

MORPHOLOGICAL IDENTIFICATION OF SOME WHEAT VARIETIES AND ITS CROSSES.

Attia, A.N.E. ; M.S.A Sultan ; M.A Badawi and A.A.K. Alfahdaway

Agronomy Department, Faculty of Agriculture, Mansoura University, Egypt.



ABSTRACT

The field experiments were conducted out during 2013/2014 and 2014/2015 seasons at the Experimental Station Farm of Agronomy Department, Faculty of Agriculture, Mansoura University, Dakahlia Governorate, Egypt to evaluate the morphological (quantitative and qualitative) characteristics for identifying 5 genotypes of wheat and their F₁ single crosses. The International Union for the Protection of New Varieties of Plants (UPOV, 2012 was used to evaluate the genetic purity of wheat genotypes and their F₁ single crosses) technique was used to evaluate the genetic purity of wheat genotypes and their F₁ single crosses. The aim of these experiments was to evaluate the morphological (quantitative and qualitative) characteristics for identifying 5 genotypes of wheat and their F₁ single crosses. The International Union for the Protection of New Varieties of Plants

The obtained results showed that the five studied wheat genotypes *i.e.* P₁(Gemmiza 7), P₂ (Sakha 93), P₃ (Giza 168), P₄ (Gemmiza 9) and P₅ (Sids 13) were significantly differed in flag leaf length, flag leaf area, plant height, stem diameter and the length of the bare region. Spike length, spike weight, number of spikelets/spike, number of grains/spike, grains weight/spike, 1000– grain weight and biological yield/plant

Coleoptile coloration with anthocyanin, plant growth habit, spike color, spike density, awns length at tip of spike, glume beak length, grain coloration with phenol and grain color for the five identified wheat genotypes and their F₁ crosses were recorded. the aim the study significantly

Keywords: Morphological Identification, Wheat Varieties, Wheat Crosses.

INTRODUCTION

Wheat (*Triticum aestivum* L.) is one of the most important nutritional cereal crops in Egypt and all over the world. Wheat is the stable food crop of the urban areas; moreover it is used widely in blending with maize flour in rural areas to make bread, macaroni, biscuit and sweets. It is also worth mentioning that wheat straw is a source of fodder for animals.

The development of varieties should be supported by the availability of high quality seeds. Genetic purity is one of the quality criteria required for successful seed production of wheat. The introduction of Plant Breeder's Rights has brought even more exacting requirements for genotype and distinctness testing in seed certification (Cooke, 1999).

To achieve this goal, it is essential to use stable international technique that will identify morphological characters at different growth stages. The international reorganization descriptor of UPOV, 2012 was followed to differentiate between the tested wheat genotypes. Since morphological attributes may be influenced by genotype environment and traditionally, morphological comparisons formed the basis of genetic purity

evaluations, but this is expensive and unreliable, and cannot provide information on the purity of specific genetic attributes that relate to grain quality of the variety (Baird *et al.*, 1995). This makes the development of new techniques for genetic purity determination and identification even more essential.

