

Morphological Features, Yield Components and Genetic Relatedness of Some Wheat Genotypes Grown in Palestine

Rezq Basheer-Salimia^{1,*}, Sayel Atawnah²

¹Department of Plant Production and Protection, Faculty of Agriculture, Hebron University, Palestine

²Union of Agricultural Work Committees (UWAC), Palestine

*Corresponding author: rezqbasheer@hebron.edu

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Abstract The objectives of the present study were to study the morphological characteristics, yield components, chemical compositions and genetic relatedness of six wheat *Triticum* spp genotypes frequently grown under rain-fed conditions at the southern highland of West-Bank, Palestine. Three local genotypes commonly known as Black-Depia, White-Depia, and White-Hetia, and three introduced ones namely Ambar, Sham-3, and Sham-5, were allocated at three different agro-ecological conditions namely Al-Arroub, Dora, and Janata using completely randomized block design, with five replications (net plot size of 25 m² areas per replicate). The results showed significant variations among the six wheat genotypes almost for all measured parameters (maturation and harvesting date, stem length, tillering, number of grains per spike, average spike weight, spike length, spike length with awns, weight of 100 seeds per genotypes, and total yields). Generally, local wheat genotypes presented better yield than the introduced ones. Black-Depia genotype showed the highest yield (grain plus hay) among the three examined sites therefore, it could be a promising cultivar for any further breeding program especially for drought tolerance; however, the lowest yields were obtained in Sham-5 and Sham-3 at Janata site, respectively. Regarding wheat quality parameters, no significant variations were observed for any conducted analyses, however, there were trends for higher protein contents in Sham-5 and White-Hetia genotypes. UPGMA dendrogram clustered the examined six wheat genotypes into two main clusters related to Black-Depia as an isolated genotype. The first cluster is composed of “Sham-5, White-Hetia and Sham-3 genotypes; and the second cluster consisted of White-Depia and Amber genotypes.

Keywords: wheat, genotypes, growth, yield, genetic relatedness

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1. Introduction

Among the history, wheat is considered as the first important and strategic crop for the majority of world's populations; in addition, it is the most widely cultivated plants. It is well documented that this crop is grown in the earliest sites of civilization and played a major role wherever societies developed. Almost one-third of the world population was depending on this crop for their daily life [1].

Wild wheat is still colonizing its primary habitats in the Fertile Crescent from Palestine and Jordan to south Turkey, Iraqi Kurdistan, and southwestern Iran [2,3]. From there, wheat primarily shifted and transported to an array of secondary habitats (open Mediterranean), and finally to the rest of the world.

In Palestine, field crops and forages occupy the largest cultivated land after fruit trees with total areas of 44,1

thousand hectares, in which wheat contributes the majority of the total field crops in terms of area covered (22,624 hectares) and total production. Recent statistics showed that 96% of its cultivation is still under rain-fed condition with an average production of 1,360 Kg per hectare [4].

Comparably, productivity of wheat in Palestine might be one of the lowest across the world due mainly to detrimental effects of biotic and abiotic stresses. Many others stated that yield of wheat can be increased either by bringing more land area under cultivation (impossible to be achieved here due to the limited total areas and high population density), and/or by increasing its yield per unit area which might be the case [5]. One promising approach toward this end is the establishment of national wheat breeding programs that depend initially on identifying markers and traits which facilitate the development of high yielding and/or stress tolerant wheat cultivars [6].

Characterization and identification of such markers could be achieved either by morphological and/or molecular markers [7,8]. Morphological markers have

been used for many years for characterization of genotypes and it continues to be the first step for the description and classification of any germplasm as well as useful tools for screening the accessions of any collection [9]. In wheat, several reports demonstrated the usefulness of these markers in documenting variability in their genotypes [6]. To date, neither morphological nor molecular markers have been identified in wheat genotypes grown in Palestine. The main goals of this

study were to examine the morphological characteristics, yield components, grain chemical compositions, and genetic relatedness of some wheat genotypes grown at three different agro-ecological conditions of the southern highland of West-Bank, Palestine, in addition, to determine the adaptability and the productivity of each wheat genotype for each location in order to help growers choose the best genotypes.

Table 1. Study sites description

	Study Sites		
	Dura Site	Al-Arroub Site	Janata Site
Location	14 km south of Hebron city between Dora and Aldhrya	9 km north of Hebron city	8 km south to east of Bethlehem city
Elevation	660 m	842 m	629 m
Latitude	46°66	32°27	34°89
Longitude	64°64	45°42	39°09
Topography	Mountainous	Valley	Hilly with moderate to steep slope
Rain-fall	350 mm	516.8 mm	260 mm

2. Materials and Methods

2.1. Plant Materials, Experimental Sites, Design and Plantation

A field investigation was carried out using six genotypes of wheat (three local commonly known as Black-Depia, White-Depia, and White-Hetia, and three introduced ones namely Ambar, Sham-3, and Sham-5), grown at three different agro-ecological sites namely Al-Arroub, Dora, and Janata (Table 1), under rain-fed conditions at the southern highland of West-Bank, Palestine. The experiment was laid out in a randomized completely block design (RCBD), with five replications using the net plot size of 25 m² area (5 m * 5 m) per replicate. To isolate the plots as well as to facilitate the follow-up process (cultural practices, measurements, etc), one meter corridors around all the plots were used. Adoption rate of 375 gram of seeds/wheat genotype/plot (equivalent to 15 kg/dunum), were manually sown.

