



Plant Production Science

ASSESSMENT OF SIX QUINOA (*Chenopodium quinoa* Willd.) GENOTYPES FOR SEED YIELD AND ITS ATTRIBUTES UNDER TOSHKA CONDITIONS

Samy A. Afiah^{*}, Wafaa A. Hassan and A.M.A. Al Kady

Pl. Breed. Unit, Pl. Genet. Res. Dept., Des. Res. Cent., El-Matareya, Cairo, Egypt

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ABSTRACT: The present work was conducted at Toshka Station, Desert Research Center, Aswan, Egypt to assess mean performance and genetic behavior of 6 quinoa genotypes (AMES22157, Q 31, AMES13761, NSL106398, Q12 and Q27) under heat stress conditions during the two growing seasons (2015/2016 and 2016/2017). The experimental design used was a randomized complete block design with three replicates. Results showed a significant differences among quinoa genotypes for all studied characters in both growing seasons. Genotypes AMES22157, Q12 and Q27 gave the highest number of secondary branches/plant, number of inflorescences/plant, seed weight/plant and biological weight/plant indicating their importance as promising genotypes in quinoa breeding programs. The high values of heritability coupled with high values of genetic advance were recorded by plant height, number of primary branches/plant, number of secondary branches/plant, seed weight/plant and biological weight/plant. Positive and highest significant correlation were observed between seed yield and each of plant height, number of primary branches/plant, number of secondary branches/plant, and number of inflorescences/plant. Results of path analysis confirmed the importance of previous characters. The cluster analysis classified the tested genotypes into two sub class groups (clusters) where the first cluster aggregated the genotypes (AMES22157, Q12 and Q27) that had the highest mean values of all studied characters except harvest index. The obtained results by GT biplot graphs were coincided with those obtained by correlation matrix and cluster analysis indicating that GT biplot graph is considered a successful and effective technique beside these analyses.

Key words: *Chenopodium quinoa* willd, genotypes, Toshka, heritability, genetic advance, correlation, path analysis, cluster, (GT) biplot.

INTRODUCTION

Quinoa (*Chenopodium quinoa* Willd.) is a pseudocereal and is one of the 250 species included in the genus *Chenopodium*, commonly known as ‘goosefoot’ genus (Giusti, 1970). It is a dicotyledonous annual species belonging to the family Amaranthaceae (formerly *Chenopodiaceae*) (Al-Naggar *et al.*, 2017a). The seeds are rich source of a wide range of minerals (Ca, Fe, K, Mg, Mn, P, Zn), vitamins, oil containing large amounts of linoleate, linolenate and natural antioxidants (Koziol, 1992; Repo-Carrasco *et al.*, 2003) and high quality protein containing ample amounts of sulphur rich amino acids (lysine, methionine, threonine) (Koziol, 1992).

Furthermore, it is tolerant to a diverse range of abiotic stresses (Rao and Shahid, 2012) such as drought, heat stress, frost and salinity (Fuentes and Bhargava, 2011; Ruiz *et al.*, 2014 and 2016). The resistance to abiotic stresses is resulting from a vast genetic diversity and unfavorable environmental conditions prevailing in the origin of the crop (Sanchez *et al.*, 2003). However, in Egypt, quinoa is under researched, under-supported and considered a neglected crop; it has not been provided due to importance. Expansion of agriculture is only available in the newly reclaimed lands in desert areas of Egypt. There is a need for cultivation of crops or cultivars that require minimum inputs including soil moisture availability. Quinoa can be termed

* Corresponding author: Tel. : +201069293837
E-mail address: wafaahassan@gmail.com

'underutilized', especially for Egypt, since in spite of its wide adaptability and nutritional superiority, its commercial potential has remained untapped (Al-Naggar *et al.*, 2017b).

Toshka is one of the cultivated areas of the South Valley of Egypt. This area differs in its soil particle distribution, chemical analyses and its fertility as well as climatic conditions than both of Delta and Nile Valley areas (Soliman *et al.*, 2005).

Knowledge of heritability and genetic advance is a basic step to identify the characters amenable to genetic improvement through selection. It is worthy to emphasize that, without considering genetic advance; the heritability would not be practically profitable in breeding program depending on phenotypic selection (Johnson *et al.*, 1955 a and b).

Improvement of a complex and low heritable character like grain yield may be more successful and fast using selection through its more heritable components, which showed significant positive association with it.

Breeding decisions based only on correlation coefficients may not always be effective since they provide only one-dimensional information neglecting the complex interrelationships among plant traits (Kang, 1994). Path analysis separates the direct effects from the indirect effects through other traits by partitioning the simple correlation coefficients (Dewey and Lu, 1959).

Cluster analysis considered as multivariate technique which grouped individuals or objects based on characteristics performance, so that different clusters classified individuals into higher homogeneity within clusters and heterogeneity between clusters (Mohammadi and Prasanna, 2003; Bhattacharai *et al.*, 2017).

Genotype x trait (GT) biplot permits the visualization of the real correlation among traits and understanding of relationships that facilitate the identification of traits that can be used in indirect selection for grain yield (Yan and Rajcan, 2002; Yan and Tinker, 2005; Yan, 2014). In addition, GT biplot gives information on the usefulness of cultivars for production as well as information that helps detect less important (redundant) traits. The present investigation aimed to: assess the genetic behavior of six quinoa genotypes under heat

stress, estimate genetic diversity among tested genotypes in order to select the appropriate genotypes as parents to design a quinoa breeding program under heat stress conditions, identify genotype and trait relationships using correlation coefficient and GT biplot, recommend the suitable genotypes can be cultivation in Toshka region.

