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Evaluation of Some Genotypes of Wheat (*Triticum Durum* L.) Under Conditions in Al Jabal Al Akhdar - Libya.

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Abstract

The experiment was conducted at the research farm of the College of Agriculture during the season (2019-2020) to evaluate the performance of six genetic compositions under semi-arid conditions using the green fodder. These compositions were obtained from the International Center for Agricultural Research in Dry Areas (ICARDA) and the International Maize and Wheat Improvement Center (CIMMYT), compared to the local variety "Ain Al-Faras." The treatments were planted according to a randomized complete block design (RCBD) with three replications. Significant differences were observed among all the genetic compositions for all the studied traits. The variety "Ain Al-Faras" outperformed the other genetic compositions in plant height, spike length, number of grains per spike, grain yield, straw yield, and biological weight, with values of 86 cm, 9.65 cm, 61 grains/spike, 1.14 tons/ha, 10.68 tons/ha, and 11.82 tons/ha, respectively. Genetic composition 2020-741 also excelled in the trait of number of grains per spike (52.33), while genetic composition D2020-72 exhibited superiority in the trait of thousand-grain weight (63.35 g). Moreover, genetic composition D2020-4 showed a higher harvest index compared to the other genetic compositions, with a value of 12.91. The results indicated that the values of phenotypic variance were close to the values of genetic variance for most of the studied traits. The highest heritability ratio was observed for the traits of number of grains per spike and grain yield. High relative genetic advance values were recorded along with high values of specific combining ability for both the number of grains per spike and grain yield. Therefore, it is possible to infer the genetic composition through morphological data, and such traits can be considered as selection criteria for improving these crops.

Keywords: *Durum wheat - Genetic compositions - Coefficient of variation - Heritability - Genetic advancement*

1. Introduction

Wheat (Triticum durum) is one of the most widely cultivated crops in the world (Tayyar, 2010). It is considered one of the most important food grains and is grown on over 220 million hectares worldwide, with more than half of this area distributed in developing countries. Wheat plays a crucial role in achieving food security. However, in Libya, the productive cultivated area is still low, accounting for only about 0.5% of the total Arab wheat production (FAO, 2020).

Due to population growth and increased food demand, it has become necessary to increase agricultural production by developing new varieties that can replace old ones or transfer desirable traits to them (Mustafa, 2003). Variability in the performance of different wheat varieties has been reported, indicating that genetic variation among the used genetic materials is the most important factor in the success of breeding programs (Dehghanl et al., 2008). Wheat varieties differ in their growth, yield, and components (Mahammed, 2000).

Several studies have shown significant genetic and phenotypic variation in wheat varieties regarding leaf area, plant height, number of grains per spike, grain weight, and grain yield (Joshi et al., 1982; Singh et al., 2018; Jahanian et al., 2019). Environmental variation was found to be low compared to genetic and phenotypic variation for these traits (Al-Anbari, 2004). In another study, high broad-sense heritability was observed for plant height, spike length, grain weight, and grain yield, ranging from 90% to 99% (Al-Anbari, 2004).

Furthermore, in his study of ten wheat varieties, Al-Anbari (2004) found high broad-sense heritability for traits such as plant height, spike length, grain weight, and grain yield, with values ranging from 99% to 90% to 98% to 99%, respectively. Similarly, Takkreeni (2000) indicated that the values of broad-sense heritability were high for all growth traits, yield traits, and their components in wheat, ranging from 88% to 99%.

These findings suggest that there is a strong genetic basis for the inheritance of plant height, spike length, grain weight, and grain yield in wheat varieties. High heritability values indicate that these traits are largely influenced by genetic factors rather than environmental conditions. This knowledge is valuable for breeders and researchers involved in wheat breeding programs, as it provides insights into the potential for improving these traits through selective breeding and genetic manipulation techniques.

In broad sense, inheritance was high for traits such as plant height, spike length, 1000-grain weight, and grain yield per plant, reaching values of 99, 90, 98, and 99, respectively. The findings of Tekrini (2000) indicated that the broad sense heritability values were high for all growth traits, yield, and its components in wheat, ranging from 88 to 99 percent.

Therefore, the aim of this study is to evaluate the performance of these genetic structures under the conditions of the Green Mountain region.

