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Agronomical characterization performance of 100 common wheat (*Triticum aestivum* L.) accessions

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Abstract

The aim of this study was to assess the agronomic characteristics of common wheat (*Triticum aestivum* L.) germplasm, maintained in *ex situ* collection at Plant Genetic Resources Institute (PGRI), Agricultural University of Tirana. Total of 100 wheat accessions were planted under field condition and their agro morphological characters (14 quantitative traits) such us, plant height, spike length, 100 kernel weight, days to maturity were recorded. The results show that the highest value of plant height trait was recorded in AGB 0150 accession (167 cm), meanwhile two accession recorded the highest number of spikelet per spike ±25.8 (AGB 0013 and AGB 0138). Positive correlation are observed among descriptors, as number of kernel per spike and kernel weight trait (r=0.85), also data show positive relation (r=0.529) between spike length and number of spikelet for spike. The divergence between accessions was observed using Cluster analyze. The accessions were gathered in 6 major groups (cluster 5 with 38 accessions and cluster 2 with 27 accessions). Based on this analyse accessions in cluster 2 and 5 were the nearest neighbour with the lowest divergence levels meanwhile wheat genotype grouped in cluster 3 and 4 presented the farthest one.

Keywords: *Triticum aestivum* L., germplasm, accessions, agro morphological, trait, cluster.

1. Introduction

Wheat because of its crucial nutritional value and its significant share in daily energy intake was one of the most important cultivated food crops and for 8 000 years has been the fundamental staple food of the majority human civilizations of Europe, West Asia and North Africa [6]. World wheat production is almost based on 2 wheat species, common or bread wheat (*Triticum aestivum* L.), which represents about 90% of world production, and durum wheat (*Triticum turgidum* subsp. *durum*), which accounts 10% of wheat production [3]. In fact, bread wheat is a very diverse and widely adaptable cereal crop [12]. Its landraces are distinguished by their genetic variability and heterogeneity. Therefore, this genetic diversity needs to be characterized and measured it may be useful in breeding programs and also conservation and management of plant genetic resources [15]. Genetic variability evaluation based on morphological characters of economic interest might be used to choose suitable materials in breeding programs for

crop improvement [7]. Also, in comparison to biochemical traits, morphological traits had crucial role in genetic study due to the ease of their identification, and their simple mode of inheritance in comparison to quantitative traits [13]. For that reason, markers to describe genetic diversity are morphological and agronomic traits celebrated as descriptors and presented by the International Plant Genetic Resources Institute (IPGRI) [11], [15]. As reported [1] quantitative traits are often used to assess and describe wheat characters due to their role in the estimation of genetic diversity and discrimination of closely related types. Albania is an area rich in crop biodiversity, it is characterized by a high diversity of climatic and agronomic conditions. Therefore a total of 100 wheat accessions were planted under field condition and their agro morphological characters (14 quantitative traits) such us, plant height, spike length, 100 kernel weight, days to maturity were recorded to evaluate morphological diversity.

2. Material and Methods

Our study is based on the characterization of the diversity of bread wheat (*Triticum aestivum* L.). The plant material is characterized by a survey on land and laboratory, during the year 2015-2016 in the experimental field of the Agricultural University of Tirana. During the crop year, the accessions were evaluated using 14 characters of quantitative type. These characters were: tillring capacity(TC), plant height (PH), spike length (SL), number of spikelet per spike(NSpkSp), number of seeds per spikelet (NSeSpk), number of seeds per spike (NseSp), seed size (SeS) and weight of seeds per spike (WseSp). Part of the survey was number of days from sowing to germination (SG), number of days from germination to spikelet (GSpk), days from spikelet to flowering (SpkF), number of days from flowering to maturity (FM), number of days from germination to maturity and days to maturity (DM). Morphological characterization of the accessions was conducted according to international standards, particularly those of the International Plant Genetic Resources Institute [9].

Statistical analyses: After transferring data over a matrix, statistical tests were carried out by the Statistical Package for Social Sciences (version 21) and JPM. *Analysis of variance (ANOVA)* was used to calculate variation among accessions, using the JPM software. *Hierarchical Ascendance Classification (HAC)* or cluster analysis, was used to calculate the mean data of accessions using the SPSS software to better classify the 100 accessions of bread wheat. *Principal components analysis (PCA)* was carried out on the correlation matrix calculating the mean data of the accessions.

