

## **GENETIC DIVERSITY OF WHEAT GRAIN QUALITY AND DETERMINATION THE BEST CLUSTERING TECHNIQUE AND DATA TYPE FOR DIVERSITY ASSESSMENT**

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Wheat is an important staple in human nutrition and improvement of its grain quality characters will have high impact on population's health. The objectives of this study were assessing variation of some grain quality characteristics in the Iranian wheat genotypes and identify the best type of data and clustering method for grouping genotypes. In this study 30 spring wheat genotypes were cultivated through randomized complete block design with three replications in 2009 and 2010 years. High significant difference among genotypes for all traits except for Sulfate, K, Br and Cl content, also deference among two years mean for all traits were no significant. Meanwhile there were significant interaction between year and genotype for all traits except Sulfate and F content. Mean values for crude protein, Zn, Fe and Ca in Mahdavi, Falat, Star, Sistan genotypes were the highest. The Ca and Br content showed the highest and the lowest broadcast heritability respectively. In this study indicated that the Root Mean Square Standard Deviation is efficient than R Squared and R Squared efficient than Semi Partial R Squared criteria for determining the best clustering technique. Also Ward method and canonical scores identified as the best clustering method and data type for grouping genotypes, respectively. Genotypes were grouped into six completely separate clusters and Roshan, Niknejad and Star genotypes from the fourth, fifth and sixth clusters had high grain quality characters in overall.

*Key words:* Genetic Diversity, Iron, Wheat, REML, Zinc

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## INTRODUCTION

Wheat is one of the most ancient crops. Its domestication marks the transition from hunting–gathering to agrarian economy in western Asia, which marks the dawn of the evolution of western civilization (DVORAK *et al.*, 2012). Today, the importance of wheat is mainly due to the fact that its grain can be ground into flour and semolina, which form the basic components of bread products, such as pastas, and hence it presents the fundamental source of nutrients to the superlative of the world population (SRAMKOVA *et al.*, 2009). Deficiencies of micronutrients such as iron, zinc, and vitamin A (“hidden hunger”) afflict over three billion people (SRAMKOVA *et al.*, 2009). Zinc shortcoming is reason for many severe health backwash, comprising impairments of bodily growth, immune system and learning potency, combined with increased venture of infections, DNA damage and cancer development (PRASAD, 2007). The results of malnutrition make immense economic and societal expenses to nations. Micronutrient malnutrition vastly increases morbidity and mortality rates, diminishes cognitive potencies of children and lowers their educational attainment, reduces labor productivity, stagnate national development efforts, contributes to continued high population growth rates and reduces the livelihood and quality of life for all those affected (WELCH and GRAHAM, 1999).

In the resent study revealed that new wild emmer wheat accessions have been identified showing simultaneously very high concentrations of Zn (up to 139 mg/kg), Fe (up to 88 mg/kg) and protein (up to 380 g/kg) in grains and high tolerance to drought stress and Zn deficiency in soil (PELEG *et al.*, 2008). This result shows that it should be possible to improve Fe and Zn levels in wheat grain through plant breeding. Supplementary study has also shown that there is no negative linkage between grain yield and Fe and Zn density in the grain (WELCH and GRAHAM, 2002). A survey of genetic diversity with the help of suitable statistical methods is absolutely necessary to start an efficient breeding program (KHODADADI *et al.*, 2014).

The Root Mean Square Standard Deviation (RMSSTD) measures the homogeneity of the cluster formed at any given step. It truly measures the compactness or homogeneity of a cluster. The smaller the RMSSTD, the more homogeneous or compact is the cluster formed at a given step. A large value of RMSSTD suggests that the cluster obtained at a given step is not homogeneous, and is probably formed by merging of two very heterogeneous and more compact clusters (SHARMA, 1996). The Semi Partial R Squared (SPR) measures the loss of homogeneity due to merging two groups to form a new group at a given step. If the value is little, then it suggests that the cluster solution obtained at a given step is wrought by merging two very homogeneous clusters. On the other hand, large values of SPR suggest that two heterogeneous clusters have been merged to form the new cluster. R Square (RS) measures the heterogeneity of the cluster solution formed at a given step. A large value represents that the clusters obtained at a given step are quite different (i.e., heterogeneous) from each other, whereas a little value would implicate that the clusters formed at a given step are not very different from each other. To find the optimal number of clusters and the quality of the clustering, the RS and the SPR measured after clustering method. While RS should be maximal, the SPR should be minimal (RUJASIRI and CHOMTEE, 2009). The objectives of this study were assessing variation of some grain quality characteristics in the Iranian wheat genotypes and identify the best type of data and clustering method for grouping genotypes.

