Detection of Quality Diversity of Durum Wheat (*Triticum durum* Desf.) Using Cluster and Principal Component Analyses

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Abstract

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The present work was carried out to study quality diversity among 15 accessions of durum wheat from the collection of the National Gene bank in Bulgaria. Cluster analysis results showed that accessions Agathe, Mauragani iraclion, [1]97102050 and the unique Kubanka were more specific. They combine high protein content with a high quality of gluten and are preferable to accessions with high protein and gluten content but insufficiently strong gluten. The results of Principal Component Analysis suggested that the most variable characters were the gluten softening of grain and semolina and the gluten compressibility of grain and semolina. They were responsible for the clustering of accessions in the present study.

Key words: cooking score, durum wheat, gluten, pigment content, protein

Introduction

Durum wheat is a main row material for pasta products due to its balanced components that interact during processing, allow receiving products with desired quality. The principal quality objectives of durum wheat variety development - protein content and gluten strength are factors in pasta cooking quality, and pasta color, as primary market traits. Varieties that combine high yellow pigments (over 7 ppm), protein concentration (over 15-16% dm) and strong gluten give pasta with a bright yellow color and good cooking quality (D'Egidio et al., 1990; Landi and Guarneri, 1992). One of the most important factors determining processing potential is the variety, which makes it necessary to breed durum wheat with high intrinsic quality that is key to market recognition (Dexter and Marchylo, 1996).

The development of the introduction

work on the collection of durum wheat maintained at the National Gene bank of the Institute of Plant Genetic Resources in Sadovo gives wide range of accessions diverse both by their origin and by a complex of biological and economic traits. Appling appropriate methods and criteria for evaluation are the base of selection valuable germplasm as an initial form for high quality breeding. The assessment of genetic diversity or similarity is not only important for the improvement crop efforts but also for effective management and protection of germplasm resources.

This information can be obtained by applying cluster analysis (Ward, 1963). Here the accessions included in the study are grouped according to the behavior of the traits in relation to average values. The implementation of cluster analysis does not give an opportunity to find out those traits that have contributed the most of grouping the accessions. This determination is necessary in order to get a better idea on quality of accessions and to determine the presence of additional traits in order to use in effective breeding programs.

The principal component analysis (PCA) is one of the multivariate approaches of grouping, based on similarity coefficients or variance-covariance of the component traits of the entries. This gives more information about major groups, while a cluster analysis provides higher resolution among closely related accessions. (Lin et al., 2001). Joint application of both analyses gives a clearer view the importance of quality traits used in clustering the accessions studied (Phillipeau, 1990; Rachovska et al., 2002).

The present work aims to determine the similarity/diversity of durum wheat accessions based on many qualitative traits and to explain the causes of the clustering.

Materials and Methods

The grain samples consisted of fifteen durum wheat accessions (*Triticum Durum Desf.*) with different origin from the collection of the National Gene bank for three crop years were studied. Ten accessions originate from France, two from Greece and each one from Bulgaria, Jordan and Russia (Table 1). The field experiments were conducted using a randomized block design with four replications and a harvest plot of 10 m^2. During the vegetation period phenological records were taken regularly according to "Descriptors for Wheat" (1994). Results were reported by Popova (2001).

Quality assessment
The grain physical characteristics (test weight and 1000-kernel weight) were

Table 1
Origin of *Triticum durum* accessions

Accession/Cat.Number	Origin
Zagorka 88102002	Bulgaria
Mauragani iraklion 97102012	Greece
Moundros 97102013	Greece
Jordan C-53 97102025	Jordan
Kubanka 1908	Russia
Agathe 87102065	France
Cham 1 94102031	France
97102041	France
97102046	France
97102050	France
97102051	France
97102055	France
97102061	France
97102065	France
97102076	France

determined according to approved Bulgarian standard methods. Wheat samples were cleaned and tempered to 16.5 % moisture and milled into semolina using an adapted QC-109 laboratory mill "Labor Mim" (Petrova, 1993). An average semolina rate, on a clean wheat basis, of 57 % was obtained. Processing of the pasta product (micro disk with 7 mm diameter) and cooked disks quality, expressed as a cooking score from 1 (very poor) to 8 (very good) were carried by the micro procedure described by Alause (1977).

