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Research Article

Agro-morphological diversity in promising wheat genotypes grown under restricted irrigated condition

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Abstract
A set of 36 promising genotypes were evaluated for 33 agro-morphological traits. Sufficient genetic variability was found for almost all the characteristics of wheat. Genetic diversity among nineteen traits of wheat genotypes was estimated using Mahalanobis D^2 analysis and principal component analysis (PCA). Sufficient genetic diversity was observed among the genotypes and grouped genotypes into five clusters by Tocher's method. Cluster I contained the maximum numbers of genotypes (32) and the remaining clusters II, III, IV and V were mono-genotypic. The lowest inter cluster distance was noticed between clusters III and I (260.57) and maximum between Cluster IV and V (891.62). The larger inter-cluster distances between clusters were considered more diverged than those with small distances. The major contributing character towards genetic divergence was found to be grain yield per plant (25.24%), followed by wet gluten (21.59%), chlorophyll content (11.11%) and protein content (10.63%). Principal component (PC) analysis resulted in eight principal components (PCs) having Eigenvalue >1 which contributed 78.67 per cent of the total variability amongst the wheat genotypes assessed for various morpho-physiological traits. The traits with the highest weight in component first were the number of tillers per plant, the number of ear per plant, grain yield per plant and harvest index which explained 15.17 per cent of the total variation. Component 2 was associated with protein content and wet gluten content which account for 13.91 per cent variation. In component 3, traits with highest weight were days to heading, days to maturity, plant height, the number of spikelets per ear, ear length and relative water content which explained 13.41 per cent of the total variation. Similarly, the traits with the highest weight in component 4 were sedimentation value; biological yield per plant in component 5; ear weight and chlorophyll content in component 6; peduncle length, 1000-grain weight and canopy temperature in component 7 was the major contributing traits which account for 8.89, 7.78, 7.20 and 6.31 per cent variability, respectively for the above traits. The result of the present study could be exploited in the planning and execution of a future breeding programme in wheat.

Key words: Principal component, genetic divergence, cluster analysis

INTRODUCTION

Wheat is the second most important cereal crop in the world and contributes substantially to National food security. In India, it is grown in an area of 29.55 m.ha with the production of 101.20 m.t and average national productivity of 3424 kg/ha. Madhya Pradesh is accounting for 16 per cent of production and 18 per cent of the area under cultivation and ranks the third largest wheat producer of India. Madhya Pradesh produces approximately 17.35 m.t wheat in an area of 5.52 m.ha and 3143 kg/ha productivity (Anonymous, 2018-19).

It is supposed that by the year 2025 around 1.8 billion people will face a shortage of water and 65 per cent of the world's population will live under a scarcity of water

(Nezhadahmadi *et al.,* 2013). The reduction in southwest monsoon showers leads to reduce the availability of water for *Rabi* crops in India. Extreme heat and water scarcity is the result of the climate change scenario causing higher soil moisture stress and more evapotranspiration. This stress of soil moisture leads to drought conditions which is one of the most important phenomena that affects crop production and yield. Wheat is very sensitive to high temperature and moisture stress, resulting in low productivity. Under the scenario of climate change, Madhya Pradesh has a need for drought tolerant and low moisture genotypes for sustainable productivity of wheat. There is great scope to increase wheat production in very late sown conditions by breeding more efficient plant types adaptable to restricted irrigated conditions. Therefore, the main objective of the modern plant breeding programme is to develop varieties that are able to use available water more efficiently and increase productivity in arid and semi-arid regions.

For enhancing the yield through genetic recombination, hybridization between selected parents followed by subsequent selection is one of the important approaches to wheat breeding. (Islam, 2004). For the selection of diverse potential genotypes in the segregating generations, several techniques such as cluster analysis, PCA and factor analysis were found most appropriate and frequently used (Eivazi *et al.,* 2007). The major objective of this study is to assess the genetic diversity among wheat genotypes by using cluster analysis and cluster analysis-PCA-based methods for the selection of promising genotypes in advanced or segregating generations. Therefore, this study was executed with the objective of identification of morpho-phenological traits and the extent of genetic variability among diverse wheat genotypes under restricted irrigated conditions.

