

Research Article



Use of Multivariate Analysis in Determining Characteristics for Grain Yield Selection in Wheat

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Abstract | Multivariate analysis was used to assess the diversity in 176 wheat genotypes for morpho-physiological traits. Simple correlation coefficients indicated that grain weight had a significant positive relationship with residual transpiration, osmotic adjustment, cell membrane stability, flag leaf weight, specific flag leaf weight, while negatively correlated with specific flag leaf area. These results indicated the importance of physiological traits and their positive influence on grain weight. Multivariate techniques, including factor analysis (FA) and cluster analysis, indicated that the magnitude of variability existing in the gene pool was satisfactory for initiating a breeding plan. Relative water content, cell membrane stability, osmotic adjustment and grain yield per plant were major contributors towards variability. Grain yield per plant was closely linked to relative water content, cell membrane stability and specific flag leaf area. Eight clusters were formed through cluster analysis, and greater genetic distance was detected among the members of cluster 6 and cluster 8 and cluster 7 and 8. Members of these two clusters can be utilised in transgressive breeding.

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Introduction

Breeding activities aiming towards increase in productivity can benefit from a thorough understanding of the genetic variability within a set of elite and wild germplasm accessions. This knowledge permits a more precise selection of the genotypes to be crossed to produce segregating populations helpful for breeding purposes and (or) to estimate the genetic nature of morpho-physiological parameters (Vuylsteke et al., 2000; Reif et al., 2003a and 2003b; Melchinger et al., 2003; Parrisaeux and Bernardo, 2004).

Various numerical taxonomic methods are being uti-

lized to classify and to determine the nature of genetic variability in wheat germplasm (Maccaferri et al., 2007). A number of suitable methods like principal component analysis, factor analysis and cluster analysis are presently available for the selection of parent, detection of genetic variability, centre of origin, study of interaction among the environments and tracking the course to crop evolution (Mostafa et al., 2011). Hierarchical clustering techniques have long been the most popular clustering method with Ward's method and average linkage probably being the best available (Milligan, 1980). Even though hierarchical techniques have been widely used, they do offer several distinct disadvantages that affect any of their cluster

solutions. Non-hierarchical methods have gained increased acceptability and usage but several shortcomings can significantly affect their use in many types of applications (Hair et al., 2006). With each approach having distinct advantages and disadvantages, it has been proposed to use both methods (hierarchical and non-hierarchical) to gain the benefits of each (Milligan, 1980; Hair et al., 2006). In addition, assessment of genetic distance is one of most suitable tools for selection of parents in a wheat crossing scheme. Selection of suitable parents is necessary for hybridization schemes to increase the genetic variability for possible yield enhancement (Mostafa et al., 2011). Aims of this research work include establishing the amount of genetic variability and interrelationships among the gene pool, screening the gene pool for morpho-physiological traits and identifying best parents to initiate a hybridization programme.

Materials and Methods

Experimental material

One hundred and seventy six wheat genotypes were evaluated for various quantitative traits at Barani Agricultural Research Station, Fatehjang, Pakistan (Easting 43°-28 minutes, Northing 37°-15 minutes, elevation 504.5m above sea level and Av. Annual Rainfall 870mm) during Rabi seasons of 07-08 and 08-09 under rainfed conditions. The germplasm included commercial varieties of Pakistan, introduced varieties, land races, advanced lines developed at Barani Agricultural Research Station, Fatehjang, Pakistan and some wide crosses selected from CIMMYT material.

Field experiment

The experiment was grown for two years in conserved moisture with lentil-fallow-wheat rotation under rainfed conditions. The field was ploughed three times to prepare the seed bed. First ploughing was done with mould board plough during monsoon (July-August). At the end of monsoon the field was ploughed with cultivator to seal the ridges formed by mould board plough and to conserve moisture. At the end of October, the crop was sown on conserved moisture after ploughing along with planking. The fertilizers in the form of urea and DAP was broadcasted at the rate of 100 kg/acre. Urea was applied in two doses. Half dose of urea was applied at sowing and other half at jointing stage after the rainfall. The experiment was laid out in an augmented design with check repeated after every 20 entries. Two meter long rows of each entry were planted. Seed rate was kept 50 kg/acre. The rows were 30 cm apart. Weedicide (Buctril Super) was

sprayed at tillering stage after rainfall to control the weeds.

Data collection

The data were recorded from 10 randomly selected guarded plants. Parameters recorded at booting included residual transpiration, relative water content, osmotic adjustment, cell membrane stability, flag leaf area (cm²), specific flag leaf area, flag leaf weight (g) and specific flag leaf weight on individual plant basis from mother shoot of selected plants. After threshing data regarding 1000-grain weight (g) and grain yield per plant (g) were recorded.

Statistical analysis

The data recorded over two years were averaged and used to compute mean values. Pearson's correlation coefficients were worked out between the traits following Snedecor (1956) with the help of SPSS 20. Multivariate techniques including factor analysis (FA) and cluster analysis were employed using statistical software 'Statistica/w 6.0.' and Past version 2.17c (Hammer et al., 2001). As measurement scales of various traits were not identical means the data were standardized as Hair et al. (2006). Then dendrogram was constructed utilizing Ward's method based on squared Euclidean distance (Kumar et al., 2009).

Results and Discussion

One hundred and seventy six wheat genotypes were used to assess the relationship among various traits and to quantify the diversity residing among the gene pool. Basic statistics for various morpho-physiological traits are presented in Table 1.

