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ANALYSIS OF GENETIC VARIATION IN BREAD WHEAT BY GRAIN YIELD COMPONENTS

SUMMARY

The aim of this research was to evaluate the genetic variability of 18 wheat (*Triticum aestivum* L.) genotypes by quantitative agro-morphological traits, and to identify factors affecting the cultivars grain yield. A two years study (2017-2019) was conducted at the Experimental Field of the Agricultural University of Tirana (altitude of 40 m above the sea level, Latitude 41°24'6.14"N and Longitude 19°44'9.93"E). Plant material used, is part of the 270 accessions of the base collection of the Institute of Plant Genetic Resources. During the growing crop years, the accessions were evaluated for different quantitative characters and morphological characterization of the accessions was conducted according to international standards. ANOVA, principal components and cluster analysis were carried out involving nine quantitative traits, such as tiller capacity, plant height, spike length, number of spikelet's per spike, number of seeds per spikelet, number of seeds per spike, weight of seeds per spike, weight of 1000 seeds and grain yield.

According to PCA, three components exhibited about 75.51% of the variability within 18 wheat genotypes. Accessions were grouped into three major clusters based on Euclidean distance, suggesting that wheat genotypes with major level of dissimilarity between them were "Generozo" and "Ejesh". The results revealed that tiller capacity, number of seeds per spikelet, weight of seeds per spike/g and weight of 1000 seeds/g were the most important characters in differentiating the genotypes.

Wheat genotypes used in this study reacted differently in the two growing seasons, giving high results in most of the traits that contribute directly in grain yield during 2017/2018 crop year. The use of principal component and correlation coefficient analysis in the wheat germplasm, simplify dependable classification of bread wheat germplasm, the identification of the superior genotypes and their relation with bio morphological traits with possibility expenditure in future breeding programs.

Keywords: variability, traits, grain yield, PC analysis

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INTRODUCTION

Common wheat (*Triticum aestivum* L.) is among the most important cereals cultivated for human consumption in most parts of the world. The crop is used by more than one billion people and it is grown on approximately 220 million hectares of land worldwide, with a total annual production of about 729 million tons (FAO, 2017). It has been projected that the demand for wheat in the developing world will increase 60 percent by 2050 which is a sobering forecast considering global wheat yields have remained constant for more than a decade (Curtis, 2002). Wheat (*Triticum aestivum* L.) because of its nutritional value is one of the most important cultivated food crops in Albania, with 70 000 ha of cultivated area which contributes to 22.5% of the country's GDP providing the income base for most of the population and serves as an employment safety net (FAO, 2017).

Genetic variability is one of the factors important for plant breeding programs. The evaluation of genetic variability based on morphological characters especially those of economic interest might be used to select appropriate materials in breeding programs for crop improvement, because in classical breeding process determination of variability between varieties is based on a large number of morphological characteristics (Dos Santos et al., 2009; Bode et al., 2013). Wheat grain yield is the result of some important physiological traits occurring in the growth and mostly is determined by the number of spikes, the number of grains and grain weight. The importance of these yield traits to wheat grain yield depends on the growth stage and management type (Okuyama et al., 2004).

The correlation coefficients analyze is a reliable statistical method, which provides tool to quantify the associations among different traits and indicate whether the influence is reflected in the yield. The evaluation of phenotypic variability by multivariate analysis gives the possibility to include a large number of accessions and to identify the most suitable resources for special traits (Goel et al., 2015). Analysis of morphological characteristics gave a clear insight into the existing genotypes diversity that can be used as a parent lines for a new selection cycle.

The objective of the present study was to provide a clear assessment of the variability and to evaluate the interrelationships among yield contributing traits through characterization of 18 accessions of wheat (*Triticum aestivum* L.) germplasm, to identify genetically divergent wheat genotypes with desirable traits that can be used as donors in hybridization for grain yield and other yield contributing components.