MATERIALS AND METHODS

A set of 36 promising genotypes (advanced lines along with checks) were planted in randomized completely block design with three replications at Seed Breeding Farm, Department of Plant Breeding and Genetics, College of Agriculture, JNKVV, Jabalpur (Madhya Pradesh) during *Rabi,* 2017-18 (**Table 1**). All the recommended agronomic practices were followed for restricted irrigation conditions, where only one irrigation was given at 45 DAS. At the time of maturity, five plants were randomly selected from each replication. The observations were recorded from the field for various morphological (plant growth habit, foliage color, ear time of emergence, ear waxiness, flag leaf length, ear shape, ear density, awns, awns length, awn color, ear color, grain color, grain shape and seed size) and quantitative traits (days to heading, days to maturity, plant height (cm), the number of tillers per plant, the number of ear per plant, the number of spikelets per ear, ear length (cm), peduncle length (cm), biological yield per plant (g), grain yield per plant (g), thousand grain weight (g), harvest index (%), relative water content (RWC%), canopy temperature (ºC), chlorophyll content index, protein content (%), wet gluten (%) and sedimentation value (ml). The significance of the mean difference between genotypes and different genetic parameters were estimated using statistical analyses. The post-harvest data of wheat lines and their characterization at the different stages of agro-morphological development are important and useful in the characterization, evaluation and identification of best lines. Genetic divergence was estimated by Euclidean cluster analysis and the grouping of the genotypes into clusters following Tocher's method as suggested by Rao (1952). The principal component analysis method explained by Massay (1965) and Jolliffie (1986) was followed in the extraction of the components and it was performed using Xl- Stat software.

RESULTS AND DISCUSSION

Though, more than 70 per cent area under wheat cultivation in Madhya Pradesh is said to have very limited irrigation facilities. However, even under a limited supply of irrigation water, farmers have no choice to grow cereal other than wheat in *Rabi* season due to their preference to grow wheat. Thus, timing the length of irrigation interval with the stages of crop growth might bring about a reduction in the number of irrigations and results in an economic crop yield. In light of these facts, the experiment was conducted to find out the promising genotypes under restricted irrigation with maximum yield.

A wide range of variation was observed for twelve qualitative traits (**Fig. 1**). Genotypes were polymorphic with respect to growth habits and were classified as erect (47.0%), semi erect (39.0%) and spreading (14.0%). Presented data revealed three types of foliage color *viz.,* pale green (11.0%), green (69.0%) and dark green (19.0%). Genotypes further showed variability for ear time of emergence like a medium (75 %) and late (25.0%). There were considerable differences among genotypes for ear waxiness medium (94.0%) and strong (6.0%) and flag leaf length (short and medium). There was large variation for ear shape namely parallel (42.0%), clubbed (39.0%), and fusiform (19.0%); ear density *viz*., lax (8.0%), medium (56.0%), dense (33.0%) and very dense (3.0%). The results of the present study were supported by earlier findings of Satyavart *et al*. (2000), Simic *et al*. (2004), Haljak *et al*. (2008) and Kumar *et al*. (2009. Variation was observed for awn length *viz*., very short (8.0%), short (25.0%), medium (28.0%), long (17.0%) and very long (22.0%). Large variations for awn color such as dull white (17.0%), light brown (61.0%) and dark brown (22.0%) were also observed. Three types of ear color *viz*., white (14.0%), light brown (61.0%) and dark brown (25.0%) were observed in the present study. Motzo and Gunta (2002) and Boudour *et al*. (2004) also observed similar results in wheat germplasm. Sufficient variations were also observed for seed size *viz*., medium, large and very large. The highest frequency was recorded in large (42.0%) seed size, followed by very large (31.0%) and medium (28.0%). A wide range of variations was also revealed with respect to grain shapes such as