MATERIALS AND METHODS

Plant Materials and Experimental Design

The present study was conducted during 2015/2016 and 2016/2017 winter seasons at Toshka Station, Desert Research Center, Aswan, Egypt, Toshka station is located on latitude 22° 25' N, 31° 05' E and elevation 181 m above the sea level to evaluate the performance and genetic behavior of yield, and its components for six quinoa genotypes namely; AMES22157, Q31, AMES13761, NSL106398, Q12 and Q27 representing a wide genetic background. Names of genotypes, code, source and origin are illustrated in Table 1. All of them were introduced from International Centre for Biosaline Agriculture (ICBA) and tested through Genetic Resources Department, Desert Research Center (DRC) breeding program. In each season, the aimed entries were laid out in a randomized complete block design with three replications. The experimental plot area was 20 m². Each plot consisted of 5 ridges, 4 m long and 1m apart. Quinoa seeds were hand sown on Nov. 3rd and 5th in the first and second seasons, respectively. Plots were kept free of weeds through hand hoeing. All recommended cultural practices of quinoa cultivation were applied at the proper time.

Before soil preparation for cultivation, some physical and chemical analyses were performed. Soil of the experimental site was sandy in texture. Chemical and physical analyses of soil and, as well chemical analysis of irrigation water at Toshka are shown in Table 2. Also, meteorological data presented in Table 3 show the monthly values for each temperature (maximum, minimum and mean), solar radiation and wind speed in both seasons.

Collected Data

At harvest time, (on 30 March in both seasons) samples of ten plants taken at random from the inner ridges from each plot to determine

Table 1. Names of the six quinoa genotypes, code, source and origin

Name of germination line	Code	Source	Origin
<i>C. quinoa</i> (Accession)	AMES22157	USDA	Chile
<i>Regalona Baer</i>	Q 31	Imported	Chile
<i>C. quinoa</i> (Accession)	AMES13761	USDA	USA
<i>C. quinoa</i> (Accession)	NSL106398	USDA	USA
<i>C. quinoa</i> (Accession)	Q 12	USDA	Colorado USA
<i>C. quinoa</i> (Accession)	Q 27	USDA	Chile

C. quinoa: *Chenopodium quinoa* Willd.

Table 2. Mechanical and chemical analyses of the experimental soil and chemical analysis of irrigation water at Toshka

Soil mechanical analysis										
Soil depth (cm)	Coarse sand (%)	Fine sand (%)	Silt (%)	Clay (%)	Textural class					
0-30	78.94	18.09	2.95	0.02	Sand					
30-60	77.23	19.97	2.77	0.03	Sand					
Soil chemical analysis										
Soil depth (Cm)	pH	EC (µS/cm)	Soluble cations (meq/l)			Soluble anions (meq/l)				
			Ca ⁺⁺	Mg ⁺⁺	Na ⁺	K ⁺	CO ₃ ⁻	HCO ₃ ⁻	Cl ⁻	SO ₄ ⁻
0-30	7.3	2.55	6.022	1.159	8.696	0.613	----	1.199	5.629	9.576
30-60	7.6	1.98	5.084	0.912	6.087	0.460	----	0.999	4.958	6.245
Irrigation water chemical analysis										
-----	6.9	1.2	4.05	0.92	2.17	0.05	0.099	1.82	2.48	3.14

Table 3. Meteorological data during 2015/16 and 2016/17 growing seasons at Toshka site

Month	T (°C)			SR (MJ/m ²)	WS (m/sec)
	Max.	Min.	Mean		
2015/16 season					
Nov. 2015	29.9	15.6	22.7	20.8	2.8
Dec. 2015	23.5	9.1	16.3	16.3	1.6
Jan. 2016	22.6	10.2	16.4	12.8	2.9
Feb. 2016	27.4	10.7	19.0	15.2	3.1
Mar. 2016	33.4	16.7	25.0	24.5	3.3
Total					
2016/17 season					
Nov. 2016	31.3	16.9	24.1	18.7	4.4
Dec. 2016	23.6	9.4	16.5	17.2	4.6
Jan. 2017	24.4	9.7	16.7	18.2	4.1
Feb. 2017	23.5	8.9	16.2	21.1	4.5
Mar. 2017	28.4	11.9	20.2	24.5	4.2
Total					

T= Temperature, RH (%) = Relative humidity percentage, SR = Solar radiation, WS = Wind speed

the following traits: plant height (PH) in cm, number of primary branches/plant (NPB), number of secondary branches/plant (NSB), Number of inflorescences/plant, 1000-seed weight (1000 SW;g), seed weight/plant (SY; g), biological weight/plant (BY; g) and harvest index (HI).

Statistical Analysis

The collected data were subjected to individual and combined analyses of variance (ANOVA) of randomized complete block design for each season and across the two seasons (**Gomez and Gomez, 1984**). Levene test (**Levent, 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 at 0.05 probability level.