3. Results and Discussion

These findings could be a result of their genetic differences. The development of different morphological traits in wheat is a highly coordinated process; therefore, for an effective breeding program, it is necessary to consider all of the important traits that have an impact on grain yield performance [14]. Mean values of quantitative traits measured for 100 *Triticum aestivum* accessions are presented in Table 1. According to the mean values for the trait days to flowering the wheat genotypes AGB0024 and AGB0025 were the earliest genotypes (37 days) and AGB0143 the latest genotype (61days). Days to maturity ranged from 207 to 223 with an average of 213.99.

A large variation was found for plant height trait among 100 wheat genotypes where genetic differences are reflected. Common wheat accessions represented a mean value of 105.097 cm for PH trait with a variation from 82.7cm (AGB0145) till a maximum of 167cm (AGB0150). Our results are higher from those reported from other authors [5,9,10]. Different results [14] obtained for wheat plant height ranging from 62 cm to 110 cm, while [2] reported a range from 71 to 79cm for plant height in different bread wheat genotypes.

The results of this study show a mean value of 2 for tillring capacity trait where AGB0151 recorded the higher value (3.7). These results are lower from those reported from [19]. According to [19] most of the variations in the wheat plant height variations are attributable to differences in internodes length rather than internodes number. Spike length varied from 5.95 cm in AGB0147 to 12.37 cm in AGB 0032 (table 1). Results of our study are higher from those reported from [19]. In terms of the spikelet number our results are within the limits reported from other authors [9,10,19]. AGB 0013 and AGB 0138 were the two wheat accessions with the higher value recorded ($\pm$25.8) for NSpkSp. Grain yield is influenced by spike properties and the spikelet number plays a very important role in wheat grain yield. The grain number for spikelet ranged from 2.00 (AGB 0146) to 4.00 (AGB 0013), and according to [20] when wheat is stressed during reproductive development, the grain number in fertile florets is reduced. As for the number of seed per spikelet trait we observed a high variation among 100 wheat genotypes (from 10 till 72.6), where AGB 0057 presented the highest value for this trait.

The grain number is regarded as the main wheat yield component and an increased grain number has been produced by spikes per unit area or more grains per spike due to a higher spikelet number or higher floret fertility. One of the main components of the wheat yield is seed size, because it affects yield and increasing grain size continues to be a major breeding target. Also the size of seeds is used to identify wheat varieties [8,17]. According to [21] seed size is a very important part of both basic plant research, since in plant reproduction, seed formation and development had significant effects, and cereal breeding, as a related trait yield and vigor. In our study length grain ranged from 3 mm to 7.33 mm (AGB0150).

Table 1. Mean values for agro morphological characters measured in 100 *Triticum aestivum* L. accessions

