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Morphological characterization of introduced quinoa genotypes under Saudi Arabia conditions

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ABSTRACT

Quinoa is a highly nutritious grain crop and has attracted attention for its strong growth potential under extremely harsh environments. Toward introducing it into Saudi Arabia's agriculture system, fifty-five quinoa genotypes were imported, and field evaluated during the winter seasons of 2016–17 and 2017–18. These genotypes were characterized by thirty-three characters using the descriptor from Bioversity International. Quinoa plant was green during the seedling stage, then pigments were scattered over many parts of the plant, and some colors changed during its life. Three colors were detected on the panicle at flowering and seven colors at maturity. Quinoa plant was between 60 and 193 cm in height, took 98 to 187 days to reach maturity, and produced 15.3 to 70.1 g of seeds per plant. Two genotypes (Ames 13747 and Ames 13720) produced high seed yields of 3.3 and 3.1 t/ha and belonged to the average maturing categories (118.1 and 122.3 days, respectively). A significant correlation was detected between seed yield and plant height, number of branches, leaf width, and leaf area. Based on K-means clustering, the genotypes were grouped into five clusters with high variation among them (87.3%) and only 12.7% within clusters. The results identified the morphological characters that could be used as selection criteria to increase the efficiency of quinoa seed yield improvement programs.

Keywords: Quinoa, morphology, description, K-means, cluster analysis

INTRODUCTION

Quinoa (*Chenopodium quinoa* Willd.) has attracted much attention in recent years because it is an excellent source of protein and of high tolerance to abiotic stresses. It is an old pseudo-grain crop cultivated in South America a thousand years ago, then the experiments to cultivate quinoa were realized in the USA and Canada and rapidly spread to 95 countries during 2015 (Bazile *et al.*, 2016). It is grown in 120 countries (Alandia *et al.*, 2020). To meet consumer demands, the cultivation area increased in the origin countries (Peru and Bolivia) by 36 and 72%, respectively (Jaikishun *et al.*, 2019). The Food and Agriculture Organization (FAO) pronounced quinoa as one of the crops destined to offer food security in the next century because of its wide adaptability and nutrition values. (Jacobsen, 2003). It can replenish part of the food gap where it is drought- and salinity-tolerant and can grow under harmful abiotic adverse factors that affect crop production (Jensen *et al.*, 2000). Geerts *et al.,* (2008) note a wide range of soil textures, ranging from sandy to clayey, and a pH range of 4.5–9 for cultivating them. In addition to its ability to grow under several photoperiods, there are short-day and day-neutral genotypes (Bertero, 2001). Furthermore, David *et al.,* (2020) reported that it can be produce in the hydroponically controlled system. Its grain content higherprotein, fat and less carbohydrate than cereal crops, with a well-balanced complement of essential amino acids (Bastidas *et al.*, 2016). Furthermore, it is gluten-free, so the gluten-sensitive or intolerant population can safely consume quinoa, and it is recommended for baby food formulations because of its enormous potential in the food industry and because it is highly nutritious (Ogungbenle, 2003 and Zevallos *et al.*, 2014). Manjarres-Hernández *et al.*, (2022) published a list of twenty-three genotypes of sweet quinoa (free of saponin) where saponin content was between 0.018 and 0.537%. Quinoa has multiple uses, including human consumption, where the grain is used in the preparation of soups, salads, cereals, alcohol, and flour (Alizadeh *et al.*, 2022). Also using it for medicinal purposes, Arafa and Elseedy, (2016) revealed that adding quinoa seed powder to bread improved weight gains, food efficiency ratio, serum glucose, kidney functions, lipid profile, liver enzyme activities, and selected minerals (calcium and total iron) in their study on rats.

Genetic erosion is an imminent risk and may further reduce the diversity of quinoa plants in cultivation (Fuentes *et al*., 2012). In addition, the genetic diversity and wide variability have a high impact on the yield and its stability (Garcıa *et al*., 2020). Thus, investigating genetic diversity and characterization of breeding materials is very crucial, and prerequisite for breeding programs. Also, defining the indicators that plant breeders may apply in the open fields to improve quinoa, for its tolerance or adaptation to different environmental stresses, remains a matter that needs much effort. Morphological characteristics are the most useful conventional tools to analyze variation among genetic materials and genetic diversity investigation (Begna, 2021). Furthermore, Stanschewski *et al*., (2021) recommended assessing quinoa varieties across years and multiple locations due to their phenotypic plasticity. The plant height was between 60 and 180cm and its duration from 98 to 177 days in Saudi Arabia (EL-Harty *et al*., 2021). High phenotypic variability among quinoa explains its ability to adapt to different agroclimatic conditions (García *et al*., 2020). This investigation aims to characterize and evaluate introduced quinoa genotypes under Saudi Arabia conditions to select and suggest genotypes for initiating breeding programs.