Jasienski *et al.* (1997) and Kercher and Sytsma (2000) indicated that several morphological traits were used to differentiate among wheat varieties. While, the morphological traits were often influenced by environmental conditions. Lima-Brito *et al.* (2006) concluded that complementary use of morphological and yield analysis, molecular cytogenetic techniques and molecular markers allowed to more accurate evaluation and characterization of wheat hybrids. Salem *et al.* (2008) evaluated genetic diversity of seven wheat (*Triticum aestivum* L.) varieties using morphological characters *i.e.* flowering time, flag leaf characters, plant height, stem diameter, number of tillers/plant, the bare region length, spike length, spike weight, number of spikelets/spike, number of grains/spike, 1000 – grain weight, grain yield/spike and grain yield/plant. They revealed that the wheat genotypes were differed in morphological characters. Hence, the identification of the genetic diversity between varieties should be a good tool of selecting these varieties in breeding programs. Aghaee *et al.* (2010) indentified and described the genetic variation among 85 durum wheat accessions based on qualitative and quantitative agro-morphological attributes. They showed that based on qualitative and quantitative measurements, there was no clear relationship between accessions and geographical diversity. The information on diversity and relationships among the agromorphological traits will be helpful to breeders in constructing their breeding populations and implementing selection strategies. Tasnuva *et al.* (2010) revealed that to differentiate four cultivars of wheat named; Bijoy, Prodip, Sourav and Shatabdi it could be used morphological identification. Where, in case of Bijoy variety, glume beak length was almost rudiment (1-2 mm), but in Prodip, its length was the highest (15-18 mm), medium length (12-15 mm) was observed in Shatabdi and Sourav showed small (8-10 mm). Growth habit of Sourav was erect, Shatabdi semi-erect and Prodip intermediate. Zarkti *et al.* (2010) showed that the disadvantages of morphological characterizations due to their low polymorphism, heritability, and sensitivity to changes in environmental conditions. Morphological characters are also often limited in number and may be controlled by epistatic and pleiotropic gene effects. Akçura (2011) stated that morphological character have been studied in order to determination of genetic diversity and selection criteria in wheat breeding. Ateş Sönmezoğlu *et al.* (2012) used many morphological characters like; plant height, stem diameter, spike length, beak shape of lower glume, shoulder shape of lower glume, hairiness of convex surface of apical rachis segment, frequency of plants with recurved flag leaves, anthocyanin coloration of auricles of flag leaf, glaucosity of sheath of flag leaf, spike density, ear glaucosity, spike color, awn presence, length of awns at tip of ear, awn color, grain color, grain shape, and glaucosity of neck of culm to characterize 20 bread wheat landraces. They showed that morphological characters could be successfully used in genetic characterization and genetic

diversity in bread wheat landraces that may be useful for wheat breeding programs as genetic resources. Siahbidi *et al.* (2012) suggested that use characters like, spike length, number of grains/spike, number of spikelet/spike, spike weight, 1000-grain weight, grain filling period, harvest index and biological yield characters as selected suitable criteria in the wheat breeding programs and production of productive varieties.

The objective of this study was to give high light on the qualitative and quantitative diversity apparent between some wheat genotypes and their crosses.

MATERIALS AND METHODS

The field experiments were conducted out during the two successive winter seasons of 2013/2014 and 2014/2015 at the Experimental Station Farm of Agronomy Department, Faculty of Agriculture, Mansoura University, Dakahlia Governorate, Egypt.

The aim of these experiments was to evaluate the morphological (quantitative and qualitative) characteristics for identifying 5 genotypes of wheat and their F₁ single crosses. The International Union for the Protection of New Varieties of Plants (UPOV, 2012) technique was used to evaluate the genetic purity of wheat genotypes and their F₁ single crosses. These genotypes were obtained from Wheat Research Department, Field Crops Research Institute, Agriculture Research Center (ARC), Ministry of Agriculture and Land Reclamation, Egypt. Key number, names and pedigree of these genotypes are presented in Table 1.

Table 1: Key number, name and source of studied wheat genotypes.

Key No.	Name	Pedigree
P1	Gemmiza 7	CMH 74A.630/5X//SERI 82 /3/ AGENT GM 4611-2GM-3GM-1GM-0GM.
P2	Sakha 93	SAKHA92/TR810328 S.8871-1S-2S-1S-0S
P3	Giza 168	MRL/BUE/SERI CM93046-8M-0Y-0M-2Y-0B
P4	Gemmiza 9	Ald "S" / Huac // Cmh 74A. 630 / Sx CGM 4583-5GM-1GM-0GM
P5	Sids 13	KAUZ"S"/TSI/SNB"S" ICW94-0375-4AP-2AP-030AP-0APS-3AP-0APS-050AP-0AP-0SD

In 22nd November 2013 growing season, the seeds of five studied wheat parents were sown in the Farm of the Agronomy Department, Faculty of Agriculture, Mansoura University. All genotypes were crossed according to a half diallel crosses mating design to obtain 5+10 crosses. In 21st November 2014 growing season, all 5+10 genotypes, which included 5 genotypes and 10 F₁ crosses were sown using the dry method (Afir).