Genotypic and phenotypic coefficient of variations were estimated using the pertinent mean square expectations according to the method suggested by **Johnson et al. (1955 a and b)**. Broad sense heritability (h^2_b) and genetic advance in terms of percentage of means (with 5 % selection intensity) were estimated as described by **Allard (1999)**.

The interrelationships among seed yield (as resultant variable) and its related characters (as casual variables) were computed using simple correlation coefficients between all pairs of traits as suggested by **Steel et al. (1997)**. Hierarchical cluster analysis was performed on the standardized data using a measure of Euclidean distance and Ward minimum variance method as outlined by **Ward (1963)**. Also path coefficient analysis methodology was used by **Dewey and Lu (1959)** in the agricultural research. GGE biplot could be used for all types of two-way data set such as genotypes with multiple traits. **Yan and Rajcan (2002)** used the genotype by trait (GT) biplot, which is an application of the GGE biplot to study the genotype by trait data. Because the traits were measured in different units, the biplot procedure was generated using the standardized values of the trait means.

RESULTS AND DISCUSSION

The test of homogeneity of error variance made using error mean squares of the two

seasons revealed that error mean squares are homogeneous for all studied characters that permits to apply combined analysis across the two seasons.

Mean Performance

Mean values of seed weight/plant and its related characters for 6 quinoa genotypes in 1st and 2nd seasons and combined across the two seasons are given in Table 4. The results revealed the absence of significant differences between the two seasons for all the studied characters except for number of primary branches/plant and 1000 seed weight. There were clear significant differences among the tested genotypes for all aimed traits indicating to the different genetic background for the studied genotypes. The interaction effect between genotypes and seasons was significant for all characters except for seed weight/plant, biological weight/plant and harvest index, meaning that the quinoa genotypes had similar behavior in the two seasons considering the abovementioned yield characters. The first season had higher mean values for all traits compared to the second one, except for the characters being plant height, number of primary branches/plant and number of secondary branches/plant which may be returned to the environmental effects.

Results in Table 4 indicate that the tallest plants in the 1st and 2nd seasons were obtained by the promising genotype Q27 followed by Q12 with averages recording 91.94 and 74.85 cm, respectively with significant difference between them, while the shortest plants across the two seasons (39.98 cm) were recorded by genotype Q31.

As presented in Table 4, genotype AMES22157 gave the greatest number of primary branches/plant (as an average across the two seasons) recording 4.36, while the lowest number of primary branches/ plant (2.05) was obtained by genotype AMES13761.

Meanwhile, the highest values of number of secondary branches/plant (13.75, 12.10 and 14.78), number of inflorescences/plant, (8.41, 9.15 and 9.40), seed weight/plant (14.29, 14.51 and 16.89 g) and biological weight/plant (43.18, 41.15 and 53.92 g) were produced by genotypes AMES22157, Q12 and Q27, respectively. The results indicated that these genotypes are the

Table 4. Mean values of seed weight/plant and its related characters for 6 quinoa genotypes combined across the two seasons.

Genotype	PH			NPB			NSB			NINF		
	S1	S2	Comb.	S1	S2	Comb.	S1	S2	Comb.	S1	S2	Comb.
AMES22157	64.67	67.06	65.86	3.28	5.43	4.36	13.03	14.47	13.75	9.23	7.58	8.41
Q 31	38.33	41.63	39.98	3.00	1.83	2.42	6.93	9.47	8.20	6.70	5.33	6.02
AMES13761	47.00	56.65	51.83	2.20	1.90	2.05	6.73	9.33	8.03	6.47	4.00	5.23
NSL106398	46.67	35.75	41.21	1.20	3.63	2.42	7.37	12.40	9.88	7.40	5.33	6.37
Q 12	72.60	77.09	74.85	2.00	4.40	3.20	10.47	13.73	12.10	9.30	9.00	9.15
Q 27	95.03	88.85	91.94	1.68	4.33	3.01	19.57	10.00	14.78	6.80	12.00	9.40
Mean	60.72	61.17	60.94	2.23	3.59	2.91	10.68	11.57	11.13	7.65	7.21	7.43
Season (S)	NS			*			NS			NS		
LSD _{0.05}	Genotype (G)			3.91			0.61			1.01		
	S x G			5.53			0.86			1.43		
	CV			5.33			17.28			7.57		
1000 SW				SY			BY			HI		
AMES22157	4.20	3.69	3.94	14.67	13.92	14.29	45.38	40.97	43.18	32.47	34.15	33.31
Q 31	2.95	2.91	2.93	8.00	7.63	7.81	21.14	20.24	20.69	37.58	37.96	37.77
AMES13761	3.88	3.52	3.70	8.00	5.55	6.78	18.89	16.02	17.46	42.15	34.78	38.46
NSL106398	3.77	3.73	3.75	9.00	7.25	8.13	22.01	18.55	20.28	41.37	39.21	40.29
Q 12	3.92	3.43	3.67	15.00	14.03	14.51	43.44	38.86	41.15	34.90	36.57	35.74
Q 27	3.67	3.35	3.51	17.48	16.30	16.89	55.59	52.25	53.92	31.71	31.17	31.44
Mean	3.73	3.44	3.58	12.02	10.78	11.40	34.41	31.15	32.78	36.69	35.64	36.17
Season (S)	*			NS			NS			NS		
LSD _{0.05}	Genotype(G)			0.16			1.58			4.38		
	S x G			0.22			NS			NS		
	CV			3.68			11.49			11.09		
* Significant at 5% level of probability, PH = plant height, NPB = No. of primary branches/plant, NSB = No. of secondary branches/plant, S1 and S2 = 1 st and 2 nd seasons NINF = No. of inflorescences/plant, 1000 SW = 1000 seed weight, SY = Seed weight/plant, BY = Biological weight/plant and HI = Harvest index.												

promising once and could be recommended to be involved in quinoa breeding programs. On the other hand, the lowest values of the aforementioned four characters were gained by the poor genotype AMES13761 recording only 8.03 secondary branches/plant, 5.23 inflorescences/plant, 6.78 g seed weight/plant and 17.46 g biological weight/plant.