## MATERIALS AND METHODS

**Plant materials and experimental design**

Thirty spring wheat genotypes supplied by the Agricultural Research Institutes Gene Bank in Karaj and used for this research in the research field of faculty of agricultural sciences, Tarbiat Modares University, Tehran, Iran in 2009 and 2010 years. The weather condition of Tehran province was presented in Table 1. The plot size was 1.5 m length with three rows, row spacing was 20 cm and seeding rate was 250 seeds per m<sup>2</sup> based on a randomized complete block design with three replications. Nitrogen and phosphorus fertilizer, were consumed at 40 and 60 Kg ha<sup>-1</sup>, respectively before planting and nitrogen fertilizer was also broadcast at the stages of tillering and stem elongation at 40 kg ha<sup>-1</sup>.

Tab. 1. Weather data for Tehran province

Year	Climatic parameters	March			April			May			June			July			August			
		Mean	Max.	Min.	Mean	Max.	Min.	Mean	Max.	Min.	Mean	Max.	Min.	Mean	Max.	Min.	Mean	Max.	Min.	
2009	Total rainfall (mm)	19.9			44.61			13.41			2.31			0			0			
	Rainfall (mm)	0.6	14.8	0.0	1.5	15.3	0.0	0.4	10.3	0.0	0.1	1.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	Min. Temperature (°C)	7.5	16.0	1.0	8.4	18.0	0.0	17.1	25.0	9.0	20.5	27.0	13.0	24.8	32.0	19.0	21.2	26.0	17.0	
	Max. Temperature (°C)	17.5	25.0	9.0	18.1	25.0	13.0	27.3	34.0	22.0	31.7	37.0	25.0	36.9	41.0	32.0	35.4	38.0	32.0	
	Min. Humidity (%)	14.8	44.0	4.0	28.8	64.0	9.0	23.0	55.0	14.0	20.3	34.0	14.0	15.2	27.0	8.0	17.1	25.0	7.0	
	Max. Humidity (%)	43.9	90.0	14.0	63.3	94.0	26.0	44.6	91.0	22.0	43.4	69.0	25.0	37.3	67.0	16.0	46.8	65.0	30.0	
	Total rainfall (mm)	34.1			51.9			12.6			1.7			0			0.1			
2010	Rainfall (mm)	1.1	11.9	0.0	1.7	12.9	0.0	0.4	5.0	0.0	0.1	1.7	0.0	0.0	0.0	0.0	0.1	0.0		
	Min. Temperature (°C)	9.8	20.0	1.0	12.5	18.0	8.0	17.8	25.0	9.0	24.1	32.0	18.0	25.5	32.0	20.0	23.5	30.0	20.0	
	Max. Temperature (°C)	18.1	28.0	10.0	22.2	26.0	16.0	27.8	35.0	21.0	35.3	39.0	31.0	37.6	42.0	33.0	33.8	39.0	30.0	
	Min. Humidity (%)	34.0	77.0	15.0	28.1	61.0	13.0	19.4	43.0	6.0	13.6	19.0	7.0	15.7	25.0	8.0	18.7	25.0	13.0	
	Max. Humidity (%)	59.0	95.0	25.0	58.4	85.0	41.0	44.3	76.0	17.0	30.8	54.0	19.0	37.3	62.0	15.0	37.2	61.0	20.0	

