

Characterization of Agronomic Traits and Grain Quality of Some Wheat Landraces

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ABSTRACT

This study was carried out at Nubaria Research Station Farm to evaluate of 12 wheat land races genotypes during two seasons 2014/15 and 2015/16. Analysis of variance was computed to measure genotypic and phenotypic coefficients of variation and broad sense heritability (h^2) for yield and its components. Also, Chemical compositions of whole meal wheat genotypes were determined. Results indicated significant differences among wheat genotypes for all studied traits except spike length (cm) in the combined data.

Results indicated that high values of genotypic (GCV) and phenotypic (PCV) coefficients of variation were obtained by grain yield (67.84 and 68.83), followed by number of spike/m² (35.54 and 38.57), number of kernel/spike (34.02 and 36.33) and 1000-kernel weight (26.50 and 29.35) respectively. High heritability coupled with high genetic advance was observed for most traits. Whole meal wheat genotype L1 contain the highest content of crude protein and ash which were (13.23 and 2.01 %) respectively. On the contrary, L1 had the lowest content (82.78%) of carbohydrates. In addition to, the L10 had the highest crude fat content compared with the other wheat genotypes.

Key words: Wheat, *Triticum aestivum*, Variance coefficient, Heritability, Genetic gain.

INTRODUCTION

Bread wheat (*Triticum aestivum* L.) is one of the most widely grown crops in the world and Egypt, the local production is about 8 million tons, however it covers less than half of the local consumption. Increasing wheat productivity is a national target in Egypt to reduce the gap between wheat consumption and production. It is not possible to increase the area under production. Hence, only alternative is left to increase the productivity by introducing superior varieties and better management of crop production to cope up with increasing demands of food. A major cause of concern to a plant breeder is the constant improvement of the best available genotypes for further enhancement in their yield potential either directly or through improvement of various factors which contribute indirectly to high yield. Therefore, the only alternative strategic solution is to increase its productivity per feddan by applying the better crop

management techniques and introducing high yielding cultivars characterized by tolerance against biotic and abiotic stresses.

Genetic diversity available in the existing germplasm determines the success of any crop improvement programme (Falconer and Mackay, 1996) and (Moose and Mumm, 2008). Therefore, quantitative assessment of genetic diversity present among population usually helps a plant breeder in choosing desirable parents for breeding programme. In whole grain wheat flour (WGWF) all the anatomical components of the grain, such as endosperm, bran and germ are present in the same proportions that exist in the intact form. Thus, WGWF contains substantially more fibers, vitamins, minerals and phytochemicals than refined wheat flour (RF). Accordingly, it is considered as an excellent source of nutritional and functional ingredients for human health with many associated benefits, including the reduction of diseases risk such as diabetes, cardiovascular diseases, obesity, and cancer (Liu, 2007).

The objective of the present study was to evaluate a set of 10 landraces and two cheiks wheat with an aim, to analysis the genetic variability, heritability, and genetic advance for yield and its component traits. Furthermore, assess various biochemical grains under Nubaria conditions.

MATERIALS AND METHODS

Plant materials and experimental design

The present work was carried out at the Nubaria Research Station Farm during the two successive seasons of 2014/2015 and 2015/2016 to evaluate the yield performance of ten wheat landraces and two released Egyptian cultivars (Gemmeiza 9 and Giza 168). The detailed description of the code and pedigree of the tested genotypes are presented in Table (1). In each season, the plant materials were laid out in a randomized complete block design, with three replicates. Each plot consisted of six rows 3.5 m long and 20 cm apart. The total grain yield (kg/m²) was measured by harvesting each plot at crop maturity. Five plants were randomly chosen from each plot to measure the other yields components traits. Sowing dates were

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Table 1. Code of ten landraces of number and pedigree of two check cultivars

No	Genotypes	Code number and /or origin
1	L1	G.S. N.3276
2	L2	G.S. N.3359
3	L3	G.S. N.3314
4	L4	Assut 2799/38
5	L5	Assut 2816/40
6	L6	Assut 74
7	L7	Assut 3737
8	L8	Assut 3745
9	L9	G.S. N.3841
10	L 10	G.S. N.3845
11	Gemmeiza 9	
12	Giza 168	