MATERIAL AND METHODS

The study is based on the characterization of the diversity of 18 genotypes of bread wheat (*Triticum aestivum* L.), part of the base collection of Plant Genetic Resources Institute (Table 1, https://www.eurisco.ipk-gatersleben.de/apex/).

Experiment carried two replications during the autumn season 2017/2018 and 2018/2019 at the Experimental Station of Valias, Tiranë (altitude of 40 m above the sea level, Latitude 41°24'6.14"N and Longitude 19°44'9.93"E). Common wheat was sown at the end of November 2017 and 2018, and standard fertilization and cultivation practices for wheat were carried out. At the beginning of June 2018 and 2019, wheat ears were manually harvested with the aim of determining yield components.

During the each crop years, the accessions were evaluated for different characters of quantitative type as: tiller capacity (TC), plant height/cm (PH), spike length/cm (SL), number of spikelet per spike (NSpkSp), number of seeds per spikelet (NSSpk), number of seeds per spike (NSSp), weight of seeds per spike/g (WSSp), weight of 1000 seeds (W1000S) and grain yield/g (GY).

Table 1. List of the 18 *Triticum aestivum* L. genotypes object of the study

Genotype Nr.	Accession code	Accession name	Acquire date	Origin
G 1	AGB 2811	Generozo"E" (YG-3072)	19990722	GRC
G 2	AGB 2812	Yecora"E"(YG-6123)	19990722	GRC
G 3	AGB 2813	Nestos	19990722	GRC
G 4	AGB 2814	Aranthos (G-05322)	19990722	GRC
G 5	AGB 2815	Ejesh (G-84909)	19990722	GRC
G 6	AGB 2822	Verjina (G-84865)	19990722	GRC
G 7	AGB 2823	Dodoni	19990722	GRC
G 8	AGB 2825	Yecora "E"	19990722	GRC
G 9	AGB 2837	Golia	20010626	ALB
G 10	AGB 2839	Galves 87	20010626	UKR
G 11	AGB 3064	IKBA_05	20101125	ALB
G 12	AGB3066	Univers 1	20101125	ALB
G 13	AGB3067	Univers 2	20101125	ALB
G 14	AGB3068	Univers 3	20101125	ALB
G 15	AGB3069	Univers 4	20101125	ALB
G 16	AGB3070	Univers 5	20101125	ALB
G 17	AGB3071	Univers 6	20101125	ALB
G 18	AGB2838	Agimi	20010626	ALB

For weather condition the data from IGEWE (www.geo.edu.al) were used (Table 2). Vegetation season 2017/2018 was specific for bread wheat growing due to mild winter and a considerable rainfall during all the season in comparison to the vegetative season of 2018/2019. In the first-year higher precipitation was noted in spring time when wheat genotypes were in phase of intensive growth and needed higher amount of water.

Morphological characterization of the accessions was conducted according to international standards (IPGRI, 1985). Statistical tests were carried out by the Statistical Package for Social Sciences (version 21).

Table 2. Weather condition of the two growing seasons

	Dec.	Jan.	Feb.	Mar.	Apr.	May	June	Total/Mean
2017/2018 crop season								
± T°C	8.8	9	10.3	12.9	19.8	22.1	25.4	13.816
±mm	126.4	70	210	200	2.5	150	100	122.7
2018/2019 crop season								
± T°C	9.9	7	9	14	18	17	26	14.414
±mm	100	100	45	0.3	100	137.4	0	68.957

RESULTS AND DISCUSSION

The genetic variability between 18 wheat genotypes conserved in the Gene Bank is assessed using different agronomic traits, especially those related to yield component. Basic statistic for quantitative traits (Table 3) were used and the estimated variation coefficient was high for agronomic traits as grain yield, number of seeds per spike, spike length, weight of seeds per spike and weight of 1000 seeds, similar with others authors (Sabaghina et al., 2014; Xhulaj et al., 2019). Wheat genotypes used in this study reacted differently in the two growing seasons, giving high results in most of the traits that contribute directly in grain yield during 2017/2018 crop year. During the growth year of 2018/2019 the wheat genotypes presented high values only for plant height trait (Table 3).

