Bulgarian Journal of Agricultural Science, 19 (No 1) 2013, 110-116
Agricultural Academy

COMPARISON AMONG CLUSTERING IN MULTIVARIATE ANALYSIS OF TRITICALE USING AGRONOMICAL TRAITS

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Abstract

DOGAN, R. and H. VURAL, 2013. Comparison among clustering in multivariate analysis of triticale using agronomical traits. *Bulg. J. Agric. Sci.,* 19: 110-116

This research has been done for determining the most suitable triticale genotypes in the triticale sowing duty system of the Marmara Region ecological conditions. 22 triticale genotypes were used in this two years long study, which has, randomize block experimental design with three replications. Data were analyzed by multivariate statistical methods. Regarding the plant height, the genotype no. 23 recorded the highest value; however, the genotype no. 21 recorded the lowest one. The genotype no. 3 recorded the highest spike length; however, the genotype no. 21 recorded the lowest values respectively. The genotype no. 3 recorded the highest value of grain number spike^{-1}. The genotype no. 4 recorded the highest value of 1000 kernel weight. The genotype no. 21 recorded the highest test weight; however, the genotype no. 7 recorded the lowest values respectively. Regarding the grain yield, the genotype no. 13 recorded the highest value (6723 kg ha^{-1}); however, the genotype no. 16 recorded the lowest one (5244 kg ha^{-1}). According to the two years results, the differences between triticale genotypes were found to be statistically sinificant in all components observed. The differences between the years were proved significant in all components. According to the results of factor analysis, triticale genotypes have similar properties significantly. Therefore, more than one major component has not been found. However, it was found one principal component (PC1) by factorial analyses. In addition, twenty-two examined cultivars were separated in two main groups by cluster analyses.

Key words: Breeding, factor analysis, triticale, yield and yield components

Introduction

Triticale (*x Triticosecale Wittmack*) is a synthetic species. Previous studies have indicated that the grain production of newer and improved triticale cultivars, both as a monocrop and in small grain mixtures, is acceptable in a wide range of environments (Pfeiffer, 1996; Juskiw et al., 2000 a,b and Barnett et al., 2006). The forage production and silage yield as well as the quality of hexaploid triticales, both as a monocrop and in small grain mixtures, have been reported to be favorable in comparison with other small grains (Juskiw et al., 2000a,b; Rao et al., 2000 and Erekul and Köhn, 2006). These studies have indicated that triticale has great potential to fit into current small-grain areas and to contribute to the improvement of grain and forage production in diverse geographical environments. Triticale is, in general, more tolerant to environmental stresses than are wheat and barley (Jessop, 1996). Additionally, triticale combines high plant productivity and grain yield (Royo et al., 1999), good flavor after backing (Gupta and Priyadarshan, 1982) and stability to environmental variations (Hoerlein and Valentine, 1995).

This research was carried out to determine the adaptation of some triticale genotypes under the ecological conditions of Marmara Region in Turkey. Milvanovic

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(1993), Yagbasanlar et al. (1988), Mützing (1989), Mergoum et al. (1992), Unver (1999), Atak and Ciftci (2006), Mut et al. (2006), Yanbeyi et al. (2006), Akgün et al. (2007) and Alp (2009) were studied some researches on the agronomical characteristics of some triticale genotypes.

In this research, multivariate statistical methods were used for determining of data to obtain more results than variance analysis. Rudimentary, exploratory procedures are often quite helpful in understanding the complex nature of multivariate relationships. Analysis of principal components is more of a means to an end rather than an end in them because they frequently serve as intermediate steps in much larger investigations. For example, principal components may be inputs to a multiple regression or cluster analysis. Moreover, principal components are one 'factoring' of the covariance matrix for the factor analysis model (Johnson and Wicherin, 1992).

Cluster analysis when searching the data for a structure of 'natural' groupings is an important exploratory technique. Grouping can provide an informal means for assessing dimensionality, identifying-outliers and suggesting interesting hypotheses concerning relationships (Johnson and Wicherin, 1992).