G. S. N. : Genetic Screening Nursery

Table 2. Mechanical and chemical characteristics of the soil at the experimental sites during 2014/15 and 2015/16

Soil depth (cm)	Particle size analysis %				Texture class	CaCO ₃ (%)	pH	E.C. (ds/m)
	Coarse sand	Fine sand	Silt	Clay				
0-30	11.4	35.7	26.4	26.5	Sandy clay loam	29.8	8.5	1.05
30-60	8.0	38.9	27.3	27.8	Sandy clay loam	30.1	8.3	0.90

18 and 20 November in the two successive seasons, respectively.

The experiment was subjected to the recommended package of agronomic and protection practices at the proper time to obtain a healthy crop.

All the cultural practices were performed as recommended. The soil of the experimental site was calcareous and its physical and chemical properties were determined according to Page (1982) and presented in Table 2.

Data collection:

During the two seasons the following data were recorded:

Mean performance:

Plant height (cm), data of number of days to 50% heading (DH) and number of days to 50% maturity (DM) were recorded on plot basis, number of spikes/m², 1000-kernel weight (g), number of kernels/spike, spike length (cm), and grain yield (GY) was determined from the whole area of the plot (10.5 m²), then converted to the unit of (ardab/fad)

Chemical analysis of samples:

Moisture, crude protein (N x 5.95), crude fat and ash content of samples were determined according to the method described in. Total carbohydrates were calculated by differences.

Statistical analysis:

Data were subjected to individual and combined analysis of variance (ANOVA) of randomized complete block design for each seasons and across them (Steel *et al.*, 1997). Levene test (1960) was run prior to the combined analysis to test the homogeneity of individual error terms. Least significant difference (LSD) test was used to detect the significant differences among genotype means. The genotypic and phenotypic variances and their corresponding coefficients of variations were estimated, using the pertinent mean square expectations, according to the method, suggested by Johnson *et al.* (1955). Broad sense heritability (h²) was estimated as described by Allard (1999).

Genetic parameters: Heritability in broad sense (h²) was determined as:

$$\sigma^2 g / \sigma^2 p$$

$$EGA = KH^2 \sigma \text{ phenotypic,}$$

$$EGA\% = \frac{EGA}{\chi} \times 100$$

The predicted genetic advance under selection (EGA) was computed.

Where: K is the selection differential and equals to 2.06 upon selection the highest 5% of the population, h²

Heritability is narrow sense and σ_{Ph} = phenotypic standard deviation.

$$\text{Phenotypic Coefficient of Variability (PCV)} = \frac{\text{Phenotypic Variance } (\sigma^2_p)}{\bar{x}}$$

$$\text{Phenotypic Coefficient of Variability (PCV)} = \frac{\text{Genotypic Variance } (\sigma^2_p)}{\bar{x}}$$

where, \bar{x} = grand mean of all entries. The PCV and GCV coefficients of variation were calculated according to Toker (1998). Genetic advance was calculated according to Allard (1960). Expected genetic advance (EGA) as percentage of the grand mean (EGA %).

RESULTS AND DISCUSSION

Field evaluation:

Table (3) shows the mean values of wheat genotypes for agronomic characters. For heading date the earliest genotype was L5 (76.67), while L1 was the latest genotype (83.83). Meanwhile the tallest genotype was Gemmeiza 9 (105) on the other hand; L10 was the shortest genotype (75.5).

For the number of kernels/spike Giza 168 had the highest value (53.12) but L1 gave the lowest value (30.03). There is no significant difference among test genotypes for spike length. With respect to number of spikes /m² L5 had the highest number of spikes/m² (569.50), while L1 had the lowest number of spikes/m² (346.33). The highest spike length (cm) gave 12.75 (cm) for each L1 and L6, while Giza 168 gave the least value 10.50 (cm). For 1000-kernel weight (g) Gem.9 gave the highest value (48.14), while L1 gave the

lowest value (34.55). With respect to grain yield (ardab/fed). Gem. 9 had the greatest value grain yield (19.08). On the other hand, L9 had the lowest grain yield (8.11).