Table 1: Descriptive statistics for the estimated variables in 176 spring wheat genotypes

Parameters	Min	Max	Mean	Standard deviation
Residual transpiration (g H ₂ O/min/cm ² /10 ⁵)	0.001	0.094	0.02	0.01
Relative water content (%)	32.59	95.63	70.18	7.92
Osmotic adjustment (g)	0.02	1.90	0.59	0.25
Cell membrane stability (%)	14.69	36.45	26.31	3.78
Flag leaf area (cm ²)	11.06	21.99	16.16	2.08
Specific flag leaf area (g)	12.46	42.35	23.20	4.27
Flag leaf weight (g)	0.34	1.61	0.72	0.19
Specific flag leaf weight	0.02	0.08	0.04	0.01
1000-grain weight (g)	27.32	56.14	40.30	5.06
Grain yield per plant (g)	32.40	178.0	101.7	26.69

Table 2: Simple correlation coefficients among morpho-physiological traits in spring wheat genotypes

	RT	RWC	OA	CMS	FLA	SLA	FLW	SLW	GWt
RWC	-0.124								
OA	0.125*	-0.608**							
CMS	0.021	0.097	-0.056						
FLA	0.025	0.214**	0.246**	-0.018					
SLA	0.044	-0.046	-0.526**	0.040	-0.262**				
FLW	0.066	0.116	0.583**	-0.017	0.712**	-0.815**			
SLW	0.048	-0.007	0.571**	-0.059	0.248**	-0.905**	0.808**		
GWt	0.296**	0.007	0.164*	0.196**	0.071	-0.142*	0.186**	0.127*	
GY	0.030	-0.016	0.023	0.053	-0.048	-0.010	-0.038	-0.004	0.009

* Significant at $p = 0.05$, ** Significant at $p = 0.01$; RT = Residual Transpiration; RWC= Relative Water Content; OA = Osmotic Adjustment; CMS = Cell Membrane Stability; FLA = Flag Leaf Area; SLA = Specific Flag Leaf Area; FLW = Flag Leaf Weight; SLW = Specific Flag Leaf Weight; 1000GWt =1000-Grain Weight; GY = Grain Yield per Plant

Correlation studies provide directional model for the selection of complex traits and is important to select an ideal plant types. Direct selection for complex parameters could be misleading, indirect selection via related parameters with simple inheritance might be more effective (Toker and Cigirgan, 2004). Residual transpiration displayed significant positive association with osmotic adjustment, while a highly significant positive association was observed among 1000-grain weight (Table 2). Higher grain weight may be selected with the help of relatively simple traits like residual transpiration and osmotic adjustment in a breeding programme. Since osmotic adjustment depicted significant positive connection with flag leaf area, flag leaf weight, specific flag leaf weight and 1000-grain weight, these traits may be selected indirectly via osmotic adjustment. However, Živčák et al. (2009) reported that osmotic adjustment had high level of correlation with grain yield. Significant correlations of osmotic adjustment with so many important traits indicated the importance of its role in moulding these traits and their subsequent selection in a breeding programme. Highly significant positive relationship was witnessed between 1000-grain weight and cell membrane stability. Highly significant positive association was also observed among flag leaf weight, specific flag leaf weight and 1000-grain weight. Highly significant negative association of flag leaf weight and grain yield was reported by Mohammadi et al. (2011) in durum wheat. Specific flag leaf weight displayed significant positive association with 1000-grain weight. It can be used as indirect selection principle for grain weight. Grain weight displayed positive significant correlation with residual transpiration, osmotic adjustment, cell membrane stability, flag leaf weight, specific flag leaf weight. These results indicated the importance of the physiological traits and their positive influence

on grain weight. Based on these results physiological traits may be recommended as an indirect measure to enhance grain weight. Mohammadi et al. (2011) reported that 1000-grain weight and grain yield had positive significant association. Simple correlation coefficient could not detect any relationship for grain yield per plant. It was necessary to utilize other statistical techniques to confirm these results or to detect probable relationship with grain yield per plant.

Table 3: Factors analysis for morpho-physiological traits in spring wheat genotypes

	Factor 1	Factor 2	Factor 3	Factor 4
Eigen value	3.42	1.57	1.34	1.03
Total variance %	34.19	15.71	13.43	10.31
Cumulative eigen value	3.42	4.99	6.33	7.36
Cumulative %	34.19	49.89	63.32	73.63

Factor analysis

The factor analysis developed by Cattell (1965), reduces a large amount of correlated variables to a few variables called factors (Leilah and Al-Khateeb, 2005). Ten morpho-physiological parameters recorded in 176 wheat genotypes were grouped into 10 factors. Four out of 10 factors were selected as their eigen values were greater than 1, which is usually considered as the criterion of significance. The scree plot graphs eigen value against the factor number, from forth factor onwards, it could be observed that the line is becoming straighter, indicating that each succeeding factor is amounting for lesser and lesser magnitude of variability (Figure 1). However, following Kaiser (1958) correction only those factors were kept whose eigen values was greater than 1. Factor 1 had the highest eigen value (3.42), the value decreased gradually in the

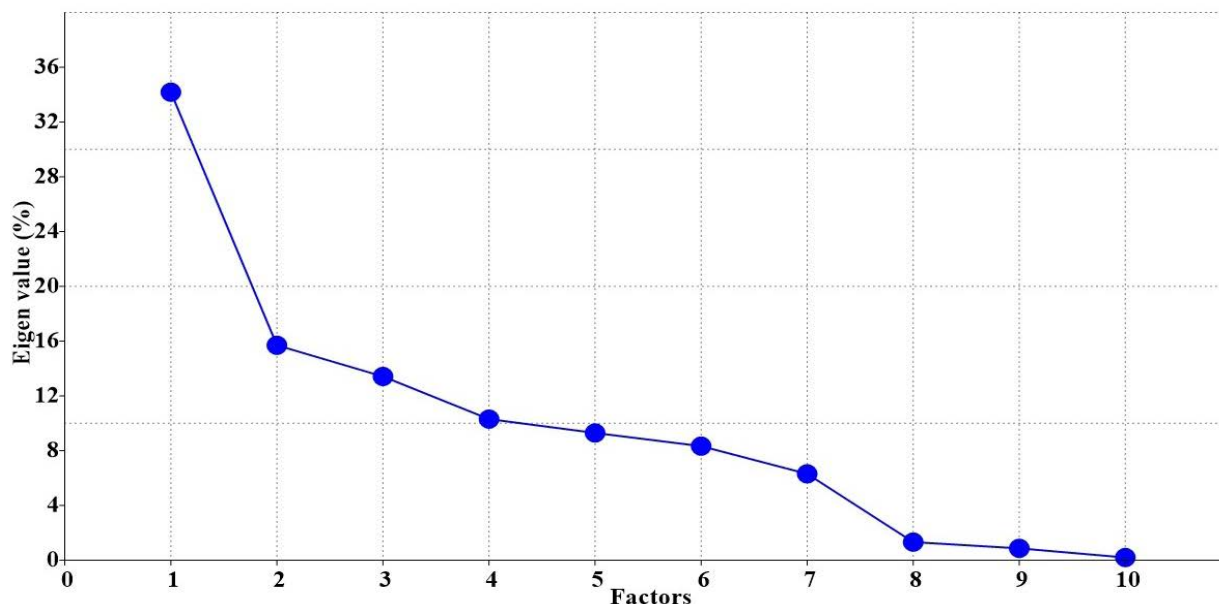


Figure 1: Scree plot diagram of eigen values constructed on 10 morpho-physiological parameters recorded in 176 spring wheat genotypes

