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Growth and fruit morpho-physicochemical diversity assessment of local melon genotypes

ABSTRACT

The genetic diversity of melon genotypes obtained from northern Iraq was assessed in 2021 at the University of Sulaimani's Directorate of Garden in Qlyasan using a Randomized Complete Block Design with three blocks, using growth and fruit morpho-physicochemical characteristics. The 57 genotypes were characterized morphologically and physiochemically, and there were high significant differences between them. The values of main stem length, lateral stem length, main stem diameter, and lateral stem diameter were ranged from 20.49 to 85.84 cm, 29.45 to 92.52 cm, 0.85 to 1.77 cm, and 0.42 to 0.74 cm, respectively. The fruit weight produced by G11 achieved the highest value (1860.72 g). Antioxidant activity was increased in genotypes with higher levels of polyphenols, titratable acidity, and total soluble solids. Principal component analysis (PCA) revealed four distinct groups of genotypes based on studied traits. PCA plot revealed that fruit thickness, fruit length, fruit width, placenta weight, fruit weight, seed length, seed width, total phenolic content, total flavonoid content, antioxidant activity, pH, and titratable acid were significant determinants of genetic diversity in the melon genotypes. Based on the majority of the fruit morpho-physicochemical traits, genotype G11 was regarded as the best performer. The results of this study suggested a significant degree of heterogeneity in Iraqi melon germplasm, which must be conserved and incorporated into future development projects.

INTRODUCTION

Cucumis is a genus of the Cucurbitaceae family, and its two economically significant species are cucumber (*Cucumis sativus*) and melon (*Cucumis melo*) (Maleki et al. 2018). Melon is a diploid plant with 24 chromosomes (2n = 2x) (Paris et al. 2012). It is possible that it was domesticated largely for the nutritional content of its seeds and subsequently experienced a period of considerable variation. Fruits provide significant health benefits in addition to basic nourishment. Several investigations have indicated that eating fruits can help prevent chronic diseases. Melon fruits are ingested by humans and are made up of different varieties, some of which bear sweet and tasty fruits and others which bear bitter and medicinally essential fruits. Melon contains a considerable quantity of biologically active substances such as ash, fiber, protein, phenolic compounds, carbohydrates, tocopherols, phospholipids, and sterols, all of which have a favorable effect on humans. As a result, melon can be thought of as effective candidates for the development

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of unique functional foods that contribute to a healthy food chain (Azhari et al. 2014; Mallek-Ayadi et al. 2018; Khalid et al. 2021; Rolbiecki et al. 2021; Sánchez et al. 2021).

Due to the diversity of the species' morphology, which includes a wide range of leaf, flower, and fruit characteristics, plant taxonomists have developed intraspecific categories based primarily on fruit characteristics (Nuñez-Palenius et al. 2008). It has been discovered by Raghami et al. (2014) and Pitrat (2016) that *C. Melo* has 19 distinct horticultural divisions within the species, comprising agrestis, kachri, chito, tibish, acidulus, momordica, conomon, makuwa, chinensis, flexuosus, chate, dudaim, chandalak, indicus, ameri, cassaba, ibericus, cantalupensis, and inodorus. For commercial purposes, the cantalupensis and inodorus melon species are the dominant ones. Tropical and subtropical regions produce the majority of the world's melon, although it is growing more popular in locations with milder weather. Northern Iraq cultivates both rain-fed (local) and non-rain-fed (commercial) melon. Non-rain-fed melon requires frequent watering throughout the growing and producing process and has a limited tolerance for water stress. Rain-fed melon thrives in sunny, warm climes and is drought resistant. It is vital to blame genetic degeneration or the loss of indigenous germplasm on the introduction of new commercial cultivars with high quality and quantity under water stress. The formation, enrichment, evaluation, documentation, and conservation of plant collections are all part of plant genetic resource management. Awareness of the extent of genetic diversity and the interactions between different local genotypes is useful for both detecting and successfully preserving genetic resources and boosting the efficacy of breeding initiatives. As a result, breeders will have a better understanding of genetic variety in order to select the best parents for their hybrids while preserving population diversity (Hill 2001; Govindaraj et al. 2015; Tian et al. 2015). To solve this problem, species diversity analysis is essential. Melon genetic diversity has been studied using a variety of morphological, phenological, physiological, sensory, and physicochemical analyses (Dantas et al. 2015; Maleki et al. 2018; Saputro et al. 2020; Singh et al. 2020; Pandey et al. 2021). The most important criterion for first assessments of genetic diversity for melon genotype categorization and identification is morphological investigation. The northern part of Iraq contains abundant melon genetic resources with different physical traits. Regardless, no research has been conducted to demonstrate the genetic variability of Iraqi native melon genotypes. As a result of the findings, there is still some confusion about the differences between melon genotypes and the relationships between different groups from the north of Iraq. Furthermore, imported melons account for the vast majority of melon genotypes grown by farmers. Farmers believe that imported melon has better attributes than local melon, hence local melon production is declining. The aim of this study was to assess the genetic diversity of melon genotypes using growth and morpho-physicochemical characteristics. This study's specific purpose was to maintain genetic variation and promote its use in breeding programs, as well as to provide essential information for GenBank population management and to establish the degree of collection diversity.