MATERIALS AND METHODS

Fifty-five quinoa genotypes were selected from the US National Plant Germplasm System (NGPS) depending on their origin Table (1) for evaluation under Saudi Arabian conditions. Field experiments were planted on November 25, 2016, and November 27, 2017, in sandy clay loam soil (pH = 8.15; electrical conductivity = 2.1 dS/m) in Dirab Experiments and Agricultural Research Station, College of Food and Agricultural Sciences, King Saud University, Riyadh, located at 24° 43′ 34″ N, 46° 37′ 15″ E, and an elevation of about 400 m above sea level. The genotypes were arranged in a random complete block design with three replications; the experiment plot comprised three rows 3 m long, keeping distances of 50 cm and 20 cm between rows and plants, respectively. After seedlings' emergence, plants were thinned out, leaving one plant per hole. Calcium superphosphate (CaH6O9P2) was applied during soil preparation at a rate of 71.4 kg P2O5/ha. Nitrogen as ammonium sulfate (60 kg/ha) was applied in two equal doses: the first with sowing and the second four weeks after planting. Plots were kept free of weeds through hand hoeing twice during the vegetative period, in addition to protecting plants from bird attacks by covering plants before the maturing stage using nets.

Genotypes were characterized by thirty-three characters using descriptions of Bioversity International & FAO, (2013). These characters were 21 qualitative characters, *viz.* growth habit (GH), branches (Br), position of branches (PBr), stem color at maturing stage (SC), stem shape (SS), stria (St), stria color (StC), pigmented axis (PA), leaf shape (LS), leaf margin (LM), leaf color (LC), leaf granule color (LGC), petiole color (PeC), panicle color at flowering (PCF), panicle color at maturity (PCM), panicle shape (PS), panicle density (PD), dehiscence degree (DD), perigonium appearance (PG), perigonium color (PC) and seed episperm color (SeC) in addition to 12 quantitative characters *viz.* plant height (PH), number of branches (NoB), stem diameter (SD), panicle length (PL), panicle width (PW), petiole length (PeL), leaf length (LL), leaf width (LW), leaf area (LA), number of teeth/leaf (NoT), number of days from sowing to 95% maturity (MD), and seed yield/plant (SY).

For the economic characters, the assumptions of parametric analysis were verified before the analysis of variance (ANOVA) for each season, and their combined was carried out according to Steel *et al*., (1997). The economic characters in this study were plant height, number of branches, and number of days to 95% maturity, and seed yield/ha (seed yield obtained from each experimental plot and converted into ton per hectare). To determine the significant differences between treatments, least significant difference test was performed at $p < 0.05$ (Steel *et al*., 1997) using XLSTAT software (Adinsoft, 2017). Pearson correlation was estimated using PAST, 4.09 software (Hammer *et al*., 2001). K-mean cluster analysis (MacQueen, 1967) was used for grouping quinoa genotypes based on their performance using XLSTAT software.

RESULTS

The morphological characters detected tremendous variation among the fifty-five genotypes Table (2). Two types of stem shape were showed, angular in 53% of genotypes and cylindrical in 46%. While leaf was triangular (67%) or rhomboidal (33%), and its margin was serrate (53%), or dentate (47%). Also, three forms of clusters (amarantiform, glomerular, and intermediate) have been recognized. Stem colors were in general yellow, green, brown at physiological stage or white, red, pink, purple, orange in some genotypes, however, strial color if present was green or purple and may be pink or red in only one and five genotypes, respectively. Regarding leaves, leaf color (LC), leaf granule color

Table 1: Genotype code number, name and origin of the fifty-five quinoa genotypes.