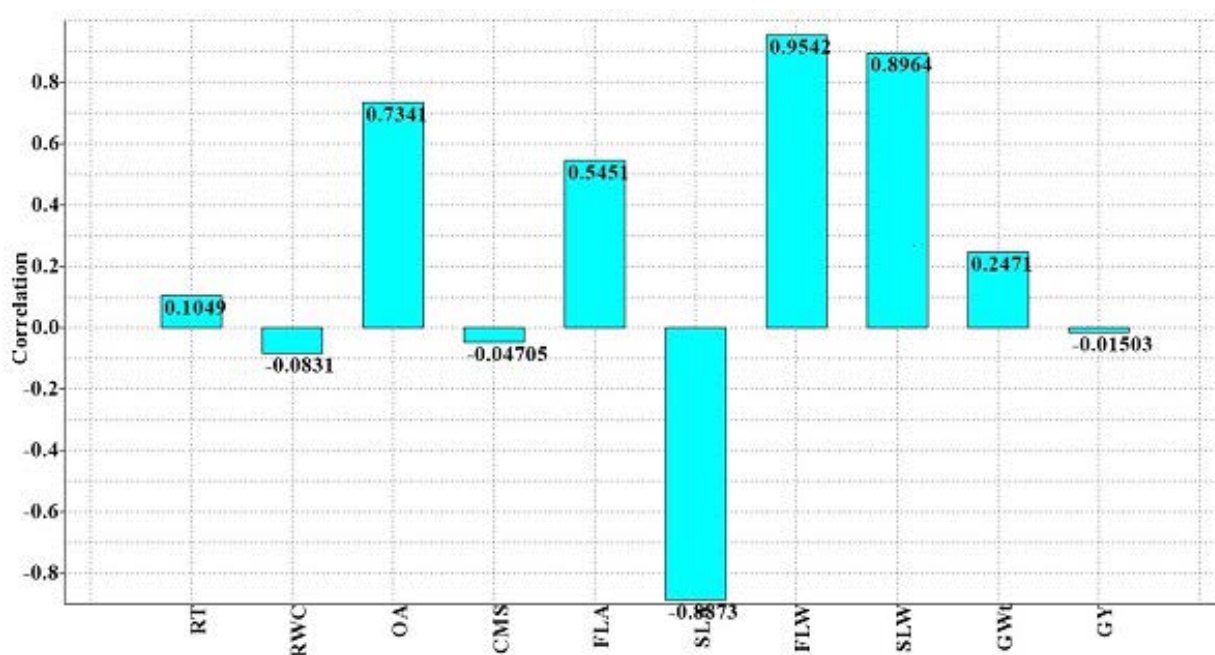


Figure 2: Factor loadings of factor 1 assessed from 10 morpho-physiological traits in spring wheat genotypes

subsequent factors. Highest total variance was observed in factor 1 (34.19%) then value decreased gradually in the succeeding factors. The four factors accumulated 73.63% of the total variability for the ten traits (Table 3).

The commonalities (Table 4) accounted for by all the factors taken together were found between 0.49 (CMS) and 0.96 (flag leaf weight). The first factor (Figure 2) which explained 34.19% of the variability, increased with increasing flag leaf weight (0.95), specific flag leaf weight (0.90), osmotic adjustment (0.73)

and flag leaf area (0.55). Hence, the suggested name for this factor is “Flag leaf”. Specific flag leaf area (-0.89) had negative load on this factor. Negative relationship between these traits was also depicted in correlation analysis. The second factor (Figure 3) which explained 15.71% of the total variability, increased with relative water content (0.91) hence named as “relative water content”. Osmotic adjustment (-0.57) exerted a negative load on this factor, indicating a negative relationship with relative water content. Correlation analysis confirmed this negative association. The third factor (Figure 4) explained 13.43% of the total

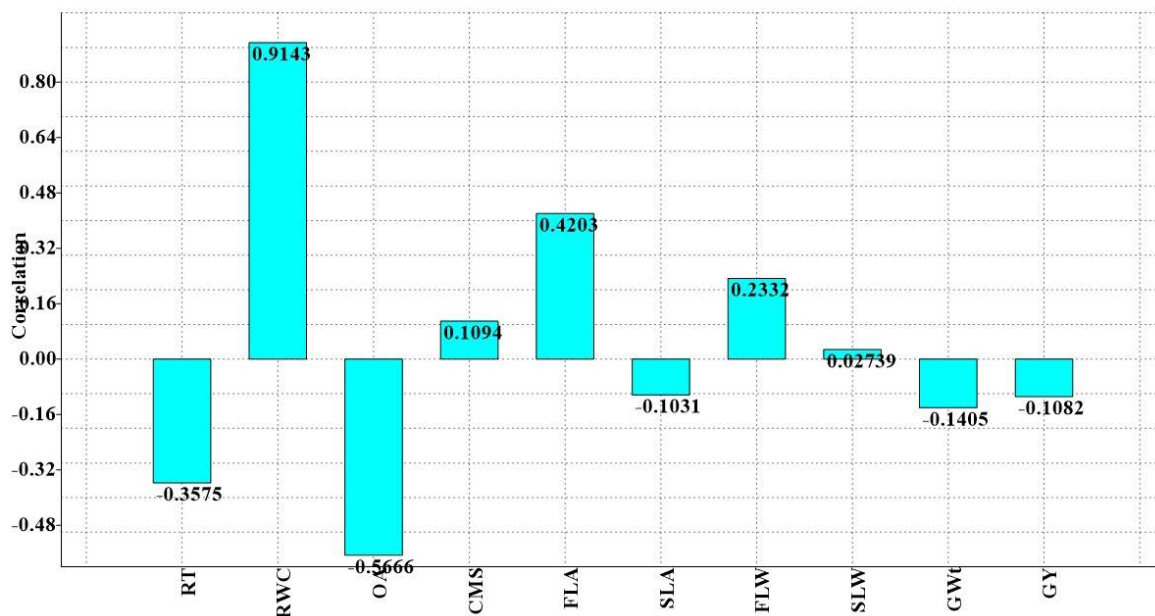


Figure 3: Factor loadings of factor 2 assessed from 10 morpho-physiological traits in spring wheat genotypes