Bank Code	TC	PH (cm)	SpL (cm)	NSpkSp	NSeSpk	NSeSp	SeS (mm)	WSeSp (g)
AGB0001	2.5	97.7	8.75	15.6	3	15.9	5.1	0.730
AGB0002	2	94.9	9.02	19.8	3.2	24.2	6.1	1.292
AGB0003	2	91	10.77	22.8	3	31.66	5.93	1.218
AGB0004	3	111.9	9.83	20	2.4	49	5	1.890
AGB0005	2.4	98.9	10.13	19.8	3	25.71	5.65	1.172
AGB0006	2.4	93.1	10.82	23.4	3.2	37.6	5.3	1.374
AGB0007	2.4	98.8	10.65	21.8	2.7	34.7	4.7	1.540
AGB0008	2.4	86.4	9.4	21.2	2.8	30.2	5.2	1.588
AGB0009	2	91.5	7.46	18.2	3.7	44.2	6.5	2.190
AGB0010	2.7	103.8	8.23	18.2	2.6	52.4	7	2.214
AGB0011	2	114.4	11.39	19.4	3	34.5	6.2	1.900
AGB0012	2.2	106	8.24	20	3.3	37.6	5.1	1.300
AGB0013	2	134.2	6.6	25.8	4	54.2	5.9	2.654
AGB0014	2	107.5	9.93	23.8	2.8	54.8	5.6	1.846
AGB0015	2	94.9	6.85	15	3	29.6	6.6	1.012
AGB0016	2	141.5	7	21	3	45.2	6.3	1.782
AGB0017	3	94	7.9	15.4	3	23.4	6.7	0.764
AGB0018	2.3	113.1	10.02	19.4	2.2	19.83	5.9	0.825
AGB0019	2.5	93.1	6	11.2	3.4	43	5	1.666
AGB0020	2.4	91.6	7.9	16	2.8	44.8	5	1.650
AGB0021	2.3	137.3	7.4	12.6	3.4	25.4	3	0.998
AGB0022	2.2	149.5	9.87	24.6	3	68	5.8	2.782
AGB0023	2.1	140.6	11.15	22.2	3.2	62.6	6.6	2.712
AGB0024	2.5	99.1	10.6	18.6	3.2	66.6	7	2.722
AGB0025	2.5	106	8.4	17.4	3	30	5.3	1.484
AGB0026	2	110.1	9.88	23	3.3	58.2	5.7	2.200
AGB0027	3	99.5	8.3	17.8	3.2	61.6	5	2.580
AGB0028	3.6	96.4	8.65	18	2.6	60.4	5	2.310
AGB0029	2.5	98.5	10.55	20.8	2.6	47.4	5	1.798
AGB0030	3.4	147.3	8.55	18	2.8	56.2	7	2.720
AGB0031	2.5	100.3	9.18	17.4	2.833	23.5	6.33	1.310
AGB0032	2	101.9	12.37	23	2.6	26.4	6.4	0.914
AGB0033	2.5	97.8	7.9	16.6	3	30.4	5	0.848
AGB0034	3.1	110.8	6.95	11.4	3	35	5	1.310
AGB0043	2	83	7.93	20.2	3.3	24	5.06	0.654
AGB0044	2.5	103.5	8.45	19.2	2.6	42.2	7	2.032
AGB0045	2	101.5	6.2	17	3	18.1	5.43	0.642

AGB0046	2	102.1	10.18	23.4	4	37.2	5.46	1.714
AGB0047	2	89.5	7.3	15.8	3	42.2	5.66	1.638
AGB0048	2	95.5	9.6	20.2	3	35.4	5.41	1.352
AGB0049	2	89.5	8	17.8	3	50.8	4.96	1.538
AGB0050	2	92.5	6.8	15.8	3	50.9	5.48	2.220
AGB0051	2.1	98	8	17	3	58.1	5.5	2.520
AGB0052	2.9	98.1	9.2	18.8	2.4	53	3	2.340
AGB0053	3	109.2	10.2	20.6	3	56.4	5.9	2.256
AGB0054	2	96.5	8.75	17.8	3	30.6	5.5	0.982
AGB0055	3.1	92.2	9.9	17.6	2.4	43.4	5	1.790
AGB0056	3	95	8.4	15.8	3	37	5.26	1.208
AGB0057	3	110	9.8	19	3	72.6	5.2	2.908
AGB0058	2.3	95.5	8.4	16.2	3	44.2	5.5	1.540
AGB0059	2.2	105.5	10.2	19.4	3	60.2	5.56	2.195
AGB0060	3	97	10.5	18.2	3	42.2	5.43	1.568
AGB0061	3	98	9.05	18.2	3	48.1	6.5	2.042
AGB0062	2	115.1	8.62	22.6	3	50.6	5.63	2.190
AGB0063	2	101	7.5	15.8	3	19.6	6.33	1.012
AGB0064	2	126.5	9.46	22.8	2.1	16.4	6.14	0.886
AGB0065	3.1	126.6	7.65	10.5	3	30.2	3	0.928
AGB0066	2	113	10.51	19.8	3.3	36.2	4.92	1.900
AGB0067	2	111.5	8.64	22.6	3.3	34.4	4.36	1.244
AGB0068	2	117.7	9.73	21	3	47.67	5.26	1.723
AGB0069	2	121.5	7.45	18.2	3	47.8	5.93	2.620
AGB0070	2.4	108.1	12.27	22.2	3	58.2	5.9	3.118
AGB0071	2	99	9.44	19.4	3.4	61	6.2	2.532
AGB0072	3	105	8.35	19	3	42.2	6.3	2.032
AGB0073	2.3	83.3	8.1	18.8	3.2	38.6	3	2.126
AGB0074	2	106.3	8.93	17	2.8	25.67	5.56	0.874
AGB0075	3.6	111.7	10.8	17.8	3.6	45.4	5	2.106
AGB0076	2	100.1	8.8	17	3	34.2	5.4	1.428
AGB0077	3.1	91.4	9.35	18.8	3.4	31	3	1.460
AGB0078	2.5	101.7	10.75	21.8	2.8	32	6.33	1.178
AGB0079	2	96.3	7	15.66	2.3	27.6	3	0.930
AGB0080	2.2	101.7	10.03	19.8	3	42	6.1	1.694
AGB0081	2	103	8.75	18.2	3	27.4	6.86	1.210
AGB0125	2	112	7.45	15.4	3	18.6	6.5	1.064
AGB0126	2.2	108	9.26	19.8	3	37.6	5.93	1.766
AGB0127	2.3	104	6.65	17	3	44.7	6.1	2.154
AGB0128	2	107	9.5	17	3	27.67	6.44	1.442
AGB0129	2.6	100.3	9.95	16.2	2.6	32.8	7	1.782
AGB0130	2	103.5	7.15	15.8	3	13.4	6.16	0.620
AGB0131	2	94.7	8.1	16.2	3	26.8	6.43	0.872
AGB0132	2.6	117.5	6.3	21	3	34.2	6.25	1.406
AGB0133	2.3	118.1	10.65	24.6	3	29	6.03	1.552
AGB0134	2.6	95	9.3	17.4	3	35.4	5.53	1.548
AGB0135	2	96.7	7.01	15.8	3	24.7	5.46	0.708