2. Materials And Methods

A field experiment was conducted at the farm of the Department of Agriculture, Omar Al-Mukhtar University, during the 2019/2020 season to evaluate the performance of six genetic structures under rainfed conditions. These structures were obtained from the International Center for Agricultural Research in the Dry Areas (ICARDA) and the International Maize and Wheat Improvement Center (CIMMYT), and were compared to the local variety "Ain Al-Faras" (Table 1). The treatments were planted according to a randomized complete block design (RCBD) with three replications. The experimental plot dimensions were 23 meters in length and contained 6 rows spaced 25 cm apart, with a row length of 3 meters. The planting was done on November 20, 2019, at a seed rate of 150 kg/ha. The recommended mineral fertilizer was added to the soil at a rate of 100 kg/ha in the form of diammonium phosphate (DAP) (18-46). Weeding and irrigation were carried out as needed

The studied traits were as follows:

1. Plant height: According to Singh & Stockopf (1971), measured at full maturity from ground level to the end of the terminal spike, excluding the awn, as an average for ten randomly selected plants from the middle rows within each experimental unit.

2. Spike characteristics: Measured at harvest from a sample consisting of ten randomly selected spikes from each experimental plot. The measurements included:

   a. Spike length (cm).

   b. Awn length (cm).

   c. Number of spikelets per spike.

   d. Number of grains per spike.

3. Yield-related traits:

The following parameters were determined for each experimental plot, excluding the edges:

a. 1000-grain weight (g): Calculated as the average weight of 500 randomly selected grains from the grain yield of each experimental plot and converted to the weight of 1000 grains, following Briggs & Aytenfisum (1980).

b. biological yield (t/ha): Calculated as the weight of plants from the two middle rows within each experimental plot covering an area of 6 m², converted to tons per hectare based on the total above-ground dry matter weight after air-drying the sample, according to Donald (1962).

c. Grain yield and straw yield (kg/ha): Estimated from the grain yield of the harvested plants from the two middle rows covering an area of 6 m² within each experimental plot, converted to kilograms per hectare.

d. Harvest index (%): Calculated as the ratio of grain yield to total yield, multiplied by 100, following Donald (1962).

Harvest index = (Grain yield / Total yield) × 100.

Statistical Analysis:

The plants were analyzed statistically using a completely randomized block design (RCBD) with the software 7 GenStat. The genetic analysis involved analyzing the variance according to Fisher (1936) and calculating the genetic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV). The heritability was determined using the method described by Burton and Devane (1953), and the genetic advance was calculated according to Al-Jibouri et al. (1958).

Using the following equations:

.$\boldsymbol{VG} = MSg - MSe/\mathrm{r}\,1$

VG = MSG - MSE/r

.$\boldsymbol{VE}$ = MSE2

VE = MSE

Where:

MSg = Mean Squares of Genetic Variance
MSE = Mean Squares of Experimental Error
r = Number of Replications
VC = Genetic Variance
VE = Environmental Variance

The components of phenotypic variance can be considered as follows, assuming no interaction between genetics and environment:

$\boldsymbol{VP} = \boldsymbol{VG} + \boldsymbol{VE}$. 3

VP = VG + VE
VP = Phenotypic Variance

Additionally, the measures of genetic and phenotypic variability are defined as:

4. Genetic Coefficient of Variation (GCV) = (Standard Deviation of Genetic Variance / Mean) × 100

GCV = (σG / $\bar{X}$) × 100

5. Phenotypic Coefficient of Variation (PCV) = (Standard Deviation of Phenotypic Variance / Mean) × 100

PCV = (σP / $\bar{X}$) × 100

And the broad sense heritability (h2b.s) is calculated as:

h2b.s = (VG / VG + VE) 6.

The interpretation of heritability values in the broad sense, according to Bahow (1997), is as follows: values less than 40% are considered low, values between 40% and 60% are considered moderate, and values greater than 60% are considered high.

Table (1) shows the genotypes used in the study

Source		Attributed	Name of genotype
Ancient settlement Atba Fazzan Valley			Ain Al-Faras
1	ICARDA	Mrb3/Tdicoccoides601116//IcamorTA0463/Zna4/4/Stj3//Bcr/Lks4/3/Ter3/6/Ossl1/S	D2020-4
2	CIMMYT	GUAYACAN INIA/POMA_2//SNITAN/4/D86135/ACO89//PORRON_4/3/SNITAN/13/BOOMER_33/ZAR/3/BRAK_2/AJAIA_2//SOLGA_8/10/PLATA_10/6/MQUE/4/USDA573//QFN/AA_7/3/ALBA-D/5/AVO/HUI/7/PLATA_ 13/8/THKNEE_11/9/CHEN/ALTAR 84/3/HUI/POC// BUB/RUFO/4/FNFOOT/11/ARTICO/AJAIA_3/	2020-741
3	CIMMYT	GUAYACAN INIA/POMA_2//SNITAN/4/D86135/ACO89//PORRON_4/3/SNITAN/5/SOOTY_9/RASCON_37//SOMAT_3.1/3/SOOTY_9/RASCON_	2020-744