Material and Method

This study was carried out at the Research and Application Center of the Agricultural Faculty, Uludag University, Bursa, Turkey, as field experiments in 2005 and 2006.

The total precipitation in the second year (564.5 mm) of the experiment during the growth season was lower than the normal value (555.6 mm), but it was approximately the same as the normal value in the first year (545.6 mm). The average temperature (10.96 °C) in the second year was lower than the normal temperature (11.59 °C), but it was close to normal in the first year (11.18 °C). Both in the first year (66.55%) and in the second year (69.14%), the relative moisture was lower than the normal value (70.98%) (Anonymous, 2008). Soil of the experimental area was clayey textured, almost without salt, rich in K, neutral in pH and poor in organic matter (Tumsavas and Aksoy, 2008).

The experiment was arrangement according to the Randomized Block Design with three replications. In the study, 22 triticale genotypes developed by crossing method in Agriculture Faculty of Uludag University (Coplu, 2001) were studied on the yield and yield components in Southern Marmara Region.

In experimental years, sowings were made by using an ojord-type sowing machine in November. The size of each plot was 6 × 1.2 m. Eight rows were sown in each plot, with row spacings of 15 cm. After sowing, a hand-driven roller was used to make the seeds to come into contact with the soil. Half of the nitrogen fertilizer was applied immediately after the sowing and other half of it at the jointing stage. The N fertilizer was ammonium nitrate (26 % N).

All data were subjected to analysis of variance for each character using MSTAT-C (version 2.1, Michigan State University, 1991) and JUMP programme. The significance of genotypes were determined at the 5 and 1% probability levels by the F-test. The F-protected least significant difference (LSD) was calculated at the 5% probability level according to Steel and Torie (1980).

So as to find the natural grouped between varieties and examining the changes in the data, principal component factor analysis and cluster analysis as multivariate statistical analysis methods have been used (Johnson and Wicherin, 1992 and Adam and Hwangs, 1999).

Principal component analysis is concerned with explaining the variance-covariance structure through a few linear combinations of the original variables. Its general objectives are data reduction, and (2) interpretation.

Clustering (or grouping) is distinct from the classification methods. Cluster analysis may serve as a tool of selection and data reduction via similarity coefficient, similar genotypes may consider one genotype in the second test of performance if they have genetic diversity among them to avoid inbreeding effect. Cluster analysis is a more primitive technique in that no assumptions are made concerning the number of groups on the group structure. Grouping is done based on similarities or distances.

Results and Discussion

According to the two years analysis results obtained from triticale genotypes, it is proved that in the whole examined features, genotypes differences are statistically significant (Table 1).

Plant height is a good indicator of vegetative growth and is a different significance for triticale. Triticale is not a cereal produced for only seed. At the same time, triticale is a cool climate cereal largely used as stalks, straw, arises in the form of feed and forage grass silage at animal feeding and marginal conditions. Therefore, the length of stem is important. It has been expressed that is a feature genotypic of plant height by many researchers (Akulov, 1988; Yagbasanlar et al., 1988 and Atak and Ciftci 2006). Still, same researchers reported that the plant height was affected from growing techniques and environment conditions (Varughese et al., 1986; Akulov, 1988 and Yagbasanlar et al., 1988). Genotype 21 (108.5 cm) was smallest in terms of plant height while genotype 23 has the most value (128.7 cm) in the same character. Akgun et al. (1997a), Atak and Ciftci (2006) and Mut et al. (2006) reported that plant height in triticale was shortened due to deficient precipitation. Similar results were obtained by some previous researchers (Unver, 1999; Paksoy, 2005; Furan et al., 2005 and Alp, 2009).

Results of the present study revealed that spike length was the highest in genotype 3 but the lowest in genotype 8 and 21. Our findings were similar to the results of (Unver, 1999; Paksoy, 2005; Atak and Ciftci, 2006 and Alp, 2009). In addition, genotype 3 has the most value in terms of spikelet number/spike while genotype 21 was the lowest value. Many previous researchers were found similar results (Paksoy, 2005 and Atak and Ciftci, 2006).