**Studied traits and their measurement**

The measured traits include grain F, Acetate, Cl, Br, Phosphate, Sulfate, Succinate, NH<sub>4</sub>, K, Mg, Ca, N, grain iron concentration, grain zinc and crude protein concentration all based on µg g<sup>-1</sup> Scale. Grain iron and zinc were measured using atomic absorption method (GUPTA, 2000) after digestion based on nitric (0.1 normal)/citric (10%) acid (MORGOUNOV *et al.*, 2007) and extraction by ion-chromatography method (SMALL *et al.*, 1975). Also, homogeneity of experimental field has confirmed and then trial was conducted. Grain F, Acetate, Cl, Br, Phosphate, Sulfate, Succinate, NH<sub>4</sub>, K, Mg and Ca contents were measured based on ZHAO *et al.* (2006) suggested method. For estimate grain crude protein content firstly grain N content was measured from NH<sub>4</sub> content (AHMEDANI *et al.*, 2009) by multiplying NH<sub>4</sub> content by N proportion in NH<sub>4</sub> (0.7765) and then N content multiplied by factor of 5.7 for wheat (SAMEEN *et al.*, 2002).

**Statistical analysis**

Statistical analysis including Normality test using Shapiro-Wilk method, estimation of variance components through restricted maximum likelihood (REML), means comparison by LSD test and cluster analysis were performed using the statistical software SPSS version 16.0 (SPSS, Chicago, USA) program. In addition, Principal component (PC), discriminate and canonical scores, RS,

RMSSTD and SPR were calculated using statistical software SAS version 9.1. Excel version 2007 was used for calculating some descriptive statistics and drawing graph. For determine the best type of data for grouping genotypes, five types of the data were used. Principal component analysis (PCA) based on covariance matrix and correlation matrix was done and for each types of PCA the first five component scores which had eigenvalues more than one selected and used for assessment of clustering methods performance and found appropriate type of data for cluster analysis. Also discriminant and canonical scores were calculated and respectively four and three component scores which had eigenvalues more than one and used for the above mentioned purposes. Three measures including RMSSTD, RS and SPR computed according to LIU *et al.* (2006) and used for detecting the best clustering technique. Broadcast heritability ( $H_b^2$ ) was estimated based on formula suggested by HOLLAND *et al.* (2003) and using SAS 9.1.

## RESULTS

Analysis of variance results showed high significant difference among varieties for all traits except for Sulfate, K, Br and Cl content, also deference among two years mean for all traits were no significant. Meanwhile there were significant interaction between year and genotype for all traits except Sulfate and F content (Tab. 2).

Tab. 2. REML estimation of variance components for studied traits in 30 spring wheat genotypes

S.O.V	Mean square														
	Crude Protein	Zn	Fe	N	Ca	Mg	K	NH <sub>4</sub>	Succinate	Sulfate	Phosphate	Br	Cl	Acetate	F
Year	0 <sup>ns</sup>	5.9 <sup>ns</sup>	0 <sup>ns</sup>	0 <sup>ns</sup>	0 <sup>ns</sup>	813.8 <sup>ns</sup>	130648 <sup>ns</sup>	0 <sup>ns</sup>	2034.0 <sup>ns</sup>	0 <sup>ns</sup>	7195.9 <sup>ns</sup>	349.6 <sup>ns</sup>	0	43354 <sup>ns</sup>	0 <sup>ns</sup>
Replication (Year)	95.1	0	3.1	2.9	0	3.1	0	4.9	464.4	0	492.36	8.3	29.68	0	11.95
Genotype	82777 <sup>*</sup>	45.5 <sup>*</sup>	17.0 <sup>**</sup>	2547.7 <sup>***</sup>	3249.2 <sup>***</sup>	7034 <sup>*</sup>	27388 <sup>ns</sup>	4225.5 <sup>***</sup>	17767.0 <sup>***</sup>	3.1 <sup>ns</sup>	88741 <sup>***</sup>	29.53 <sup>ns</sup>	516.19 <sup>ns</sup>	18898 <sup>*</sup>	413.1 <sup>**</sup>
Genotype × Year	106072.2 <sup>***</sup>	87.2 <sup>***</sup>	21.5 <sup>***</sup>	3264.7 <sup>***</sup>	732.7 <sup>***</sup>	1101.6 <sup>**</sup>	95729 <sup>***</sup>	5414.8 <sup>***</sup>	6870.3 <sup>**</sup>	9.9 <sup>ns</sup>	32702 <sup>**</sup>	331.9 <sup>***</sup>	1586.3 <sup>**</sup>	24819 <sup>*</sup>	316.4 <sup>ns</sup>
Error	49970	12.4	10.1	1538	590.7	1257.2	37516	2550.9	8628.1	33.7	42031	60.5	2602.6	55866	994.29