Table 1. List of genotypes used in the experiment

S.No.	Genotype name	Pedigree	Origin
1	GW 1350	GW1234/HI8699	SDAU, Vijapur (Gujarat)
2	JW 3173 (C)	HI 1011/WH 965-1	JNKVV, Jabalpur
3	NIDW 1149	NIDW 295 /NIDW 15	MPKV, Niphad (Maharashtra)
4	MP 3508	MP 3051/JW 17	JNKVV, Jabalpur
5	HI 8815	HI 8627/ HI 8663	IARI Regional Station, Indore
6	UAS 470	JUPARE C 200* 2 / KHAPLI / 5 / PLATA6 / GREEN_17 // SNITAN / 4/YAZI_1 / AKAKI4// SOMAT_3 / 3 / AUK / GUIL // GREEN	UAS, Dharwad (Karnataka)
7	HI 8814	HI 8627/ HI 8663	IARI Regional Station, Indore
8	DBW 280	BABAX/LR42//BABAX*2/3/PAVON 7S3, +LR47/4/ND643/ 2* WBLL1 /5/ BABAX/ LR42 // BABAX*2/3/PAVON 7S3,+LR47	IIWBR, Karnal (Haryana)
9	DBW 276	AKAW 4006/F81513/MILAN	IIWBR, Karnal (Haryana)
10	MP 1346	SOKOLL/ROLF07/GW190	JNKVV, Powarkheda
11	GW 512	GW 394 / MP 1156	SDAU, Vijapur (Gujarat)
12	HD 3297	DBW17 / PBW550	IARI, New Delhi
13	MP 1345	BABAX/LR42//BABAX/3/ER2000/4/PAURAQUE#1	JNKVV, Powarkheda
14	HI 1605 (C)	BOW/VEE/5/ND/VG9144//KAL/BB/3/YACO /4/CHIL/6/ C ASKOR/ 3/CROC_1/ AE.SQ (224)// OPATA /7/ PASTOR/ MILAN/ KAUZ/3/BAV92	IARI Regional Station, Indore
15	MPO 1347	GW1189/NIAW79	JNKVV, Powarkheda
16	UAS 466 (C)	Amruth/Bijaga Yellow//AKDW 2997-16	UAS, Dharwad (Karnataka)
17	MACS 4075	MACS 2496 / Raj 4037 // DBW 35	ARI, Pune (Maharashtra)
18	NIAW 3386	BECARD/QUAIU#1	MPKV, Niphad (Maharashtra)
19	CG 1030	KAMB1*2/BRAMBLING/SUJATA	IGKVV, Bilaspur (Chhattisgarh)
20	HD 3296	HI1500/DBW43	IARI, New Delhi
21	AKAW 5082	AKAW-2344 X Raj-4000/AKAW-4103-2-1-5	PDKV, Akola (Maharashtra)
22	MACS 6719	MACS 2846 / UAS 410	ARI, Pune (Maharashtra)
23	DBW 277	NI 5439/ MACS 2496	IIWBR, Karnal (Haryana)
24	HI 1531 (C)	HI 1182/CPAN 1990	IARI Regional Station, Indore
25	HP 1970	DBW-28/DBW-52	IARI Regional Station, Pusa (Bihar)
26	DBW 110 (C)	KIRITAT/4/2*SERI*2/3/KAUZ*2/BOW//KAUZ	IIWBR, Karnal (Haryana)
27	DDW 47	PBW34/RAJ1555//PDW314	IIWBR, Karnal (Haryana)
28	MP 1331	PBW343*2/KUKUNA//KITE	JNKVV, Powarkheda
29	MP 3288 (C)	DOVE/BUC/DL 788-2	JNKVV, Jabalpur
30	HI 8627 (C)	HD 4672/PDW 233	IARI Regional Station, Indore
31	UAS 466	AMRUTH//BIJAGA YELLOW/AKDW299-16	UAS, Dharwad (Karnataka)
32	NIAW 3170	SKOLL/ROLF07	MPKV, Niphad (Maharashtra)
33	MP 3493	35IBWSN159 / DBW17 (35 IBWSN 159= CROC_1/ Ae. Squarrosa (205)//KAUZ/3/ATTILA)	JNKVV, Jabalpur
34	MP 3503	23 ESWYT 18 / DBW 17	JNKVV, Jabalpur
35	MP 3497	35 IBWSN162 / 20 SAWSN 81 (35 IBWSN162 =CROC _1/Ae. Squarrosa (205)//KAUZ/3/MUNIA20 SAWSN 81= FASAN/2*TEPOCA/3/CHEN/ Ae. squarrosa (TAUS)//BCN)	JNKVV, Jabalpur
36	MP 3507	35 IBWSN 159 / 34 IBWSN 23 (35 IBWSN 159= CROC_1/ Ae. Squarrosa (205) //KAUZ/3/ ATTILAH021222 (34 IBWSN 23)= ALTAR84/ AE.SQUARROSA (219)//SERI)	JNKVV, Jabalpur