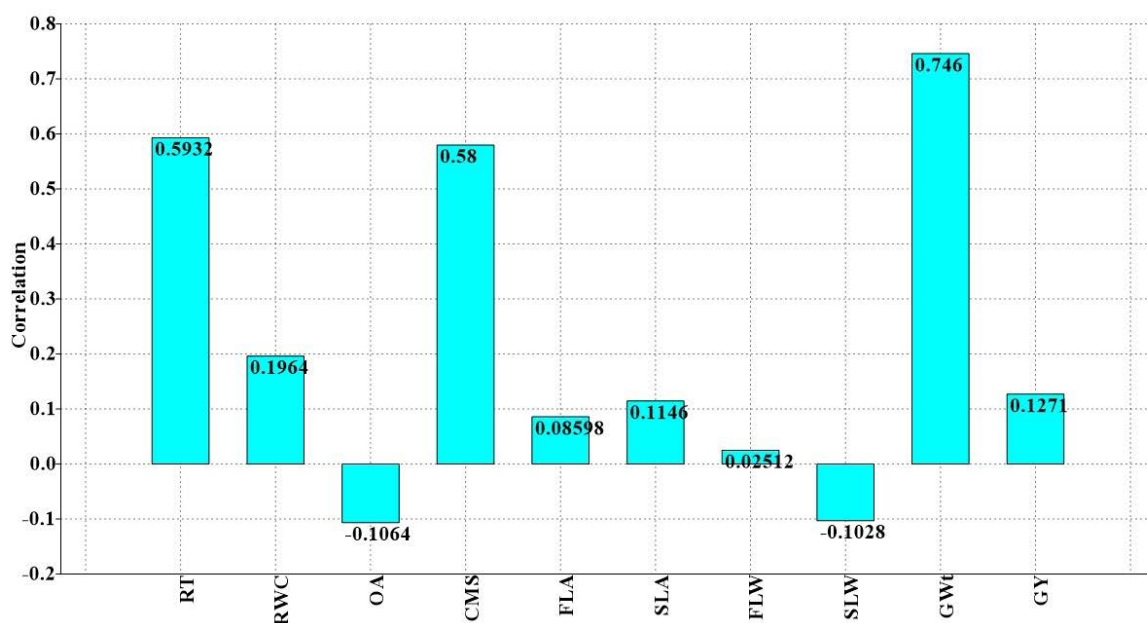


Figure 4: Factor loadings of factor 3 assessed from 10 morpho-physiological traits in spring wheat genotypes

variability. Thousand grain weight (0.75) and cell membrane stability (0.58) exerted maximum load on third factor. This factor is viewed as a measure of “grain weight”. Positive relationship between 1000-grain weight and cell membrane stability was depicted by simple correlation coefficient analysis. Residual transpiration (-0.59) exercised negative load on this factor. The fourth factor (Figure 5) included grain yield per plant (0.80) which accounted for 10.31% of the total variability, hence considered as a measure of “grain yield”. Residual transpiration and flag leaf area showed negative load on this factor. A short summary of factors loading for morpho-physiological traits in current studies is presented in Table

5. The data showed that specific flag leaf weight, flag leaf weight, osmotic adjustment, specific flag leaf area, relative water content, 1000-grain weight and grain yield per plant had the highest communalities, their contribution to variability was relatively higher in the gene pool. Maximum communalities for spike length, number of spikes per meter square, harvest index, biological yield and grain weight per spike were observed by Leilah and Al-Khateeb, (2005) these traits showed maximum role in the improvement of grain yield in wheat.

Cluster analysis

Numerous authors have criticized variable based ap

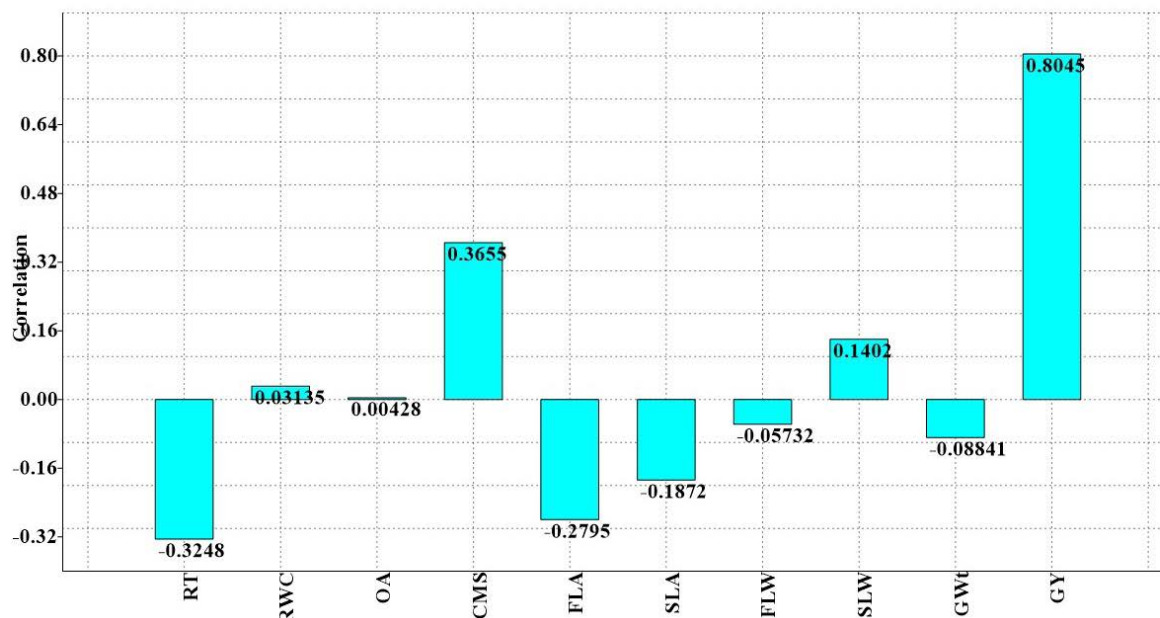


Figure 5: Factor loadings of factor 4 assessed from 10 morpho-physiological traits in spring wheat genotypes