Accession AGB 2823 (Dodoni) during the first year of crop production, resulted with highest values measured in four traits as plant height (±111.6cm), weight of seeds per spike (±3.12g), number of seeds per spike (±80.2) and grain yield (±400g). This genotype presented lower values not only for the same traits in the second year (2018/2019) but also among the 18 genotypes had the lowest tiller capacity measured. Aranthos wheat cultivar (G4) represent the highest values measured in traits (during 2017/2018 crop year) as number of seeds per spikelet (±4), weight of 1000 seeds (±51.2g) and grain yield (400g).

The wheat genotype IKBA_05 (G11) resulted with the higher number of spikelet per spike (±20) and weight of seeds per spike (±2.1g) traits among the 18 common wheat genotypes during the 2019 season, meanwhile for the first year of crop growth it differs from the other genotypes for the NSSpk trait (±4). Grain yield is influenced by spike properties and the spikelet number plays a very important role in the wheat grain yield (Sabaghina et al., 2014).

Albanian cultivar Univers 1 presented low measured values for some characters in the first year of planting, as tiller capacity, weight of seeds per spike and weight of thousand seeds, while we see an improvement in the second year of production in compare with other wheat genotypes part of the study, for components such as grain yield (148g) and weight of thousand seeds (47.1g).The results objectively present key results, without interpretation, in an orderly and logical sequence using both text and illustrative materials (tables and figures).

Table 3. Descriptive statistics and ANOVA of quantitative traits in 18 genotypes of bread wheat (*Triticum aestivum* L.) measured in two years of crop growth

	Bio-morphological traits																	
	±TC		±PH		±SL		±NSpkSp		±NSSpk		±WSSp		W 1000 S/g		±NSSp		GY/g/m²	
Nr.	I	II	I	II	I	II	I	II	I	II	I	II	I	II	I	II	I	II
G 1	2.4	2.5	87.3	102	9.37	6.7	21.4	15.6	3	3	2.2	0.9	42.8	30	56.8	33	250	15
G 2	2.6	2	84.2	92.5	12.24	8.88	19.6	15.8	3	2	2.26	1.16	49.7	35	47.8	29.6	320	50
G 3	2.4	2.7	91.1	102.2	9.31	8.58	20	17.6	3	3	2.24	1.28	39.3	35	64	44.4	300	47
G 4	2.3	2.5	96.4	96.4	10.64	8.95	22.8	16.2	4	3	2.52	0.82	51.2	23	61	27.2	400	138
G 5	2.5	2.7	106	135.5	6.65	9.2	19	17	3.4	3	2.54	2.08	42	39	75.8	65.4	330	110
G 6	2.4	2.1	99.4	114.3	8.46	7.83	20.6	15.2	4	3	2.54	0.9	47	34	58	27.4	310	48
G 7	2.8	2	111.6	111.6	11.2	8.15	20.2	16.8	3.5	3	3.12	1.88	49	40.2	80.2	45.6	400	56
G 8	2.4	2	92.4	85.8	9.1	10.11	20.2	16.4	3.4	3	2.02	0.28	45	20.1	47.8	10.2	200	28
G 9	2	2	72.5	71.2	8.5	6.15	21.4	15.4	3	3	2.26	0.66	34	30	57.8	27.6	170	53
G 10	3	2	103.6	122.6	11.1	9.44	22	18.2	3	3	2.66	1.14	44	31	66.4	35.8	190	58
G 11	2.4	2.7	102.3	115	10.15	8.73	16.2	20	4	3	2.61	2.1	47	44.1	66.4	40.8	300	145
G 12	2	2	101.7	101.4	13.72	8.8	23.4	15.8	2	3	1.42	1.62	30.1	47.1	38	44.6	73	148
G 13	2	2	73.5	78.6	11.32	9.39	22.6	20	3	3	1.44	0.98	35.2	25.9	50	48.4	200	120
G 14	2	2.3	71.7	101.9	7.1	9.16	20.4	17.8	2	3	1.96	1.06	34	25	55.8	43.6	68	55
G 15	2	3	93.5	105.5	9.54	8.69	19.8	18.4	2	3	1.46	1.3	31.1	44.2	18.6	59.4	150	95
G 16	2.2	2.5	83.3	93.7	10.92	6.7	22.6	16.6	3	3	1.84	1.62	41.3	30	56.4	52.6	132	83
G 17	2	2	73.5	117.3	12.19	8.21	23.2	17.6	3	3	1.88	0.7	39.1	29	69	27.8	135	64
G 18	2.4	2	88	92.2	11.4	8.9	22.2	13	4	2	2.72	0.74	39	32	72.4	28	190	41
Mean	2.32	2.27	90.66	102.2	10.16	8.476	20.9	16.8	3.1	2.8	2.21	1.17	41.2	33.1	57.9	38.4	228.7	75.2
Stdv	0.29	0.33	12.39	15.81	1.830	1.044	1.79	1.71	0.6	0.32	0.47	0.51	6.43	7.56	14.5	13.5	102.1	41.1
CV%	13	14.8	13.7	15.5	18.0	12.3	8.6	10.2	20.9	11.2	21.7	43.2	15.6	22.9	25.0	35.3	44.6	54.6
std.er	0.06	0.07	2.92	3.72	0.43	0.24	0.42	0.41	0.15	0.07	0.12	0.12	1.52	1.78	3.41	3.19	24.1	9.67
F-Stat	0.17766		5.93749		11.51572		49.43897		1.92876		38.82968		12.06041		17.39823		35.08276	
P-Val.	0.676NS		<.02021*		<.00176*		<.00001*		0.173NS		<.00001*		<.00142*		<.00019*		< .00001*	