AGB0136	3	95.5	6.7	16.2	3	40.7	5.73	2.116
AGB0137	2	104	9.19	23.4	3.8	47.8	6.06	2.254
AGB0138	2.3	99.5	9.56	25.8	4	54	6.4	2.154
AGB0139	2	103.2	8.8	17.4	3	36.6	6.04	1.620
AGB0140	2	99.5	8.1	19	3	39.5	5.88	1.912
AGB0141	2	91.5	9.56	22.2	3.3	54	5.51	2.154
AGB0142	2.6	91	8.2	22.4	3	30.6	5.8	1.398
AGB0143	2.4	91.5	6.4	10.5	3.4	29.4	5	0.734
AGB0144	2.7	102.5	7.5	17.22	2.4	10	3	0.700
AGB0145	3.4	82.7	8.4	16.8	2.8	18.8	3	0.652
AGB0146	2.2	90.8	6.75	6.8	2	10	6.13	2.100
AGB0147	3.3	148.5	5.95	19.8	3	17.8	5.6	0.882
AGB0148	2.6	92.7	7.55	13.3	2.2	31.8	3	0.782
AGB0149	3.3	148	6.75	22	3.4	47.2	5	2.556
AGB0150	2	167	7.7	21.4	3	36.4	7.33	2.180
AGB0151	3.7	99	8	18.6	2.8	41.8	7	2.298

Regarding weight of grains per spike, genotype AGB 0070 showed the higher value (3.11 g). Seed weight parameter is one of the important parameters in wheat that increases seed germination percent, seedling emergence, tillring, density, spike and yield. According to [18] the grain number and weight as two main components in wheat grain yield are determined at different times of the growing season. This author suggested that seed weight best explained genotype by environment interaction for wheat grain yield.

Selection of wheat genotypes regarding grain yield would be as effective as selection for its components, as the number of spikes and its length per plant, grain number per spike and seed weight. The relation of these traits with grain yield and the interrelationships have special importance as the basis for selecting high yielding genotypes. In this study the morphological variation of different traits among 100 wheat genotypes were studied and indicated that there were large genetic variations as it is proved using ANOVAs analysis (Table 2).