Accession no.	Plant name	Origin	Status	Accession no.	Plant name	Origin	Status
Ames 13719	27 GR	US, New Mexico	I G	PI 587173	LP 128	Argentina, Jujuy	Cultivar
Ames 13720	TUNDRI	US, New Mexico	I G	PI 596293	Colorado 407D	US, Colorado	Cultivar
Ames 13722	7ALC	US, New Mexico	I G	PI 596498	Rosa Junin	Peru, Cuzco	Landrace
Ames 13723	37TES	US, New Mexico	I G	PI 614002	Ames 10334	Bolivia,	Landrace
Ames 13725	115R	US, New Mexico	I G	PI 614880	QQ065	Chile, Los Lagos	Cultivar
Ames 13728	136R	US, New Mexico	I G	PI 614882	QQ67	Chile	Landrace
Ames 13733	168R	US, New Mexico	I G	PI 614884	QQ87	Argentina, Jujuy	Landrace
Ames 13736	144R	US, New Mexico	I G	PI 614886	QQ74	Chile, Maule	Landrace
Ames 13741	3P	US, New Mexico	I G	PI 614888	QQ61	Chile, Bio-Bio	Landrace
Ames 13745	Kaslaea	US, New Mexico	I G	PI 614901	CQ101	Bolivia, Oruro	Landrace
Ames 13746	Pison	US, New Mexico	I G	PI 614922	Sayana	Bolivia, La Paz	Cultivar
Ames 13747	Apelawa	Bolivia	I G	PI 614925	CQ 125	Bolivia, La Paz	I G
Ames 13748	Copacabana	US, New Mexico	I G	PI 614938	CQ 139	Bolivia, Oruro	Landrace
Ames 13749	32ALC	US, New Mexico	I G	PI 634919	Pichaman	Chile	Landrace
Ames 13750	31TES	US, New Mexico	I G	PI 634920	Faro	Chile	Cultivar
Ames 13759	20ALC	US, New Mexico	I G	PI 634925	UDEC-3	Chile	Landrace
Ames 13762	172R	US, New Mexico	I G	PI 665272	Bianra de Juny	Australia	I G
PI 470932	Pasan Ralle	Bolivia	Cultivar	PI 665273	Line 2-31	Bolivia, La Paz	I G
PI 510532	de Quiaca.	Peru	Cultivar	PI 665275	Line 0692	Bolivia, La Paz	I G
PI 510540	Grande	Peru	Cultivar	PI 665276	Line 1376	Bolivia, La Paz	I G
PI 510542	Quiona Rojo	Peru	Cultivar	PI 665283	Col. #6197	US, Colorado	I G
PI 510543	Amarillo	Peru	Cultivar	PI 674265	Chucapaca	Bolivia, La Paz	Cultivar
PI 510544	Sajama	Peru	Cultivar	PI 674266	DE-1	Ecuador	Cultivar
PI 510545	Sajama Jusi	Peru	Cultivar	PI 677096	537 BK60-B	US, Maryland	Cultivar
PI 510546	RB-80	Peru	Cultivar	PI 677097	NSSL 86649	US, Carolina	Cultivar
PI 510547	Silvestre	Peru	Cultivar	PI 677099	NSSL 91567	US, New York	Cultivar
PI 510548	Blanca	Peru	Cultivar	PI 677100	Japanese strain	US, Washington	Cultivar
PI 510551	Quinua	Peru	Cultivar				

I G, improved genotype. *, name of the cultivar by FAO.

(LGC), petiole color (PeC) was identified. Furthermore, color of panicle at flowering (PCF) differed during maturity (PCM), with 76% of genotypes being green during flowering and 55% Orange during maturity. Seed color was cream in most of genotypes (62% of genotypes) followed by coffee (31%) or black, and red (4% for each one). The average, stander error (S.E.), and frequency distribution for each quantitative character are presented in Table 3. Plant height was between 60 and 193 cm, and the number of branches was in the range of 4-23. Seed yield per plant was in the range of 15–70 g; however, most genotypes (76%) produced average seed yield, followed by 15% of genotypes in the high production category. Highly variation for number of days to mature was recorded, the earliest genotypes take 98 to mature while the latest genotypes taking 187 days.