2.2. Measured and Evaluated Parameters

Maturation and harvesting date (when the moisture contents of the seeds reaches 15%); stem length (from the stem base up-to the stem apex); tillering (using randomly one square meter frame-quadrant per plot); number of grains per spike; average spike weight (spike with awns); spike length and spike with awns length; and weight of 100 seeds were measured. In addition total yield (grain plus hay), total grain and total hay production were also recorded in kilograms/plot/genotype, and accordingly calculated per dunum.

For grain quality parameters, representative seed samples from only Al-arroub site were used in this experiment. Seeds were ground in a Wiley mill and then stored in sealed jars according to [10]. Chemical analysis including: dry matter [11]; total nitrogen (using Kjeldahl procedure; [10]; crude protein (determined by estimating nitrogen content using Kjeldahl procedure); percentage of crude protein (obtained by multiplying the nitrogen concentration by 6.25 (NX 6.25) according to [10,12]; ash content (using igniting in muffle furnace at 550°C for 8 h); and moisture content were evaluated. Furthermore,

nutritional values including: Ca, Mg, K, Na, P, Fe, Zn, Mn, Cu, and B: Calcium (Ca) and Magnesium (Mg) contents were determined with an atomic absorption spectrophotometer (Unicam, model SP9, UK) using the wet digestion method with a mixture of nitric, sulfuric and perchloric acids.

Iron (Fe), Zinc (Zn), Manganese (Mn), and copper (Cu) were determined by Atomic Absorption Spectrophotometry, using the wet-digested method (HNO₃-HClO₄). The digestion procedure is adapted from [13]. Potassium (K) and sodium (Na), concentrations were measured colorimetrically by flame photometer [14]. Phosphorus (P) content was determined by the ammonium metavanadate-ammonium molybdate procedure [15]. Using spectrophotometric method, the vanadomolybdate reagents produce a stable yellow color with phosphates [16]. Boron (B) is measured by dry ashing [17] and subsequent measurement of B by using a spectrophotometer.

2.3. Data Analysis

The data were statistically analyzed using the one-way analysis of variance (ANOVA) and means were separated using the Tukey's pairwise comparisons at a significance level of $P \leq 0.05$ using the MINITAB package system. For genetic variations and relatedness, each morphological and yield trait (descriptor) was scored as 1 for presence and 0 for absence; accordingly, the relatedness among genotypes was estimated based on Jaccard's similarity coefficient using the multilocus fingerprinting data sets containing missing data (FAMD) software version 1.108 beta. Consequently, cluster analysis was made using the un-weighted pair-group method with arithmetic averages (UPGMA) [18] and the Tree view software (Win32, version 1.6.6).

3. Results

3.1. Morphological Parameters

Maturation and consequently harvesting date was earlier at Janata site followed by Dora and Al-arroub sites, respectively. All examined wheat genotypes reached the

maturity stage at Janata site in a shorter time compared with the other two sites. In contrast, maturation and harvesting date was delayed by 3-12 days (depending on the wheat genotypes); at Al-arroub site (Table 2).

Table 2. Maturation and harvesting date of six wheat genotypes cultivated at three different sites

Maturation and harvesting/day	Sites		
	Dora	Al-arroub	Janata
Black-Depia	176	188	174
White-Depia	175	185	174
White-Hetia	175	187	176
Ambar	169	180	169
Sham-5	181	185	178
Sham-3	181	184	178

In general, the six wheat genotypes planted at Al-arroub site revealed significantly higher values of stem length, number of tillers, average spike weight, spike length, and weight of 100 seeds, followed by Dora and Janata sites, respectively (Table 3, Table 4, Table 5, Table 6, and Table 7).

Table 3. Comparison between six wheat genotypes planted in three different sites (Dora, Al-arroub and Janata) in terms of stem length (cm), (Mean* ± S.E)

Genotypes	Sites			P-value
	Dora	Al-arroub	Janata	
Black-Depia	85.58 ^b ± 0.91	101.56 ^a ± 0.44	64.18 ^c ± 0.86	0.001
White-Depia	82.28 ^b ± 0.69	88.30 ^a ± 0.92	70.76 ^c ± 0.65	0.001
White-Hetia	75.10 ^b ± 0.55	80.30 ^a ± 0.46	60.66 ^c ± 0.58	0.001
Ambar	79.54 ± 0.09	88.98 ± 0.48	77.90 ± 11.6	0.473NS
Sham-5	81.28 ^b ± 0.16	92.54 ^a ± 1.10	79.04 ^b ± 1.28	0.001
Sham-3	73.68 ^b ± 0.75	88.72 ^a ± 0.39	65.26 ^c ± 0.69	0.001

*: Means within rows using different letters are differ significantly at the $P \leq 0.05$ level (using one way ANOVA analysis)

Table 4. Comparison between six wheat genotypes planted in three different sites (Dora, Al-arroub and Janata) in terms of tillering, (Mean* ± S.E)