Table 2. Anova data of quantitative traits measured in 100 common wheat accessions

Traits	Cluster		Error		F	SIG.
	Mean Square	df	Mean Square	df		
TC	.169	5	.218	94	.776	.569
PH	4037.376	5	47.981	94	84.145	.000
SpL	4.790	5	1.897	94	2.525	.034
NSpkSp	32.841	5	8.801	94	3.732	.004
NSeSpk	.215	5	.123	94	1.745	.132
NSeSp	2602.478	5	61.709	94	42.173	.000
SeS	1.213	5	1.013	94	1.198	.316
WSeSp	4.312	5	.184	94	23.492	.000
SG	.292	5	.367	94	.794	.557
GSpk	54.603	5	9.627	94	5.672	.000
SpkF	2.358	5	1.555	94	1.516	.192
FM	15.059	5	16.061	94	.938	.460
GM	30.384	5	10.292	94	2.952	.016
DM	28.129	5	11.046	94	2.546	.033

Table 3. Correlations between traits measured in common wheat genotypes

Traits	TC	PH	SPL	NSK/SP	NSE/SPK	NSE/SP	SES	WSE/SP	SG	GSPK	SPKF	FM	GM	DM
TC	1	.03	-.03	-.21*	-.15	.13	-.21*	.14	.16	.09	-.11	-.13	-.07	-.04
PH	.03	1	-.04	.26**	.08	.16	.19	.27**	.10	.22*	.01	.04	.30**	.31**
SpL	-.03	-.04	1	.52**	-.03	.27**	.13	.23*	-.04	-.12	.03	-.19	-.31**	-.31**
NSpkSp	-.21*	.26**	.52**	1	.20*	.31**	.27**	.37**	-.04	-.01	.08	-.04	-.01	-.01
NSeSpk	-.15	.08	-.03	.20*	1	.27**	.08	.22*	-.05	-.01	.09	-.07	-.09	-.10
NSeSp	.13	.16	.27**	.31**	.27**	1	.13	.85**	.13	.14	.01	-.17	-.03	-.01
SeS	-.21*	.19	.13	.27**	.08	.13	1	.26**	-.01	.05	.05	-.01	.09	.08
WSeSp	.14	.27**	.23*	.37**	.22*	.85**	.26**	1	.14	.11	.05	-.16	-.01	.01
SG	.16	.10	-.04	-.04	-.05	.13	-.01	.14	1	-.21*	.10	.17	.01	.23*
GSpk	.09	.22*	-.12	-.00	-.01	.14	.05	.11	-.21*	1	-.48**	-.51**	.24*	.20*
SpkF	-.11	.01	.03	.08	.09	.01	.05	.05	.10	-.48**	1	.20*	.09	.10
FM	-.13	.04	-.19	-.04	-.07	-.17	-.01	-.16	.17	-.51**	.20*	1	.63**	.64**
GM	-.07	.30**	-.31**	-.01	-.09	-.03	.09	-.01	.05	.24*	.09	.63**	1	.98**
DM	-.04	.31**	-.31**	-.01	-.10	-.01	.08	.01	.23*	.20*	.10	.64**	.98**	1

According to the data (Table 2) statistical variations are proved for traits as plant height, number of spikelet per spike, number of seed per spike as for weight of seeds per spike etc.

Strong positive correlation are observed among descriptors, as number of kernel per spike and kernel weight trait (r=0.85) and seed germination to days to maturity (r=0.98). Data in Table 3 show positive significant relation (r=0.529) between spike length and number of spikelet for spike and days to germination and days to flowering (r= 0.63) also days to flowering and days to maturity trait (r= 0.64). Strong negative relations is observed among several trait as in spikelet to flowering period trait and days to germination/spikelet formation (r= -0.48) and between GSpk trait and flowering to maturity period (r= -0.51)

Positive medium relations are observed between number of seeds per spike and number of spikelet per spike (r=0.31), weight of seeds per spike and number of spikelet per spike (r=3.78), among plant height ad days to germination to maturity (r=0.3) (*Correlation is significant at the 0.05 level/1-tailed :**Correlation is significant at the 0.01 level /2-tailed).