\*\*\*, \*\* and \* significant at 0.1%, 1%, 5% level of probability and non significant, respectively

Results of mean comparison of traits showed that Mahdavi genotype in the second year (3397.34, 767.59 and 596.03) and Chamran genotype in the first year (793.77, 179.34 and 139.26) had the highest and the lowest crude protein, NH<sub>4</sub> and N content respectively. Also, for Zn, Fe, Ca, Mg, K, Succinate, Phosphate, Br, Acetate content the Falat (71), Star (55.07), Sistan (351.04), Chamran (428.41), Sholeh (3164.01), Sistan (901.3), Sholeh (1940.35), Bahar (115.04), Marvdasht (1698.72) genotypes in the first year yielded the highest mean value, respectively. The Sepahan in the second year yielded the highest Cl (293.22) and Star yielded the highest F (134.05) content (Data not shown).

The Ca (0.94) and Br (0.29) content showed the highest and the lowest  $H_b^2$ , respectively (Tab. 3). For compare reliability and efficiency of RMSSTD, RS and SPR, standardized mean values of these measures were computed for each of the clustering techniques and then variances of these data were computed for each of measures (Tab. 4).

Tab. 3. REML estimation of broadcast heritability on a Family Mean Basis

	Crude Protein	Zn	Fe	N	Ca	Mg	K	NH <sub>4</sub>	Succinate	Sulfate	Phosphate	Br	Cl	Acetate	F
H <sub>b</sub> <sup>2</sup>	0.76	0.71	0.77	0.77	0.94	0.69	0.55	0.77	0.90	0.42	0.90	0.29	0.51	0.68	0.76
Se <sub>H<sub>b</sub></sub>	0.11	0.15	0.11	0.11	0.2	0.16	0.27	0.11	0.04	0.39	0.04	0.53	0.31	0.17	0.12

H<sub>b</sub><sup>2</sup>: Broadcast heritability

Tab. 4. Standardized mean value and variance of these mean values for the SPR, RS and RMSSTD for clustering techniques

Measure	Variance	Ward	Centroid	Complete Linkage	Average linkage	Median	Single Linkage
SPR	0.17	2.03	1.39	1.73	1.30	1.53	2.38
RS	0.21	3.46	2.18	2.75	2.40	2.47	2.94
RMSSTD	39.23	5.01	6.54	5.36	6.33	6.74	21.25

In this study, six clustering techniques efficiency were compared based on three above mentioned criteria. The results showed that Ward method yielded the lowest RMSSTD and highest RS, whereas SPR value for all methods were close and the lowest for Single Linkage and Ward methods (Tab. 5). In addition increasing in the number of clusters tended to increase the efficiency of all clustering techniques until reaching to sixth cluster whereas from the sixth to the seventh cluster efficiency of the clustering techniques were constant in the most cases and in a few cases decreased (Fig. 1). Therefore the sixth cluster was diagnosed as Dendrogram cut off point and these criteria can be used as appropriate method to find out optimum number of clusters.

Tab. 5. Mean value of the SPR, RS and RMSSTD for clustering techniques

Measure	Ward	Centroid	Complete Linkage	Average linkage	Median	Single Linkage
SPR	0.08	0.09	0.10	0.10	0.10	0.06
RS	0.58	0.46	0.54	0.51	0.48	0.35
RMSSTD	46.31	49.84	49.54	46.49	47.60	55.65

Note: a lower RMSSTD and SPR and higher RS value means that the clustering technique is better.

Also, in this study for identification the best type of data for cluster analysis, five types of data were compared based on RMSSTD, RS and SPR criteria. Standardized mean values of these criteria were computed for each type of data (Tab. 6). Because of the least value of RMSSTD and highest value of RS for canonical scores, this type of data indicated as the best data type for cluster analysis.