MATERIALS AND METHODS

Plant materials and experimental design

The research was carried out on 57 local melon genotypes gathered in northern Iraq. These genotypes have been planted throughout Iraq's northern areas (Sulaimani, Erbil, and Duhok governorates). Because no information about their parents is available, these samples are considered genotypes rather than varieties or cultivars. The melon genotypes belonged to six horticultural groups of *Cucumis melo* L., based on the botanical classification of Pitrat (2016) and Raghami et al. (2014), including cantalupensis, inodorus, Ameri, Dudiam, Charentais, and Chandalak. The experiment conducted on the field of the University of Sulaimani's Directorate of Garden in Qlyasan from May 10 to August 31, 2021. Seeds (3 seeds) from various genotypes were sown per hole in the field soil on May 10, 2021 using a Randomized Complete Block Design with three blocks. There were 171 plots in the blocks. A block and a plot had 342 and 6 m^2 of area, respectively. Each genotype had seven plants, spaced 1.00 m apart, in each plot. Before tillage, a representative soil sample was obtained from the experiment field at a depth of 0–30 cm, air dried, sieved with 2 mm sieves, and packed for analysis. As stated in Table 1, some physical and chemical

properties were investigated at the Soil and Water Sciences Department, Faculty of Agricultural Sciences, University of Sulaimani. Table 2 depicts the climate trend of Qlyasan from January to December during the season of 2021. Following the emergency of seedlings, one plant was kept in each hole. These plants were only irrigated once after seeding, and then the irrigation was switched off for all growth and productive phases.

Table (1): Shows some of the physical and chemical features of the soil at the cultivation region

Soil properties	Quantity
Sand (g Kg^{-1})	42.60
Silt (g Kg^{-1})	435.90
Clay (g Kg^{-1})	534.80
O.M (g Kg^{-1})	22.77
Available phosphate (mg Kg^{-1})	6.15
Total N (mg Kg^{-1})	1.17
pH	7.27
E.C. (dS m^{-1})	0.60
Soluble cations and anions (Mmole L^{-1})	
$CaCO_3$ (g Kg^{-1})	102.50
Calcium (Ca^{+2})	0.37
Potassium (K^{+})	0.13
Sodium (Na^{+})	0.33
Carbonate ($CO_3^{=}$)	0.00
Bicarbonate ($HCO_3^{=}$)	3.13
Chloride (Cl^{-})	0.45
Sulphate ($SO_4^{=}$)	0.71

Table (2): Meteorological data of the year 2021.

	Temperature (° C)			Humidity (%)			Vapor (mm)			
Month	Min	Max	Average	Min	Max	Average	Min	Max	Average	Precipitation (mm)
January	2.68	15.32	9.00	40.00	77.13	58.56	5.04	7.72	6.38	65.40
February	4.58	17.48	11.03	44.21	81.75	62.98	6.61	9.21	7.91	71.40
March	7.72	20.19	13.96	38.74	75.77	57.26	7.10	9.91	8.51	30.40
April	13.89	29.44	21.66	24.63	60.50	42.57	8.23	12.12	10.18	10.70
May	20.32	35.40	27.86	18.48	47.90	33.19	9.10	12.85	10.98	4.20
June	22.58	40.01	31.30	15.07	39.93	27.50	9.45	13.33	11.39	0.00
July	27.43	43.25	35.34	17.97	39.32	28.65	13.10	17.42	15.26	0.00
August	26.57	42.97	34.77	16.77	39.03	27.90	11.97	15.94	13.95	2.00
September	21.04	36.15	28.59	17.57	48.03	32.80	9.17	13.32	11.25	0.00
October	16.59	28.49	22.54	26.06	54.52	40.29	8.69	11.66	10.18	18.50
November	9.81	20.19	15.00	39.23	72.20	55.72	7.79	10.37	9.08	17.20
December	5.71	14.85	10.28	47.71	84.00	65.85	6.52	8.74	7.63	72.10