Results showed that the heaviest 1000 seed weight was obtained by that genotype AMES22157 recording 3.94 g (as an average

across the two seasons) while the lightest weight (2.93 g) was registered by genotype Q31. Also, genotypes; AMES13761and NSL106398 gave the highest values of harvest index across the two seasons recording 38.46 and 40.29, respectively while the lowest value was attained by genotype Q27 (31.44 g).

On the other hand, all the coefficients of variation (CV's) were laid out in the acceptable statistically range indicating to the validity of collected data.

The current results are in agreement with those obtained by **Jacobsen et al. (2003)**, **Bhargava et al. (2006)**, **Razzaghi et al. (2012)**, **Omar et al. (2014)**, **Al-Naggar et al. (2017 a and b)** and **Fghire et al. (2017)** who found significant differences among quinoa genotypes for most studied agronomic characters.

Genetic Parameters

Estimates of grand mean, phenotypic (PCV) and genotypic (GCV) coefficients of variation, broad sense heritability (h^2_b), and expected genetic advance (EGA) expressed as percent of grand mean at 5% selection intensity are presented in Table 5.

In general, the values of (PCV) were slightly higher than their corresponding values of (GCV) for most studied characteristics. The magnitude of this difference was low for all studied characters except harvest index indicating that the marked influence of environmental factors on the phenotype expression was weak and this give a good chance to improve these traits through selection based on the phenotypic performance because their phenotypic variations were mostly attributed to genetic makeup rather than environmental effect.

The highest estimates of phenotypic (PCV) and genotypic (GCV) coefficients of variation were obtained by number of primary branches/plant (15.87% and 14.79%) and biological weight/plant (15.20% and 14.74%), respectively indicating a wide pattern of genotypic variation among tested genotypes considering the previous two characters. In accordance, the selection among the tested genotypes would be successful and effective to improve these traits. Meanwhile, moderate values of PCV and GCV were recorded by plant height (10.94% and 10.80%), number of secondary branches/plant (11.44% and 11.05%), number of inflorescences/plant (10.79% and 9.28%) and seed weight/plant (12.62% and 12.02%), respectively. On the other hand, the lowest estimates of PCV and GCV (< 5%) were obtained by 1000 seed weight and harvest index.

It is important to emphasize that, without considering genetic advance (GA), the heritability values (h^2) would not be practically valuable in the selection depends on phenotypic appearance. **Johnson et al. (1955a and b)** confirmed that heritability estimates in conjunction with genetic

advance would give more reliable index of selection value.

In the present investigation, the h^2_b values ranged from 17.07% for harvest index and 97.49% for plant height, while the values of genetic advance (%) ranged between 5.26% and 88.46% for harvest index and biological weight, respectively. The highest estimates of heritability and genetic advance may be returned to the wide differences among the tested genotypes considering most studied characters.

The high values of heritability ($h^2 \geq 80$) coupled with high values of genetic advance (GA ≥ 60) were recorded by plant height, number of primary branches/plant, number of secondary branches/plant, seed weight/plant, and biological weight/plant. These results may be due to the great differences among average values of these traits which allow running successful selection among them.

However, number of inflorescences/plant recorded high heritability value (73.93), but it accompanied with moderate genetic advance value (49.36), while 1000 seed weight registered high heritability value (88.96), and low genetic advance value (20.21). The lowest heritability and genetic advance values were recorded by harvest index as above shown. From these results, it is obvious the limited scope for improvement of these traits among the tested genotypes. The current conclusions are supported by **Hassan et al. (2016)** and **Al-Naggar et al. (2017a)** who confirmed that plant breeders can safely make their selection when they take in consideration high values of heritability and genetic advance.

Correlation Matrix

Simple correlation coefficients among seed weight/plant and its related attributes i.e. plant height, number of primary branches/plant, number of secondary branches/plant, number of inflorescences/plant, 1000 seed weight estimated across the two seasons are given in Table 6.