Table 4: Factor loadings and communalities of morpho-physiological traits in spring wheat genotypes

Variables	Factor 1	Factor 2	Factor 3	Factor 4	Communalities
RT	0.10	-0.36	-0.59	-0.32	0.59
RWC	-0.08	0.91	-0.20	0.03	0.88
OA	0.73	-0.57	0.11	0.01	0.87
CMS	-0.05	0.11	0.58	0.37	0.49
FLA	0.55	0.42	0.09	-0.28	0.57
SLA	-0.89	-0.10	0.11	-0.19	0.85
FLW	0.95	0.23	0.03	-0.06	0.96
SLW	0.90	0.03	-0.10	0.14	0.84
1000GWt	0.25	-0.14	0.75	-0.09	0.65
GY	-0.02	-0.11	0.13	0.80	0.67

RT = Residual Transpiration; RWC= Relative Water Content; OA = Osmotic Adjustment; CMS = Cell Membrane Stability; FLA = Flag Leaf Area; SLA = Specific Flag Leaf Area; FLW = Flag Leaf Weight; SLW = Specific Flag Leaf Weight; 1000GWt=1000-Grain Weight; GY = Grain Yield per Plant

proach which usually utilizes the application of regression analysis and assume causal homogeneity among the parameters (Abbott, 2001; Ragin, 2006; Cooper, 2011; Dymnicki and Henry, 2011). In reply to this criticism, scientists have devised newer case-based methods (Byrne and Ragin, 2009), for instance cluster analysis, which recognizes and explains groups of cases elaborated by resemblances or differences on several dimensionalities. It forms groups that increases within group resemblance and reduces between-group resemblance (Henry et al., 2005). Gorman-Smith et al. (1998) used a two-step clustering

method i.e., hierarchical Cluster analysis followed by K-means non-hierarchical splitting.

Table 5: Summary of factors loading, percentage of the variance explained by a factor and factor name in factor analysis for 10 morpho-physiological traits in wheat

Characters	Loading	Variance (%)	Suggested factor name
Factor 1			
Flag leaf weight	0.95	34.19	Flag leaf
Specific flag leaf weight	0.90		
Osmotic adjustment	0.73		
Flag leaf area	0.55		
Specific flag leaf area	-0.89		
Factor 2			
Relative water content	0.91	15.71	Water content
Factor 3			
1000-grain weight	0.75	13.43	Grain weight
Residual transpiration	-0.59		
Cell membrane stability	0.58		
Factor 4			
Grain yield per plant	0.80	10.31	Grain yield

Hierarchical method

The cluster diagram showed 3 main clusters (Figure 6). Cluster 1 included osmotic adjustment, flag leaf area, flag leaf weight and specific flag leaf weight showing close relationship. Due to lowest linkage distance flag leaf weight and specific flag leaf weight were closest of all the ten traits. Osmotic adjustment

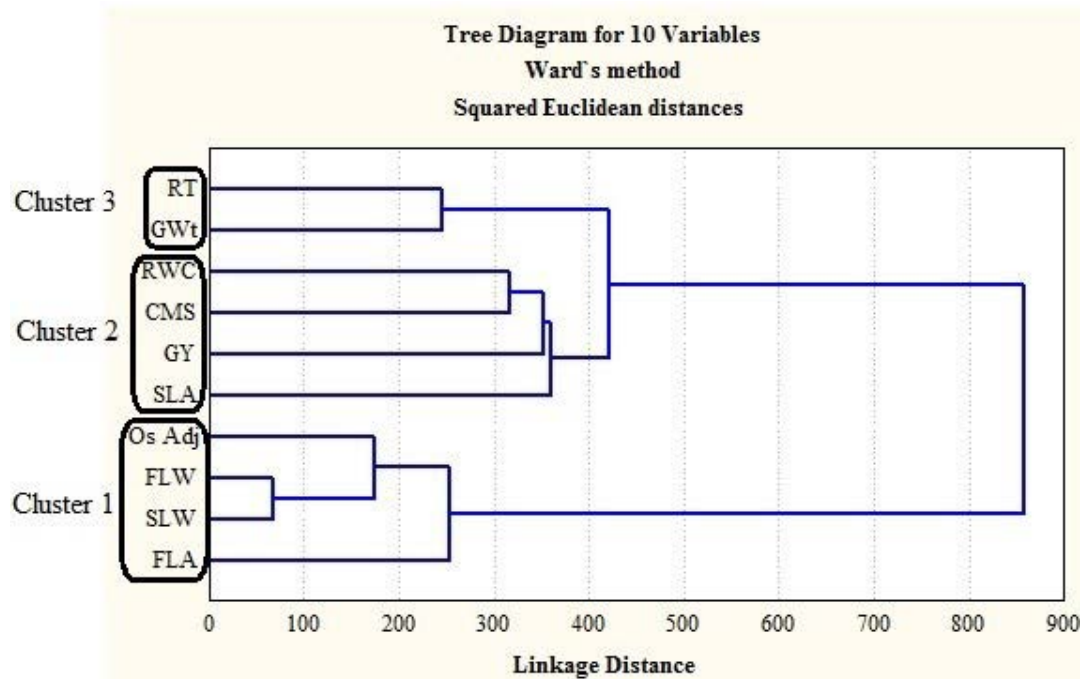


Figure 6: Tree diagram based on 10 morpho-physiological traits in spring wheat genotypes using Ward's method