TC - tiller capacity; PH - plant height/cm; SL - spike length/cm; NSpkS - number of spikelet per spike; NSSpk - number of seeds per spikelet; NSSp - number of seeds per spike; WSSp – weight of seeds per spike/g ,WS-weight of 1000 seeds/g and GY-grain yield/g; I-2017/2018 season; II-2018/2019 season. F ratio values significant at the P0.05 level of the probability (*); NS-non significant.

Despite genetic composition, also climate factors as rainfall and temperature plays an important role in determining crop growth and influence

grain yield. Rainfalls play a significant role in both vegetative and reproduction stages of plant growth. Other studies (Liu et al., 2003) identified that wheat yield and quality was affected by average rainfall during seed planting time, flowering and grain-filling time. Moisture stress during the flowering, pollination, and grain-filling stages is especially harmful to wheat crop. Temperature is a modifying factor in all stages of wheat development including germination, tillering, booting, ear emergence, anthesis and maturity since it can influence the rate of water supply and other substrates necessary for growth, but varies with plant species, variety and phenological stages (Wahid et al., 2007).

We observed that all our genotypes produced higher grain yield during the first season in compare to the second growing season. In terms of total precipitation during the entire growing season, there exist differences between the two years of crop growth where main rainfall at the level of ±127.7mm is observed during the first season (2017/2018) and a lower value of precipitation (±68.95mm) during 2018/2019 crop year (Table 2).

Differences exist also in the distribution of precipitation between the two growth stages that vegetative and reproductive within one season, followed with visible differences between two years of crop production. During 2018 season the vegetative stage was characterized by high precipitation (±135 mm), meanwhile during 2019 this stage was associated with a lower level of precipitation (±81.66 mm) with a difference of ±53.8mm of rainfall. Little differences is observed for the air temperature at the level of ±0.73°C between year's crop for the same stage.

Regarding reproductive stage of our wheat genotypes, during 2018 this phase was related with a level of ±117.5mm of precipitation in comparison with the second year (2018/2019) where low level of rainfall was recorded (±79.23 mm) during the same phase. Data observed (Table 2) reveal a difference of 1.93°C in air temperature between the two growing seasons. Results suggest that our wheat genotypes to produce higher grain yield need moderate rainfall and air temperature.