Genetic parameters

Table 4. Presents the genetic parameters studied. The phenotypic coefficient of variation (PCV) was greater than genotypic coefficient of variation (GCV) for all the studied characters indicating role of environmental interaction in the expression of the characters. These results were in agreement with (Gollen *et al.* 2011). A perusal coefficients of variation revealed that the highest GCV and PCV were observed for grain yield (67.84%, 68.83%) followed by , number of spikes/m²(34.02-36.33), number of kernels per spike (34.02%, 36.33%),and 1000-grain weight (26.5-29.35). Similar results were harmony with (Kaul and Singh, 2011 and Kumar *et al.* 2013).

Table (4) shows that high values of heritability were found for grain yield followed by, days to heading, number of kernels/spike, and number spikes/m². This shows the presence of additive gene effect and selection may be made for the improvement of these traits. Although low heritability exhibited that the characters were highly influenced by environmental effect and genetic improvement through selection will be difficult due to effect of environment (Arya *et al.*, 2017).

The expected genetic advance (EGA %) ranged from 12.75 to 67.47%. The highest EGA was observed for spike length and grain yield. High heritability coupled with high genetic advance as percent mean were revealed for number of spikes/m², 1000- kernel weight, number of kernels/spike and grain yield.

Table 3. Mean performance of ten wheat landraces and two check cultivars for agronomic characters (combined data)

Genotype	Number of days to heading	Plant height (cm)	Number of kernels/spike	Number of spikes/m ²	Spike length (cm)	1000 Kernel weight (g)	Grain yield (ardab/fad)
L1	83.83	82.83	30.03	346.33	12.5	34.55	8.78
L2	81.00	77.33	45.89	463.33	12.75	43.25	9.56
L3	80.50	79.03	45.45	455.67	11.75	39.24	9.43
L4	76.83	82.33	38.57	487.67	12.25	34.64	6.31
L5	76.67	84.42	35.30	569.50	11.92	41.70	14.59
L6	81.17	80.08	40.02	548.00	12.75	47.03	12.30
L7	79.33	76.17	35.98	406.67	11.67	35.33	12.20
L8	80.67	76.16	41.02	413.00	11.33	44.93	10.85
L9	82.17	76.58	39.69	384.33	11.25	37.04	8.11
L10	78.67	75.50	41.02	447.83	11.92	43.23	15.73
Gem. 9	82.00	105	48.80	541.00	11.08	48.14	19.08
Giza 168	79.00	95	53.12	455.50	10.50	36.08	17.41
LSD at (0.05)	2.55	5.198	7.10	78.67	N.S	6.129	3.185

Table 4. Genetic parameters of grain yield and its related characters computed from ten landraces and tow check cultivars across both seasons combin

Characters	Genetic parameters					
	Grand mean	G CV %	Ph CV %	H ² %	Genetic advance	
					EGA	EGA %
Days to heading	80.153	6.45	6.72	92.09	10.22	12.75
Plant height (cm)	78.68	10.27	12.39	68.68	13.78	17.52
Number of kernels/spike	40.52	34.02	36.33	87.71	10.30	25.42
Number of spikes/m ²	459.90	35.54	38.57	84.90	310.30	67.47
Spike length (cm)	11.81	12.97	14.35	81.67	2.84	24.12
1000-Kernel weight (g)	43.43	26.50	29.35	81.52	13.24	30.49
Grain yield (ardab/fad)	15.148	67.84	68.83	97.00	20.84	37.58

Similar results were reported by Nagireddy and Jyothula, (2009) and Khokhar *et al.*, (2010). This indicates substantial contribution of additive gene action in the expression of the characters (Kuobaili and Khoury 2005).

Chemical composition of whole meal wheat genotypes (g/100g on dry weight basis)

The chemical composition of whole meal wheat genotypes was determined and the results are recorded in Table (5). The moisture content of whole meal wheat genotypes ranged from (11.26 to 12.71%).

