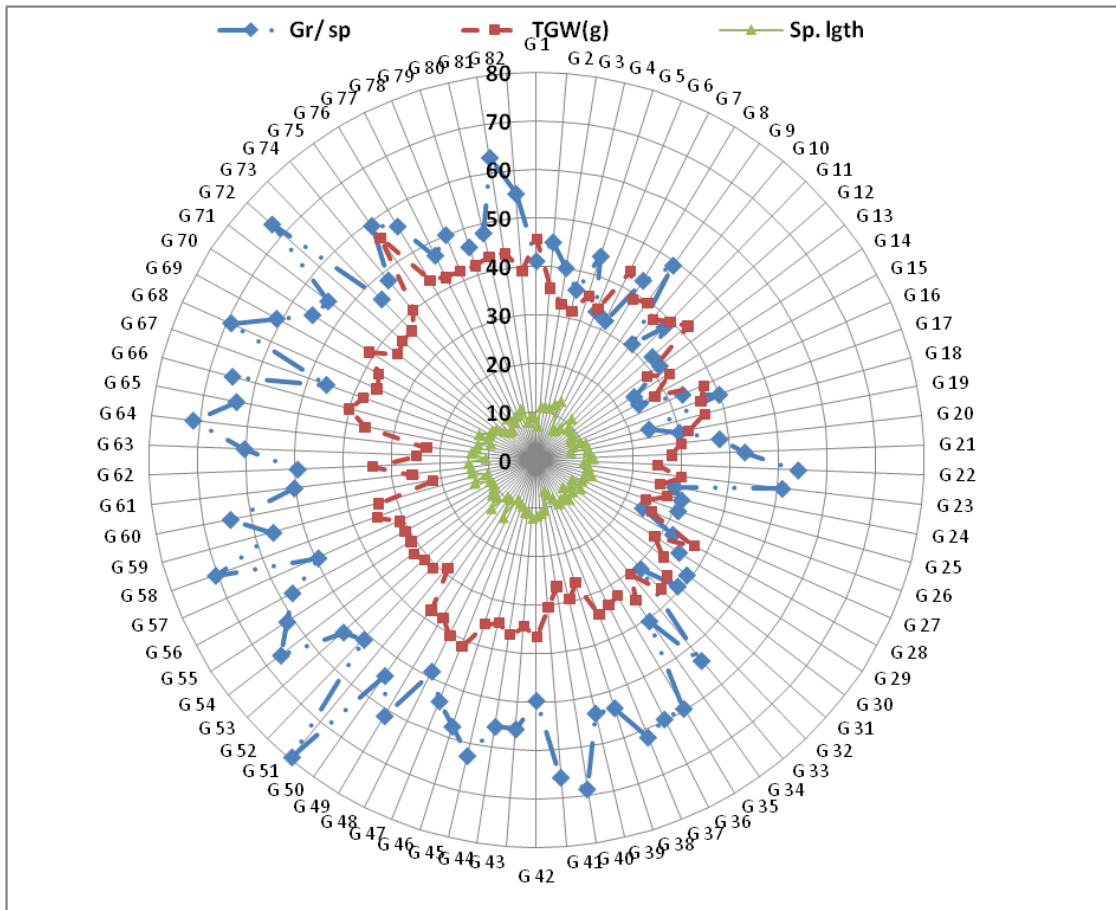


Fig. 2. Variation in grains per spike, thousand grains weight and spike length

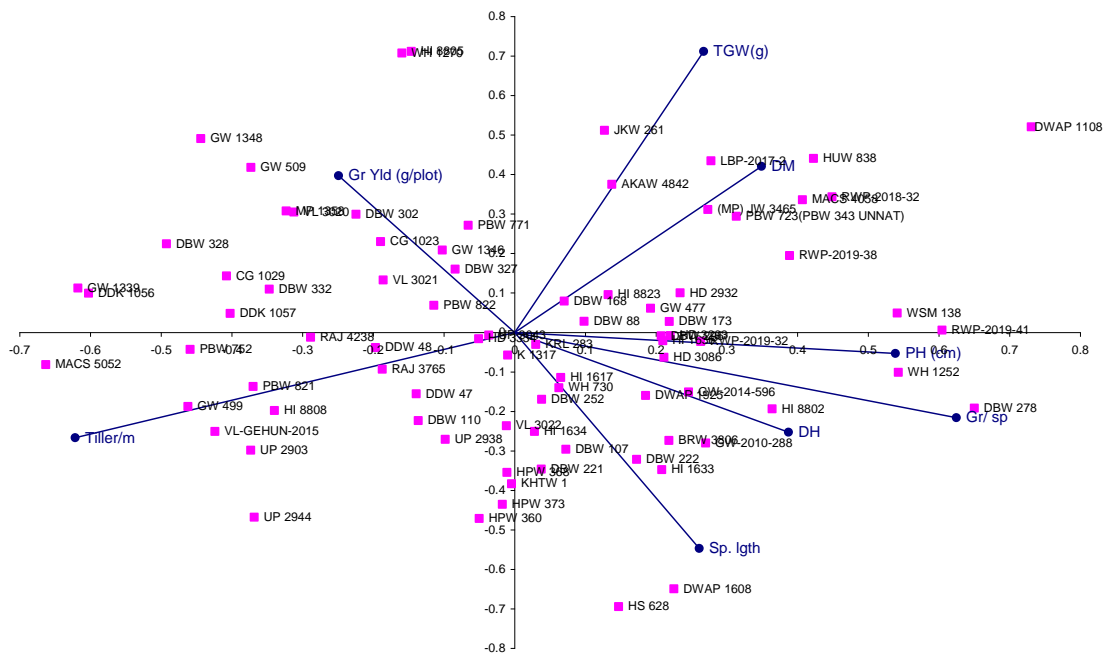


Fig. 3. Genotypes and traits under biplot analysis

Table 3. Loadings of yield related traits as per first two significant principal components

Traits	PC1	PC 2
Days to Heading	0.3121	-0.2194
Days to Maturity	0.2813	0.3652
Plant Height (cm)	0.4339	-0.0461
Tiller per /m	-0.5009	-0.2319
Grains/ spike	0.5034	-0.1876
Thousands Grain Weight (g)	0.2153	0.6185
Spike length	0.2103	-0.4754
Grains Yield (g/plot)	-0.2007	0.3448
% contribution	29.64	21.93