Results showed that the most effective relationships to quinoa breeder were those between seed weight/plant and each of plant height (0.87**), number of primary branches/plant (0.35*), number of secondary branches / plant (0.63**), and number of inflorescences/ plant (0.75**). Therefore, seed weight/plant of

Table 5. Estimates of genetic parameters of seed weight/plant and its related characters for 6 quinoa genotypes computed across the two seasons

Yield character	Genetic parameters				
	Grand mean	PCV (%)	GCV (%)	h^2_b (%)	EGA (5%)
Plant height	60.94	10.94	10.80	97.49	65.99
No. of primary branches/plant	2.91	15.87	14.79	86.90	85.33
No. of secondary branches/plant	11.13	11.44	11.05	93.20	66.00
No. of inflorescences/plant	7.43	10.79	9.28	73.93	49.36
1000 seed weight	3.58	3.67	3.46	88.96	20.21
Seed weight/plant	11.40	12.62	12.02	90.81	70.91
Biological weight/plant	32.78	15.20	14.74	94.01	88.46
Harvest index	36.17	4.98	2.06	17.07	5.26

PCV= Phenotypic coefficients of variation, GCV = Genotypic coefficients of variation, h^2_b = Broad sense heritability and EGA = Expected genetic advance

Table 6. Correlation coefficients among seed weight/plant and its related characters for 6 quinoa genotypes (combined across the two seasons)

Character	PH	NPB	NSB	NINF	1000 SW
NPB	0.23				
NSB	0.64**	0.27			
NINF	0.59**	0.44*	0.14		
1000 SW	0.20	-0.02	0.22	0.18	
SY	0.87**	0.35*	0.63**	0.75**	0.30

* and ** Significant at 5% and 1% level of probability, respectively, PH = plant height,
NPB = No. of primary branches/plant, NSB = No. of secondary branches/plant,
NINF = No. of inflorescences/plant, 1000 SW = 1000 seed weight,
SY = seed weight/plant, BY = biological weight/plant and HI = harvest index.

these quinoa genotypes may be raised through selection for the tallest plants and those had more branches and inflorescences. However, positive and insignificant association was obtained between seed weight/plant and 1000 seed weight indicating that this character may be independent in their genetic behavior than seed weight/plant under the tested genotypes.

The seed yield components exhibited various trends of associations among themselves. Highly positive and significant associations were observed among plant height and each of number of secondary branches/plant (0.64**), and number of Inflorescences/plant (0.59**) revealing that the tallest genotypes had often

more branches and inflorescences. There was positive and significant association (0.44*) between number of primary branches/plant and number of inflorescences/plant.

On the other hand, the magnitude of the correlation coefficients among other traits was trivial and insignificant. The breeder should be aware about the nature of associations seed yield components. These results concur with those reported by **Bhargava et al. (2007)**, **Mignone and Bertero (2007)**, **De Santis et al. (2009)**, **Gambin and Borras (2010)**, **Omar et al. (2014)**, **Hassan et al. (2015)** and **Al-Naggar et al. (2017a)**.

Path Analysis

In the present investigation, the resultant variable was seed weight/plant while the above correlated characters represented the causal variables. The relative importance of direct and joint effects for the five yield characters on seed weight/plant are shown in Table 7. Results exhibited that the maximum relative importance on seed weight/plant were obtained by plant height (14.36) followed by number of secondary branches/ plant (8.95), and number of inflorescences/plant (20.66). Accordingly, the indirect selection of the above three mentioned characters toward seed yield would be effective for quinoa improvement. On the other hand, the relative contributions of the other two yield characters *i.e.* number of primary branches/plant and 1000 seed weight were very small and low magnitude.

With respect to the considerable components of the indirect effects, it is noted that plant height had the highest contribution on seed yield through its indirect effects with number of secondary branches/plant (14.49), and number of inflorescences/plant (20.32). Meanwhile, a moderate influence on seed yield was indirectly recorded by number of secondary branches/plant (3.92) *via* number of inflorescences/plant. Trivial values of relative importance were observed for the other direct and indirect effects.

Totally, the studied yield characters explained 86.23% of seed yield variation. In accordance, the residual part may be attributed to unknown variation (random error), committing of errors during measuring the studied characters and/or some other traits that were not incorporated in the present investigation.

An overall view on the results of path analysis, it revealed that the three yield components *i.e.* plant height, number of secondary branches/plant and number of inflorescences/plant had the maximum influence directly and indirectly toward seed yield in quinoa crop.

Cluster Analysis

The cluster analysis was used as an efficient procedure to emerge the structural relationships among tested genotypes and provides a hierarchical classification of them. In the present work, the distance of 6 quinoa genotypes were estimated based on seed yield and its related characters. The six genotypes were classified

into two primary groups (clusters) where each group contained the genotypes that showed similar phenotypic performance. The clustering pattern of these genotypes is tabulated in Table 8 and diagrammatically displayed as dendrogram graph in Fig. 1. Results showed that each primary cluster consisted of three genotypes. The first cluster included the genotypes of AMES22157, Q12 and Q27 while the second contained Q31, AMES13761 and NSL106398.

The first cluster aggregated the genotypes that had the highest mean values of all studied characters except harvest index, reinforcing their importance as promising genotypes that could be exploited in quinoa breeding programs. The mean values of these genotypes for the different characters were recorded as plant height (77.55 cm), number of primary branches/plant (3.52), number of secondary branches/plant (13.54), number of inflorescences/plant (8.99), 1000 seed weight (3.71 g), seed weight/ plant (15.23 g), biological weight/plant (46.08 g) and harvest index (33.8).

In contrary, the three genotypes of the secondary cluster gave the lowest mean values of all studied characters except harvest index recording plant height (44.34 cm), number of primary branches/plant (2.29), number of secondary branches/plant (8.71), number of Inflorescences/plant (5.87), 1000 seed weight (3.46 g), seed weight/plant (7.57 g), biological weight/plant (19.48 g), and harvest index (36.45).