The experimental design was Randomized Complete Block Design (RCBD) with three replicates. One row which is the 3-meter long and contains

30 plants is repeated 3 times, the distance between the plant and other 10 cm and between the rows 60 cm.

The preceding winter crop was maize (*Zea mays* L.) in both seasons. The optimum agricultural practices for wheat were performed during the two growing seasons as described by the recommendations of Ministry of Agriculture and Land Reclamation.

STUDIED CHARACTERS:

MORPHOLOGICAL IDENTIFICATION (UPOV, 2012):

The morphological identification was conducted usually using the guidelines for the conduct of tests for distinctness, uniformity by International Union for the Protection of new Varieties of Plants (UPOV, 2012).

A- Quantitative characters:

Three random replicates each consists of 10 plants, were used for determination the following characters:

1- Growth characters:

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|---|--|
| 1.1- Flag leaf length (cm).(50_51) | 1.2-Flag leaf width (cm).(55_65) |
| 1.3- Flag leaf area (cm ²). (50_51) | 1.4- Plant height (cm). (75_92) |
| 1.5- Stem diameter (mm). | 1.6-The length of the bare region (cm).. |

2- Yield and its attributes:

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|----------------------------------|-------------------------------|
| 2.1- Spike length (cm). | 2.2- Spike weight (g). |
| 2.3- Number of spikelets/spike. | 2.4- Number of grains/spike. |
| 2.5- Grains weight/spike (g). | 2.6- 1000 – grain weight (g). |
| 2.7- Biological yield (g/plant). | |

B- Qualitative characters:

Three random replicates, each of ten plants were used for estimating qualitative characters using the descriptors issued by International Union for the Protection of New Varieties of Plants (UPOV, 2012).

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|--|------------------------|
| 1. Coleoptile coloration with anthocyanin. | 2. Plant growth habit. |
| 3. Spike color. | 4. Spike density. |
| 5. Awns length at tip of spike. | 6. Glume beak length. |
| 7. Grain coloration with phenol. | 8. Grain color. |

STATISTICAL ANALYSIS:

All obtained data were statistically analyzed according to the technique of analysis of variance (ANOVA) for the Randomized Complete Block Design with three replicates as published by Gomez and Gomez (1984) by using "MSTAT-C " computer software package. New Least Significant of Difference (NLSD) method was used to test the differences between treatment means at 5 % level of probability as described by Waller and Duncan (1969).

RESULTS AND DISCUSSION

A- Quantitative characters:

1- Growth characters:

The means of flag leaf length, flag leaf width, flag leaf area, plant height, stem diameter and the length of the bare region for the five identified wheat genotypes and their F₁ crosses are presented in Table 1.

Table 1: Differences in flag leaf length, flag leaf width, flag leaf area, plant height, stem diameter and the length of the bare region for identified wheat genotypes and their crosses.

Characters Genotypes	Flag leaf length (cm)	Flag leaf width (cm)	Flag leaf area (cm ²)	Plant height (cm)	Stem diameter (mm)	The length of the bare region (cm)
P ₁	23.00	1.25	21.93	90.00	4.27	19.33
P ₂	21.33	1.50	24.00	92.33	4.26	17.33
P ₃	20.66	1.41	21.93	89.00	4.72	17.33
P ₄	18.33	1.08	14.68	89.00	4.37	18.00
P ₅	20.00	1.16	17.37	79.00	5.33	15.66
C ₁	19.00	1.33	19.00	85.66	5.96	14.33
C ₂	32.00	1.66	40.00	99.00	5.83	21.66
C ₃	19.33	1.50	21.50	89.00	4.78	15.33
C ₄	23.33	1.66	30.50	88.00	5.35	18.66
C ₅	20.00	1.50	22.25	95.00	5.24	14.66
C ₆	20.00	1.33	20.37	91.33	4.18	14.66
C ₇	18.66	1.16	16.37	78.66	5.52	13.00
C ₈	29.33	1.41	30.94	91.66	5.33	19.00
C ₉	20.00	1.33	20.37	76.00	4.85	11.66
C ₁₀	19.66	1.66	24.50	72.33	5.50	12.66
F. test	*	NS	*	*	*	*
NLSD at 5%	2.93	-	11.49	6.05	0.84	3.92

The five studied wheat genotypes *i.e.* (Gemmiza 7), (Sakha 93), (Giza 168), (Gemmiza 9) and (Sids 13) were significantly differed in flag leaf length, flag leaf area, plant height, stem diameter and the length of the bare region (Table 1).