		37//STORLOM/4/SOOTY_9/RASCON_37//GUAYACAN INIA/3/SOOTY_ 9/RASCON_37//LLARETA INIA	
4	ICARDA	Quabrach1/4/IcamorTA0462/3/Maamouri3//Vitron/Bidra1/5/Murlago st2	D2020-7
5	ICARDA	Ter1//Mrf1/Stj2/3/Icasyr1	D2020-2
6	ICARDA	Saadi/Adnan2ICD10-003-BLMSD-0AP-4AP-0TR-8STR-0TR	D2019-101 D.01

3. Results and Discussion

Plant Height (cm):

Significant differences were observed among the genetic structures under study in terms of plant height, as indicated in Table (2). The local variety, "Ain Al-Faras," exhibited the highest average plant height, reaching 86 cm. On the other hand, the genetic structure D2020-7 recorded the lowest average plant height (58.93 cm) compared to the other genetic structures. These differences in plant height can be attributed to genetic variations, environmental factors, and changes in growth conditions. These factors have contributed significantly to the phenotypic and significant variation in this trait among the introduced genetic structures (Gholamin et al., 2010). Changes in plant phenotypic characteristics, such as plant dwarfism or increased height, and the occurrence or absence of a wax layer, have been observed when exposed to low temperatures or changes in growth conditions (Almeselmani et al., 2012).

Grain Length (cm):

Table (2) shows that the comparison variety, "Ain Al-Faras," exhibited a significant superiority in grain length with an average of 9.65 cm compared to the other genetic structures, especially the genetic structure D2020-7, which recorded the lowest average grain length (5.94 cm). The inherent nature of these genetic structures may have been the cause or responsible factor for the variation in average grain length. The genetic and environmental differences among the varieties are considered one of the main reasons for the variation in crop traits, yield components, and biological yield (Ahmad et al., 2005; Gulzar et al., 2010).

Number of Spikelets per Meter:

The data presented in Table (2) indicate significant differences among the genetic structures under study compared to the local variety, "Ain Al-Faras," in terms of spikelet production. It was found that the local variety, "Ain Al-Faras," outperformed the other introduced genetic structures with a higher number of spikelets per meter (61 spikelets/meter). This could be attributed to genetic variations and the environmental genetic interaction, which helps to express certain traits that may not be present in the previously derived crop environment (Longove et al., 2014; Report of Progress 1108, 2014).

Number of Grains per Spike:

The results demonstrate significant and notable differences, as shown in Table (1), in the trait of the number of grains per spike. The genetic structure D2020-741 exhibited the highest average (52.33 grains/spike), while it decreased to the lowest average (25.66 grains/spike) in the genetic structure D2020-744. It appears that genetic composition plays a role in interacting with the environment to enhance fertilization success, in addition to the genetic structure's ability to utilize the products of photosynthetic processes for grain formation (He et al., 2012).

Weight per Grain (grams):

The results presented in Table (2) reveal significant and notable differences in the trait of weight per grain (grams) among the introduced genetic structures and the local variety, "Ain Al-Faras." The genetic structure D2020-2 demonstrated superiority by providing the highest average weight per grain with a mean of 63.35 grams compared to the other genetic structures. Conversely, the genetic structure D2020-741 exhibited the lowest average weight per grain with a value of 40.03 grams. This variation in weight per grain can be attributed to the efficiency of the genetic structures in utilizing the products of photosynthetic processes and perhaps the duration of grain filling, which is influenced by the surrounding environment. This finding is supported by the study conducted by Kamaluddin et al. (2007) (Kamaluddin et al., 2007).

Grain Yield (tonnes/hectare):

Based on the data in Table (2), significant and notable differences are observed among the introduced genetic structures and the local variety, "Ain Al-Faras," in terms of grain yield. The local variety, "Ain Al-Faras," exhibited the highest average grain yield with a value of 1.14 tonnes/hectare compared to the other introduced genetic structures. On the other hand, the genetic structure D2020-7 had the lowest average grain yield (0.54 tonnes/hectare). These variations can be attributed to genetic factors that manifest between different structures cultivated under the same conditions, or due to the multiple phenotypic variations within the same genetic structure in different environments. It is also possible that these differences are a result of genetic and environmental interactions that can have either positive or negative effects, depending on the necessary genetic expression of the genes and their ability to tolerate new environmental conditions (Guendouz et al., 2013; Queensland, 2012).

Straw and Biomass Yield (tonnes/hectare):

The results indicate significant and notable differences in straw yield, as shown in Table (2). The variety "Ain Al-Faras" outperformed other genetic structures with the highest average yield (10.68 tonnes/hectare), while the genetic structure D2019-101 had a lower yield (6.80 tonnes/hectare) compared to the other introduced genetic structures. The genetic and environmental variations among the studied varieties are among the primary factors contributing to the differences in growth traits and yield components (Ahmad et al., 2005; A. Gulzar et al., 2010).