Genotypes	Sites			P-value
	Dora	Al-arroub	Janata	
Black-Depia	8.16 ^b ± 0.37	9.48 ^a ± 0.38	8.58 ^{ab} ± 0.09	0.032
White-Depia	6.44 ^a ± 0.24	6.86 ^a ± 0.16	5.48 ^b ± 0.12	0.001
White-Hetia	6.46 ^b ± 0.13	6.90 ^a ± 0.13	4.88 ^c ± 0.09	0.001
Ambar	7.16 ^b ± 0.29	8.40 ^a ± 0.36	4.94 ^c ± 0.17	0.001
Sham-5	8.10 ^a ± 0.21	6.90 ^b ± 0.68	6.32 ^c ± 0.13	0.001
Sham-3	8.05 ^a ± 0.04	6.06 ^b ± 0.07	5.32 ^c ± 0.12	0.001

*: Means within rows using different letters are differ significantly at the $P \leq 0.05$ level (using one way ANOVA analysis)

Table 5. Comparison between six wheat genotypes planted in three different sites (Dora, Al-arroub and Janata) in terms of average spike weight (gram), (Mean* ± S.E)

Genotypes	Sites			P-value
	Dora	Al-arroub	Janata	
Black-Depia	3.62 ^b ± 0.006	4.58 ^a ± 0.008	1.79 ^c ± 0.01	0.001
White-Depia	1.83 ^b ± 0.008	3.61 ^a ± 0.01	1.74 ^c ± 0.01	0.001
White-Hetia	2.99 ^a ± 0.02	2.83 ^b ± 0.03	1.96 ^c ± 0.01	0.001
Ambar	3.33 ^b ± 0.01	3.93 ^a ± 0.02	1.49 ^c ± 0.006	0.001
Sham-5	2.66 ^a ± 0.02	2.15 ^b ± 0.03	1.22 ^c ± 0.02	0.001
Sham-3	3.23 ^a ± 0.02	3.00 ^b ± 0.02	1.23 ^c ± 0.01	0.001

*: Means within rows using different letters are differ significantly at the $P \leq 0.05$ level (using one way ANOVA analysis)

Table 6. Comparison between six wheat genotypes planted in three different sites (Dora, Al-arroub and Janata) in terms of weight of 100 seeds/wheat genotype (gram), (Mean* ± S.E)

Genotypes \ Site	Dora	Al-arroub	Janata	P-value
Black-Depia	4.36 ^b ± 0.07	5.50 ^a ± 0.19	4.24 ^b ± 0.09	0.001
White-Depia	3.23 ^b ± 0.06	4.28 ^a ± 0.10	2.88 ^c ± 0.04	0.001
White-Hetia	3.19 ^b ± 0.09	5.02 ^a ± 0.15	3.39 ^b ± 0.06	0.001
Ambar	4.28 ^b ± 0.20	5.26 ^a ± 0.08	3.46 ^c ± 0.06	0.001
Sham-5	3.32 ^b ± 0.12	4.52 ^a ± 0.16	3.09 ^b ± 0.04	0.001
Sham-3	3.76 ^b ± 0.10	5.20 ^a ± 0.08	3.60 ^b ± 0.03	0.001

*: Means within rows using different letters are differ significantly at the P ≤ 0.05 level (using one way ANOVA analysis)

Table 7. Comparison between six wheat genotypes planted in three different sites (Dora, Al-arroub and Janata) in terms of spike length (cm), (Mean* ± S.E)

Genotypes \ Sites	Dora	Al-arroub	Janata	P-value
Black-Depia	5.19 ^c ± 0.06	8.65 ^a ± 0.02	7.51 ^b ± 0.03	0.001
White-Depia	8.67 ^c ± 0.05	10.7 ^a ± 0.02	8.92 ^b ± 0.05	0.001
White-Hetia	7.79 ^b ± 0.06	9.01 ^a ± 0.1	6.05 ^c ± 0.05	0.001
Ambar	6.59 ^b ± 0.03	8.67 ^a ± 0.01	4.90 ^c ± 0.06	0.001
Sham-5	7.72 ^a ± 0.05	5.82 ^b ± 0.09	4.83 ^c ± 0.06	0.001
Sham-3	7.11 ^a ± 0.02	7.03 ^a ± 1.19	4.84 ^b ± 0.14	0.065

*: Means within rows using different letters are differ significantly at the P ≤ 0.05 level (using one way ANOVA analysis)

At the wheat genotype level, significant variations were noticed almost for all measured morphological parameters. Black-Depia presented significantly higher stem length at Al-arroub site followed by Dora and Janata sites, respectively. It was also noted that Sham-5 exhibited the highest stem length at Janata site. The other wheat genotypes presented a moderate stem length (Table 3).

Black-Depia presented the highest number of tillers (branching) at the Dora site; however, White-Hetia as well as Ambar genotypes exhibited the lowest tillers number at Janata site.

White-Depia contained the significantly highest number of grains per spike at Al-arroub site (74.28) followed by Amber (70.56). Conversely, Sham-3 and Sham-5 revealed the lowest number of grains per spike at Janata site (Table 4).