The tallest blade of flag leaf (23.00 cm) was resulted from sowing (Gemmiza 7). On the other hand, the shortest blade of flag leaf (18.33 cm) was obtained when sowing (Gemmiza 9). The arrangement of other studied genotypes concerning flag leaf length was as follows; (Sakha 93), (Giza 168) and (Sids 13).

The maximum flag leaf area was produced from sowing P₂ genotype (Sakha 93), which result was 24.00 cm². On the other side, the lowest flag leaf area (14.68 cm²) was resulted from sowing genotype (Sids 13). It could be also noticed that P₁ (Gemmiza 7) and P₃ (Giza 168) genotypes resulted in the same flag leaf area (21.93 cm²).

The tallest wheat plants (92.33 cm) were resulted from sowing P₂ genotype (Sakha 93). On the other direction, the shortest wheat plants (79.00 cm) was obtained when sowing P₅ genotype (Sids 13). The other studied wheat genotypes that used as parents; (Gemmiza 7), (Giza 168) and (Gemmiza 9) were insignificantly differed in the plant height.

The thickest stems were produced from sowing genotype (Sids 13), which result was 5.33 mm. On the other side, the thinnest stems (4.26 mm) was resulted from sowing genotype (Sakha 93). It could be also noticed that (Gemmiza 7), (Giza 168) and (Gemmiza 9) were insignificantly differed in their stem diameter.

The longest bare region (19.33 cm) was resulted from sowing (Gemmiza 7). On the other hand, the shortest bare region (15.66 cm) was obtained when sowing P₅ (Sids 13). The arrangement of other studied genotypes concerning length of the bare region was as follows; (Gemmiza 9) then (Sakha 93) and (Giza 168).

Wheat F₁ crosses were significantly differed too in flag leaf length, flag leaf area, plant height, stem diameter and the length of the bare region as shown from results tabulated in Table 1.

The tallest blade of flag leaf (32.00 cm) was recorded by sowing cross (Gemmiza 7) X (Giza 168). At the same time as, the shortest blade of flag leaf (18.66 cm) was resulted from sowing cross (Sakha 93) X (Sids 13). From the results showed in the same Table, it could be noticed that no significant differences were detected among the following crosses; C1, C6 and C9 in their length of flag leaf.

The highest flag leaf area was obtained from sowing cross (Gemmiza 7) X P₃(Giza 168). Where, the corresponding result was 40.00 cm². Meanwhile, the lowest flag leaf area (16.37 cm²) was produced from sowing cross P₂ (Sakha 93) X P₅ (Sids 13). It is worthy to mentioned that, the differences among the following crosses; C5, C8, C6, C8, C4, C9 and C10 concerning their flag leaf area did not reached the level of significance.

The tallest wheat plants (99.00 cm) was recorded by sowing the cross (Gemmiza 7) X (Giza 168). Whilst, the shortest wheat plants (72.33 cm) was resulted from sowing cross (Gemmiza 9) X (Sids 13). From the results showed in the same Table, it could be noticed that no significant differences were detected among the following crosses; C5, C3, C6 and C8 in their plant height.

The thickest wheat stems were obtained from sowing the cross (Gemmiza 7) X (Sakha 93). Where, the corresponding result was 5.96 mm. Meanwhile, the thinnest wheat stems (4.18 mm) was produced from sowing cross P(Sakha 93) X Gemmiza 9).

The longest bare region (21.66 cm) was recorded by sowing cross (Giza 168) X (Gemmiza 7). At the same time as, the shortest bare region (11.66 cm) was resulted from sowing cross (Giza 168) X (Sids 13).