Furthermore, significant variation was observed among the genetic structures in biomass yield. The variety "Ain Al-Faras" exhibited the highest average biomass yield (11.82 tonnes/hectare) compared to the other genetic structures, particularly the genetic structure D2019-101, which had the lowest value (7.39 tonnes/hectare). This variation can be attributed to genetic and environmental factors and their interaction, which significantly influenced the variation among the genetic structures (Raza et al., 2012; Mumtaz et al., 2010).

Harvest Index:

The significant and notable differences in biomass and grain yield per unit area were positively reflected in the variation of this trait among the genetic structures, as illustrated in Table (2). The genetic structure D2020-4 exhibited the highest average harvest index (%12.91), while the genetic structure D2020-7 had the lowest average for this trait (%6.69). This confirms that the genetic structures with relatively equivalent grain and biomass yield have achieved higher efficiency in the distribution of dry matter and its conversion into grains

Table (2) shows the averages of the studied traits in some durum wheat genotypes

Genetic structures	Plant height(cm)	Spike length (cm)	Number of spikes	Number of grains per spike	The weight of a thousand grain (g)	Grain yield (tons/ha)	Straw yield (tons/ha)	Biological weight (ton/ha)	Harvest Guide
D2020-4	72.38	7.93	55.33	41.33	47.86	1.11	7.59	8.72	12.91
2020-741	66.38	7.01	48.66	52.33	40.03	1.08	9.05	9.78	11.13
2020-744	63.60	6.22	35.66	25.66	51.19	0.60	8.19	8.79	6.88
D2020-7	58.93	5.94	44	31.33	53.76	0.54	7.57	8.11	6.69
D2020-2	68.77	6.29	47.33	28.66	63.35	1.08	9.94	11.03	9.84
D2019-101	70.37	6.25	31	31	61.48	0.59	6.80	7.39	8.07
Ain Al-Faras	86	9.65	61	38.33	62	1.14	10.68	11.82	9.62
f	**	**	**	**	**	**	**	**	**
LSD0.05	8.85	1.52	10.76	5.71	7.71	0.17	1.67	3.11	7.18

Some genetic constants of the studied traits:

The genetic and non-genetic variations in the genetic structures of the studied traits can be divided using genetic indicators such as the coefficient of genetic and phenotypic variation, heritability, genetic advance, etc., to determine the suitability of these genetic structures as a source of desirable traits for breeding programs in the future. The selection of parents is based on desired agricultural features and the degree of inheritance of crop traits in which the environmental interaction is involved, as the degree of inheritance and genetic advance change as a result of the environmental interaction. Direct selection for grain yield often poses a contradiction in breeding programs due to the influence of the crop's components (Mustafa, 2007 & ELsheikh).

It was observed through Table (3) that the coefficients of genetic and environmental variation were high between the crop and its components for most of the studied traits, including grain yield (10.53) (11.05), number of grains (8.47) (8.89), number of grains per spike (7.21) (8.20), harvest index (7.75) (8.84), spike length (5.94) (6.96), biological weight (5.33) (6.23), straw yield (5.12) (6.08), 1000-grain weight (5.12) (5.65), and plant height (3.91) (4.45). The values of the coefficients of genetic variation for all traits were lower than the values of the coefficients of environmental variation, indicating that most of the variation in these traits was due to environmental factors. However, the environment still plays a role in influencing the studied traits. It is also noteworthy that the heritability values were high for all studied traits, indicating a significant genetic contribution to the total phenotypic variation (Raha & Ramgiri, 1998 - Sharma & Garg, 2002). This suggests that the selection for these traits can be effective in improving the desired characteristics, considering the high heritability values (Rasal et al., 2008).

Table (3) Some statistical and genetic constants for the characteristics of the studied genotypes

	Plant height(cm)	Spike length (cm)	Number of spikes	Number of grains per spike	The weight of a thousand grain (g)	Grain yield (tons/ha)	Straw yield (tons/ha)	Biological weight (ton/ha)	Harvest Guide
Genetic variation	66.42	1.57	99.69	81.65	69.63	0.07	1.37	2.25	4.69
Phenotypic variation	86.19	2.16	128.9	89.88	84.64	0.08	2.43	3.07	6.1
Coefficient of genetic variation	3.91	5.94	7.21	8.47	5.12	10.53	5.12	5.33	7.75
Coefficient of phenotypic variation	4.45	6.96	8.20	8.89	5.65	11.05	6.08	6.23	8.84
Degree of heritability	77.05	72.97	77.33	90.84	82.27	90.78	71.09	73.22	76.92
Relative genetic progress	7.07	10.46	13.06	16.64	9.58	20.67	8.90	9.39	14.01

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