Table 1
Average values of quantitative characteristics (2005-2006)

Genotypes	1	2	3	4	5	6	7	8
1	113.3	12.6	21.7	39.2	1.7	42.6	71.2	5315
2	116.1	13	22.5	46.4	2.09	43.1	69.4	5487
3	118.7	14	24.3	54.9	2.43	41.8	70.1	6481
4	117.8	13.2	23.1	45.5	2.19	45.1	69.9	6081
5	115.6	12.4	22	43.1	2.12	41.2	70	6026
6	120.8	13	22.4	46.9	2.15	44.2	70.3	6598
7	111.4	12.8	22.4	47.4	2.03	39.9	69.1	5932
8	119.8	11.9	23.3	52.3	2.34	42.7	70.7	6621
9	121.9	12.6	22.8	48	2.27	42.9	71.5	6138
10	118.1	12.7	21.7	50.1	2.2	40.8	70	6095
11	113.9	12.6	22	48.5	2.09	40.8	70.4	6593
12	116.1	12.2	21	46.4	2.07	44.2	70.6	6717
13	118	12.8	23.5	48	2.25	44.1	71.3	6723
14	120.3	12.4	21.9	48.8	2.11	41.6	70.7	6453
15	112.8	12.7	22.9	47.2	2.05	43.4	69.5	6642
16	114.7	12.4	21.6	46.6	2.1	40.8	69.8	5244
17	115.9	13.1	21.9	47.3	2.25	36	70.6	6027
18	118.4	13.5	20.8	47.5	2.38	45	71.2	6537
19	114.2	12.7	22.6	45.7	2.06	43.6	70.6	6400
20	117.3	13.3	21.7	43.1	2.11	42.1	70.7	5753
21	108.5	11.9	20.7	48.6	2.06	41	72.1	6281
22	128.7	12.7	22.4	46.5	2.21	44.3	71.2	6438
Average	116.9	12.8	22.2	47.2	2.15	42.3	70.5	6208
LSD (%5)	6.419	1.599	2.654	7.745	0.4622	6.654	2.781	123.3

Note: 1. Plant Height (cm), 2. Spike lenght (cm), 3. Number of Spikelet spike $^{-1,}$ 4. Number of Grain Spike $^{-1,}$
5. Weight of Grain Spike $^{-1}$(g) , 6. 1000 Kernel Weight (g), 7. Test Weight (kg 100 L^{-1}) , 8. Grain Yield (kg ha $^{-1}$)

The differences among the genotypes in terms of grain number spike^{-1} were found statistically significant. Grain numbers spike^{-1} levels of the genotypes ranged from 39.2 to 54.9. According to mean of two years, Genotype 3 gave the highest value with 54.9. In triticale, grains number spike^{-1} is an important yield component. Atak and Ciftci (2006), Yanbeyi and Sezer (2006) and Alp (2009) were reported similar results.

The differences between the genotypes in terms of grain weight spike^{-1} were found significant. The grain weight spike^{-1} of genotypes ranged from 1.70 to 2.43 g. The grain weight spike^{-1} was maximum in line Genotype 3. Akgun et al. (1997a) reported that spike number m^{-2}, grain number spike^{-1} and grain weight spike^{-1} is important factor for grain yield. Our results are in agreement to the findings of Akgun et al. (1997a) and Furan et al. (2005).

In this study, it was determined that the differences between the lines were insignificant in 1000 kernel weight. As seen in Table 1, 1000 kernel weight was ranged from 36.0 to 45.1 g according to the genotypes. It was obtained that Genotype 4 was high value (45.1 g); but Genotype 17 has small value (36.0 g) for 1000 kernel weight. Many previous researchers were reported similar results (Furan et al., 2005; Atak and Ciftci, 2006; Yanbeyi and Sezer (2006) and Akgun et al., 2007**)**.

Significant differences were found between the test weights of genotypes. The test weight of genotypes ranged from 69.1 to 72.1 kg. When we look at to see the test weight of genotypes, Genotype 21 was the highest (72.1 kg) while Genotype 7 has the least values. In triticale, the test weight is low because the grains are thin and wrinkle. Tosun et al. (1993), reported that the grain wrinkly had the complex genetic structure (cytological and physiological factors) in triticale. Nevertheless, they reported almost equal value of the test weight of genotypes improved in last years (Yagbasanlar et al., 1988). Our results were similar to the results of Akgun et al. (1997a), Tosun et al. (2000) and Mut et al. (2006).