The grand differences in growth characters between (Gemmiza 7) X(Gemmiza 9) as well as the crosses C7 and C2 supplies useful information for crosses identification and could be easily recognized them with their growth characters and it is considered an important trait for morphological identification. The possible reason for the observed differences among wheat genotypes in growth characters could be due to the amount of diversity among them which could be manipulated for further improvement in wheat breeding. These results are in agreement with those recorded by Salem *et al.* (2008).

2- Yield and its attributes:

The means of spike length, spike weight, number of spikelets/spike, number of grains/spike, grains weight/spike, 1000–grain weight and biological yield/plant for the five identified wheat genotypes and their F₁ crosses are shown in Table 2.

Table2:Differences in spike length, spike weight, number of spikelets/spike, number of grains/spike, grains weight/spike, 1000–grain weight and biological yield/plant for identified wheat genotypes and their crosses.

Characters Genotypes	Spike length (cm)	Spike weight (g)	Number of spikelets/spike	Number of grains/s pike	Grains weight/s pike (g)	1000 – grain weight (g)	Biologic al yield (g/plant)
P ₁	12.66	3.71	18.33	73.33	2.376	74.03	6.40
P ₂	17.00	2.73	20.00	72.66	2.052	57.27	6.71
P ₃	14.33	3.42	20.00	66.33	2.387	70.68	7.02
P ₄	16.00	3.72	20.00	72.66	2.732	67.34	7.06
P ₅	13.00	3.04	20.33	81.33	2.066	50.57	5.04
C1	17.00	4.70	21.33	77.00	2.740	77.45	8.04
C2	18.33	4.39	22.00	88.00	3.369	70.83	9.37
C3	14.00	3.74	21.00	63.00	2.395	63.56	7.06
C4	17.00	3.05	22.00	79.66	2.396	63.91	5.74
C5	16.33	5.40	22.00	88.00	4.059	77.02	9.71
C6	13.00	3.37	19.00	69.66	2.394	70.59	7.37
C7	14.33	3.03	18.00	66.66	2.394	70.59	7.37
C8	14.66	3.35	22.00	73.33	2.699	57.58	6.03
C9	14.66	3.05	21.00	70.33	3.053	43.84	6.04
C10	13.00	3.71	21.00	70.33	3.712	60.38	6.71
F. test	*	*	*	*	*	*	*
NLSD at 5%	2.97	1.07	1.52	3.90	1.09	1.41	1.93

Spike length, spike weight, number of spikelets/spike, number of grains/spike, grains weight/spike, 1000– grain weight and biological yield/plant were significantly differed among the five studied wheat genotypes *i.e.* (Gemmiza 7), (Sakha 93), (Giza 168), (Gemmiza 9) and (Sids 13) as clearly seen from results in Table 2.

The maximum spike length was produced from sowing P₂ genotype (Sakha 93), which result was 17.00 cm. On the other side, the shortest spike (12.66 cm) was resulted from sowing P₁ genotype (Gemmiza 7). It could be also noticed that the differences between (Gemmiza 7) and (Sids 13) genotypes and also between (Giza 168) and (Gemmiza 9) were insignificant regarding their spike length.

The heaviest spike (3.72 g) was resulted from sowing (Gemmiza 9). On the other hand, the lightest spike (2.73 g) was obtained when sowing (Sakha 93).

The maximum number of spikelets/spike was produced from sowing P₅ genotype (Sids 13), which result was 20.33. On the other direction, the lowest number of spikelets/spike (18.33) was resulted from sowing P₁ genotype (Gemmiza 7). It could be also noticed that (Sakha 93), (Giza 168), (Gemmiza 9) and (Sids 13) genotypes did not significantly in their number of spikelets/spike.

The highest number of grains/spike (81.33) was resulted from sowing P₅ (Sids 13). On the other hand, the lowest number of grains/spike (66.33) was obtained when sowing (Giza 168).

The maximum grains weight/spike was produced from sowing P₄ genotype (Gemmiza 9), which result was 2.732 g. On the other hand, the lowest grains weight/spike (2.052 g) was resulted from sowing P₂ genotype (Sakha 93).