According to the above mentioned conclusion, canonical scores were obtained from original data, and cluster analysis done based on ward method. By incision dendrogram at 6 units distance the genotypes categorized into six completely separate clusters (Fig. 2) suggesting considerable amount of genetic diversity among material. To determine the cutoff point, in addition to above mentioned results, discriminant analysis was used (KHODADADI *et al.*, 2011). Mean and standard deviations of traits for groups were presented in Table 7.

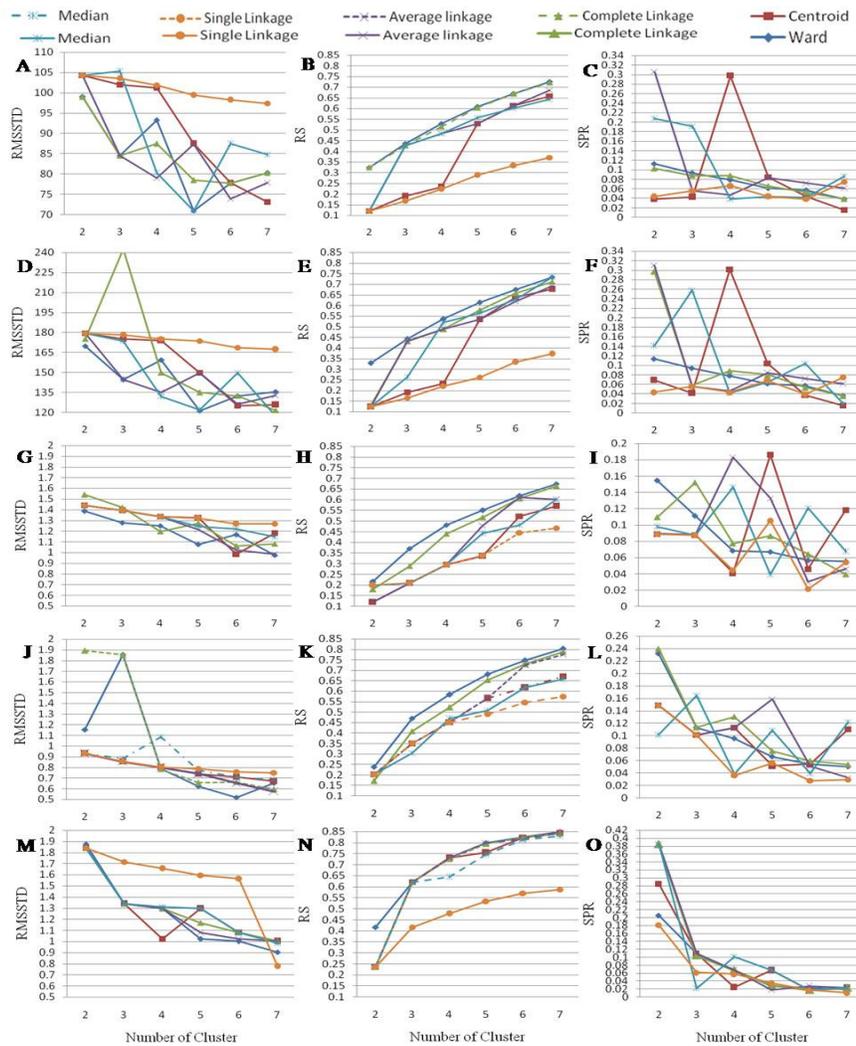


Fig. 1. Chart of average RMSSTD, RS and SPR values; A, B and C; RMSSTD, RS and SPR of the 15-variable, original dataset respectively; D, E and F; RMSSTD, RS and SPR of the 5-variable, PC Scores based on covariance matrix dataset respectively; G, H and I; RMSSTD, RS and SPR of the 5-variable, PC scores based on correlation matrix dataset respectively; J, K and L; RMSSTD, RS and SPR of the 3-variable, Canonical Scores dataset respectively; M, N and O; RMSSTD, RS and SPR of the 4-variable, discriminant scores dataset respectively.