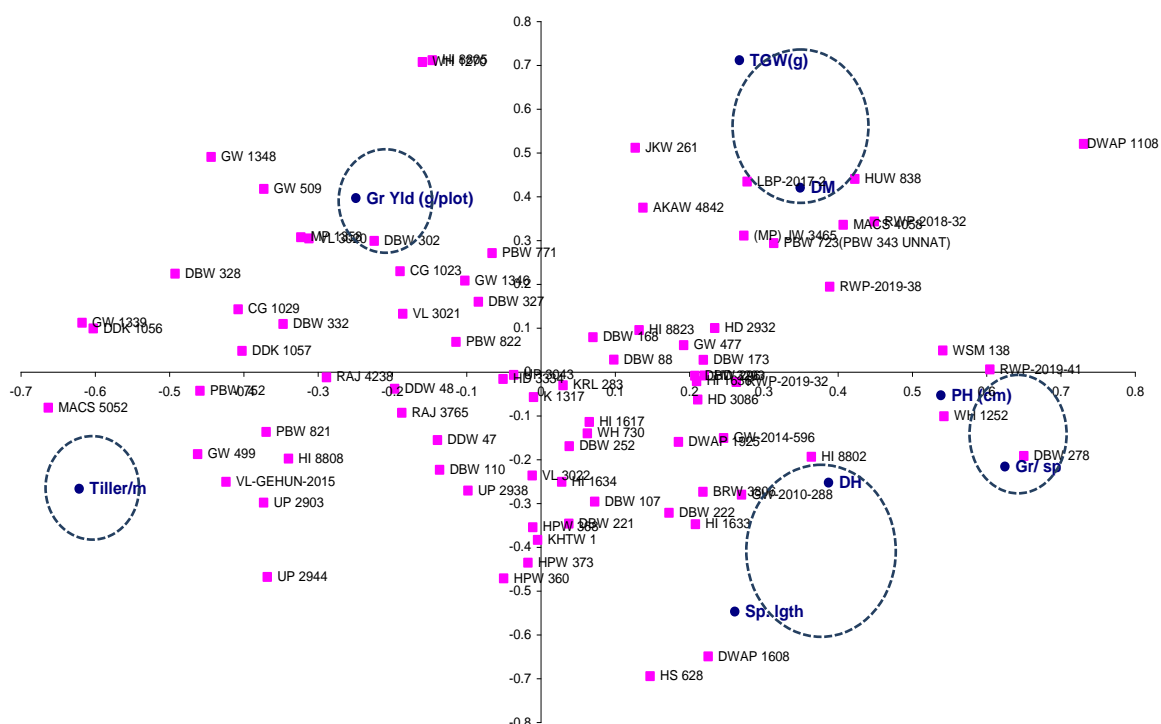


Fig. 4. Association analysis among traits

The high positive correlation of days to heading has been observed for spike length, grains per spike, plant height (Fig. 3). Positive association also observed between days to maturity with thousands grains weight, grains per spike with grain filling period, plant height with spike length and grain yield per plot, TGW. No association had expressed by spike length to grains yield per plot. Nearly similar type of relationship was exhibited by tillers per meter row length with plant height. Negative correlation showed by spike length (cm) with thousands grains weight (gm). Days to maturity with grains yield per plot (gm) also maintained similar type of relationship. Also plant height (cm) exhibited negative relation with to grains yield per plot (gm). The difference

between the biplot origin and genotype position in the biplot is the vector length of the genotype and it is a measure of the distinctiveness of the genotype from other genotypes as reviewed by Smith *et al.*, 2021. DWAP1108, GW1348, DWAP1608, HS 628, MACS 5052 observed far from other wheat genotypes. Mainly three clusters of small and moderate sizes observed in biplot analysis. Tillers per meter row length placed in first cluster as placed in first quadrant. Second cluster comprises of spike length, plant height, days to maturity, days to heading and grains yield per plot placed in second quadrant. Third cluster consisted of TGW, starch, bold grains, tillers per meter were observed in next quadrant (Fig. 4).

