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Study of wheat genetic variation in base collections

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Abstract

The aim of this study was to investigate the main morphologic and biometric parameters, and the production index, in 20 wheat accessions (*Triticum aestivum* L.), from the base collection of the Gene Bank in Albania. The studied morphological parameters were: plant height (PH), spikelet for spike (SS), grain weight per spike (GWS), spike weight (SW), 1000 grain weight, days to maturity (DM). Collected data indicated that genotypes present significant differences for PH; the number of SS, there is a high difference of GWS (g per spike). High differences were presented for days to maturity (DM). Also some genotypes have high protein content (12-15.2%) and the gluten content with an average 21.6-35.6 %. Results taken were analyzed for relations between characters in wheat genotypes. Hierarchical Cluster Method was used to observe relation and distance among genotypes. The collected data by this study will be as additional information for Gene Bank and to be used in the plant improvement programs.

Keywords: accessions, base collection, Cluster method.

1. Introduction

The Albanian Gene Banks offer the main means to store PGR, protect genetic materials and to provide the raw material for the plant breeders. The study of the base collection showed that there is a high genetic diversity of wheat cultivars, bean populations, and the collection of the medicinal and aromatic plants [6]. Base collection contains more than 650 wheat accessions. Wheat landraces in Albania have been planted in a considerable number (about 60 nominations) until the 1950' [11]. In the '60 – '80-s of the last century, a considerable number of wheat lines and cultivars are created in the Agriculture Research Institute of Lushnja and in the Plant Breeding Department of the Agriculture University of Tirana. The wheat cultivars created in the country were almost entirely cultivated in the whole surface of Albania for over 20 years. In the '90-s, the surface cultivated with wheat decreased, the usage of wheat cultivars created in the country was reduced and the public investments for the creation of new varieties dropped. In such conditions, the Gene Bank was set up and nearly all the wheat cultivars created in the country was deposited in it, Gene Bank. The majority of this material is not characterized and evaluated for the features of the genotypes preserved, which are in storage. The study of the variation presence in the collections of wheat cultivars is carried out using biomorphologic characterization [9]. Understanding the diversity conserved worldwide of the germplasm collections (*in-situ*, *ex-situ*, *on-farm*) and harnessing its potential for improving and adapting crops to meet the challenges faced by the world populations will highly accelerate food and nutrition security, thus contributing in this way to alleviating poverty and to a better nourishment through a more balanced and healthy diet. It is a prerequisite to accomplish harmonious and sustainable development [2]. Singh and Dewivedi [12] have reported significant positive association of grain yield plant^{-1} with number of spikes bearing tillers plant^{-1} both at genotypic and phenotypic levels. The investigation of morphological treat (plant height, index of 1000-kernel weight, grain per spike, etc) is very significant to evaluate wheat germoplasm [13]. In the domestic wheat accessions, the content of wet gluten is also high, and ranges from 21.60 % to 38.80 %, with an average value 28.40 % [10]. Improvement of the production traits may be effective for the selection of the genotypes for higher grain production [8]. The study of the base collection showed that there is a high genetic diversity of wheat cultivars [4].

The protein content, as an indicator of the quality of grain, ranges from 12.47 % to 17.00% with an average value 14.18%, which are considered high values [1]. The study of the new wheat cultivars in different areas of cultivation in our country has indicated significant differences in their adaptation to the eco-climatic conditions of each area [5]. Every year, the Gene Bank undertakes the study of a certain number of these genotypes. The goal of this study was to evaluate different components, production elements, the extension of the vegetative period and chemical parameters content of the twenty wheat genotypes on trial. The results of the study are deposited in the Gene Bank. The information gathered will be useful by breeders for the future wheat genetic improvement programs.

2. Materials and methods

For this study is studied wheat collection that breeder by Albanian Research Institute and conserved at Gene Bank. During 2012 and 2013 are selected twenty wheat genotypes and carried out characterization and evaluation to genotypes list (table 1).

Table 1. List of twenty wheat genotypes with their origin and source

Genotyp	*Code of genotypes*	*Source*	*No*	*Code of genotypes*	*Source*
G01	AGB0505	AGB	G11	AGB0516	AGB
G02	AGB0506	AGB	G12	AGB0517	AGB
G03	AGB0507	AGB	G13	AGB0519	AGB
G04	AGB0508	AGB	G14	AGB0520	AGB
G05	AGB0509	AGB	G15	AGB0521	AGB
G06	AGB0510	AGB	G16	AGB0522	AGB
G07	AGB0511	AGB	G17	AGB0523	AGB
G08	AGB0512	AGB	G18	AGB0524	AGB
G09	AGB0513	AGB	G19	AGB0525	AGB
G10	AGB0515	AGB	G20	AGB0526	AGB

AGB = Albanian Gene Bank

The field experiments were carried out at the Didactic Experimental Economy of the Agriculture University of Tirana (ordination. Latitude 041^0 23’ N; Longitude 019^0 47’ E; Altitude 4.5 m). The seeds were sown on November 19. Each plot was planted in five rows; the plot size was 5 m × 1.2 m. Normal agro technical practices were applied to the experimental material throughout the vegetative period. Harvesting was done by uprooting of plants and boarder rows/plants were omitted for collection of samples. Observation was made from ten randomly selected plants and data were taken on plant height (PH), spikelet’s per spike (SPS), grains per spike (GS), 1000 kernel weights (1000 W), days to maturity (DM) and yield kv/ha (YKH) (with moisture 14 %).. Analysis was performed by Multivariate Principal Components Analysis. Scatter plot was used for determined Correlation coefficients between days to maturity with various characters. The dendrogram were estimated according to Hierarchical Clustering Method.