ovate (17.0%), oblong (75.0%) and elliptical (8.0%). All the genotypes showed a wide range of variability for morphological traits. Qualitative traits are controlled by a few genes with large effects and their expressions are constant across environments and could be due to genotypic differences.

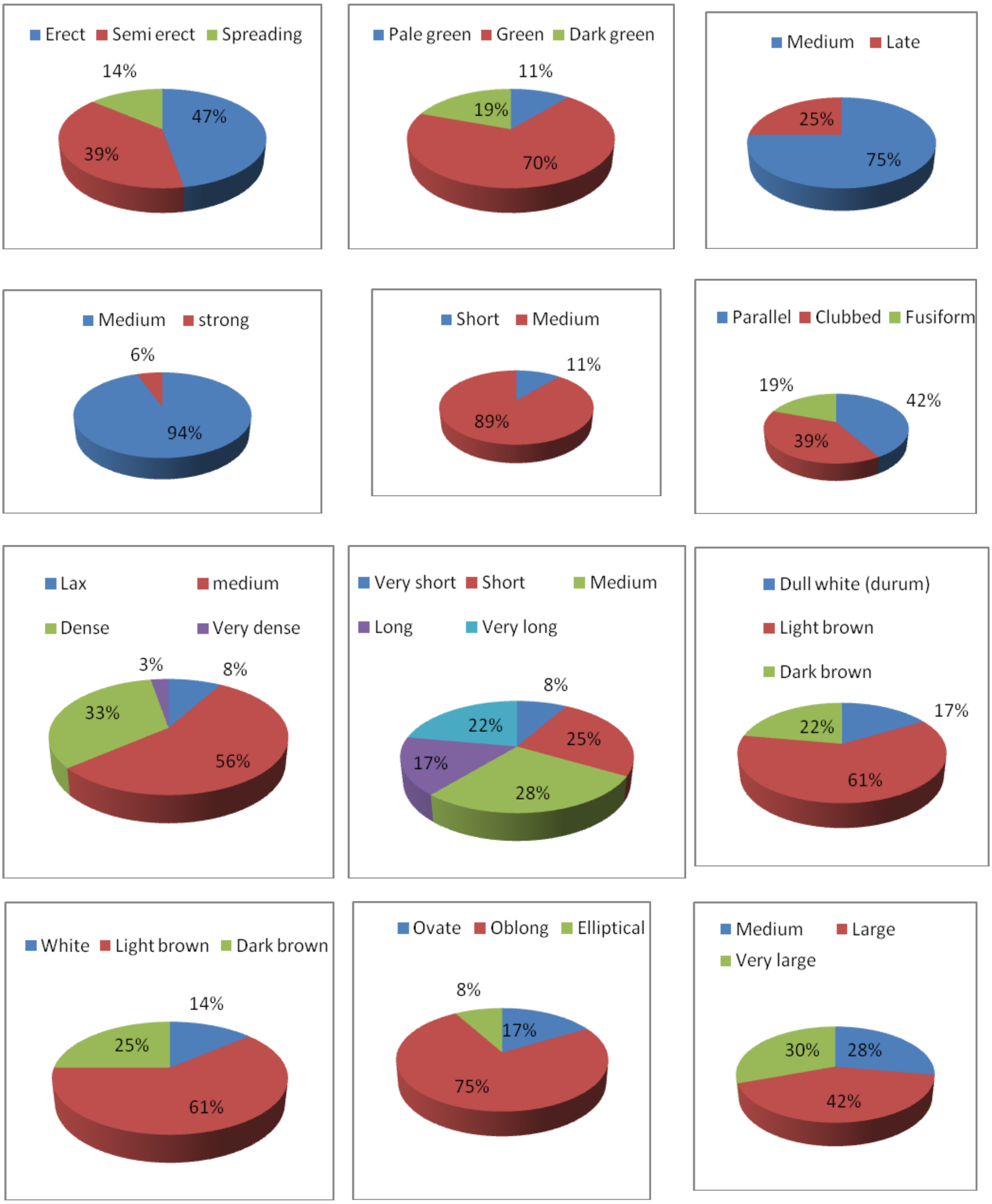

Fig. 1. Variation for growth habit, foliage color, ear time of emergence, ear waxiness, flag leaf length, ear shape, ear density, awns length, awns color, ear color, grain shape & seed size

Descriptive statistics for nineteen quantitative traits demonstrated that means for all traits comprising of their minimum and maximum values, comparable along with the values of standard deviation (**Table 2**). Plant height exhibited a maximum standard deviation (6.60), followed by relative water content (5.47) and harvest index (4.92) showing a maximum variation to the data recorded. Maximum variation was recorded for plant height, relative water content and harvest index, indicating the presence of sufficient variability in the present investigation. The variations present among the wheat genotypes depicted the scope of variation for the improvement in yield and yield related traits by selection.

The genetic divergence analysis is used for the quantification of genetic distance among the selected germplasm and to find out the relative contribution of specific traits towards divergence. These D-square statistics (D^2) developed by Mahalanobis (1936) technique has been used to categorize germplasm on the basis of similarity/ dissimilarity into similar or distinct groups. The