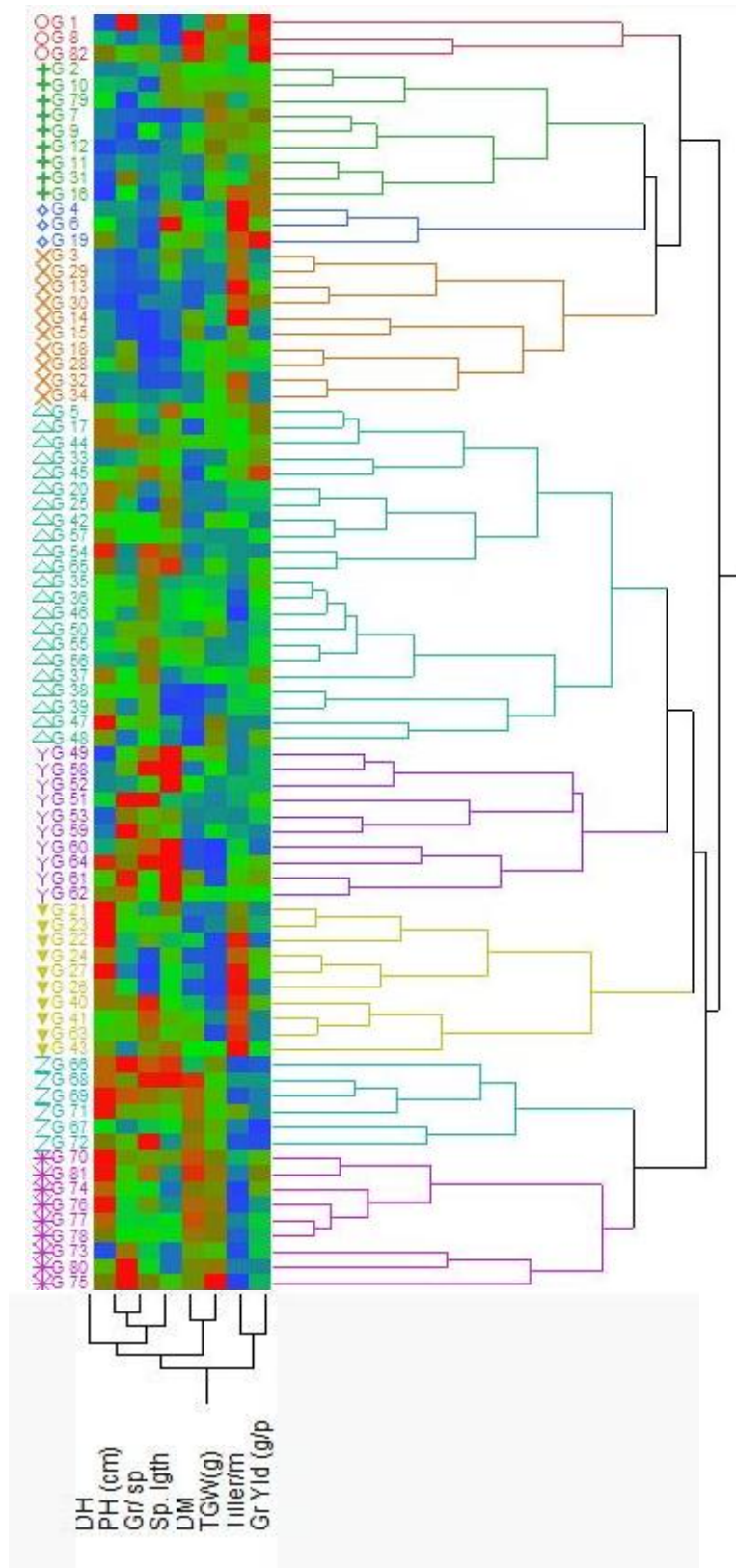


Fig. 5. Multivariate hierarchical clustering of genotypes vis-à-vis traits

3.4 Multivariate Hierarchical Clustering

The appropriate classification of the diverse genotype's based on a set of studied important traits carried out by cluster analysis so as to keep alike genotypes in the similar group. The cluster analysis has no mechanism for distinguishing irrelevant and relevant variables. The Ward's method had been exploited under multivariate clustering of genotypes. Using cluster analysis, 82 wheat cultivars were divided into nine different clusters based on important morphological traits. First group consisted of three genotypes (G1, G8, G82) while the last one contained nine genotypes (G70, G81, G74, G76, G77, G78, G73, G80, G75). Only three genotypes G4, G6, G19 placed in third cluster whereas largest cluster of twenty three genotypes was the fifth one. Six genotypes were observed in second last cluster. Remaining clusters have occupancy of nine, ten, ten, ten genotypes (Fig. 5). Thousands grain weight expressed as point of dissection of studied traits as tillers per meter and grain yield per plot in one side and days to heading, days to maturity, grain per spike, plant height on other side. Identification of wheat genotypes based on simultaneous selection among yield contributing traits will improve the grain yield in wheat [13,14].

4. CONCLUSIONS

From the study, it was found that grain yield per plot had a positive correlation with number of tillers per row length, plant height, and thousand grains weight. These traits are important yield contributing traits. More over the plant height is having negative correlation with grain yield per plot. Therefore the simultaneous selection among yield contributing traits would improve the wheat crop behaviour and the selection of diverse genotypes from this set would be beneficial for a further wheat improvement programme.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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