Black-Depia revealed significantly higher average spike weight at Al-arroub site. In contrary, Sham-3 and Sham-5 showed the lowest average spike weight at Janata site (Table 5).

Black-Depia presented significantly higher seed weight (weight of 100 seeds), among the three different sites, however, White-Depia genotype revealed the lowest weight at Janata site (Table 6).

Regarding spike length, Al-arroub presented higher spike length for all examined genotypes except with Sham-5 and Sham-3 genotypes which revealed lower

spike length (Table 3). However, the lowest spike length was significantly presented with Sham-5 and Sham-3 genotypes at Janata site with an average of 4.83 and 4.84, respectively (Table 7).

Amber showed significantly higher spike length with awns at Al-arroub site (21.09 cm) compared with other examined genotypes. In contrast, White-Depia presented the shortest spike length with awns at Al-arroub and Janata sites (Table 8).

3.2. Yield Parameters

In general, Black-Depia showed the highest yield (grain plus hay) among the three different sites, however, the lowest yield was presented in Sham-5 and Sham-3 by 330.4 and 408 kg at Janata site, respectively (Table 9 and Table 10). At Dora site, Black-Depia showed the highest yield (grain plus hay) followed by Sham-5. However, Amber presented the lowest production. At the grain production level, significant variation in Black-Depia genotype per site was observed (Table 11 and Table 12). Black-Depia genotype at Al-arroub site presented significantly the highest grain production (416 kg). Sham-5 genotype in Janata site as well as White-Hetia genotypes at Dora site significantly exhibited the lowest grain production by 99.12 kg to 215.68 kg respectively.

Table 8. Comparison between six wheat genotypes planted in three different sites (Dora, Al-arroub and Janata) in terms of spike length with awns (cm). (Mean* ± S.E)

Genotypes \ Sites	Dora	Al-arroub	Janata	P-value
Black-Depia	16.51 ^b ± 0.06	20.24 ^a ± 0.12	20.07 ^a ± 0.09	0.001
White-Depia	16.88 ^a ± 0.10	14.07 ^b ± 0.26	14.56 ^b ± 0.09	0.001
White-Hetia	19.01 ^a ± 0.06	18.65 ^a ± 0.33	17.28 ^b ± 0.13	0.001
Ambar	16.82 ^b ± 0.08	21.09 ^a ± 0.06	16.31 ^b ± 0.28	0.001
Sham-5	17.79 ^a ± 0.08	16.81 ^b ± 0.10	15.72 ^c ± 0.12	0.001
Sham-3	18.71 ^a ± 0.09	16.39 ^c ± 0.17	17.65 ^b ± 0.09	0.001

*: Means within rows using different letters are differ significantly at the P ≤ 0.05 level (using one way ANOVA analysis).

Table 9. Comparison between six wheat genotypes planted in three different sites (Dora, Al-arroub and Janata) in terms of total yield production (grain and hay) at harvesting (Mean* ± S.E)

Genotypes Sites	Dora	Al-arroub	Janata	P-value
Black-Depia	816.0 ^{ab} ± 80.6	1022.1 ^a ± 89.0	632.0 ^b ± 15.0	0.007
White-Depia	755.2 ^a ± 27.6	829.2 ^a ± 29.1	568.0 ^b ± 23.3	0.001
White-Hetia	672.8 ^b ± 23.8	883.2 ^a ± 25.9	592.0 ^b ± 15.0	0.001
Ambar	693.0 ^a ± 40.6	808.8 ^a ± 47.6	488.0 ^b ± 29.4	0.001
Sham-5	807.0 ^a ± 22.0	745.6 ^a ± 28.6	330.4 ^b ± 28.9	0.001
Sham-3	775.2 ^a ± 49.0	727.2 ^a ± 24.3	408.0 ^b ± 15.0	0.001

*: means within rows using different letters are differ significantly at the $P \leq 0.05$ level (using one way ANOVA analysis)

Table 10. Comparison between total six wheat genotypes planted in the same site in terms of total yields production (grain and hay), (Mean* ± S.E)

Genotypes Sites	Dora	Al-arroub	Janata
Black-Depia	816.0 ^{ab} ± 80.6	1022.1 ^a ± 89.0	632.0 ^a ± 15.0
White-Depia	755.2 ^b ± 27.6	829.2 ^{bc} ± 29.1	568.0 ^{ab} ± 23.3
White-Hetia	672.8 ^b ± 23.8	883.2 ^{ab} ± 25.9	592.0 ^a ± 15.0
Ambar	693.0 ^b ± 40.6	808.8 ^b ± 47.6	488.0 ^b ± 29.4
Sham-5	807.0 ^b ± 22.0	745.6 ^{bc} ± 28.6	330.4 ^c ± 28.9
Sham-3	775.2 ^b ± 49.0	727.2 ^c ± 24.3	408.0 ^{bc} ± 15.0
P-value	0.001	0.002	0.001

*: means within columns with different letters differ significantly at $p \leq 0.05$ level (using one way ANOVA analysis)

Regarding the total hay production, significant variation in Black-Depia per site was observed (Table 13). For the three examined sites, Black-Depia genotype gave significantly the highest hay production. However, the

lowest hay production obtained significantly at Janata site with Sham-3 genotypes. Moreover, Sham-5 and Sham-3 exhibited slightly better hay production at Dora site than at Al-arroub site (Table 14).