Tab. 6. The standardized mean value of SPR, RS and RMSSTD for five types of data

Measure	Original data	PC Scores based on covariance matrix	Discriminant scores	Canonical scores	PC scores based on correlation matrix
SPR	4.27	4.28	4.83	6.25	8.22
RS	3.98	4.08	7.52	8.89	6.33
RMSSTD	13.91	13.20	12.44	7.39	24.60

Note: a lower RMSSTD and SPR and higher RS value means that the data type is better.

The first group contains 13.3% of genotypes (Fig. 2). The average values for all traits except for acetate, Mg and Ca were less than the total means (Tab. 7). The second group contains 50% of genotypes (Fig. 2). Grain quality state of this group in all case except for Mg, Fe, Ca, Succinate, Cl and F were better than the first group. In overall this group has no any special feature and was in the range of the other group values (Tab. 7). The third group contains 26.6% of genotypes (Fig. 2). This group showed the lowest mean value for K. The fourth group contains only the Roshan genotype that had the highest mean values for Ca, K, Sulfate, Phosphate and Br minerals (Tab. 7). The fifth group contains the Niknejad genotype that had the highest mean values for crude protein, Zn, N, NH<sub>4</sub> and acetate. The sixth group contains the Star genotype that had the highest mean values for Fe, Succinate, Cl and F and the lowest mean values for crude protein, Zn, Ca and acetate (Tab. 7).

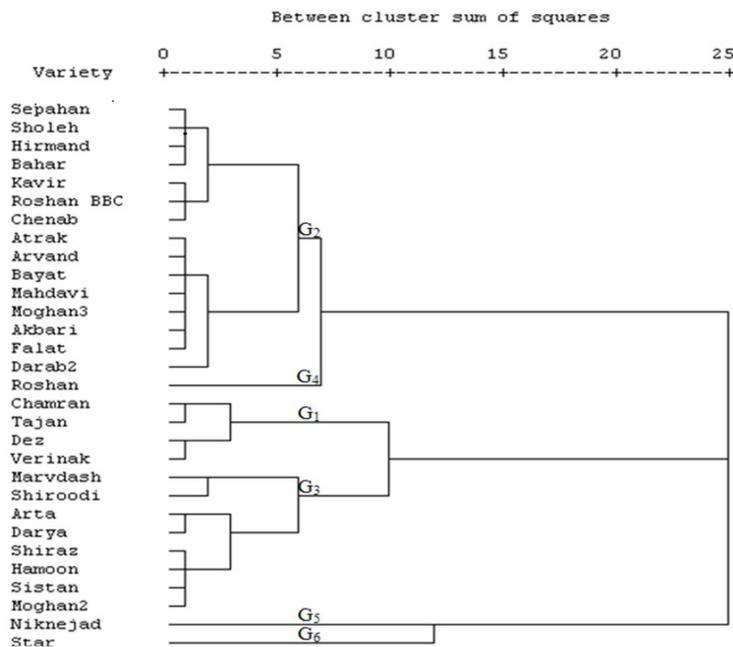


Figure 2. Dendrogram showing the genetic relationship between 30 spring wheat for studied traits using ward method based on canonical scores

Tab. 7. Mean, standard deviation, Deviation from total mean and mean comparison results