Combined analysis of variances indicated highly significant (p 0.01) among genotypes for plant height, number of branches, panicle size, days to maturity, and seed yield/ha. The mean performance of the quinoa genotypes is presented in Table (4). Five genotypes were early maturing (between 98.2 and 106.4 days), viz. Ames 13723, PI 587173, PI 596293, PI 614886, and PI 614880. The highest seed yield (3.9, 3.5, 3.3,

and 3.1 t/ha) produced by four genotypes *i.e.* PI 470532, PI 470932, Ames 13747, and Ames 13720, respectively. Figure (1) shows the correlation matrix for the twelve characters; the positive correlations are displayed in blue, and the negative correlations are in red. The size and color intensity of the circle are relatively proportional to the correlation. The results showed positive and significant correlations between seed yield and plant height (r = 0.69), number of branches (r = 0.60), leaf width, and area (r = 0.55 and 0.52, respectively). The plant height was correlated with most of the studied characters: number of branches, petiole length, leaf length, leaf area, stem diameter, leaf width, number of teeth, and number of days to maturity. K-mean analysis of the studied genotypes was carried out using XLSTAT software for all characters. The genotypes were partitioned into five clusters, with high variation between clusters (87.3%) and only 12.7% within clusters. The highest variation (9351.9) and the highest average distance to the central genotype (86.2 units apart) were in the first cluster (I) that contained eight genotypes (Ames 13719, Ames 13720, Ames 13728, Ames 13747, PI 470932, PI 510532, PI 510540, and PI 665283) from Bolivia, Peru, and the US states of New Mexico and Colorado. On the other side, the lowest variation (901.2) as well as the lowest average distance to the central genotype (26.9 units apart) were recorded between seven genotypes (Ames 13722, Ames 13725, Ames 13733, Ames 13736, PI 587173, PI 596293, and PI 614888) of the second cluster (II). These genotypes are improved genotypes or cultivars in Argentina, the US, Colorado, New Mexico, and Chilean landraces (PI 614888) Table (5).

Table 2. Classification of the fifty-five quinoa genotypes based on relative frequency distributions (%) of discrete variables of morphological characters

Character	Descriptor	Absolute frequency	Relative frequency	Character	Descriptor	Absolute frequency	Relative frequency
PBr	Curved	25	45	**Pr**	Present	55	100
	Oblique	30	55	**DD**	Light	11	20
GH	Br to2/3 of MS	55	100		Regular	35	64
SS	Angular	29	53		Strong	9	16
	Cylindrical	26	47	**PS**	Amarantiform	25	45
St	Absent	8	15		Glomerulate	10	19
	Present	47	85		Intermediate	20	36
StC	Green	29	52	**PD**	Compact	5	9
	Pink	1	2		Intermediate	22	40
	Purple	12	22		Lax	28	51
	Red	5	9	**PG**	Clossed	28	51
SC	White	3	5		Opened	27	49
	Yellow	19	35	**PCF**	Green	42	76
	Red	2	4		Mixture	8	15
	Pink	1	2		Red	5	9
	Purple	1	2	**PCM**	Black	1	2
	Orange	2	4		Green	1	2
	Green	18	32		Orange	1	2
	Brown	9	16		Red/pink	4	7
Pa	Absent	36	65		Yellow	14	26
	Present	17	31		Orange	30	55
	Undetermined	2	4		Red	4	7
LS	Rhomboidal	18	33	**PC**	Black	2	4
	Triangular	37	67		Coffee	6	11
LM	Dentate	26	47		White	1	2
	Serrate	29	53		Yellow	5	9
LC	Green	40	73		Red	6	11
	Green/red	8	15		Orange	7	13
	Red	7	12		Green	2	4
LGC	Absent	10	18		Grey	1	2
	Purple	9	16		Cream	25	45
	Red	3	6	**SeC**	Black	2	4
	White	33	60		Coffee	17	31
PeC	Green	50	91		Cream	34	62
	Red	5	9		Red	2	4

Growth Habit (GH), branches (Br), position of branches (PBr), stem color at maturing stage (SC), stem shape (SS), stria (St), stria color (StC), pigmented axis (PA), leaf shape (LS), leaf margin (LM), leaf color (LC), leaf granule color (LGC), petiole color (PeC), panicle color at flowering (PCF), panicle color at maturity (PCM), panicle shape (PS), panicle density (PD), dehiscence degree (DD), perigonium appearance (PG), perigonium color (PC) and seed episperm color (SeC).

Table 3. Mean ± standard deviation (S.D.) and frequency distribution for the quantitative characters.