extent of diversity present between germplasms determines the extent of improvement gained through selection and hybridization. The more divergent the two germplasms are the more will be the probability of improving through selection and hybridization.

The 36 wheat genotypes used in the study were classified into five groups based on D^2 analysis (**Table 3**). It was indicated that the tested entries were moderately divergent. Maximum numbers of entries i.e. 32 were grouped into cluster I. Other clusters, clusters II, III, IV and V were mono-genotypic having one genotype each. This indicates that the crossing between superior

Table 2. Descriptive statistics seed yield and its attributes in 36 wheat genotypes

Trait	Mean	Minimum	Maximum	Standard deviation
Days to heading	67.53	61.33	76.33	3.35
Days to maturity	116.75	111.33	121.00	2.87
Plant height (cm)	98.41	80.00	112.00	6.6
Number of tillers per plant	7.44	4.33	10.33	1.4
Number of ears per plant	6.68	4.33	10.33	1.24
Number of spikelets per ear	17.85	15.00	21.00	1.68
Ear length (cm)	10.09	6.50	15.23	2.12
Ear weight (g)	2.62	2.10	3.67	0.3
Peduncle length (cm)	15.71	9.00	25.00	3.02
Biological yield per plant (g)	43.66	36.63	48.67	2.96
Grain yield per plant (g)	13.29	9.37	18.17	2.05
1000 grain weight (g)	42.98	36.30	57.70	4.36
Harvest index (%)	30.54	20.80	44.73	4.92
Canopy temperature (ºC)	22.45	18.37	26.60	2.06
Chlorophyll content (SPAD 502)	44.64	34.17	53.37	4.35
Relative water content (%)	66.74	54.20	77.93	5.47
Protein content (%)	13.01	11.67	14.43	0.56
Wet gluten (%)	31.19	26.77	37.47	2.67
Sedimentation value (ml)	48.83	40.93	55.50	4.13