Table 6: Analysis of variance as revealed by K-means clustering for 10 morpho-physiological traits in various clusters

Parameters	Between cluster SS	d f	Within cluster SS	d f	F-value	Probability
RT	0.00	7	0.02	168	0.87	0.53
RWC	4612.56	7	6356.46	168	17.42**	0.00
OA	1.92	7	8.92	168	5.16**	0.00
CMS	233.19	7	2262.82	168	2.47*	0.02
FLA	37.49	7	716.69	168	1.26	0.28
SLA	41.46	7	3154.19	168	0.32	0.95
FLW	0.10	7	5.94	168	0.42	0.89
SLW	0.00	7	0.01	168	0.62	0.74
1000GW _t	274.36	7	4207.02	168	1.57	0.15
GY	117402.06	7	7278.42	168	387.12**	0.00

RT = Residual Transpiration; **RWC**= Relative Water Content; **OA** = Osmotic Adjustment; **CMS** = Cell Membrane Stability; **FLA** = Flag Leaf Area; **SLA** = Specific Flag Leaf Area; **FLW** = Flag Leaf Weight; **SLW** = Specific Flag Leaf Weight; **1000GW_t** =1000-Grain Weight; **GY** = Grain Yield per Plant

and flag leaf area were outliers in this cluster. Second cluster included relative water content, cell membrane stability, grain yield per plant and specific flag leaf area. This cluster emphasised the importance of physiological traits in indirect selection of a complex trait like grain yield. These physiological traits are relatively easy to analyse and select. Other statistical techniques like correlation analysis and factor analysis could not explain the relationship among grain yield per plant and other traits with such clarity as cluster analysis, although factor analysis showed some relationships but the correlation values were too small and indistinctive. Third cluster exhibited relation between grain weight and residual transpiration. A strong correla-

tion was also observed between the two traits by correlation and factor analysis.

Tree diagram based on 176 genotypes of wheat indicated eight clusters (Figure 7). Cluster 1 included 17 members. This cluster included 3 sub-clusters, the variety Barani-79 was an outlier and stemmed alone in the sub-cluster. Cluster 2 consisted of 32 genotypes of wheat. This cluster further divided into 2 sub-clusters and 4 sub-sub-clusters. Cluster 3 contained 17 genotypes of wheat as members. The cluster further divided in sub-clusters. The variety Fakhar-e-Sarhad stemmed alone in the sub-cluster as outlier. Cluster 4 had 29 members. It additionally divided into 2 sub-clusters

Table 7: Euclidean distances between clusters as revealed by K-means based on morpho-physiological traits in spring wheat genotypes

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7
Cluster 2	4.90						
Cluster 3	4.83	5.74					
Cluster 4	8.27	5.98	4.78				
Cluster 5	5.41	6.03	9.58	11.72			
Cluster 6	12.48	11.33	7.86	5.52	16.76		
Cluster 7	20.23	18.91	15.51	13.01	24.48	7.80	
Cluster 8	13.48	14.45	18.06	20.30	8.65	25.40	33.12

Table 8: Members of each cluster constituted by K-means based on morpho-physiological traits in spring wheat genotypes

Cluster No	No. of members	Members
1	18	Babax 1, Bahawalpur-94, Bahawalpur-2000, Bakhtawar-93, Bhrikuti, Chakwal-86, Chakwal-97, Fakhar-e-Sarhad, GA-2002, Gatcher, Jupateco-73R, Jupateco-73S, Khyber-87, Pastor, Saughat-90, Sutlaj-86, Tonichi-81, LLR9
2	32	Gauarab, Kaghan-93, Kohsar-95, MH-97, Moomal-2002, Noshera-96, Opata-85, Pak.81, Parula, Parwaz-94, Pasban-90, Shaheen-94, Wafaq-01, Zarlashazta, WC4, WC5, WC6, WC9, WC11, WC14, WC15, WC17, WC18, WC22, WC23, 8970, 92R10, BARS-2009, 02FJ12, 02FJ13, 02FJ23, 03FJ26
3	26	Abadgar-93, Anahuac-75, Annapurna, AS-2002, Bahawalpur-97, Barani-79, Blue Silver, Chanab-70, Chapio, Darawar-07, Faisalabad-83, Frontana, Pirsabak-2005, Punjad-1, Rawal-87, Rohtas-90, Saleem-2000, Sarsabz, Sehar-2006, SH-2002, Sind-81, Super Kauz, Takbeer, Tatara, LLR17, WC3
4	24	Alter-84D, Barani-83, Kohinoor-83, Inqilab-91, Kirin-95, Bhakhar-2002, Faisalabad-85, Iqbal-2000, LU-26, Lyallpur-73, Magalla-99, Manthar-3, Mexipak-65, Noroeste, Super Seri-82, Watan-94, WC1, WC7, WC13, WC26, 8973, 02FJ06, 03FJ05, 05FJS315
5	28	Avocet+YrA, Avocet-YrA, Babax 2, Genaro-81, Kohistan-97, Mehran-89, Pasang Lamu, Pavon-76, Pirsabak-91, Pirsabak-2004, Potohar-93, Punjab-85, Sariab-92, Tandojam-83, Trap 1, Tukuru, Zardana, LLR23, WC16, WC24, WC25, 94R30, 98FJ13, 02FJ02, 02FJ08, 04FJH07, 04FJH17, Patra
6	19	Buck Buck, C-591, Cartens V, Iumillo-D, Kakatsi, Kukuna, Milan/SHA, Punjab-96, SA-42, Seri-82, Shahkar-95, Sonalika, Soorab-96, Suleman-96, Yecora-70, WC2, WC8, WC12, WC20
7	11	Inia-66, Kanchan, Manitou, Marvi-2000, Shafaq-2006, Sonora-64, Transec, LLR45, WC10, 03FJ13, NR-268
8	18	Amadina, Anmol-91, Atilla, Auqab-2000, PBW-373, WL711, Zarghoon, LLR5, WC19, WC21, 03FJ27, 04FJH161, 04FJH226, 04FJH270, 04FJS26, 04FJS35, Chakwal-50, NARC

and 4 sub-sub-clusters. Cluster 5 constituted 17 genotypes, with 2 sub-clusters and 4 sub-sub-clusters. Cluster 6 was relatively a small cluster comprising of 10 members. The cluster further divided into 2 sub-clusters and 4 sub-sub-clusters. The genotype Transec descended alone in a sub-cluster. Cluster 7 was formed of only 13 members. Cluster 8 was the biggest of all the clusters containing 41 members, the can be divided into sub-clusters, sub-sub-clusters and further. Similarly, [Khodadadi et al. \(2011\)](#) categorized wheat cultivars into seven groups. [Yousuf et al. \(2008\)](#) formed four distinct clusters to arrange seventy wheat genotypes.