Characters	Mean ± S.D.	Descriptors	Absolute frequency	Relative frequency (%)
Plant height (PH)	109.5 ±25.0	Short (60 to 84)	8	15
		Average (85 to 133)	40	73
		Tall (134–193)	7	13
Number of branches (NoB)	12.8 ± 4.3	Low (4–9)	26	47
		Average (10–17)	21	38
		High (18–23)	8	15
Number of days maturity (MD)	125.9 ± 18.4	Early (98–108)	6	11
		Average (108–144)	43	78
		Late (145-187)	6	11
Seed yield/plant (SY)	30.6 ± 12.7	Low (15-17)	5	9
		Average (18-42)	42	76
		High (43-70)	8	15
Number of teeth/leaf (NoT)	13.0 ± 3.8	Low (6–9)	29	53
		Average (10–17)	17	31
		High (18–21)	9	16
Leaf width (LW)	7.8 ± 1.4	Narrow (5–6)	4	7
		Average (7–9)	42	76
		Wide (10–11)	9	16
Leaf length (LL)	9.0 ± 1.4	Short (6–8)	9	16
		Average (9–10)	38	69
		Tall (11–12)	8	15
Leaf area (LA)	40.6 ± 11.5	Narrow (21–29)	11	20
		Average (30–52)	34	62
		Wide (53–66)	10	18
Petiole length (PeL)	7.2 ± 1.5	Short (5–6)	6	11
		Average (7–9)	42	76
		Tall (10–11)	7	13
Stem diameter (SD)	15.7 ± 4.2	Thin (8–12)	11	20
		Average (13–20)	37	67
		Thick (21–27)	7	13
Panicle length (PL)	22.9 ± 3.8	Short (17–19)	9	16
		Average (20–27)	33	60
		Tall (28–32)	13	24
Panicle width (PW)	8.0 ± 2.0	Narrow(5–6)	8	15
		Average (7–10)	41.0	75
		Wide (11–15)	6.0	11

Table 4: Mean performance of the fifty-five genotypes across the two seasons.

Genotypes	Plant height (cm)	No. of branches /plant	No. of days to maturity	Seed yield (t/ha)	Genotypes	Plant height (cm)	No. of branches /plant	No. of days to maturity	Seed yield (t/ha)
Ames 13719	127.7	17.0	114.4	2.8	**PI 587173**	119.0	13.0	100.0	2.1
Ames 13720	124.3	17.0	118.1	3.1	**PI596293**	126.7	13.0	100.0	2.0
Ames 13722	119.7	17.0	113.9	2.0	**PI 596498**	116.0	7.7	130.0	1.5
Ames 13723	77.0	8.4	98.5	1.4	**PI 614002**	109.3	19.0	130.0	1.7
Ames 13725	136.3	20.0	114.0	1.8	**PI 614880**	129.0	15.0	106.0	1.7
Ames 13728	141.7	19.0	118.0	2.7	**PI 614882**	144.0	13.0	114.0	1.4
Ames 13733	97.0	13.2	123.0	2.1	**PI 614884**	89.0	8.4	120.0	1.2
Ames 13736	131.3	19.0	130.0	2.1	**PI614886**	130.7	13.0	105.0	1.1
Ames 13741	129.7	15.0	126.0	1.7	**PI 614888**	124.0	9.6	124.0	2.1
Ames 13745	125.3	15.0	126.0	1.5	**PI 614901**	62.0	9.0	124.0	1.9
Ames 13746	99.7	18.0	110.0	1.2	**PI 614922**	81.0	7.0	140.0	1.8
Ames 13747	98.0	13.0	122.3	3.3	**PI 614925**	86.7	7.0	140.0	1.4
Ames 13748	108.0	14.0	118.0	1.3	**PI 614938**	94.0	10.0	125.0	1.2
Ames 13749	90.7	13.0	113.0	1.3	**PI 634919**	111.3	12.0	116.0	1.8
Ames 13750	112.0	15.0	125.0	1.2	**PI 634920**	129.3	16.0	115.0	1.7
Ames 13759	115.3	11.4	110.0	1.3	**PI 634925**	135.7	10.0	115.0	1.5
Ames 13762	110.0	14.0	113.0	1.8	**PI 665272**	100.7	10.0	143.0	1.0
PI 470932	177.0	10.6	175.0	3.5	**PI 665273**	135.3	17.0	150.0	1.7
PI 510532	193.2	23.0	187.2	3.9	**PI 665275**	180.0	18.0	170.0	1.6
PI 510540	172.3	23.0	167.4	2.8	**PI 665276**	105.7	10.0	142.0	1.7
PI 510542	84.3	12.0	132.0	0.8	**PI 665283**	127.3	17.0	124.0	2.8
PI 510543	81.0	12.0	132.0	0.9	**PI 674265**	106.7	14.0	115.0	1.6
PI 510544	68.7	6.0	140.0	1.0	**PI 674266**	109.3	22.0	153.0	1.5
PI 510545	92.3	7.0	134.0	0.9	**PI 677096**	132.7	15.0	116.0	1.3
PI 510546	93.3	9.0	134.0	0.9	**PI 677097**	71.3	9.0	113.0	1.2
PI 510547	97.0	9.0	132.0	1.1	**PI 677099**	92.7	11.0	130.0	1.2
PI 510548	87.3	9.0	132.0	1.4	**PI 677100**	59.7	6.7	110.0	1.1
PI 510551	88.0	5.9	132.0	1.1	**$LSD_{0.05}$**	12.9	5.4	14.2	0.9