Table 11. Comparison between six wheat genotypes planted in three different sites (Dora, Al-arroub and Janata) in terms of total grain production. (Mean* ± S.E)

Genotypes Sites	Dora	Al-arroub	Janata	P-value
Black-Depia	244.4 ^{ab} ± 39.2	416.0 ^a ± 27.1	185.6 ^b ± 16.1	0.027
White-Depia	249.6 ^a ± 18.7	294.4 ^a ± 14.7	172.8 ^b ± 9.5	0.001
White-Hetia	215.6 ^b ± 7.8	324.8 ^a ± 30.7	177.6 ^b ± 4.4	0.001
Ambar	240.8 ^{ab} ± 30.9	312.8 ^a ± 69.4	146.4 ^b ± 8.8	0.037
Sham-5	239.8 ^a ± 15.4	186.4 ^a ± 19.4	99.12 ^b ± 8.6	0.001
Sham-3	238.1 ^a ± 32.1	214.1 ^a ± 23.3	122.4 ^b ± 4.4	0.006

*: means within rows using different letters are differ significantly at the $p \leq 0.05$ level (using one way ANOVA analysis)

Table 12. Comparison between six wheat genotypes planted in the same site in terms of total grains production (Mean* ± s.e)

genotypes sites	Dora	Al-arroub	Janata
Black-Depia	244.4 ^{ab} ± 39.2	416.0 ^a ± 27.1	185.6 ^a ± 16.1
White-Depia	249.6 ^a ± 18.7	294.4 ^{ab} ± 14.7	172.8 ^{ab} ± 9.5
White-Hetia	215.6 ^b ± 7.8	324.8 ^{ab} ± 30.7	177.6 ^{ab} ± 4.4
Ambar	240.8 ^{ab} ± 30.9	312.8 ^{ab} ± 69.4	146.4 ^b ± 8.8
Sham-5	239.8 ^b ± 15.4	186.4 ^b ± 19.4	99.12 ^c ± 8.6
Sham-3	238.1 ^b ± 32.1	214.1 ^b ± 23.3	122.4 ^{bc} ± 4.4
P-value	0.04	0.002	0.001

*: means within columns using different letters are differ significantly at the $p \leq 0.05$ level (using one way ANOVA analysis)

Table 13. Comparison between six wheat genotypes planted in three different sites (Dora, Al-arroub and Janata) in terms of total hay production. (Mean* ± s.e)

Genotypes	Dora	Al-arroub	Janata	P-value
Black-Depia	572.0 ^{ab} ± 41.8	606.1 ^a ± 68.9	446.4 ^b ± 17.8	0.002
White-Depia	505.6 ^a ± 13.8	558.8 ^a ± 23.7	395.2 ^b ± 15.5	0.001
White-Hetia	457.1 ^b ± 23.6	558.4 ^a ± 11.5	414.4 ^b ± 10.5	0.001
Ambar	416.2 ^b ± 40.8	496 ^a ± 23.7	341.6 ^b ± 20.6	0.001
Sham-5	567.2 ^a ± 7.7	559.2 ^a ± 9.6	231.3 ^b ± 20.3	0.001
Sham-3	537.1 ^a ± 20.5	513.1 ^a ± 21.8	285.6 ^b ± 10.5	0.001

*: means within rows using different letters are differ significantly at the $p \leq 0.05$ level (using one way ANOVA analysis)

Table 14. Comparison between six wheat genotypes planted in the same site in terms of total hay production. (Mean* ± S.E)

Genotypes	Dora	Al-arroub	Janata
Black-Depia	572.0 ^a ± 41.8	606.1 ± 68.9	446.4 ^a ± 17.8
White-Depia	505.6 ^{ab} ± 13.8	558.8 ± 23.7	395.2 ^{ab} ± 15.5
White-Hetia	457.1 ^{ab} ± 23.6	558.4 ± 11.5	414.4 ^a ± 10.5
Ambar	416.2 ^b ± 40.8	496.0 ± 23.7	341.6 ^b ± 20.6
Sham-5	567.2 ^a ± 7.7	559.2 ± 09.6	231.3 ^c ± 20.3
Sham-3	537.1 ^{ab} ± 20.5	513.1 ± 21.8	285.6 ^{bc} ± 10.5
P- value	0.003	0.261 NS	0.001

*: means within columns with different letters differ significantly at $p \leq 0.05$ level (using one way ANOVA analysis)

Table 15. Chemical analysis of grain quality parameters, (Mean* ± SD)