Table 3. Distribution of wheat genotypes into five clusters (Ward)

Cluster Number	Name of genotypes	Number of genotype
I	GW 1350, DBW 110, NIDW 1149, MP 3508, HI 8815, HI 8814, DBW 280, DBW 276, MP 1346, GW 512, HD 3297, HI 1605, MPO 1347, UAS 466, MACS 4075, NIAW 3386, CG 1030, HD 3296, AKAW 5082, MACS 6719, DBW 277, HI 8627, HP 1970, DBW 110, DDW 47, MP 1331, MP 3288, HI 8627, UAS 466, NIAW 3170, MP 3493, MP3497	32
II	MP 1345	1
III	MP 3507	1
IV	UAS 470	1
V	MP 3503	1

genotypes from diverse clusters might provide desirable recombinants for developing high yielding bread wheat varieties. Similarly, Dutamo *et al.* (2015) grouped 68 germplasm into 6 clusters; Phougat *et al.* (2017) grouped 44 genotypes into 5 clusters and Rajshree and Singh (2018) grouped 33 genotypes of bread wheat into 6 clusters.

The average intra and inter cluster distance D^2 values are presented in **Table 4.** Intra-cluster distance ranged from 0.00 to 147.49. The maximum intra cluster D^2 value was present in cluster I (147.49), whereas minimum in cluster II, III, IV and cluster V (0.00), which shows the absence of genetic variability within these clusters.

The inter cluster distance was ranged from 260.57 to 891.62. Cluster IV and V showed maximum inter cluster distance of 891.62, followed by cluster IV and cluster II (668.09), cluster IV and cluster III (562.06), cluster III and cluster II (549.22), cluster III and cluster V (493.91), cluster V and cluster II (329.32), cluster IV and cluster I (337.31), cluster V and cluster II (329.32) and cluster II and cluster I (278.47). Cluster III and cluster I (260.57) reported the lowest inter cluster distance. This result agreed with the findings of Ajmal *et al.* (2013), Khan *et al.* (2015) and Phougat *et al.* (2017). The crosses between the genotypes having maximum distance can be used in breeding programs to achieve heterosis. For the selection of genotypes to be used in a hybridization programmes with the objective to recover new recombinants with desired traits, more emphasis should be given to clusters IV and V.

The mean values of the traits for each cluster were estimated and are presented in **Table 5.** Early maturing and high biological yield per plant is a characteristic feature of cluster II. Cluster III had characteristic features of earliness in days to heading, tall plant type, high number of spikelets per ear, ear length, wet gluten and sedimentation value as compared to other clusters. Cluster IV showed high values of ear weight, 1000-grain weight, chlorophyll content and relative water content.

Table 4. Average Intra and Inter-cluster D^2-Values

Cluster number	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
I	**147.49**	278.47	260.57	337.31	443.63
II		**0.00**	549.22	668.09	329.32
III			**0.00**	562.06	493.91
IV				**0.00**	891.62
V					**0.00**

Table 5. Cluster mean values for different traits

Trait	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Days to heading	67.51	65.00	61.33	68.00	76.33
Days to maturity	117.02	113.00	113.33	118.00	114.00
Plant height (cm)	98.89	80.00	103.30	102.67	92.23
Number of tillers per plant	7.33	7.67	8.33	8.00	9.00
Number of ears per plant	6.61	7.33	7.67	6.00	7.67
Number of spikelets per ear	17.90	16.33	18.33	17.67	17.67
Ear length (cm)	10.26	6.70	11.80	6.83	9.53
Ear weight (g)	2.62	2.53	2.50	2.90	2.30
Peduncle length (cm)	15.65	17.00	13.10	15.27	19.37
Biological yield per plant (g)	43.88	47.33	36.63	43.00	40.63
Grain yield per plant (g)	13.10	13.60	14.50	12.93	18.17
Thousand grain weight (g)	42.78	40.07	39.90	57.70	40.63
Harvest index (%)	29.88	28.73	39.57	30.10	44.73
Canopy temperature (ºC)	22.21	22.40	24.57	24.00	26.60
Chlorophyll content (SPAD Units)	44.96	38.73	43.00	50.20	36.53
Relative water content (%)	67.21	59.00	61.27	77.47	54.20
Protein content (%)	13.05	12.50	12.87	12.07	13.53
Wet glutin (%)	31.34	26.77	32.47	31.20	29.37
Sedimentation value (ml)	48.99	45.17	54.70	47.00	43.50