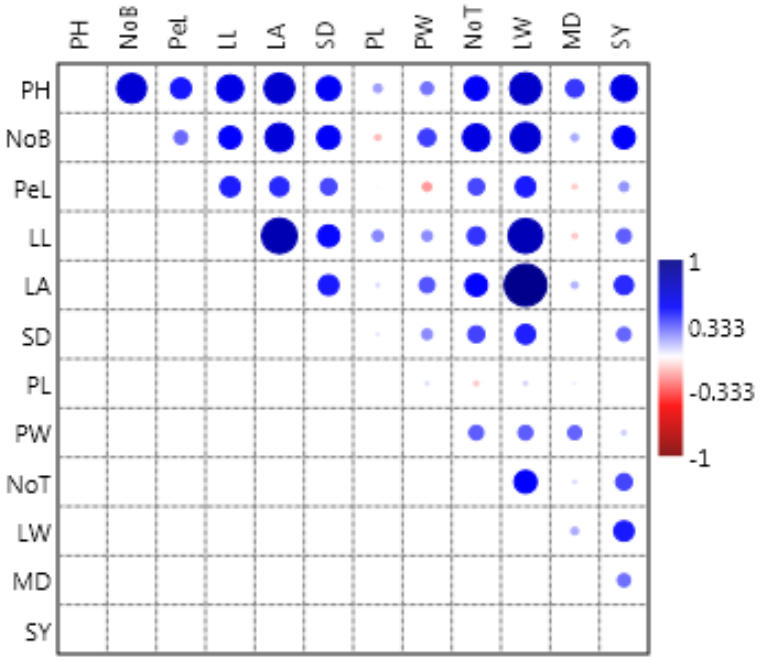

Fig. 2. Correlation matrix among the quantitative characters for the studied quinoa genotypes.

Table 5: General summary results for the k-mean classes.

Class	I	II	III	IV	V
Genotypes	8	7	12	11	17
Within-class variance	9351.9	901.2	1661.5	1180.1	1316.2
Minimum distance to centroid	45.7	17.0	16.8	13.7	12.1
Average distance to centroid	86.2	26.9	34.9	29.5	33.7
Maximum distance to centroid	135.5	39.6	83.7	63.1	46.9
	Ames 13719	Ames 13722	Ames 13723	Ames 13741	Ames 13746
	Ames 13720	Ames 13725	Ames 13745	Ames 13762	Ames 13749
	Ames 13728	Ames 13733	Ames 13748	PI 614002	Ames 13750
	Ames 13747	Ames 13736	Ames 13759	PI 614880	PI 510542
	PI 470932	PI 587173	PI 510548	PI 614901	PI 510543
	PI 510532	PI 596293	PI 596498	PI 614922	PI 510544
	PI 510540	PI 614888	PI 614882	PI 634919	PI 510545
	PI 665283		PI 614925	PI 634920	PI 510546
			PI 634925	PI 665273	PI 510547
			PI 665275	PI 665276	PI 510551
			PI 674266	PI 674265	PI 614884
			PI 677096		PI 614886
					PI 614938
					PI 665272
					PI 677097
					PI 677099
					PI 677100