Group	G.M	Descriptive statistics	Crude Protein (%)	Zn	Fe	N	Ca	Mg	K	NH <sub>4</sub>	Succinate	Sulfate	Phosphate	Br	Cl	Acetate	F
1	4	Mean	17.27	36.61	29.77	302.90	116.34	336.29	2158.71	390.08	194.37	8.39	145.90	10.28	54.32	818.16	6.56
		DfTM	-0.93	-2.49	-0.93	-17.30	6.84	40.99	-97.09	-22.22	-7.33	-1.51	-191.10	-7.02	-11.18	92.86	-6.74
		SD	2.50	3.66	2.92	43.88	35.36	67.01	434.05	56.51	66.08	1.49	65.34	4.31	22.08	93.74	6.05
2	15	Mean	18.63	39.45	29.55	326.86	104.69	285.45	2310.86	420.95	171.61	10.93	349.68	16.49	50.87	760.26	8.42
		DfTM	0.43	0.35	-1.15	6.66	-4.81	-9.85	55.06	8.65	-30.09	1.03	12.68	-0.81	-14.63	34.96	-4.88
		SD	2.48	7.26	2.48	43.48	27.31	30.77	205.18	56.00	67.02	2.42	117.67	5.97	17.56	162.24	5.54
3	8	Mean	17.98	39.79	33.11	315.44	107.87	302.25	2110.94	406.23	269.15	10.07	426.12	21.78	91.35	650.21	13.28
		DfTM	-0.22	0.69	2.41	-4.76	-1.63	6.95	-144.86	-6.07	67.45	0.17	89.12	4.48	25.85	-75.09	-0.02
		SD	1.32	3.87	3.99	23.12	38.70	6.39	192.55	29.77	64.40	2.62	154.70	5.37	32.09	165.79	14.92
4	1	Mean	18.10	35.35	28.04	317.61	155.20	237.73	2700.73	409.03	158.60	11.26	581.15	21.80	36.24	689.99	1.26
		DfTM	-0.10	-3.75	-2.66	-2.59	45.70	-57.57	444.93	-3.27	-43.10	1.36	244.15	4.50	-29.27	-35.31	-12.04
		SD	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5	1	Mean	19.83	49.78	28.93	347.97	141.77	307.25	2485.39	448.13	71.84	2.70	61.73	12.14	78.04	877.27	65.92
		DfTM	1.63	10.68	-1.77	27.77	32.27	11.95	229.59	35.83	-129.86	-7.20	-275.28	-5.16	12.54	151.97	52.62
		SD	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6	1	Mean	17.18	31.02	35.64	301.42	90.44	268.69	2303.54	388.19	315.53	6.04	228.73	21.59	139.78	314.67	71.65
		DfTM	-1.02	-8.08	4.94	-18.78	-19.06	-26.61	47.74	-24.12	113.83	-3.86	-108.27	4.29	74.28	-410.63	58.35
		SD	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

DfTM: Deviation from total mean; SD: Standard Deviation; GM: Group members

## DISCUSSION

Based on ANOVA results, variation among genotypes was appropriate for grain chemical characters to use in breeding programs for improvement of these characters. GLUHOVTSEV *et al.*, (2010) estimated high protein content (15-17%) in them study on variability of spring wheat grain quality that it is in range of this study results. ZHAO *et al.* (2009) reported that grain protein, Fe and Zn content ranged 12.5-20 (%), 28-50 ( $\mu\text{g g}^{-1}$ ) and 12-35 ( $\mu\text{g g}^{-1}$ ) in bread wheat lines respectively. Results of previous studies on wheat grain iron and zinc concentration are in accordance with this research and obtained 38.0 and 37.2  $\mu\text{g g}^{-1}$  for grain iron and 28.0 and 30.7  $\mu\text{g g}^{-1}$  for grain zinc content (WELCH and GRAHAM, 2002; MORGOUNOV *et al.*, 2007). In addition, CAKMAK *et al.* (2004) showed that cause of increasing in grain iron and zinc concentration is for presence of 6A, 5B and 6B chromosomes. Whereas previous studies on tetraploid wheat (*Triticum dicocoids*) showed that Fe and Zn respectively ranged 15-109 and 35-100 ( $\mu\text{g g}^{-1}$ ) (CAKMAK *et al.*, 2004), 20-75 and 40-112 ( $\mu\text{g g}^{-1}$ ) and grain protein content, Ca, Mg and K respectively ranged 18-30 (%), 250-650, 1500-2200 and 4100-6500 ( $\mu\text{g g}^{-1}$ ) (CHATZAV *et al.*, 2009). By comparison results of CHATZAV *et al.*, (2009) and present study, it can be concluded that nutrients uptake vigor in tetraploid wheat (wild wheat) is higher than hexaploid wheat (domesticated wheat). This conclusion has been approved by CHATZAV *et al.* (2009). Also have been said that the wheat genome contains three NAM genes, but modern wheat varieties carry a non-functional NAM-B1 allele, which inducement delayed leaf senescence and lower levels of grain protein, Fe and Zn in modern wheat varieties compared with wild emmer wheat (ZHAO *et al.*, 2009). Therefore we can use wild wheat accessions to improving bread wheat quality with retain high grain yield by appropriate breeding methods such as chromosome substitution, chromosome segment substitution and etc. Because of

significant interaction between year and genotype, progeny test in multiple environments was suggested to raise protein, Zn, Fe and Ca content through breeding programs.