In the light of previous results, it is exhibited the presence of considerable genetic diversity among the tested genotypes which giving a good chance to achieve sufficient scope for improvement of quinoa through the hybridization among genotypes taken from divergent clusters. Similar results were obtained by **Ajmal et al. (2013)** and **Bhattarai et al. (2017)** who reported that genotypes which had high performance positively associated were yield and its attributes which grouped in one cluster.

Genotypes x Traits (GT) Biplot Graph

Genotype comparison (polygon graph)

Recently, the biplot graphs can be used to compare genotypes on the basis of multiple traits (seed yield and its related characters) and

Table 7. The relative importance (RI %) according to path analysis of seed weight/plant and its related characters for 6 quinoa genotypes (combined across the two seasons)

Character		Relative importance (%)
Direct effects		
Plant height (PH)		14.36
Number of primary branches/plant (NMB)		0.08
Number of secondary branches/plant (NSB)		8.95
Number of inflorescences /plant (NINF)		20.66
1000 seed weight (1000 SW)		0.43
Indirect effects		
	NMB	0.50
Plant height via	NSB	14.49
	NINF	20.32
	1000 SW	0.99
	NSB	0.46
No. of primary branches/plant via	NINF	1.16
	1000 SW	0.01
No. of secondary branches/plant via	NINF	3.92
	1000 SW	0.86
No. of inflorescences /plant via	1000 SW	1.04
Direct + indirect		88.23
Residuals		11.77
Total		100

Table 8. Mean values of seed weight/plant and its related characters for the two groups resulted from cluster analysis

Cluster No.	Included genotypes	Cluster average							
		PH	NPB	NSB	NINF	1000 SW	SY	BY	HI
1	AMES22157	77.55	3.52	13.54	8.99	3.71	15.23	46.08	33.80
	Q12 and Q27								
	Q31								
2	AMES13761	44.34	2.29	8.71	5.87	3.46	7.57	19.48	36.45
	NSL106398								

PH = Plant height, NPB = No. of primary branches/plant, NSB = No. of secondary branches/plant, NINF = No. of inflorescences/plant, 1000 SW = 1000 seed weight, SY = Seed weight/plant, BY = Biological weight/plant and HI = Harvest index.

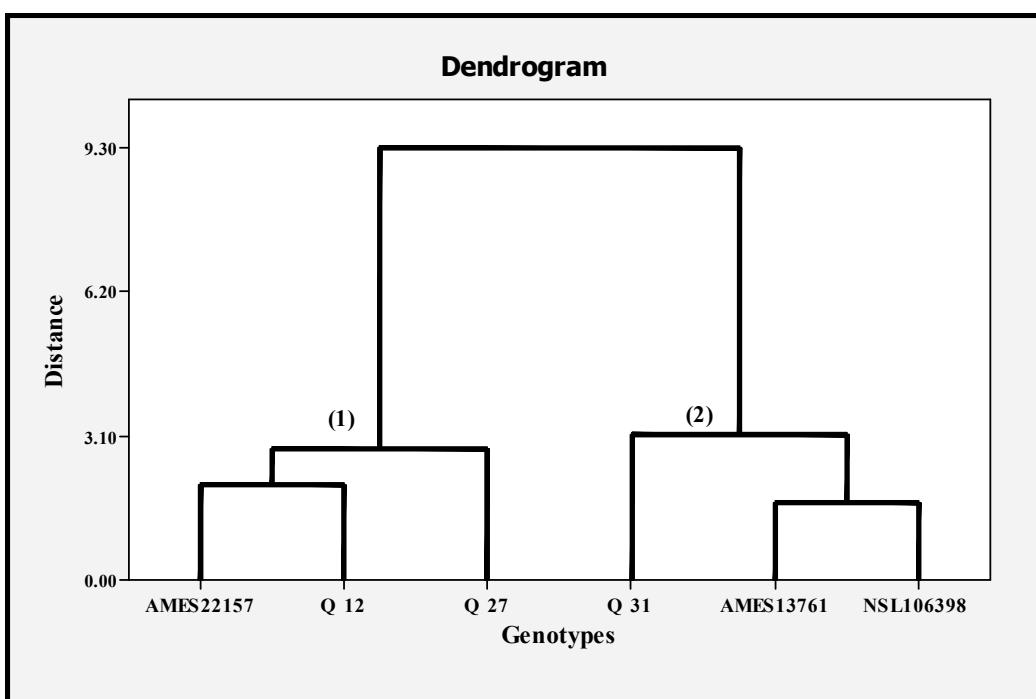


Fig. 1. Dendrogram showing the distance among 6 quinoa genotypes based on grain yield and its related attributes

to identify genotypes that are particularly good for one or more characters and therefore can be nominee for selection and hybridization in quinoa breeding program (**Yan and Rajcan, 2002; Yan and Tinker, 2005**).

The polygon view of a genotype by trait (GT) biplot graph is an effective tool to visualize the interaction patterns between genotypes and traits provided the biplot should explain a sufficient amount of the total variation.

The biplot graph (Fig. 2) presents the relationship among the aimed quinoa genotypes using the seed weight/plant and its related attributes. The GT biplot of the mean performance of the quinoa data explained 91.58% of the total variation of the standardized data. The first and two principal components (PC1 and PC2) explained 78.67% and 12.90%, respectively. **Yan and Kang (2003)** mentioned that the first two PC's should reflect more than 60% of the total variation in order to achieve the goodness of fit for GT biplot model.