Protein content of grain and semolina (N x 5.7, % dm basis) was determined by the Kjeldahl method. Wet gluten content (at 14 % mb) was determined on 25 g samples using a gluten washer and distilled water (BDS 13375-90). The gluten strength was assessed by a SDS-sedimentation test of whole meal and viscoelasticity of wet gluten BDS 13375-90. The SDS-sedimentation value was determined according to the ICC Standard method 151, but using a 3 % solution of SDS (Dexter et al., 1980). The grain gluten strength was graded by IDK apparatus compressibility with scores ranging from 0 to 120 as follows: 45–75 units = strong; 20-40 and 80-100= middle; 0-15 and 105-120 = weak gluten. The grading according to gluten softening was 5-8 mm = strong, 9-12 mm = middle and over 12 mm = weak gluten. The yellow pigment content of grain was determined by the ICC Standard method 152 as b-carotene from a standard curve.

Statistical analyses

After standardization of the data a hierarchical cluster analysis UPGME for average values was performed considering to the complex effect of the analyzed traits. The computer software STATISTICA FOR WINDOWS 4.3 was used. The genetic distinctiveness was calculated by determine the Euclidean distance between two objects in the multidimensional space, defined by the studied traits, and was illustrated by a dendrogram. A principal component analysis leading to a respective clustering was made.

Results and Discussion

The dendrogram in Figure1 visualized the hierarchical grouping of the evaluated accessions for three years. At a relatively low level of 3 distant units, they group in four clusters.

The cluster I consisted of French accessions with numbers 97102076, 97102061, 97102041 grouped along with accession from Bulgaria cultivar 'Zagorka'. They were described as heaving heavy grain, high test weight and protein content, and satisfactory to good cooking quality, but have weak gluten, poor viscoelasticity and low SDS-sedimentation value (Table 2). Genotypes [1]97102076 and [1]97102061 were early to mature. The [1]97102076 was also high yielding, an average of 4.25 t/ha (Popova, 2001).

The dendrogram showed close similarity among the accessions '[1]97102050', 'Agathe' and 'Mauragani iraclion' in the cluster II, grouped according to the 13 studied traits. They were characterized by heavy grain, high test weight and a low yellow pigment concentration (5.35 ppm), according to present standards (Table 2). These accessions had also the highest protein and wet gluten content, and the strongest gluten. This definitely reflected in superior cooking quality to rest of the accessions.
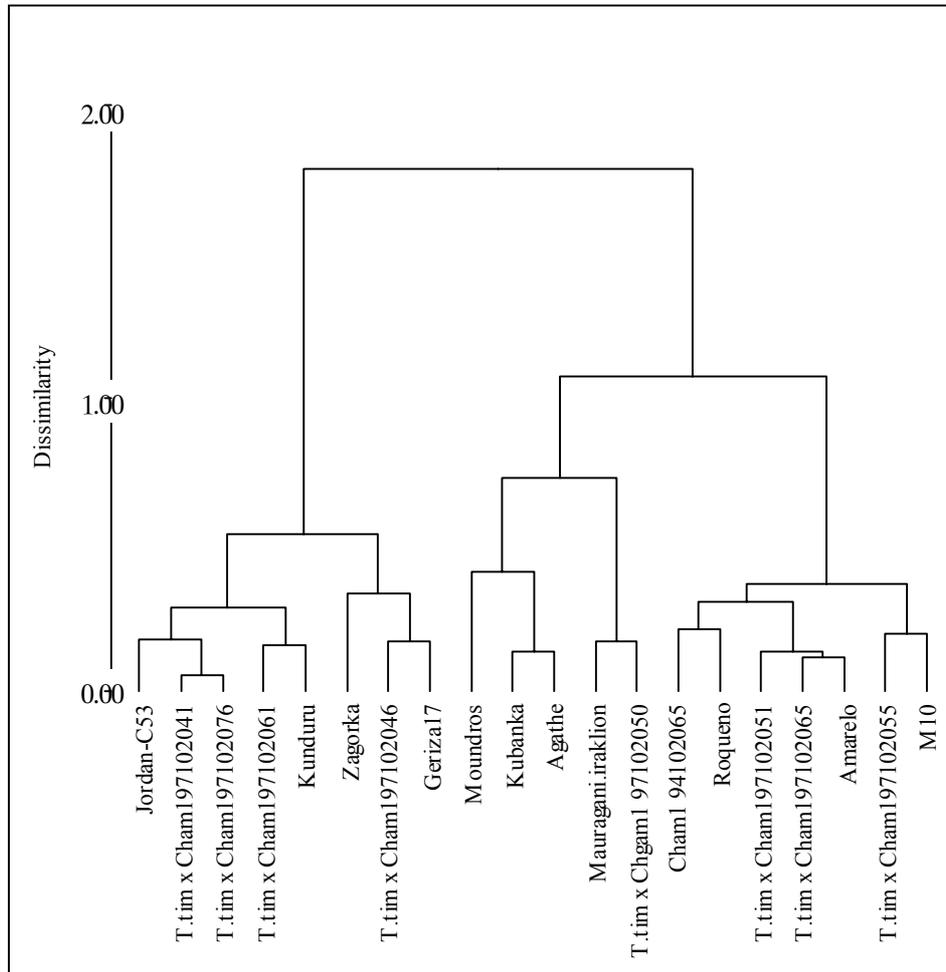
So '[1]97102050', 'Agathe' and