We observed that the highest grain yield level during 2017/2018 in compare to 2018/2019 was associated with the highest vegetative precipitation and air temperature, also with highest reproductive stage precipitation (Table 2).

Analysis of morphological quantitative characters: ANOVA analysis found the presence of significant differences between wheat genotypes for most of the bio-morphological characters at the probability of P 0.05 (Table 2). Significant differences are observed within the genotypes for plant height, spike length, number of spikelet's per spike, weight of 1000 seeds, number of seeds per spike and grain yield.

The results show that the genotypes with the highest grain yield as "Aranthos" cv. (G4), "Ejesh" (G5), "Dodoni" (G7) and IKBA_05 (G11) were those with high values in TC, WSSp. WS, and NSSpk (Figure 1). According to this analyze strong positive correlation is observed between grain yield and

NSSpk (0.623*); tiller capacity (0.524*); weight of seeds per spike (0.625*) and weight of 1000 seeds (0.680*).

Correlation coefficient analysis: The correlation analyze is useful to identify agronomic traits that are positively related with yield (Bode et al., 2013). According to the multivariate correlation analyze different traits exhibited positive relations between them (Table 4), as tiller capacity of the wheat genotypes with weight of seeds per spike (r=0.64) and weight of thousand seeds (r=0.59). Strong positive correlations are observed between weight of thousand seeds and weight of seeds per spike (r=0.7) and also between number of seeds per spike and weight of seeds per spike (r= 0.751). Strong negative correlations existed among NSpkSp traits and most of the other traits as PH (r=-0.21), TC (r=-0.34), WSSp (r=-0.41), WS (r=-0.46), and GY (r=-0.23), same results are reported from previous studies (Xhulaj et al. 2017).
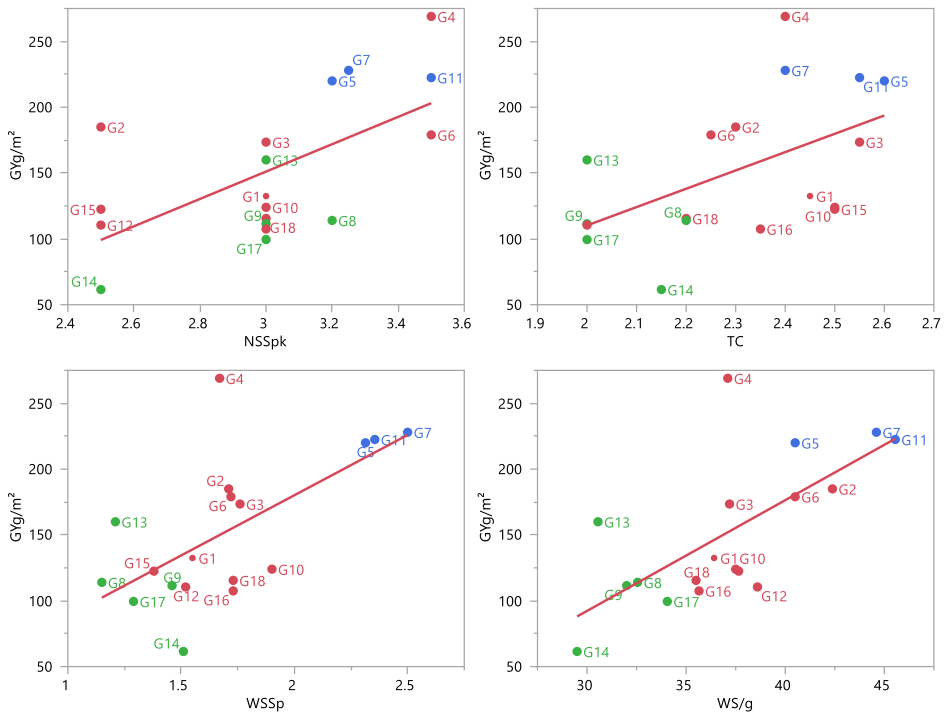