Two-year results of our study indicated that there were statistically significant differences among grain yields of genotypes. In general, the first experimental year gave higher values for all characters although mean values the first year equal to the second year. The most important reason of this, total precipitation of March, April and May (156.5 mm) in first year were more than that of second year (79.3 mm).

Genotype 13 has the most grain productivity value (6723 kg ha^{-1}) whereas Genotype 16 has the least value (5244 kg ha^{-1}). Our results showed paralleling to the findings of Coplu (2001), Ozer et al. (2005), Paksoy (2005), Mut et al. (2006), Atak, and Ciftci (2006) but these results are contrast to the findings of Yanbeyi and Sezer, (2006) and Akgun et al. (2007).

Grain yield of genotypes obtained using 8 features were analyzed by multivariate statistical methods. The purpose of multivariate analysis was to determine the similarities and differences between genotypes. According to other characteristics specified, triticale genotypes were obtained in itself homogeneous classes. For classification, cluster analysis of matris based on to hierarchical algorithm of twenty-two genotypes has been performed. According to the results of factor analysis, only a cluster has been obtained (95% of total variance). Therefore, ignorant information lost is low degree in research (4.94%) (Table 1). KMO test has been 68.6% (0.686). Value of 68.6 is greater than 0.50. Accordingly, datas have been determined to be suitable for factor analysis. Bartlett's test is significant (Table 3). There are high correlations between genotypes. In other words, this datas are suitable for the factor analysis. According to the results of factor analysis, genotypes studied have similar properties significantly. Therefore, more than one principal component (PC) has not been found (Table 2). However, rankings of genotypes according to their importance can be made by arrangement with varimax rotation. Genotype 9 has been the most important genotype, Genotype 6 and 15 has been following it. Communality values were obtained for to find the common variance between genotypes. The highest common variance values were determined at Genotype 9 and 16. Genotype with the lowest common variance, or the different genotypes, Genotype 5 and 7 are genotypes. The emergence of very low variance matrix values is indication of high reliability degree of the data. Accordingly, the results are statistically significant.

According to the dendogram results produced by cluster analysis, the highest similarity ones between genotypes are; Genotype 17 and 11, Genotype 19 and 14, Genotype 8 and 6, Genotype 9 and 2, Genotype

Table 2
Principal components and communalities rates

	Principal		Variance matrix, ε_{i}, Ψ	Varimax Rotasyonu
Varieties	Components Coefficients	Communalities, h_i^2		
Genotype 1	0.9746	0.9798	0.0502	Genotype 9
Genotype 2	0.9753	0.9512	0.0488	Genotype 6
Genotype 3	0.9758	0.9521	0.0473	Genotype 15
Genotype 4	0.9742	0.9491	0.0509	Genotype 11
Genotype 5	0.9703	0.9415	0.0585	Genotype 17
Genotype 6	0.9765	0.9536	0.0464	Genotype 3
Genotype 7	0.9729	0.9465	0.0535	Genotype 18
Genotype 8	0.9757	0.952	0.045	Genotype 8
Genotype 9	0.9768	0.9542	0.0458	Genotype 13
Genotype 10	0.9754	0.9514	0.0486	Genotype 10
Genotype 11	0.9759	0.9523	0.0477	Genotype 16
Genotype 12	0.9742	0.9491	0.0509	Genotype 2
Genotype 13	0.9754	0.9515	0.0485	Genotype 19
Genotype 14	0.9752	0.9509	0.0491	Genotype 14
Genotype 15	0.9764	0.9534	0.0466	Genotype 22
Genotype 16	0.9753	0.9512	0.0488	Genotype 1
Genotype 17	0.9759	0.9523	0.0477	Genotype 20
Genotype 18	0.9758	0.9521	0.0479	Genotype 4
Genotype 19	0.9752	0.951	0.049	Genotype 12
Genotype 20	0.9743	0.9492	0.0508	Genotype 21
Genotype 21	0.9738	0.9482	0.0518	Genotype 7
Genotype 22	0.975	0.9506	0.0494	Genotype 5
Prp. Total	20.913			
Exp. Var.		0.9506		