The perpendicular lines to the polygon sides facilitate comparison between neighboring vertex genotypes. It is obvious that genotype

Q27 recorded the highest values considering all studied characters except number of primary branches/plant, 1000 seed weight and harvest index. Also, genotype Q12 located in the same sector and reflected similar behavior toward the same traits. It is noted that the points of these genotypes and traits placed into one sector and the angles among them were acute reflecting the above associations among them.

Results of GT biplot graph appeared that genotype AMES22157 was the best one in terms of number of primary branches/plant and 1000 seed weight. However, the three genotypes; Q31, AMES13761 and NSL106398 were located in the left side of the graph far from most studied traits (obtuse angles) indicating to their poor performances while the three genotypes gave the highest values considering harvest index.

It is worth mentioning that the current results coincided with those above obtained by the part of mean performance. Also, these results (genotype groups) are consistent with those obtained by the cluster analysis. Undoubtedly, GT biplot graph is preferred because it easy to interpret and more informative.

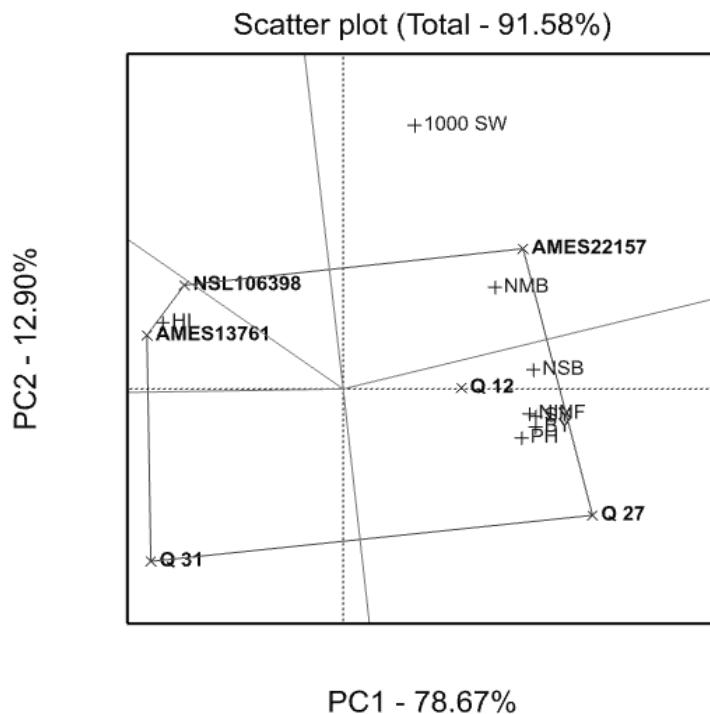


Fig. 2. Polygon view genotype by trait (GT) biplot showing which genotype had the highest values for which traits for 6 quinoa genotypes

Trait relations (vector graph)

In this graph of GT biplot (Fig. 3), a vector is drawn from the biplot origin to each marker of the traits to visualize the relationships among them (Yan and Tinker, 2005). Accordingly, any two traits are positively correlated if the angle between their vectors is an acute angle ($< 90^\circ$) while they are negatively correlated if their vectors formed an obtuse angle ($> 90^\circ$) and close to 90° no correlation (Yan and Kang, 2003). Hence, the associations among traits could easily be visualized from the biplot graph. These associations would be compared and confirmed by correlation coefficients between any two traits (Table 6).

Results revealed that the three traits of plant height, number of inflorescences/plant, seed weight/plant and biological weight/plant had strong and positive associations as shown by the acute angles among their vectors. Meanwhile there were very weak associations among the previous four characters from one side and 1000 seed weight from the other side as indicated by near perpendicular vectors among them ($r = \cos 90^\circ = 0$). In addition, there was positive association

between number of primary branches/plant and number of secondary branches/plant as indicated by acute angles. On the other hand, the associations between harvest index and all other traits were negative as shown by the large obtuse angles among their vectors.

These results coincided with those obtained by correlation matrix indicating that the GT biplot graph is a good substitute procedure for correlation coefficients for interpreting the interrelationships among the studied traits.

It is clear that the biplot methodology is an excellent tool for visual data analysis. Compared with conventional methods of data analysis, the biplot approach has some advantages *i.e.*, 1) its graphical presentation of data, which greatly enhances our ability to understand the patterns of the data, 2) it is more interpretative and facilitates pair-wise genotype comparisons, 3) it facilitates identification of possible genotypes or traits groups and 4) it gives a complete picture about the interrelationships among genotypes and traits. The current results are in harmony with those obtained by Yan (2014).