Genotypes Parameter	Ca	Mg	Fe	Zn	Cu	Mn	P	B	Na+	K+	Total Nitrogen	Protein	Moisture	Dry Matter	Ash
Black-Depia	0.25 ± 0.19	0.12 ± 0.008	136.06 ± 84.58	25.14 ± 0.96	10.94 ± 5.59	95.34 ± 9.57	0.213 ± 0.02	64.79 ± 0.45	0.01 ± 0.009	0.25 ± 0.01	2.04 ± 0.25	12.77 ± 1.62	9.35 ± 0.22	90.65 ± 0.22	3.24 ± 1.65
White-Depia	0.31 ± 0.21	0.12 ± 0.006	183.93 ± 86.25	21.49 ± 4.16	9.85 ± 4.55	139.6 ± 32.7	0.223 ± 0.01	64.50 ± 2.02	0.01 ± 0.005	0.24 ± 0.02	2.05 ± 0.18	12.86 ± 1.17	9.74 ± 0.34	90.25 ± 0.34	3.34 ± 1.52
White-Hetia	0.25 ± 0.13	0.12 ± 0.007	113.26 ± 90.30	23.23 ± 1.16	12.47 ± 5.17	75.1 ± 31.28	0.213 ± 0.02	64.06 ± 0.45	0.03 ± 0.019	0.26 ± 0.03	2.07 ± 0.07	12.94 ± 0.44	9.57 ± 0.33	90.43 ± 0.33	2.57 ± 1.13
Ambar	0.21 ± 0.13	0.12 ± 0.002	93.18 ± 52.98	27.77 ± 4.12	10.42 ± 2.18	93.3 ± 43.8	0.233 ± 0.01	65.00 ± 1.07	0.01 ± 0.004	0.26 ± 0.01	2.06 ± 0.23	12.91 ± 1.44	9.60 ± 0.52	90.39 ± 0.52	2.17 ± 0.45
Sham-5	0.15 ± 0.03	0.12 ± 0.001	117.08 ± 60.07	26.49 ± 1.31	13.2 ± 4.09	102.8 ± 38.4	0.243 ± 0.01	62.90 ± 0.22	0.01 ± 0.004	0.29 ± 0.01	2.10 ± 0.17	13.11 ± 1.08	9.61 ± 0.51	90.39 ± 0.51	2.09 ± 0.13
Sham-3	0.17 ± 0.03	0.12 ± 0.005	54.32 ± 11.22	23.07 ± 6.75	10.8 ± 4.13	83.71 ± 27.28	0.226 ± 0.03	63.77 ± 1.99	0.01 ± 0.01	0.27 ± 0.03	2.02 ± 0.11	12.66 ± 0.72	9.55 ± 0.65	90.44 ± 0.65	2.14 ± 0.24
P-value	0.778	0.12	0.388	0.37	0.93	0.279	0.543	0.408	0.714	0.2	0.997	0.998	0.938	0.938	0.522

*: Means within columns using different letters are not differ significantly at the $p \leq 0.05$ level (using one way ANOVA analysis)

3.3. Chemical Composition and Grain Quality Parameters

Among all of the examined wheat genotypes, no significant variations were observed for any conducted analyses including: Ca, Mg, Fe, Zn, Cu, Mn, P, B, Na+, Total Nitrogen, Protein, Moisture, Dry Matter and Ash.

However, slightly higher “but not significant” protein contents were revealed in Sham-5 (13.11) and White-Hetia (12.94) genotypes, whereas, the lower protein contents was registered in Sham-3 (12.66) genotype. Additionally, Black and White-Depia presented slightly higher ash content (Table 15).