K-mean clustering

After observing clustering behaviour of the wheat genotypes through hierarchical cluster analysis

by K-mean was performed. The genotypes were also grouped into eight clusters based on 10 morpho-physiological traits. Analysis of variance for 10 morpho-physiological traits indicated that relative water content, osmotic adjustment, cell membrane stability and grain yield per plant were significantly variable traits inside various clusters ([Table 6](#)). Euclidean distances between the clusters are shown in [Table 7](#). Cluster 7 and 8 were the most diverse clusters having highest genetic distance (33.12) followed by cluster number 6 and 8 with the linkage distance of 25.40. Members of these clusters can be utilized in transgressive breeding programmes.

Scattering of various clusters mean lines indicated that relative water content, cell membrane stability and

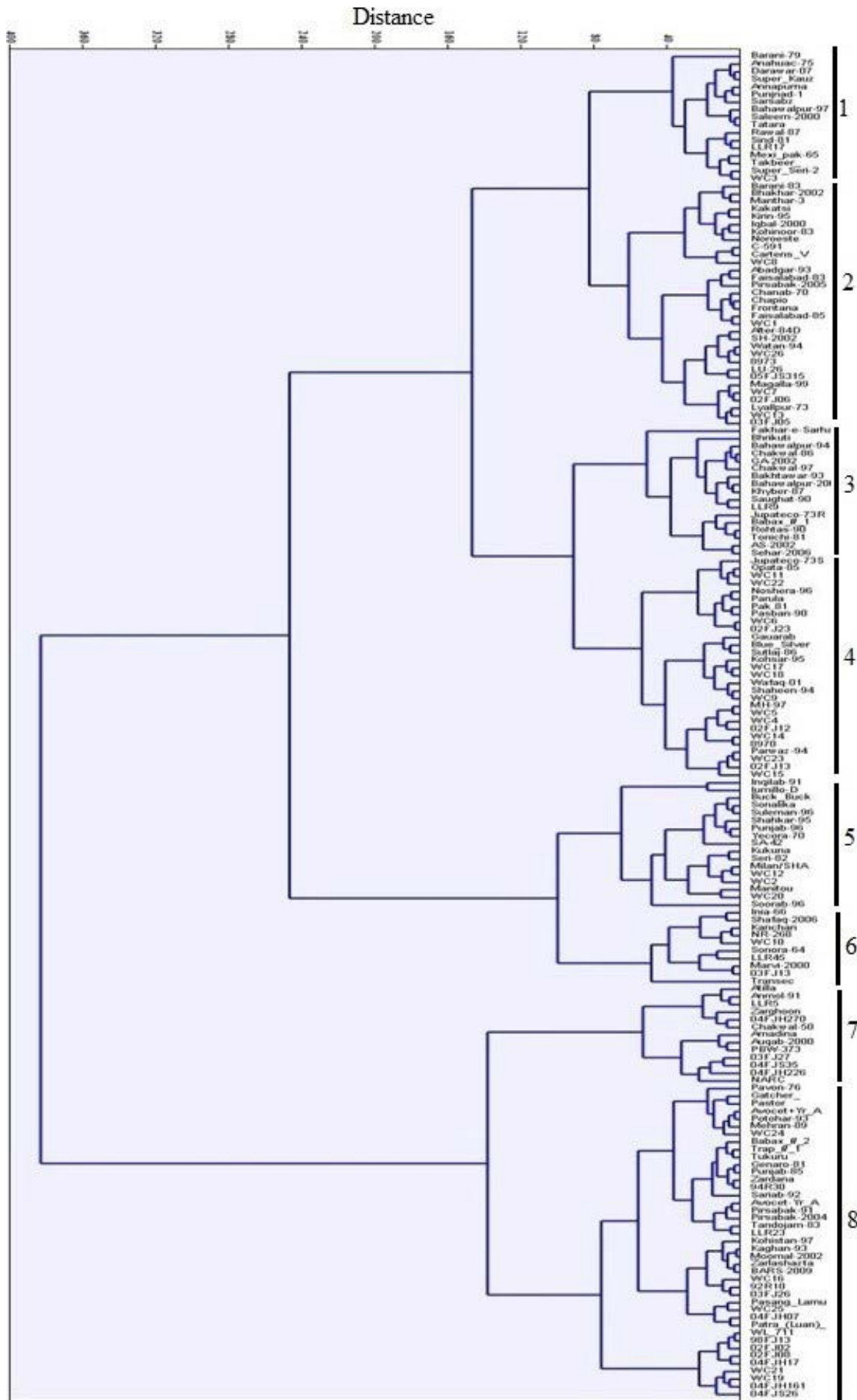


Figure 7: Tree diagram based on 176 spring wheat genotypes using Ward's method

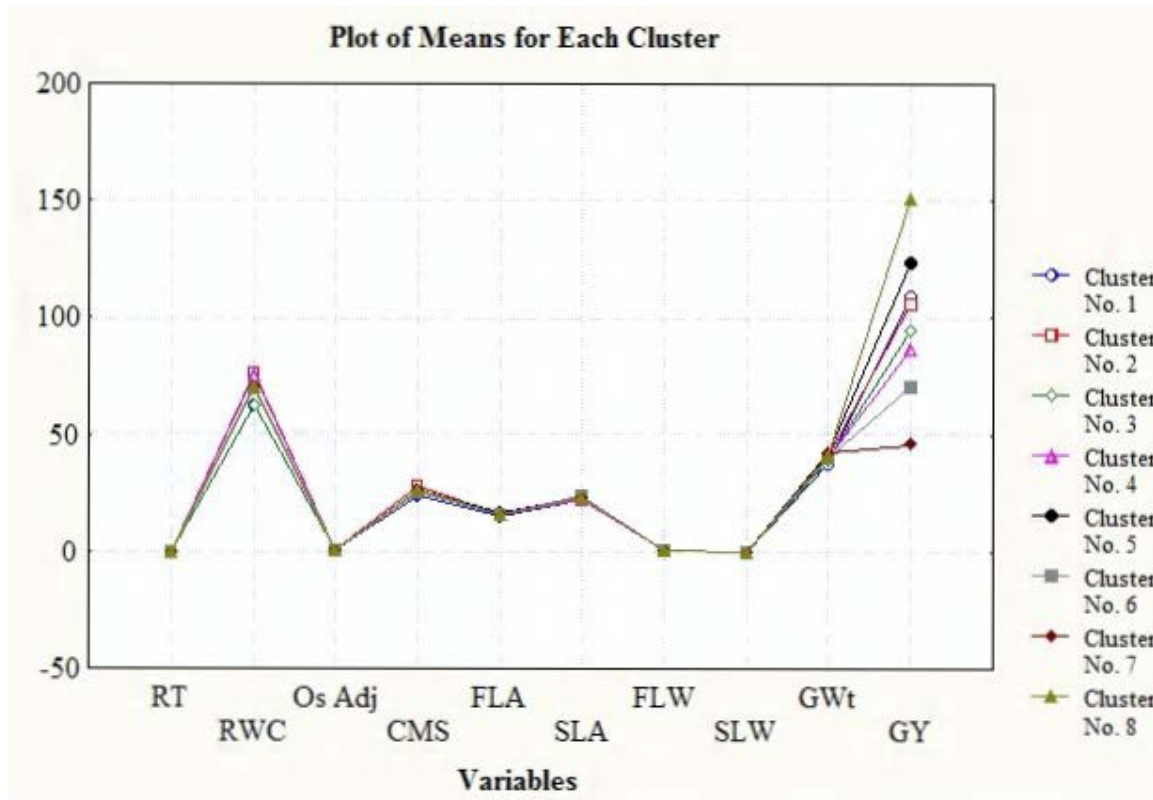


Figure 8: Plot of cluster means as revealed by K-means clustering for 10 morpho-physiological traits in spring wheat genotypes

grain yield per plant were diverse parameters among the clusters, with grain yield per plant being the most diverse (Figure 8). The variation in these traits indicated that they could be improved in breeding programme with ease.

A total of eight clusters were formed by K-mean clustering (Table 8). Cluster 1 had 18 members with highest mean value among the clusters for osmotic adjustment. This cluster included some of the known drought tolerant varieties like Chakwal-86, Chakwal-97, Fakhar-e-Sarhad and GA-2002. Most of the members of this cluster are included in cluster 3 when compared to hierarchical clustering (Figure 7). Grouping of genotypes in same clusters using different statistical techniques confirmed their relationship. Cluster 2 contained 32 members. It had the highest mean value among the clusters for cell membrane stability and relative water content (Table 8), both the traits are known to be present in drought tolerant genotypes. Pak.81, Pasban-90, BARS-2009 and most of the synthetic wide crosses were included among the members of this cluster. Pak.81 is a famous variety with 1BL.1RS translocation, incorporated in Veery and sibs and released in many countries with different names. Pasban-90 is known for its salt tolerance and is recommended for salt-affected soils of Paki-