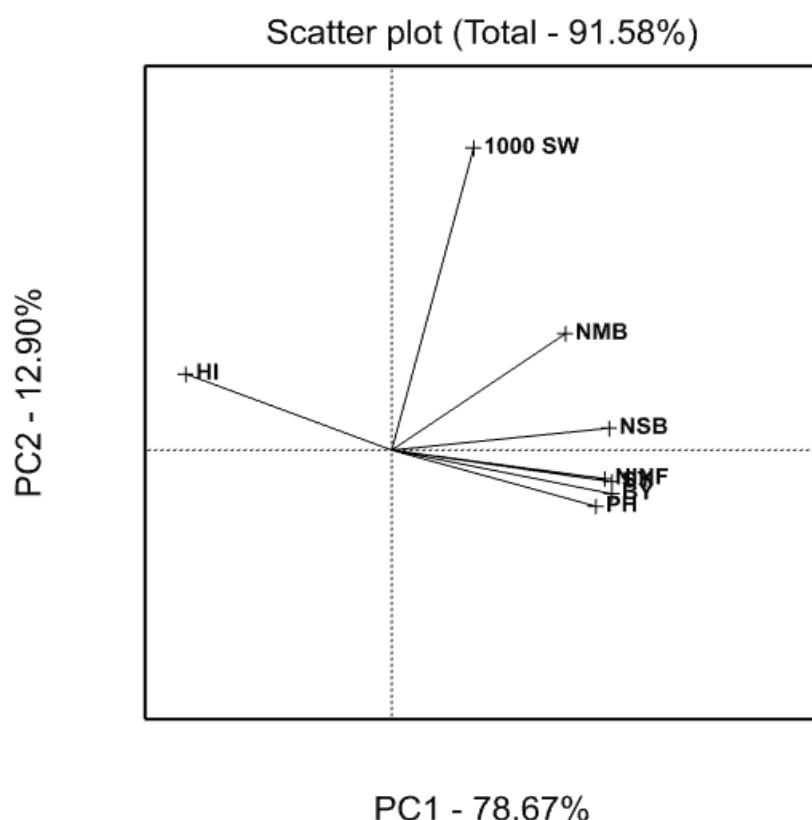


Fig. 3. Vector view genotype by trait biplot showing the interrelationship among the studied traits for 6 quinoa genotypes

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تقييم ستة تراكيب وراثية من الكينوا لمحصول البذور ومكوناته تحت ظروف توشكى

سامي عبد العزيز عافية - وفاء عبدالله حسن - عبد الرحيم أحمد محمد القاضي

وحدة تربية النبات - قسم الأصول الوراثية النباتية - مركز بحوث الصحراء - المطيرية - القاهرة - مصر

أجريت هذه الدراسة في محطة بحوث توشكى التابعة لمركز بحوث الصحراء في موسمى ٢٠١٦/٢٠١٥ و ٢٠١٧/٢٠١٦، بهدف تقييم ستة تراكيب وراثية مختلفة من الكينوا مستوردة من المركز الدولي للزراعة الملحة (ICBA) لتحمل الحرارة العالمية والمحصول ومساهماته، هذه التراكيب هي: Q 27، AMES22157، Q 31، AMES13761، NSL106398، Q 12، Q 27 زرعت في تصميم القطاعات كاملة العشوائية في ثلاثة مكررات، أظهرت النتائج وجود فروق معنوية بين التراكيب الوراثية لجميع الصفات تحت الدراسة كمتوسط لكلا الموسمين، وقد سجلت التراكيب الوراثية Q12، AMES22157، Q12، AMES22157 أعلى القيم لصفات عدد الأفرع الثانوية/نبات، عدد التورات/النبات، وزن البذور/نبات (جم)، الوزن البيولوجي/نبات (جم)، مما يشير إلى أهمية استخدامها في برامج التربية لتحسين صفة المحصول، وأشارت النتائج إلى أن أعلى القيم لكل من كفاءة التوريث العامة والتحسن الوراثي المتوقع قد سجلت لصفات طول النبات، عدد الأفرع الأولية/نبات، عدد الأفرع الثانوية/نبات، وزن البذور/نبات (جم)، الوزن البيولوجي/نبات (جم)، في دلاله على فعالية الانتخاب في الأجيال المبكرة لهذه الصفات، أوضحت نتائج تحليل معامل الإرتباط وجود تلازم موجب ووجود تباين معنوي بين صفة محصول البذور وكل من صفات طول النبات، عدد الأفرع الأولية/نبات، عدد التورات/نبات وقد جاءت نتائج تحليل معامل المرور مؤكدة لنتائج معامل الإرتباط البسيط، إستناداً إلى نتائج التحليل العنقودي أمكن تقسيم التراكيب الوراثية المختبرة إلى مجموعتين (متشابهة في داخلها متباعدة فيما بينها) وذلك تبعاً لصفة محصول البذور ومكوناته، وقد تضمنت المجموعة الأولى تحديداً على ثلاثة تراكيب وراثية (Q27، Q12، AMES22157) سجلت نباتاتها أعلى القيم لكل الصفات تحت الدراسة عدا صفة دليل الحصاد، هذا وقد تشابهت نتائج طريقة المحاور الثانية بإستخدام الرسوم البيانية (GT) مع النتائج التي تم الحصول عليها عن طريق مصفوفة الإرتباط والتحليل العنقودي مشيراً إلى أن الرسوم البيانية (GT) تعتبر طريقة ناجحة وفعالة بجانب هذه التحليلات.

الم吼ون :

١- أ.د. السيد السيد حسن
٢- أ.د. حسن عوده عواد

أستاذ المحاصيل - كلية التكنولوجيا والتنمية - جامعة الزقازيق.
أستاذ ورئيس قسم المحاصيل - كلية الزراعة - جامعة الزقازيق.