Cluster V had characteristic features of lateness in heading, high values in terms of number of tillers per plant, the number of ears per plant, peduncle length, harvest index, canopy temperature, protein content and grain yield per plant. The results of the present findings are in agreement with the earlier findings of Ali *et al.* (2008), Kumar *et al.* (2009), Hailegiorgis *et al.* (2011) and Uddin *et al.* (2015). Therefore, intercrossing of genotypes involved in these clusters could be practised for inducing variability in the respective characters and their rationale improvement for increasing grain yield.

The relative contribution of traits towards divergence was depicted in **Fig. 2**. The trait grain yield per plant (25.24%) contributed maximum towards genetic divergence, followed by wet gluten (21.59 %), chlorophyll content (11.11%), protein content (10.63%), peduncle length (5.4%), plant height (5.24%), canopy temperature (4.29), ear length (3.33%), days to maturity (2.86%), 1000 grain weight and sedimentation value (2.86%) and biological yield per plant (2.22%). The remaining traits (number of tillers per plant, days to heading, the number of spikelet per spike, relative water content and harvest index) exhibited very low or negligible contribution towards divergence. There is no contribution of the number of ears per plant and ear weight towards genetic divergence. These results are in compliance with the findings of Aharizad *et al.* (2012), Ajmal *et al.* (2013), Ali *et al.* (2015), Waiker and Arun (2015), Phougat *et al.* (2017), Gurjar and Marker (2018) and Rajshree and Singh (2018).

The principal component analysis reflects the importance of the largest contributor to the total variation at each axis for differentiation (Sharma, 2018). Eight principal components, out of 19 extracted, having eigenvalues greater than one were retained and contributed 78.67 per cent variation among 36 wheat genotypes for all parameters (**Table 6**). It was noted that PC 1 contributed 15.17 per cent, while, PC 2, PC 3, PC 4, PC 5, PC 6, PC 7 and PC 8 exhibited 13.91, 13.41, 8.89, 7.78, 7.20, 6.31 and 5.97 per cent variability, respectively for the studied traits.

The data depicted in **Table 6** showed that most of the yield contributing traits were found in the first principal component of the number of tillers per plant, the number of ears per plant, grain yield per plant and harvest index; whereas protein content and wet gluten content contributed more in the second PC. Likewise, days to heading, days to maturity, plant height, the number of spikelets per ear, ear length and relative water content in the third PC; sedimentation value in the fourth PC; biological yield per plant in the fifth PC; ear weight and chlorophyll content in the sixth PC and peduncle length, 1000-grain weight and canopy temperature in the seventh PC were the major contributing traits in each principal components. Similar findings of grouping wheat genotypes by the principal component analysis were reported by Fellahi *et al.* (2013), Getachew *et al.* (2017) and Sharma *et al.* (2018).

From the present investigation, it can be concluded that considerable genetic variation among genotypes for all the studied traits were present. For restricted irrigated conditions, the promising high yielding genotypes *viz*., NIAW 3386, MACS 6719 and MACS 4075 were