However, whole meal wheat genotype L1 contains the highest content of crud protein which was (13.23 %) followed by whole meal wheat genotype L9 which recorded (12.85%) while the lowest value of crud protein was (10.96%) for whole meal wheat genotype

L8. These results are in line with those Nemat, *et al.* (2011). They reported that, crude protein of wheat seeds were ranged from 10.2 to 12.6 % depending on genotypes .

Apparent also from the same table that, whole meal wheat genotypes contain (1.58 to 2.18 %) crud fat, In addition to; the L10 gave the highest crud fat content compared with the other wheat genotypes.

The highest content of ash was recorded for the genotype L1 (2.01%) followed by L10 (1.99%) while, the Giza 168 had the lowest value; 1.67%. These results were in the same trend with those reported by (Protonotariou, *et al.*, 2016 and Bressiani, *et al.*, 2017).

Results also revealed that the highest carbohydrates content was found in L8 (85.55 %) compared with L1 which had the lowest content (82.78%).

Table 5. Proximate chemical composition (%) of whole meal wheat genotypes (on dry weight basis)

Genotypes	Moisture%	crude Protein%	crude Fat%	Ash%	Total carbohydrates ** %
L1	11.26 b	13.23 a	1.98 a	2.01 a	82.78 e
L2	12.25 ab	11.91 b	1.87 ab	1.72 b	84.50b
L3	11.28 b	11.69 bc	1.82 ab	1.85 ab	84.64b
L4	12.51 a	11.23 c	1.58 b	1.83 ab	85.36a
L5	12.60 a	12.65 ab	2.01 a	1.75 b	83.59 d
L6	12.21 ab	11.51 c	1.81 ab	1.85 ab	84.83 b
L7	11.36 b	12.81 ab	2.06 a	1.73 b	83.40 d
L8	12.02 ab	10.96 c	1.67 b	1.82 ab	85.55 a
L9	11.28 b	12.85 ab	2.07 a	1.75 b	83.33 d
L10	12.71 a	11.83 bc	2.18 a	1.99 a	84.00 c
Gem. 9	11.65 b	12.01 b	2.15 a	1.89 ab	83.95 c
Giza 168	11.48 b	12.40 b	1.86 ab	1.67 b	84.07 c

* Each value is an average of three determinations.

+ Values followed by the same letter in Colum are not significantly different at $P \leq 0.05$

**Total carbohydrates was calculated by difference.

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الملخص العربي

توصيف بعض صفات المحصول والجودة لبعض سلالات القمح

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٦٧,٨٤ و ٦٨,٨٣ ثم عدد السنابل/م^٢ ٣٥,٥٤ و ٣٨,٥٧ ثم عدد الحبوب/سنبله ٣٤,٠٢ و ٣٦,٣٣ ووزن ١٠٠٠ حبه ٢٦,٥٠ و ٢٩,٣٥ على التوالي في كلا الموسمين.

ولوحظ ارتفاع درجة التوريث الى جانب التقدم الوراثي في معظم الصفات وأظهر التحليل الكيميائي ان السلالة L1 أعطت أعلى محتوى من البروتين والرماد ١٣,٢٣ و ٢,٠١% على التوالي وقل محتوى من الكربوهيدرات ٨٢,٧٨%. بالإضافة إلى أن السلالة L10 أعطت أعلى محتوى من الدهن مقارنة بالتراكيب الوراثية الأخرى من سلالات القمح.

أجريت هذه الدراسة في المزرعة البحثية بمحطة بحوث بالنوباريه لتقييم ١٢ تركيب وراثي خلال الموسمين المتتاليين ٢٠١٤/٢٠١٥ و ٢٠١٥/٢٠١٦ وتم حساب معامل الإختلاف الوراثي والمظهرى ودرجة التوريث بالمعنى الواسع للمحصول ومكوناته وأيضاً التحليل الكيماوى للحبوب.أوضحت النتائج وجود فروق معنوية بين كل الصفات المدروسة في كل التراكيب الوراثية ماعدا صفة طول السنبله.

أشارت النتائج إلى أن أعلى قيمه للتباين الوراثي والمظهرى تم الحصول عليها من خلال محصول الحبوب