Table 3
KMO and Bartlett's Test

Kaiser-Meyer-Olkin Measure of Sampling Adequacy		0.686
Bartlett's Test of Sphericity	Approx. Chi-Square	3041.21
	Df	231
	Sig.	0.000

20 and 7, Genotype 4 and 1 (Figure 1). The correlation between Genotype 9 and 2 have been very high found. This result shows that there is a similarity between the two genotype. Therefore, breeding study is done between these two genotypes can say that it is unnecessary. To obtain new superiority genotypes, dissimilar genotypes should be considered in breeding programmes. In this study, Genotype 1 and 5 have been determined as genotypes the most distant to each other. According to the results of the cluster analysis with complete linkage method, examined genotypes are divided two main clusters (Figure 2). Main clusters are divided into two sub-clusters. Therefore, genotypes can be classified into four sub-clusters. The first main cluster 15, the second main cluster is located in the seven genotypes. Genotypes show a high degree of similarity. However, according to the results of cluster analysis, although the small, there are differences between genotypes. Therefore, the genotypes are divided into 14 sub-classes.

Conclusion

In our study, regarding the plant height, spike length, grain number spike-^{1},1000 kernel weight, test weight and

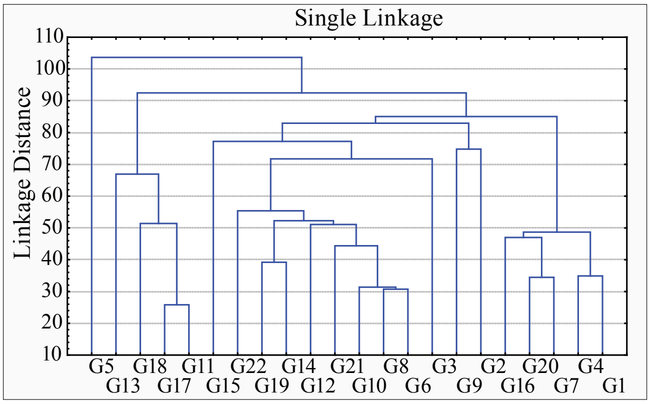

Fig. 1. Dendogram obtained by cluster analysis on the initial data

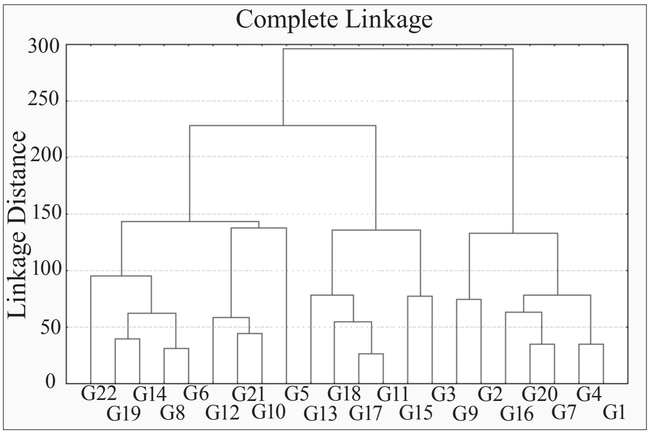

Fig. 2. Dendogram obtained by cluster analysis on the initial data

grain yield recorded the highest value (respectively; the genotype no. 23, 3, 31 ,4, 21 and 13). According to the two years results, the differences between triticale genotypes were found to be statistically sinificant in all components observed. The differences between the years were proved significant in all components. According to the results of factor analysis, triticale genotypes have similar properties significantly. Therefore, more than one major component has not been found. However, it was found one principal component (PC1) by factorial analyses. In addition, twenty-two examined cultivars were separated in two main groups by cluster analyses.

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Received June, 2, 2012; accepted for printing January, 7, 2013.