Scientists usually have tried to use the best and accurate statistical methods to assess genetic diversity. For example, in some previous studies tried to define better clustering method (MOHAMMADI and PRASANNA, 2003) and use intermediate analysis and applied clustering technique based on changed data (KHODADADI *et al.*, 2011). RUJASIRI and CHOMTEE (2009) used RS and RMSSTD criteria for comparing five clustering techniques including Hierarchical, K-means, Kohonen's Self-Organizing Maps, K-medoids and K-medoids method integrated with dynamic time warping for simulated and real datasets with a multivariate normal distribution.

By look at measures variance presented in table 4 clearly can indicate that RMSSTD is more efficient than RS and RS efficient than SPR in determining the best clustering technique. Because the highest variance for RMSSTD means that this measure had a good ability to separate clustering methods from together. Mean value of the first group for the important ingredients of human diets such as crude protein, Zn, Fe, Phosphate and sulfate were low. Therefore members of this group don't suitable for breeding programs. While in case of Mg it is proper. Also phosphate and Br content was the least amount in this group.

In some studies showed that insufficient supply of Ca and phosphate is normally associated with impaired skeletal development (YANNAKOULIA *et al.*, 2004) and approximately 99% of skeleton built from Ca (PARSONS, 2005). Also Phosphorus is an important constituent of grain of cereal crops and is the most necessary for seed development (SENG *et al.*, 1994). Therefore the fourth group genotype is suitable for Ca and Phosphate but it had minimum value of Fe. Also it must be noted that the majority of P (w80%) in wheat grain is in the form of phytate stored mainly in the aleurone cells (O'DELL *et al.*, 1972) and Phytate reduces the bioavailability of Zinc and Iron to monogastric animals and humans (FAIRWEATHER, 2004).

Three genotypes from The fourth, fifth and sixth groups yielded the highest and lowest values of the grain mineral and other contents, by cross and back cross mating between Roshan, Niknejad and Star genotypes and subsequently selection among generations we can reach to variety with high protein, Zn, Fe, Ca and some other contents mentioned in introduction section that are essential for human's nutrition. At the end it can be said that both directly by enhancing micronutrient availability and indirectly through improved agronomic performance and crop yields (WELCH and GRAHAM, 1999; GOMEZ-GALERA *et al.*, 2010) we can reach to appropriate modern varieties and in this way it is vital to explore the genetic resources of the wild relatives of crop plants as they harbor a vast allelic richness of desirable genes.

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**GENETIČKA DIVERGENTNOST KVALITETA ZRNA PŠENICE I ODREĐIVANJE  
NAJBOLJE TEHNIKE GRUPISANJA I TIPA PODATAKA ZA UTVRĐIVANJE  
DIVERZITETA**

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**Izvod**

Predmet istraživanja su bili ocena variranja nekih karakteristika kvaliteta zrna genotipova pšenice u Iranu i identifikacija najboljeg tipa podataka i metoda grupisanja genotipova. Ispitivanja su vršena gajenjem 30 ozimih genotipova pšenice u slučajnom blok sistemu sa tri ponavljanja u toku 2009 i 2010. godine. Vršena su merenja sadržaja gvožđa, acetate, hlora, broma, sulfata, sukcinata, amonijaka, kalijuma, magnezijuma, kalcijuma, azota, koncentracija gvožđa, cinka i sirovih protein u zrnu. Na osnovu dobijenih rezultata genotipovi su se grupisali u šest potpuno različitih dendograma. Najbolji kvalitet zrna je utvrđen za genotipove Roshan, Niknejad i Star iz četvarte, pete i šeste grupe klastera.

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