The divergence between accessions was observed using Cluster analyze (Table 4). The 100 wheat accessions were gathered in 6 major groups. Cluster 5 with 38 accessions, cluster 2 with 27 accessions, in cluster 1 are grouped 18 wheat genotypes, in cluster 3 only 4 accessions, cluster 4 with 7 wheat genotypes and at last in cluster 6 are present 6 *Triticum aestivum* L.accessions. Based on this analyse accessions in cluster 2 and 5 were the nearest neighbour with the lowest divergence levels meanwhile wheat genotype grouped in cluster 3 and 4 presented the farthest one. Wheat genotype AGB 0150 belonging at cluster 3 presented significant divergence in trait measured in compare with other wheat genotypes of our study. This divergence are mostly based in values of plant height trait and grain size (highest value) as for till ring capacity (lowest value).

We take note that at Figure 1 the PCA of 100 wheat genotypes is reflecting a high level of statistical significance. We also note that PCA represents 77.09% of the information used for statistical processing and it is very significant (Table 5).

Table 4. Distances between final clusters centres in 100 wheat genotypes

CLUSTER	1	2	3	4	5	6
1		17.889	46.537	42.565	23.356	57.816
2	17.889		53.792	26.770	15.152	54.636
3	46.537	53.792		58.912	41.999	33.040
4	42.565	26.770	58.912		21.901	44.368
5	23.356	15.152	41.999	21.901		39.977
6	57.816	54.636	33.040	44.368	39.977	

Table 5. Eigen values data for 100 wheat (*Triticum aestivum)* genotypes

Number	Eigenvalue	Percent	Cum Percent	ChiSquare	DF	Prob>ChiSq
1	2.643	26.43	26.43	282.871	44	<.0001
2	1.6803	16.803	43.233	200.749	38.808	<.0001
3	1.2749	12.749	55.982	160.458	32.069	<.0001
4	1.1542	11.542	67.524	134.944	25.47	<.0001
5	0.9573	9.573	77.097	106.747	19.482	<.0001
6	0.7933	7.933	85.03	81.534	13.984	<.0001
7	0.5947	5.947	90.976	57.154	9.347	<.0001
8	0.444	4.44	95.416	39.185	5.437	<.0001
9	0.3416	3.416	98.833	24.927	2.093	<.0001
10	0.1167	1.167	100	0	.	.

According to this analyze as it is shown (Table 5 & Figure 1) there are 5 main components that influence the genetic variability among 100 wheat genotypes. Traits as Weight of Seeds per Spike, Number of Seed per Spike, Number of Spikelet per Spike and Spike Length, part of the major component effect the diversity at 26.43% level. Whereas character as Germination to Spikelet and Tillring Capacity represent 16.8% of the statistical significance, also an important role plays plant height trait at the level of 9.57%.
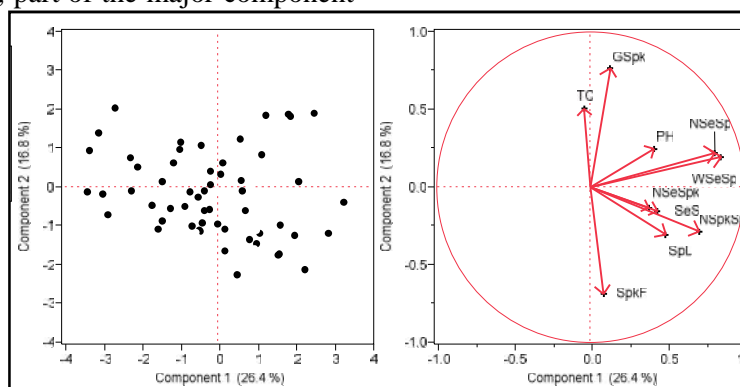
Figure 1. Graphic distibution of PCA in 100 *Triticum aestivum* L. accessions according to the average of different charachters

4. Conclusions

In this study we analysed the variability of 100 bread wheat genotypes, part of accessions found of Institute of Plant Genetic Resources on the basis of the morphological traits, and the indirect estimation of genetic variation through morphological characterization showed high variability, which provides a good background for future studies of quantitative traits. Analysis of the agro morphological characteristics in wheat genotypes revealed that a majority of the measured characteristics exhibited

high variation. This variability among genotypes is expressed in differences of plant height, number of spikelet per spike, number of seed per spike, weight of seed per spike, days from germination to spikelet, days to maturity and they could be used to select favourable traits for crosses in the genetic improvement programs. Further research based on biochemical or molecular markers must be performed in the future to grasp the genetic variation in our wheat genotypes.

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