The maximum 1000 – grain weight value (74.03 g) was resulted from sowing (Gemmiza 7). On the other hand, the minimum 1000 – grain weight value (50.57 g) was obtained when sowing (Sids 13).

The maximum biological yield/plant was produced from sowing P₄ genotype (Gemmiza 9), which result was 7.06 g. On the other side, the lowest biological yield/plant (5.04 g) was resulted from sowing P₅ genotype (Sids 13). It could be also noticed that (Gemmiza 7), (Sakha 93), (Giza 168) genotypes did not significantly differed in biological yield/plant.

From statistical analysis of obtained results, it could be stated that wheat F₁ crosses resulted from half diallel model among the five studied wheat genotypes (10 crosses) were significantly differed in spike length, spike weight, number of spikelets/spike, number of grains/spike, grains weight/spike, 1000–grain weight and biological yield/plant as shown from results found in Table 2.

The longest spike was obtained from sowing cross (Giza 168) X (Gemmiza 7). Where, the corresponding result was 18.33 cm. Meanwhile, the shortest spike (13.00 cm) was produced from sowing cross (Gemmiza 9) X (Sakha 93) or (Sids 13) X (Gemmiza 9). It is worthy to mentioned that, the differences among the following crosses; C1, C2, C5. and C4 and also C3, C6, P₄ C8, C7, C9 and C10. concerning their spike length did not reached the level of significance.

The highest value of spike weight (5.40 g) was recorded by sowing cross (Giza 168) X (Sakha 93). On the contrary, the lowest value of spike weight (3.03 g) was resulted from sowing cross (Gemmiza 9) X P₃ (Giza 168). From the results showed in the same Table, it could be noticed that no significant differences were detected among the following crosses; C3, C6, C8, C4, C7, C9. and C10 in their spike weight.

The highest number of spikelets/spike (22.00) was obtained from sowing the following crosses C2, C5, C4 and C7. Meanwhile, the lowest number of spikelets/spike (18.00) was produced from sowing cross P₄ (Gemmiza 9) X P₃ (Giza 168). It is worthy to mentioned that, the differences among the following crosses; C1, C2, C5, C3, C4, C7, C9 and C10 concerning their number of spikelets/spike did not reached the level of significance.

The highest number of grains/spike (88.00) was recorded by sowing cross C2. or C5. Along with, the lowest number of grains/spike (63.00) was resulted from sowing cross (Gemmiza 9) X (Gemmiza 7). From the results showed in the same Table, it could be noticed that no significant differences were detected among C2, C5, C4 and C1 crosses or among C8, C6, C9 and C10 in their number of grains/spike.

The highest grains weight/spike was obtained from sowing cross (Giza 168) X (Sakha 93). Where, the corresponding result was 4.059 g. Meanwhile, the lowest grains weight/spike (2.699) was produced from sowing cross P₅ (Sids 13) X P₂ (Sakha 93). It is worthy to mentioned that, the

differences among the following crosses; C5, C2, C8, C9 and C10 concerning their grains weight/spike did not reached the level of significance.

The minimum value of 1000 – grain weight (43.84) was resulted from sowing cross (Sids 13) X (Giza 168). From the results showed in the same Table, it could be noticed that no significant differences were detected between the following crosses; C1 and C5 in their 1000 – grain weight.

The highest biological yield/plant was obtained from sowing cross (Giza 168) X (Sakha 93). Where, the corresponding result was 9.71 g. Meanwhile, the lowest biological yield/plant (5.74 g) was produced from sowing cross (Sids 13) X (Gemmiza 7). It is worthy to mentioned that the differences among C5, C2 and C1. crosses or among C3, C6, C8, C7, C9 and C10 crosses concerning their biological yield/plant did not reached the level of significance.

The great differences in yield and its attributes among wheat genotypes and their F₁ crosses may be due to the amount of diversity among them, and it supplies useful information for genotypes and their F₁ crosses identification and could be easily recognized them with their yield and its attributes. The results are in line with those of Salem *et al.* (2008), Ateş Sönmezoğlu *et al.* (2012) and Siahbidi *et al.* (2012).