Figure 1: ANOVA analyses bivariate fit of grain yield by traits

Principal Component Analyses: Results of PCA suggest that 75.51% of the variability is exhibited among 18 common wheat genotypes by three components (Table 5) where the two first components influenced mostly the variability (PC1 48.82% and PC2 15.004% Figure 2). The variability presence within the first component was basically related with traits as weight of seeds per spike/g and weight of 1000 seeds/g, also by plant height/cm or grain yield, but poor variability in number of spikelet's per spike.

Table 4. Correlation matrix among the morphological traits (Pearson (n))

	TC	PH	SL	NSpkSp	NSSpk	WSSp	WS	NSSp	GY
TC	1.00	0.65	-0.23	-0.34	0.28	0.64	0.59	0.42	0.52
PH	0.65	1.00	0.05	-0.21	0.32	0.71	0.72	0.50	0.46
SL	-0.23	0.05	1.00	0.37	-0.21	-0.10	0.16	-0.20	0.05
NSpkSp	-0.34	-0.21	0.37	1.00	-0.16	-0.41	-0.46	0.01	-0.23
NSSpk	0.28	0.32	-0.21	-0.16	1.00	0.40	0.30	0.26	0.62
WSSp	0.64	0.71	-0.10	-0.41	0.40	1.00	0.79	0.75	0.62
WS	0.59	0.72	0.16	-0.46	0.30	0.79	1.00	0.32	0.68
NSSp	0.42	0.50	-0.20	0.01	0.26	0.75	0.32	1.00	0.35
GY	0.52	0.46	0.05	-0.23	0.62	0.62	0.68	0.35	1.00

TC - tiller capacity; PH - plant height/cm; SL - spike length/cm; NSpkS - number of spikelet per spike; NSSpk - number of seeds per spikelet; NSSp - number of seeds per spike; WSSp –weight of seeds per spike/g ,WS-weight of 1000 seeds/g and GY-grain yield/g.

This last trait followed by spike length strongly contributes at the genotype's variability in the second component, but this PC was very poor in number of seeds per spikelet and in tiller capacity. The third principal component exhibited positive effects for number of seeds per spike and number of spikelet's per spike. According to this analyze, the variables that effect most the variability within the three components is number of seeds per spike.

Table 5. Eigen values and % total variance for PCA in 18 wheat genotypes

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9
Eigenvalue	4.39	1.35	1.05	0.96	0.52	0.37	0.18	0.11	0.03
Variab. (%)	48.8	15.0	11.6	10.7	5.78	4.14	2.03	1.32	0.43
Cumul. %	48.8	63.8	75.5	86.2	92.1	96.2	98.2	99.5	100
Eigenvectors									
PH	0.38	0.21	0.01	-0.23	0.33	-0.62	-0.25	-0.42	-0.10
SL	-0.06	0.79	-0.2	0.05	-0.14	-0.02	0.51	-0.11	0.03
NSpkSp	-0.21	0.47	0.60	0.07	0.33	0.09	-0.32	0.35	-0.12
NSSpk	0.26	-0.2	0.22	0.74	0.04	-0.41	0.29	0.20	0.12
WSSp	0.44	0.02	0.08	-0.17	-0.35	0.01	0.11	0.33	-0.73
WS	0.41	0.21	-0.4	-0.05	-0.12	-0.01	-0.38	0.52	0.46
NSSp	0.31	0.01	0.62	-0.29	-0.38	0.11	0.17	-0.20	0.45
GY	0.37	0.14	-0.04	0.47	-0.03	0.544	-0.32	-0.45	-0.12