Fig. 1. Dendrogram

'Mauragani iraclion' belong to durum wheat of excellent pasta quality, and they can be recommended to breeders as gene source of high protein and pasta quality. In addition, these genotypes had a good agronomic performance. Agathe and '¹97102050' had good tillering capacity and cultivar Mauragani iraclion was high yielding (4.05 t/ha). The spike length of genotype '¹97102050' was great, leading to an increased grain spike numbers as

well as a heavier overall seed weight per plant (Popova, 2001).

The cluster III consisted of accessions with catalog numbers 97102065 and 97102051. The first one was high productive with a large number of kernels in spike (Popova, 2001). Both genotypes had high protein/gluten content, middle to strong gluten and good cooking quality. In the other hand they formed grain with the lower test and kernel weight but with

Table 2
Average values of traits for each of four identified main clusters

Qualitative traits	Cluster 1	Cluster 2	Cluster 3	Cluster 4
Grain				
Test weight	78.4	77.9	76.1	77.9
1000 kernel weight	38.6	40.9	34.9	39.4
Protein content	15.8	16.9	16.3	14.9
SDS -sedimentation value	27.9	49	40.3	40.2
Wet gluten	30.1	33.1	31.4	28.8
Gluten softening	11.3	6.3	8.6	7.8
Gluten compressibility, IDK	94.8	76.4	84.5	83.9
Semolina				
Protein content	14.8	15.9	15.2	14
Wet gluten	32.2	35.1	33.5	30.7
Gluten softening	14.5	7.2	9.1	9.1
Gluten compressibility	105.5	79.4	87.5	88.4
Pigment content	6.59	5.35	6.72	4.93
Pasta disk				
Cooking score	5.6	8	7.3	6.7
Cooking score	0.378	0.503	0.48	0.479

highest content of yellow pigment in semolina. The average value of yellow pigment for ¹97102065 amounted to 7.52 ppm db while maximum value was 8.9 ppm db. Therefore, the accessions of the third cluster could be used as a source of high protein content and ¹97102065 in particular as an initial material of deep yellow pigment in the breeding.

In the IV cluster French accessions 'Cham1' and '¹97102055' were most closely connected at a level less than 2.1 distant units. They were described as having large kernel and high test weight, gluten of middle strength, good cooking quality, lowest protein and gluten content in grain and semolina, lowest pigment content in semolina, than the accessions of the other clusters (Table 2).

The great distance between four main clusters in the dendrogram showed genetic diversity of the studied accessions. Those from the second, third and forth clusters were linked at a high level - 5.1 units and in their turn were linked at higher distant units - 5.6 with the accessions from the first cluster.