DISCUSSION

The morphological characters detected tremendous variation among the fifty-five genotypes. However, all genotypes were branched (Br), and the branches are higher than 2/3 of the main stem and may reach the height of the main stem (GH). Quinoa plants are green during the seedling stage, then have pigments scattered over many parts of the plant. Pigments started on the green stem in the stria (StC), then pigment covered the entire stem in some genotypes in the maturing stages; in the case of the red stria in genotypes G37 and 40, the stem and the plant were colored red even before maturity. Stem color could be one of fourteen colors (Bioversity International & FAO, 2013); this study presented only eight colors. Concerning leaf shapes Manjarres-Hernández *et al.*, (2021) recorded four shapes, viz., rhomboidal, lanceolate, triangular, and oval; different shapes were found on the same plant. This is because they include the young leaves in the descriptor. Leaf shape divided the evaluated genotypes into two groups with triangular shape (67%) or rhomboidal (33%), also its margin was serrate (53%), or dentate (47%). In some genotypes, leaf granule color (LGC) gives leaves a bright sheen that is present

only during the seedling stage but remains lukewarm until flowering. The panicles demonstrated high variation for color at flowering (PCF) and maturity (PCM), as well as for panicle shape (PS) and panicle density (PD). Granular vesicular pubescence rich in calcium oxalate covers the panicle and is the reason for the colors purple, pink, and white (Montes *et al*., 2018). These morphological characters are useful in breeding programs for detection and keeping maintenance pure genotypes, especially characters in the early stage like LGC and StC and before flowering and outcrosses. Furthermore, seed perisperm color is where it is important to recognize genotypes, and it generally was cream (62%), followed by coffee (31%), and only two genotypes were red (Ames 13747 and, PI 470932), and black (PI 665276 and, PI 677097); all these colored genotypes were from Bolivia, except PI 677097 from the USA; however, all colors had high gradation in each color. The results showed that among the 21 qualitative characters, the ones with the highest variability were stem color at the maturing stage (SC), panicle color at maturity (PCM), and perigonium color (PC). These results are in agreement with Garca *et al.*, (2020), who found highly phenotypic variability and genotypes can be easily recognized by the pigmentation of the plant, inflorescences and seeds, shape and size of seeds, and panicles. Manjarres-Hernandez *et al.*, (2021) reported that morphological character variables could be used as selection tools to increase the efficiency of quinoa improvement programs, oriented to the characteristics of agronomic importance, and determined their usefulness.

All studied quantitative characters showed high variability for all studied characters. Plant height was between 60 and 193 cm, and the number of branches was in the range of 4-23; these wide variations allow plant breeders to select cultivars suitable for different conditions. Despite being a tall plant with a high number of branches and having characteristics related to productivity and high biological mass, short plants are characterized by resistance to lodging and ease of harvesting, and their few branches enable an intercropping system. Leaf, like other parts of the plant, has a wide variability, and a number of characters could be use as selection criteria: leaf width, length, and area, as well as number of teeth per leaf, also petiole length. Low number of genotypes had (6–9 teethes/leaf) that belong to dentate leaves. The study also described two of the yield components' characteristics (panicle length and width), which are easy to recognize and could be using for select high-yielding genotypes. The main stem panicle length and width were in the ranges of 16–32 and 5–23 cm, respectively. The tallest and widest panicle are found in the improved genotypes, PI 665275 and PI 510532. Manjarres-Hernández *et al*., (2021) mentioned that the variables that contributed most to observed phenotypic variation were the panicle length, yield, seed diameter, and seed index. Garca *et al*., (2020) mentioned that the most variable characteristics were panicle, color, size of the seed, number of days to maturity, and the nutritional value of the grain. The variation in yield components may be helpful for the breeder to increase quinoa's potential under different conditions. These results are in agreement with many investigators. In Egypt, quinoa takes 115-160 days to mature, with a height of 76-146 cm and 12 to 25 branches (Shams, 2018), also under Toshka conditions Afiah *et al*., (2018) estimated 39.98 to 91.9cm height, 4.4 to 2.1 main branches and 16.9 to 6.7g seed yield per plant. Plant height ranged from 60 to 180cm, and number of days to maturity from 98 to 177 in Saudi Arabia (EL-Harty *et al*., 2021), plant height was between 78–116cm in Turkey (Mustafa and Temel, 2018). Quinoa mature after 144 and 189 days, and the high seed yield/plant was 62.0 g in Colombia (Manjarres-Hernández *et al*., 2022).