B- Qualitative characters:

Coleoptile coloration with anthocyanin, plant growth habit, spike color, spike density, awns length at tip of spike, glume beak length, grain coloration with phenol and grain color for the five identified wheat genotypes and their F₁ crosses are shown Table 3.

The results showed that (Gemmiza 7) genotype was absent or very weak of coleoptile coloration with anthocyanin. Whereas, other studied genotypes *i.e.* (Sakha 93), (Giza 168), (Gemmiza 9) and (Sids 13) were weak in coleoptile coloration with anthocyanin.

It is clearly show that (Sids 13) genotype was semi-erect in growth habit. While, the other studied genotypes *i.e.* (Gemmiza 7), (Sakha 93), (Giza 168) and (Gemmiza 9) were erect in growth habit.

Spike color of all identified wheat genotypes was white.

(Giza 168) genotype had lax spikes. While, (Sakha 93) genotype had very lax spikes. On the other direction the other studied genotypes *i.e.* (Gemmiza 7), (Gemmiza 9) and (Sids 13) were medium in spike density.

The five identified wheat genotypes *i.e.* (Gemmiza 7), (Sakha 93), (Giza 168), (Gemmiza 9) and (Sids 13) had a long awns at tip of spike.

(Gemmiza 9) and (Sids 13) genotypes had short glume beak. While, the other studied genotypes *i.e.* (Gemmiza 7), (Sakha 93) and (Giza 168) genotypes had long glume beak.

The results showed that all identified wheat genotypes *i.e.* (Gemmiza 7), (Sakha 93), (Giza 168), (Gemmiza 9) and P (Sids 13) were absent or very light in grain coloration with phenol.

All identified wheat genotypes *i.e.* (Gemmiza 7), (Sakha 93), (Giza 168), (Gemmiza 9) and (Sids 13) had white grains.

With respect to wheat F₁ crosses, The results indicated that C2 cross was medium in coleoptile coloration with anthocyanin. Meanwhile, other studied F₁ crosses of wheat which resulted from a half diallel crosses were weak in coleoptile coloration with anthocyanin.

The results indicated that P₃ x P₁ cross was medium in coleoptile coloration with anthocyanin. Meanwhile, other studied F₁ crosses of wheat which resulted from a half diallel crosses were weak in coleoptile coloration with anthocyanin.

C2 and C10 crosses were erect in growth habit. Whilst, C7 and C9 crosses were semi-prostrate in growth habit. On the other hand, the other studied F₁ crosses of wheat were semi-erect in growth habit.

The obtained results indicate that all F₁ crosses of wheat had white spike.

C2, C5, C3, C6, C8 and P₃ x P₁ crosses were dense in spike density. At the same time as other studied F₁ crosses *i.e.* C1, C4, C7, C9, C10 and C9 crosses were medium in spike density.

All studied F₁ crosses of wheat had medium length of awns at tip of spike .

All studied F₁ crosses of wheat had medium length of glume beak.

All studied F₁ crosses of wheat were absent or very light in grain coloration with phenol.

All studied F₁ crosses of wheat were white in grain color.

The possible reason for the observed differences in qualitative characters for the five identified wheat genotypes and their F₁ crosses may be due to the variation in their genetic makeup. The results are in line with those of Ateş Sönmezoğlu *et al.* (2012), they also showed that morphological characters could be successfully used in genetic characterization and genetic diversity in bread wheat landraces that may be useful for wheat breeding programs as genetic resources.

CONCLUSION

Morphological traits used to identification genotypes of wheat plants. When identification between genotypes, morphological methods using firstly, followed by the modern bio-chemical methods, especially when differences among morphological characteristics unclear.