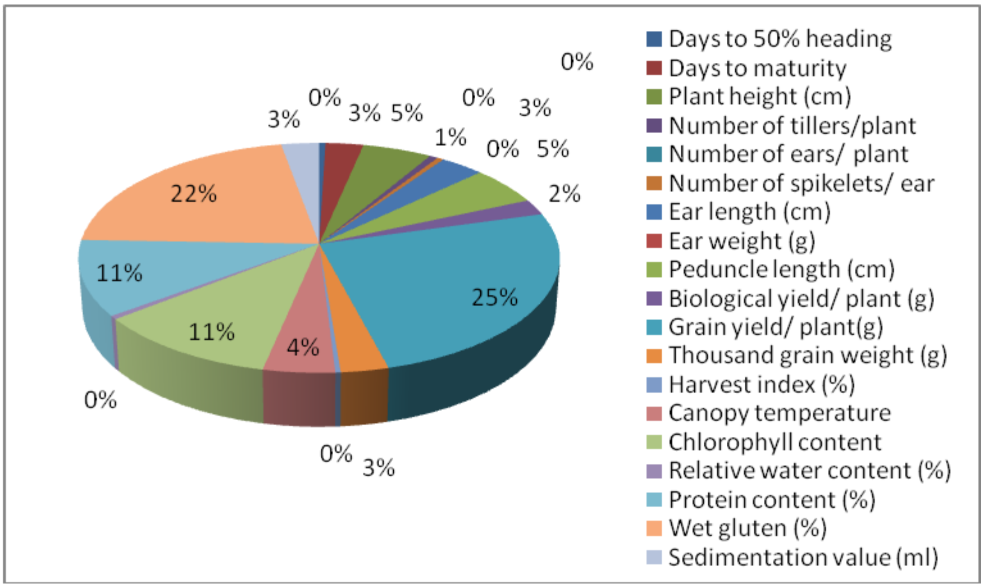

Fig. 2. Per cent contribution of the individual traits towards divergence

Table 6. Principal components for 36 genotypes on 19 traits

Variables	PCI	PC2	PC3	PC4	PC5	PC6	PC7
Days to heading	0.035	0.334	0.669	-0.104	0.563	-0.033	-0.009
Days to maturity	-0.079	0.375	0.724	-0.125	0.423	0.184	-0.065
Plant height	-0.108	-0.029	0.481	-0.284	-0.464	-0.041	-0.075
Number of tillers per plant	0.797	-0.168	0.365	0.084	-0.082	-0.120	-0.321
Number of ears per plant	0.847	-0.183	0.169	0.169	-0.059	-0.091	-0.269
Number of spikelets per ear	0.093	0.160	0.604	0.150	-0.261	-0.246	0.129
Ear length	-0.022	0.280	0.437	-0.467	-0.313	-0.189	0.108
Ear weight	-0.113	0.312	-0.263	-0.390	-0.011	0.580	-0.042
Peduncle length	-0.039	-0.455	0.058	0.399	0.157	-0.358	0.510
Biological yield per plant	0.095	-0.524	0.047	0.260	0.554	-0.236	0.197
Grain yield per plant	0.851	0.148	-0.234	0.039	0.133	0.231	0.250
Thousand grain weight	0.068	-0.487	0.372	-0.167	-0.285	0.183	0.518
Harvest index	0.774	0.439	-0.214	-0.085	-0.032	0.046	0.154
Canopy temperature	0.288	0.418	-0.153	-0.338	-0.172	-0.020	0.474
Chlorophyll content	0.002	-0.314	0.297	0.182	-0.518	0.396	-0.257
Relative water content	-0.190	0.172	0.540	0.277	-0.052	0.203	0.180
Protein content	-0.126	0.596	-0.311	0.455	-0.109	-0.235	0.015
Wet gluten	-0.104	0.504	0.107	0.421	-0.277	0.121	0.080
Sedimentation value	-0.057	0.530	0.042	0.531	-0.146	0.290	0.016
Eigen Value	2.88	2.64	2.55	1.69	1.47	1.36	1.19
Individual percentage	15.17	13.91	13.41	8.89	7.78	7.20	6.31
Cumulative Percentage	15.17	29.09	42.51	51.40	59.19	66.39	72.70

identified. Maximum variations (78.67 %) were explained by the first eight principal components and the major yield contributing traits were associated with the first principal component. Overall, the existence of substantial differences for agro-morphological and yield related traits, positive and significant association among agronomic traits with seed yield among the genotypes in this study, shows that the studied genotypes can be exploited for future breeding programmes of wheat.

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