The shortest genotypes produced the lowest number of branches per plant and seed yield per hectare with an average number of days to maturity except the Bolivian landraces (PI 614901) and cultivar (PI 614922), which produced 1.9 and 1.8 t/ha, respectively. Four genotypes (PI 470532, PI 470932, Ames 13747, and Ames 13720) were in the first rank for seed yield/ha with mean values of 3.9, 3.5, 3.3, and 3.1 t/ha, respectively. The first two genotypes were cultivars from Peru and Bolivia, taking 187.2 and 175.0 days to maturity, respectively, with huge growth like bushes (high number of branches and tallest plant). While the genotypes Ames 13747 and Ames 13720 from the USA and Bolivia combined high seed yield with average maturing times (118.1 and 122.3 days, respectively) and average plant height. However, among the studied twelve characters only plant height, number of branches, leaf width and area associated with seed yield indicate the ability to improve seed yield using these characters. The same relationship between yield and plant height, number of branches per plant, and leaf area was detected by Bhargava and Ohri (2016), Shams, 2018, and Afiah *et al*., (2018).

K-mean analysis partitioned genotypes into five clusters, the highest variation (9351.9) was in the first cluster (I) that contained eight genotypes (Ames 13719, Ames 13720, Ames 13728, Ames 13747, PI 470932, PI 510532, PI 510540, and PI 665283) from Bolivia, Peru, and the US states of New Mexico and Colorado. This cluster includes the highest seed yield genotypes. On the other side, the lowest variation (901.2) as well as the lowest average distance to the central genotype (26.9 units apart)

were recorded between seven genotypes (Ames 13722, Ames 13725, Ames 13733, Ames 13736, PI 587173, PI 596293, and PI 614888) of the second cluster (II). These genotypes are improved genotypes or cultivars in Argentina, the US, Colorado, New Mexico, and Chilean landraces. The maximum intercluster distance (396.6) was recorded between clusters I and V, and the minimum intercluster distance (53.9) was recorded between clusters II and IV. These groups are important for initiate breeding program or further study. These results agree with Afiah *et al*., (2018), EL-Harty *et al*., (2021) and Manjarres-Hernandez *et al*., (2021), who found that clusters do not correspond to the collection area or origin.

CONCLUSION

Quinoa showed a wide variation for all characters under study except type of branches; this study initiates a database for quinoa genotypes including qualitative and quantitative characters. The high variation confirmed the fact that quinoa is cultivated in different environments. Quinoa plant height ranged from 60 to 193 cm, and the number of days to mature was between 98 and 187. Regarding seed yield and its components, highly positive and significant correlations were recorded between seed yield and plant height (0.69), number of branches (0.60), leaf width, and area (0.55 and 0.52, respectively). The high-yield genotypes were PI 510532 (3.9 t/ha) and PI 470932 (3.4 t/ha) however, they take about six months to mature. The best genotypes were Ames 13747, and Ames 13720 produced 3.3 and 3.1 t/ha and matured after 12 2.3 and 118.1 days. These four genotypes were grouped in one cluster according to the K-mean analysis.

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التوصيف المظهري للتراكيب الوراثية المستوردة من الكينوا تحت ظروف المملكة العربية السعودية

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الملخص

وبهدف ادخالها الي الزراعة في السعودية تم جمع خمسة وخمسون تركيب وراثي من الكينوا وتم تقييمها حقليا خلال الموسمين الشتويين 17/2016 و 18/2017. تم توصيف هذه التراكيب الوراثية بثلاثة وثلاثون صفة طبقا لتوصيف Bioversity International. كانت الكينوا خضراء خلال مرحلة الشتلات ثم انتشرات الأصباغ على أجزاء كثيرة من النبات ، وقد تتغير بعض الألوان خلال دورة حياة النبات. اكتشف ثلاثة ألوان للعناقيد عند التزهير وسبعة ألوان عند النضج. كان ارتفاع نبات الكينوا من 60 إلى 193 سم وتستغرق 98-187 يومًا الي النضج ومحصول بذور 15.3 – 70.1جرام/النبات. انتج التراكيبان الوراثيان Ames 13747 و Ames 13720 محصول عالي من البذور قدره 3.3 و3.1 طن / هكتار علي التوالي وينتميان الي فئة متوسطة النضج (118.1 و 122.3 يومًا على التوالي). كان هناك ارتباط معنوي بين محصول البذور وارتفاع النبات وعدد الأفرع وعرض الورقة ومساحة الورقة. بناءً على تحليل K-mean ، تم تقسيم التراكيب الوراثية الي خمس مجموعات مع تباين كبير بينها (87.3٪) وفقط 12.7% داخل المجاميع. عرضت النتائج الخصائص المورفولوجية التي يمكن استخدامها كمعايير انتخابية لزيادة كفاءة برامج تحسين محصول الكينوا.

الكلمات المفتاحية: الكينوا و الصفات الوصفية و التوصيف و التحليل العنقودي