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التمييز المورفولوجي لبعض أصناف القمح

احمد نادر السيد عطية، محمود سليمان سلطان، محسن عبد العزيز بدوي و
عبدالرحمن علي خلف
قسم المحاصيل الحقلية - كلية الزراعة - جامعة المنصورة

أجريت التجارب الحقلية خلال الموسمين ٢٠١٣/٢٠١٤ و ٢٠١٤/٢٠١٥ في مزرعة محطة البحوث والتجارب الزراعية قسم المحاصيل الحقلية، كلية الزراعة، جامعة المنصورة، محافظة الدقهلية، مصر لتقييم الخصائص المورفولوجية (الكمية والنوعية) لتمييز التراكيب الوراثية لخمس أصناف من القمح والهجن الفرديه لهم. F1 وتم باستخدام تقنيه الاتحاد الدولي لحماية الأصناف النباتية الجديدة (UPOV) ، 2012 لتقييم النقاء التركيب الوراثي لخمس اصناف من القمح والهجن الفرديه الناتجه منها لهم. F1

درست خمسة تراكيب وراثيه من القمح درست، هي (جميزه٧)، (2p سحا ٩٣) (P3) جيزه ١٦٨ ()، (4p جميزه ٩) و (5p سدس ١٣) وتم اجراء التهجين بين الاصناف الخمسه كهجن نصف دائريه في الموسم لاول وفيه المسم الثاني تم زراعه لاصناف التراكيب الوراثيه الناتجه من الهجين واستخدام تصميم RCBD ثم درست الصفات المرفولوجيه الكمييه النوعيه للاصناف الهجن الناتجه منها وتتلخص اهم النتائج بالنسبه للاباء الخمسه وختلفت لاصناف الخمسه وقد كانت هناك اختلافات بشكل كبير في طول ورقة العلم، منطقة ورقة العلم، ارتفاع النبات، قطر الساق وطول المنطقة العاربية.

طول السنبله، وزن السنبله، وعدد السنبيلات / السنبله، عدد الحبوب / سنبله و وزن الحبوب / السنبله، وزن ١٠٠٠ - الحبة والمحصول البيولوجي / النبات حيث كان هناك اختلاف كبير بين الخمس مورثات من اصناف القمح المدروسة. اما بالنسبه للصفات المرفولوجيه النوعيه للاصناف والهجن الناتجه منها وتم تسجيل صبغات Coleoptile مع الأنثوسيانين، وطبيعة نمو النبات، لون السنبله وكثافة السنبله، طول السفا في طرف السنبله، طول تلوين الحبوب بالفينول ولون الحبوب لخمسه ابااء ولهجن الناتجه منها.

Table 3: Differences in coleoptile coloration with anthocyanin, plant growth habit , spike color, spike density, awns length at tip of spike, glume beak length, grain coloration with phenol and grain color for identified wheat genotypes and their crosses.

Characters Genotypes	Coleoptile coloration with anthocyanin	Plant growth habit	Spike color	Spike density	Aw ns length at tip of spike	Glume beak length	Grain coloration with phenol	Grain color
P ₁	absent or very weak	erect	w hit	medium	long	long	absent or very light	w hit
P ₂	w eak	erect	w hit	Very lax	long	long	absent or very light	w hit
P ₃	w eak	erect	w hit	lax	long	long	absent or very light	w hit
P ₄	w eak	erect	w hit	medium	long	short	absent or very light	w hit
P ₅	w eak	semi-erect	w hit	medium	long	short	absent or very light	w hit
C ₁	w eak	semi-erect	w hit	medium	medium	medium	absent or very light	w hit
C ₂	medium	erect	w hit	dense	medium	medium	absent or very light	w hit
C ₃	w eak	semi-erect	w hit	dense	medium	medium	absent or very light	w hit
C ₄	w eak	semi-erect	w hit	dense	medium	medium	absent or very light	w hit
C ₅	w eak	semi-erect	w hit	dense	medium	medium	absent or very light	w hit
C ₆	w eak	semi-erect	w hit	dense	medium	medium	absent or very light	w hit
C ₇	w eak	semi-erect	w hit	medium	medium	medium	absent or very light	w hit
C ₈	w eak	semi-prostrate	w hit	medium	medium	medium	absent or very light	w hit
C ₉	w eak	semi-prostrate	w hit	medium	medium	medium	absent or very light	w hit
C ₁₀	w eak	erect	w hit	medium	medium	medium	absent or very light	w hit