3. Results and discussion

The extent of variability for any character is very important for the improvement of a crop through breeding. The data for some characters revealed for all the genotypes presented on the table 2.

Analyzing the morphological parameters, differences among the genotypes are noticed. Plant height ranged were between 68.4 minimum (G01) to 94.8 maximum (G18). The results reported by Fetahu *et al.* [7] for plant height have been from 70.8 to 79.05 cm. Spikelets per spike were from 15.6 to 20.8 while the grain per spike was from 27 to 54.2. The number of grains per spike and the weight of 1000 grains are the main contributors in the grain production of wheat [3].The value for the of 1000-grain weight were between 35 to 49.2 and days to maturity were min. 183 days (G02 and G03) to max. 199 (G07). Genotypes showed highly significant differences for grain yield kv-1 (Table 2). Mean data showed that grain yield kv^{-1} ranged from 46 kv ha^{-1} to 66 kv ha^{-1}. In Table 3, it is presented the correlations among the parameters evaluated.

Correlation coefficients were computed among 5 traits (Table 3). There were positive correlations and significantly between the number of spikelet’s per spike with grains per spike, value of correlation (r = 0.49*, and r = 0.54* $P \leq 0.05$).

Table 2 Mean performance for morphological parameters, evaluated in twenty wheat genotypes.

GT	*PH*	*SS*	*GS*	*1000 GW*	*DM*	*YKH*
G01	68.4	20.6	35.4	38	184	52
G02	85	16.4	27	40	183	46
G03	71.4	16.6	27.8	39.4	183	47
G04	75.4	17.2	36.8	49.2	195	58
G05	78.4	15.8	37.4	46.2	198	47
G06	89	16.6	30	37	198	52
G07	78.8	20.4	51.8	38	199	62
G08	80	18	45.2	42.4	197	56
G09	72.4	18.8	50.2	36.4	197	63
G10	91.8	18	40.4	37	197	53
G11	91.2	20.8	54.2	35	195	66
G12	90.2	18.2	45	39.2	196	53
G13	88	18.4	36	44.4	184	46
G14	81.2	18.4	39.8	41.8	198	52
G15	93	19.6	44.6	39	198	55
G16	92.8	17.8	37.2	39.6	197	51
G17	85	19.4	36.2	40.2	196	47
G18	94.8	20.2	47.6	41.4	196	58
G19	78	15.6	27.6	36.4	194	48
G20	83.8	18.8	44	42	195	62

Table 3. Analysis of correlation coefficients

	PH	*SS*	*GS*	*1000 GW*	*DM*
SS	0.23				
GS	0.24	0.44			
1000 GW	-0.14	-0.35	-0.15		
DM	0.33	0.05	0.54*	-0.05	
YKH	0.06	0.49*	0.83**	-0.22	0.45*

Table 4. Multivariate Principal Components Analysis

Nr.	*Eigen value*	*Percent*	*Percent*	*Cum Percent*
1	2.2102	44.204		44.204
2	1.0695	21.391		65.595
3	0.9209	18.418		84.012
4	0.6622	13.244		97.256
5	0.1372	2.744		100.000