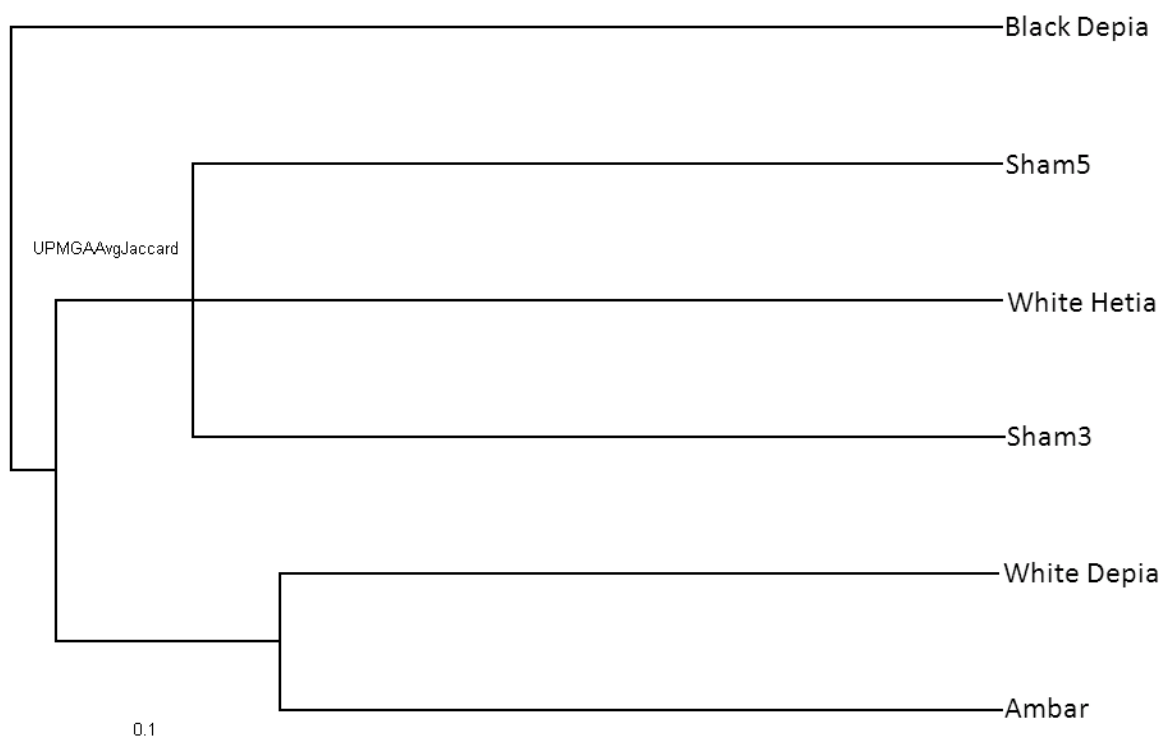


Figure 1. Dendrogram of different wheat genotypes constructed by UPGMA

3.4. Genetic Relatedness and Jaccard's Distances Index

UPGMA dendrogram clustered the examined six wheat genotypes into two main clusters related to Black-Depia as an isolated genotype (Figure 1). The first cluster is composed of "Sham-5, White-Hetia and Sham-3 genotypes; and the second cluster consisted of White-

Depia and Amber genotypes. In addition, Jaccard's distances index among the examined genotypes was found to be high. Indeed, the genetic distances matrix showed an average distance range from 0.688 to 0.955 with a mean of 0.822 (Table 16). The maximum genetic distance value of 0.955 was registered between Black-Depia and Sham-5 genotypes, whereas the lowest similarity of 0.688 was exhibited between White-Depia and Amber genotypes.

Table 16. Jaccard's distances index generated for the 6 examined wheat genotypes

	Black Depia	White Depia	White Hetia	Ambar	Sham-5
White-Depia	0.952				
White-Hetia	0.850	0.833			
Ambar	0.789	0.688	0.706		
Sham-5	0.955	0.833	0.842	0.952	
Sham-3	0.905	0.950	0.706	0.842	0.706

4. Discussion

Wheat is considered as one of the most important cereal crops in Palestine. Even though, its productivity might be one of the lowest across the world. Establishment of a national wheat breeding program is a crucial step toward increasing wheat quantity and quality. Initially, this depends on identifying morphological and/or molecular markers which facilitate the development of high yielding and/or stress tolerant wheat cultivars [6]. Identification of such markers (traits) could be achieved either by morphological and/or molecular markers [7,8]. Here, we make the first step in identifying markers and traits at morphological, yield components, grain chemical compositions, and genetic relatedness of some wheat genotypes grown at three different agro-ecological conditions of West-Bank, Palestine.

The earlier maturation and harvesting date of the six examined wheat genotypes exhibited at Janata sites, followed by Dora and Al-arroub sites, respectively, could be attributed to the differences in climatic conditions among the three examined sites (Table 1). The harsh and dry conditions which characterize the Janata site, directly affected the maturity of wheat crop [19]. In fact, higher temperatures at the end of the crop cycle induced terminal stress that affects the kernel growth and thereby leads to early maturation. Moreover, it is stated that, drought severely exaggerated the various stages of wheat growth throughout germination to maturity stages [20].

Concerning stem length parameter, it is argued that plant height was positively and significantly correlated with grain yield [21]. Their results concluded that characteristics of stem length could be used as selection criteria for genotypes to increase grain yield in bread wheat varieties. In this study, the significantly higher stem

length in the six wheat genotypes planted at Al-arroub site in general and the significant higher stem length revealed at Black-Depia genotype in particular, could be attributed either to the genetic variations and/or environmental conditions. At the genetic level, it is well documented that, the genetic make-up affects the whole qualitative and quantitative characteristics of any plant [22]. Indeed, plant heights significantly varied among different wheat genotypes [23,24,25]. In addition, environmental conditions especially higher average rainfall at Al-arroub site could probably also explain the higher stem length at this site. Similar results have been also reported by [26,27,28] who pointed out that the stem length stage is more affected by drought; in the event of increased drought it leads to reduced stem length of field crop.

A parallel trend goes also with the number of tillers (significantly higher at Al-arroub site, followed by Dora and Janata sites respectively). Many authors [29,30] pointed out that tillering (branches) is dependent mainly on water availability. However, the different tillering and performance of the examined genotypes (Black-Depia genotype presented the highest number of tillers at Dora site; whereas, White-Hetia as well as Ambar genotypes exhibited the lowest branching number at Janata site.), could be genetically controlled rather than environmentally related.

For spike characteristics, variations could also be attributed to the water deficit around the anthesis which might reduce spike and spikelet number and weight as well as the fertility of surviving spikelets [31]. Furthermore, seed weight is a direct result of the spikes growth and development which influenced mainly by the agro-climatic conditions that usually lead to an increase or decrease the size and weight of the seeds in the spikes [32]. In addition, the rate of grain number and growth in genotypes was the main factor influencing the final grain weight [33].

It is well documented that both environmental conditions as well as genetic background of breeding material affect many spike characteristics including spike length, which showed a positive direct effect on grain yield [34,20]. Therefore, Sham-5 and Sham-3 genotypes could be excluded from any future breeding programs that depend in spike length character since they significantly presented the lowest spike length, whereas, the remaining genotypes including Black-Depia, White-Depia, White-Hetia, and Amber could be promising genotypes.