In addition to cluster analysis, biplot (genotype by trait data) has been applied to explain the percentage variance associated with each principal component obtained by drawing a graph between Eigen values and Principal components number. The vector view of the biplot suggest a strong positive correlation among traits, as indicated by the small obtuse angles between their vectors, especially between weight of thousand-seeds of the genotypes and weight of seeds per spike. Also, this positive relation (r=cos 0= +1) is observed

through weight of seeds per spike and thousand-seed weight and number of seeds per spikelet.
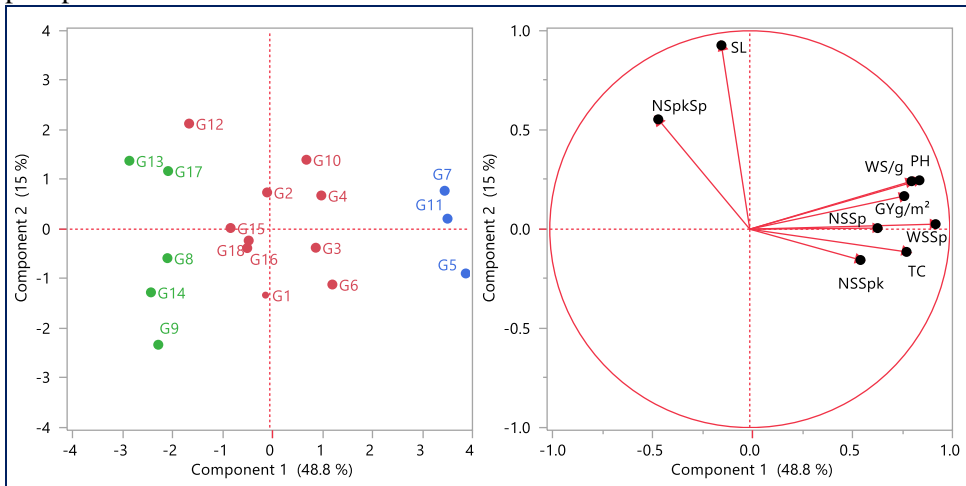

Figure 2: Principal component biplot of 18 wheat (*Triticum aestivum* L.) genotypes

The correlation between spike length and others traits as plant height, weight of thousand seeds, and finally grain yield, was near zero (r=cos 90= 0) as indicated by the near perpendicular vectors. The existence of a strong negative correlation of the vectors, indicated by the near angle of approximately 180 degrees is observed between spike length and number of seeds per spiklet, also among NSpkSp and NSSpk. The biplot (Figure 2) suggest that the best or the incompatible wheat genotypes in most of the traits, since they had the longest distance from the origin for the two principal components were Ejesh (G5), IKBA_05 (G11), Univers 1 (G12) and Univers 2 (G13). Therefore, it seems that for the first PC wheat genotypes (numbered at Figure 2) IKBA_05 (G11) and Ejesh (G5) have the highest values mostly for weight of seeds per spike, weight of thousand seeds and tiller capacity traits.

Cluster analysis: Genetic diversity among wheat germplasm was calculated after Agglomerative hierarchical clustering (AHC, Wards method, Figure 3). The 18 wheat genotypes were grouped in three major clusters. The first cluster include 10 bread wheat accessions, similar for different bio morphological traits (observed in two years of plants growth), the two wheat genotypes within this cluster with the lowest dissimilarity level observed are Generozo "E" (G1) and "Nestos" (G3). The 18 wheat genotypes were grouped in three major clusters. The first cluster include 10 bread wheat accessions, similar for different bio morphological traits (observed in two years of plants growth), the two wheat genotypes within this cluster with the lowest dissimilarity level observed are Generozo "E" (G1) and "Nestos" (G3).
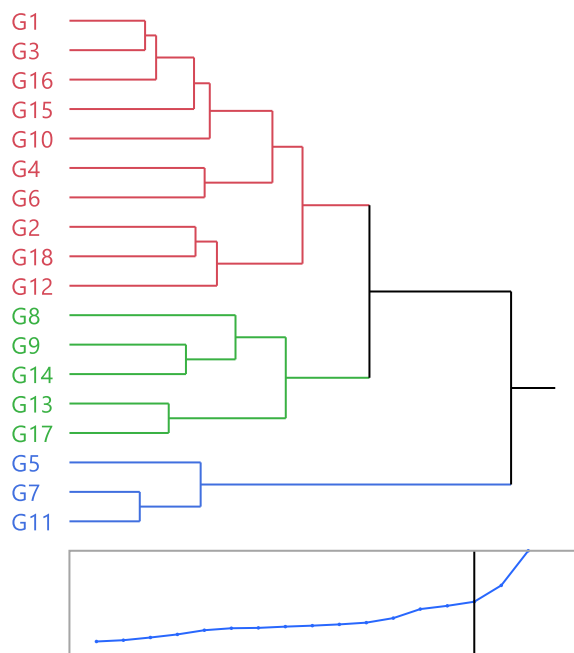
Figure 3: Dendrogram from cluster analysis of 18 bread wheat genotypes