stan. It is believed that salt tolerant varieties are also drought tolerant. BARS-2009 is a rust resistant and high yielding cultivar recommended for rainfed areas of Punjab in Pakistan. Members of this cluster are included in Cluster 4 when compared to hierarchical clustering (Figure 7). Cluster 3 had 26 members having highest mean value for osmotic adjustment. Some of the famous varieties included in this cluster were Chanab-70, AS-2002, Blue Silver, Faisalabad-83, Frontana, Rawal-87 and Sehar-2006. These members are shared by cluster 1 and 2 of hierarchical cluster diagram. Cluster 4 contained 24 genotypes. Members of cluster 4 had higher mean value of 1000-grain weight, cell membrane stability and relative water content.

Higher relative water content indicated an extensive root system for these genotypes. The cluster included widely grown varieties of recent past like Inqilab-91, LU-26, Lyallpur-73 and Mexipak-65; all these varieties are now susceptible to different races of rusts. It is estimated that Inqilab-91 was once cultivated on 70% of the country's wheat cultivated area before it became susceptible against yellow rust (Yr27 virulence). It is now widely used in hybridization programmes of many research institutes. LU-26 is known for its salt tolerance. Inqilab-91 stemmed with Iumillo D in dendrogram (Figure 7) while the other members

of this cluster are included in cluster 2. Twenty-eight genotypes constituted cluster 5, cluster 6 was comprised of 19 genotypes, and cluster 7 contained 11 genotypes. Members of cluster 7 had the maximum 1000-grain weight. These genotypes are early in their flowering habit; earliness provides longer grain filling period resulting in higher grain weight. These genotypes can be utilized to induce earliness and higher grain weight in breeding populations.

Maximum genetic distance was observed between cluster 7 and 8 showing diverse genotypes that could be utilized in transgressive breeding. Cluster 8 included 18 high yielding genotypes of diverse origin. This cluster included approved varieties (local and exotic), a land race, wide crosses and some advanced lines, for example, Atila, Auqab-2000, PBW-373, LLR5, WC19, WC21, 03FJ27, 04FJH161, 04FJH226, 04FJH270, 04FJS26, 04FJS35 and Chakwal-50.

Conclusions

Adequate variability exists in the wheat gene pool studied to initiate a breeding programme. Cell membrane stability, osmotic adjustment, relative water content and grain yield per plant had the highest contributions towards variability. Grain yield per plant is associated with relative water content, cell membrane stability and specific flag leaf area. The greatest genetic distance was detected among cluster 6 and cluster 8 and cluster 7 and 8, hence members of these clusters could be exploited in transgressive breeding.

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