'Moundros' (¹9710213) at level 3.4 units; 'Kubanka' at 3.5 units; '¹97102046' at 4.4 units and 'Jordan C 53' at level 4.5 units formed separate clusters. Accession 'Moundros' (Greece) had very strong

Table 3
Average value of traits of accessions at separate clusters

Qualitative traits	Moundros	Kubanka	97102046	Jordan C53
Grain				
Test weight	77.3	78.4	71.7	77.8
1000 kernel weight	38.9	36.6	34.6	37.6
Protein content	15.0	18.0	16.7	17.7
SDS sedimentation value	57.0	61.0	32.0	27.3
Wet gluten	28.3	35.7	31.3	33.8
Gluten softening	4.5	7.7	13.2	12.0
Gluten compressibiliti,IDK units	69.0	83.0	100.7	96.7
Semolina				
Protein content	13.94	16.84	15.7	16.56
Wet gluten	30.2	37.6	33.0	35.5
Gluten softening	5.8	8.5	17.2	14.8
Gluten compressibility,IDK un.	72.7	87.7	113.2	107.8
Pigment content,ppm db	3.38	5.33	7.19	4.98
Pasta disk				
Cooking score,1-8	7.0	8.0	5.7	7.0
Cooking score/prot.cont.of smolina	0.502	0.475	0.363	0.423

gluten and a very good cooking quality, but showed the lowest color potential of semolina (Table 3).

Despite the high stem (141 cm) and low grain productiveness (an average of 1.53 t/ha) 'Kubanka' (Russia) was unique with high values of SDS-sedimentation, protein, and gluten content in grain and semolina as well as excellent cooking score. It can be successful donor in breeding programs for good quality.

Accessions '¹97102046' (France) and 'Jordan C 53' (Jordan), which were also form separate clusters, have high protein content, very poor gluten described as having low SDS-sedimentation value and poor visco-elastic properties. Accession '¹97102046' could ensure a lot of yellow pigment to durum wheat breeders, whereas 'Jordan C-53' proved good cooking quality but very low content of yellow pigment in semolina, and this would affects undesirable color of end-used products.

The principal component analysis was applied to specify the causes of the separation of the accessions. In our study 98.5 % of the variation in the estimates of similarity was revealed by the first two components indicated the suitability of qualitative traits used. In Table 4 was shown that the characters of gluten strength, such as - gluten softening of grain and semolina, and gluten compressibility of grain and semolina had the greatest impact as far as clustering is concerned.

Table 4
Results of Principal Component Analisis

Properties	Principal	Compon.
Protein content of grain, % db	-0.195	0.969
Protein content of semol., % db	-0.200	0.968
SDS sedimentation value, cm3	-0.890	0.090
Wet gluten of grain, %	-0.353	0.920
Wet gluten of semolina, %	-0.337	0.915
Gluten softening of grain, mm	0.944	0.306
Gluten softening of semol, mm	0.955	0.206
Gluten copr. of grain, IDK un.	0.949	0.277
Gluten copr. Of semol., IDK un	0.947	0.239
Cooking score, 1-8	-0.873	0.234
Pigment content, ppm db	0.648	0.260
1000 kernel l weight, g db	-0.295	-0.337
Test weight, kg	-0.224	-0.255
% of the total variance expl.	96.700	1.800

The relatively variation of these characters correlated very strongly with the first principal component which has explained about 96.7% of the total variation. Approximately 1.8% of variation was explained by the second component that most closely correlated with relatively variation of protein and gluten content in grain and semolina.

The analyses made accurately differentiate the excellent durum wheat accessions from all others. The results obtained suggested that 'Agathe', 'Mauragani iraclion', '97102050' and the unique 'Kubanka' were more specific, combining high protein content with a high quality of gluten. Their genes of adaptivity determined the quality diversity and were preferable than accessions with high protein and gluten content but insufficiently strong gluten.

Mutual application of cluster and principal component analyses can advance research work on the evaluation of quality diversity in wheat collections and provides more opportunity for effective breeding programs.

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