A positive correlation between number of grains per spike and grain yield has been observed [33,21]. However, natural factors, mainly drought and water shortage, negatively influence these correlations [35]. Additionally, the differences in number of grains per spike were probably due to variation in genetic potential among varieties [36].

Significant differences in grains per spike among different wheat varieties were also observed by [24,37,38,39,40,41]. In this study, White-Depia and Amber could be recommended as promising genotypes since they presented significantly the higher number of grains per spike; whereas, Sham-3 and Sham-5 could be avoided.

Regarding the yield parameters, generally our local wheat genotypes (Black-Depia, White-Depia, and White-Hetia), presented higher yields compared with the

introduced Sham-3, Sham-5 and Amber genotypes. This could be attributed to the adaptability of the local genotypes among the history which found to have a significant role in the formation of yield [42].

The higher yield obtained at Al-arroub site followed by Dora and Janata sites respectively might be related to the environmental conditions (higher average rainfall) at the site rather than the genetic make-up since we have the same wheat genotypes [43,44,45]. Generally, the yield component and resource capture methods of understanding yield are complementary because often grain numbers, and possibly also potential grain size, are in balance with the resources captured. However, harsh but transient climatic conditions at anthesis can reduce grain set and yield [46], this indeed, could explain the low yield production at Janata site which has been characterized by high temperature and drought conditions during the last decades.

Similar results confirmed by [47] who stated that variation in the wheat yield is mainly related to the average rainfall. In another similar study, it is stated that drought and mainly the limited water availability is the main factor limiting crop production [48]. Moreover, it is found that grain weight is commonly considered to be influenced by the environment conditions as well as the agronomic inputs throughout different growth stages of the crop [49].

At the genotype level, it is obvious that Black-Depia is a promising genotype for any future breeding program since it presented the highest yield at the three examined sites, which might imply its high adaptability. This result found to be in agreement with [50,51,52,53] who stated that almost all plants are tolerant to drought stress but its extent varies from species to species and even within species.

Generally, grain and hay yields are highest at higher number of tillers [20]. In addition, it is reported that hay yield of wheat is the function of an accumulated effect of growth parameters like tillers per unit area and final plant height [54]. In fact, almost similar trends were also observed for all tested wheat genotypes between total number of tillers as well as plant height and total hay production. However, the variations throughout the different tested genotypes might relate to the genetic potential for each genotype.

Durum wheat is used mainly to produce bread products; in general good milling and cooking quality is related to grain quality characteristics [55]. It is well documented that, quantity characteristics are influenced mainly by environmental factors, while the quality ones are largely genetically determined [49]. In fact, findings on the nature of genetic control are rather controversial, although all scientists agree that this is undoubtedly a complex subject and one that is difficult to study, due to the strong influence of the environment upon its expression [56].

Since the quality characteristics of the six examined wheat genotypes were based on samples collected from the same site "Al-arroub site", therefore, we assume that the very narrow "un-significant" variations for almost all quality conducted analysis (Ca, Mg, Fe, Zn, Cu, Mn, P, B, Na⁺, total nitrogen, protein, moisture, dry matter and ash), is rather genetically determined. A similar result was confirmed by [54] who stated that the variations in grain

characteristics were mainly due to genotype differences and to a lesser extent to differences among harvest years.

However, the slightly higher “but not significant” protein contents revealed in White-Hetia and Amber wheat genotypes could be an added value characteristic these two genotypes compared with the others. In fact, our average level of protein content (12.7-13.1%) is in the acceptable range (12-14%) of world averages. It is stated that the high level of proteins yield a satisfactory final product [55].

Some results indicate that protein content is a quantitative trait governed by several genes distributed throughout the genome [57,58]. On the other hand; [59,60] claimed that the character is governed by a few major genes, without however excluding the action of many other genes of minor effect. In general, genes for low grain protein content show weak dominance over those for high protein content [61].

Regarding the ash content, Black and White-Depia’s presented slightly higher ash content which indeed is considered as the most important aspect of durum wheat quality for milling [62]. Several reports have already pointed out the environmental effects [63,64] noted a high genotypic influence. Other studies proved that there is a strong genotype-by environment interaction on the ash content [65].

According to UPGMA Jaccard’s distance index, Black-Depia was isolated as a unique genotype. Interestingly, this genotype showed the highest yield among the other examined genotypes as well as a cross the three different examined climatic regions which implies its high adaptability to our region, therefore, would be a promising genotype for any future wheat breeding program. Based on the high genetic similarities (around 82%) between the other five evaluated genotypes “Sham-5, White-Hetia and Sham-3” as well as “White-Depia and Amber”, the number of the genotypes would be reduced which thereby, saving time and efforts for any future wheat breeding program in Palestine [66].

5. Conclusions

It is obvious that drought and mainly the limited water availability is the main factor limiting wheat production in Palestine. Compared with the introduced wheat genotypes, our local ones presented better production in general and Black-Depia genotype in particular, therefore, the latest could be a promising cultivar for any further breeding program since it presents high productivity even under drought conditions.

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