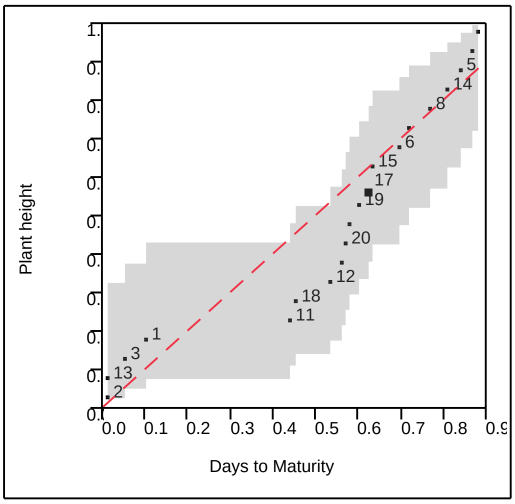

Figure 1. Scatterplot, Days to Maturity and Plant height

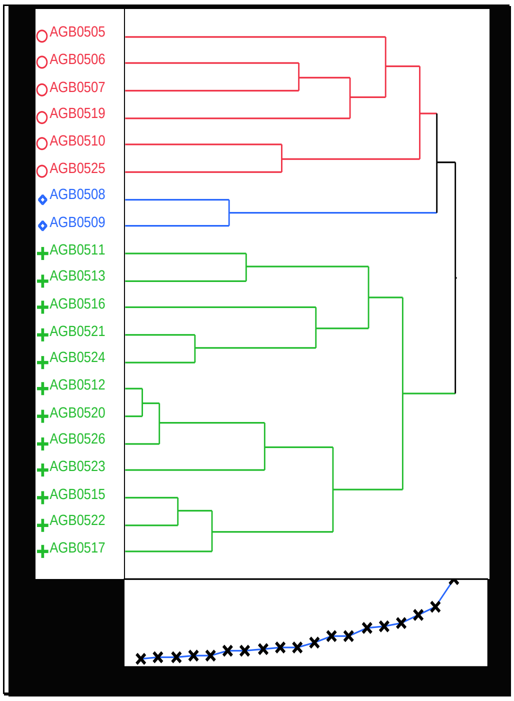

Figure 2. Dendrogram for twenty wheat genotypes

Highly significant correlation showed between grains spike with yield hectare^{-1}, levels in r = 0.83** $P \leq 0.01$). There were negative correlation between plant height with grain per spike and spikelet‘s per spike, 1000 grain weights.

Based on Principal Components Analysis (PCA), it is indicated that the two components (1) make up 44.2 % of the variability impact among the genotypes, thus the impact of these features is estimated to be significant. In the graph below (Figure 1), it is shown the correlation observed between the plant height and the days to maturity.

Analyzing the correlation between the plant height and the days to maturity, showed that four genotypes (G01, G02, G03 and G13) have weak negative correlation for the feature plants with short body with the days to maturity while the other genotypes have positive correlations. While all the other genotypes are within significant the limits. To determine the genetic distance between the genotypes and to identify the variation within the population, the hierarchical analysis Hierarchical Clustering Method = Ward was applied.

Dendrogram (Figure 2) consists of genotypes average values and shows the hierarchical relationship among and within the genotypes which resulted in three groups. The first group included in the 1st group-cluster was similar between them and they showed characteristics of were of six genotypes; second were two genotypes and the third group were of twelfth genotypes.

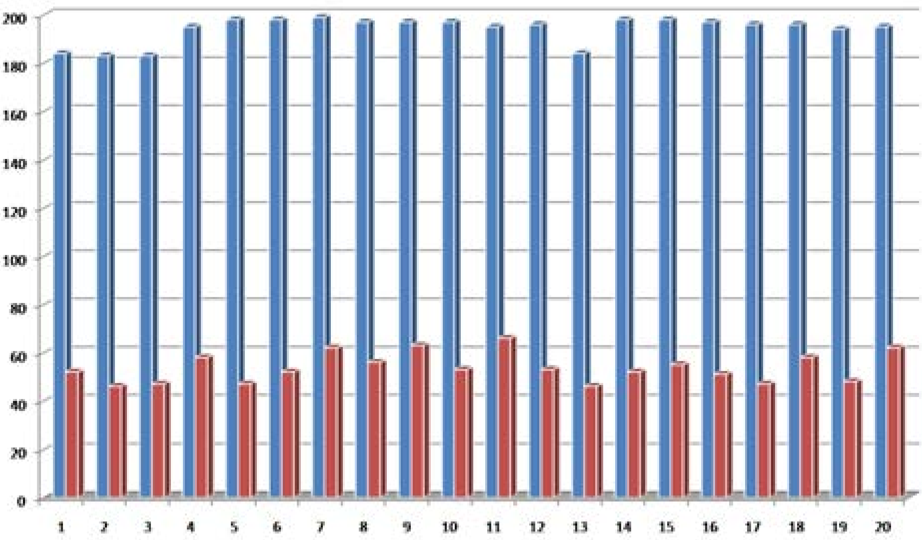

Figure 4. Days to maturity and yield kv ha^{-1} for twenty wheat genotypes

Correlation between the days to maturity and the yield kv ha^{-1} is presented in graphic (Figure 3). The data show that there are not the correlation between the days to maturity and the yield kv ha^{-1}. The positive correlations observed between length of the period days to maturity with grain yield at G07, G09, G11 and G20 but the negative correlations observed at G05, G06, G10, G17 and G19.

The indicators of the quality of grain

Also some genotypes have high protein content 12 % - 15.2% and the gluten content with an average 21.6-35.6 %. The evaluation results of twenty wheat genotypes are conformity with results reported by Arapi V.et. [1] to the protein content and by Përmeti M.[10] for the content of wet gluten.

4. Conclusions

Twenty accessions of wheat collection have been evaluated for quality and quantity indicators. Wheat genotypes are characterized by high genetic variability for morphological treat, vegetative period and yield capacity. Based on achieved results from field trial, showed differences as results of genetic diversity. The information and the results of this study increase usage value of the genetic collection conserved in Gene Bank and can be used in developing programs on wheat breeding in the future.

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