The results suggest that the high similarity among them consists mostly in traits as tiller capacity, plant height/cm, spike length/cm, number of seeds per spikelet and weight of seeds per spike/g. These two accessions were joined from another genotype as "Univers 5" (G16) for similarity in weight of 1000 seeds/g and number of seeds per spike too. Within this cluster the two wheat genotypes with the highest level of dissimilarity observed are Generozo "E" (G1) and Yecora "E" (G2) basically for plant traits as height/cm, spike length/cm, weight of seeds per spike/g, weight of 1000 seeds/g, numbers of seeds per spike, grain yield g/m2.

The second cluster grouped five accessions whereas "Univers 2" (G13) and "Univers 6" (G17) presented the lowest distance among them, for similarity in tiller capacity and number of spikelets per spike. The third cluster included only three wheat genotypes, sub-clustered at this group with lowest level of dissimilarity observed not only within this cluster but also among the 18 wheat genotypes part of this research are "Dodoni" (G7) and "IKBA-05" (G11). These two accessions presented similarity in traits related to grain yield as weight of 1000 seeds/g, number of seeds per spikelet's, tiller capacity and spike length/cm.

The results reveal that the highest genetic distance exist between accessions part of the first cluster "Generozo E" (G1) and third cluster "Ejesh" (G5). These wheat genotypes were different in most of the agro bio-morphological traits as, plant height/cm, spike length/cm, weight of seeds per spike/g, weight of 1000 seeds/g, number of seeds per spike and grain yield g/m^2.

CONCLUSIONS

The results revealed that tiller capacity, number of seeds per spikelet, weight of seeds per spike/g and weight of 1000 seeds/g were the most important characters in differentiating the genotypes. Wheat genotypes used in this study reacted differently in the two growing seasons, giving high results in most of the traits that contribute directly in grain yield during 2017/2018 crop year. According to PCA, three components exhibited about 75.51% of the variability within 18 wheat genotypes. Accessions were grouped into three major clusters based on Euclidean distance, suggesting that wheat genotypes with major level of dissimilarity between them in most of the agro bio-morphological traits as, plant height/cm, spike length/cm, weight of seeds per spike/g, weight of 1000 seeds/g, number of seeds per spike and grain yield g/m2 were "Generozo" and "Ejesh". The results show that the genotypes with the highest grain yield as "Aranthos" cv. (G4), "Ejesh" (G5), "Dodoni" (G7) and IKBA_05 (G11) were those with high values in tillering capacity, weight of seeds per spike/g, weight of thousand seeds/g and number of seeds per spikelet's. According to ANOVA analyse strong positive correlation is observed between grain yield and NSSpk (0.62*); tiller capacity (0.52*); weight of seeds per spike (0.62*) and weight of 1000 seeds (0.68*). The use of principal component and correlation coefficient analysis in the wheat germplasm, simplify dependable classification of bread wheat germplasm, the identification of the superior genotypes and their relation with bio morphological traits with possibility expenditure in future breeding programs.

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