Growth and fruit characters assessment

The growth traits including main stem length (MSL, cm), lateral stem length (MSL, cm), main stem diameter (MSD, cm), lateral stem diameter (LSD, cm), number of lateral stems (NLS), leaf length (LL, cm), leaf width (LW, cm) were estimated at the flowering stage from five randomly selected plants per plot, while fruit phenotypic characters such as number of fruits per plant (NFP), fruit length and width (FL and FW, cm), fruit length/fruit width ratio (FL/FW), fruit weight (FW, g), flesh thickness (FT, cm), rind thickness (RT, cm), placenta weight (PW, g), seeds length and

width (SEL and SEW, cm), fruit juice volume (FJA, % (v/w)), and moisture content (MC, %) were assessed at maturity stage from five randomly selected plants per plot.

Physicochemical traits measurement

The mature fruits of various genotypes were harvested. The flesh was separated and homogenized after the rind was removed. In a nutshell, a measured quantity of flesh fruit (5.00 g) was sliced, and the juice was taken from the fruits by pulping and compressing. For 10 min, the samples were centrifuged at 8000 rpm, and the clear supernatant was taken for physicochemical analysis.

Total phenolic content (TPC) measurement

The total phenolics in juice were determined using the Folin–Ciocalteu reagent, as reported in our earlier paper (Lateef et al. 2021) with some modifications. Three replications were used to get the mean value of each genotype. The results were expressed as the equivalent of µg gallic acid (GAE) per gram of flesh fresh weight using the following formula: TPC (µg GAE g^{-1} FW) = $\frac{\text{Volume of juice (mL)}}{\text{Fresh weight of flesh (g)}}$ x Concentration from standard curve of gallic acid (µg/mL).

Total flavonoid content (TFC) estimation

The TFC in each extract was calculated using our earlier paper (Lateef et al. 2021) with some modifications. Each juice's total flavonoid concentration was reported as µg quercetin (QE) per gram of fresh flesh matter using the following formula: $\frac{\text{Volume of juice (mL)}}{\text{Fresh weight of flesh (g)}}$ x Concentration from standard curve of quercetin (µg/mL). Three replications were used to create each genotype's mean value.

Antioxidant activity (AC) evaluation by DPPH

The antioxidant capacity of the flesh juice was estimated using the 1-diphenyl-2-picrylhydrazyl (DPPH) radical-scavenging method outlined in our article (Lateef et al. 2021), with some enhancements. Three replications were used to create each genotype's mean value. The antioxidant potential of various juices was quantified as Trolox equivalents per gram of fresh flesh weight using the following equation: $\frac{\text{Volume of juice (mL)}}{\text{Fresh weight of flesh (g)}}$ x Concentration from standard curve of Trolox (µg/mL). Each number in this experiment is the average of three measurements.

Soluble sugar content (SSC) measurement

Soluble sugar content was determined using the method given by Lateef et al. (2021). Three replications have been used to determine the average value of each genotype. The soluble sugar concentration was given as µg g^{-1} of fresh flesh weight using the following formula: SSC (µg g^{-1} FW) = $\frac{\text{Volume of juice (mL)}}{\text{Fresh weight of flesh (g)}}$ x Concentration from standard curve of glucose (µg/mL).

Ascorbic acid content (ASC) determination

The ASC of fresh flesh was measured using the methods mentioned previously by Abbasi et al. (2019). The ASC was defined as µg g^{-1} of fresh flesh weight. Three replications have been used to calculate the average value of each genotype.

Quantification of carotenoid content (CAC)

The CAC of fresh flesh was calculated using the methods stated previously by Ferrante et al. (2008). The carotenoid concentrations were expressed as µg per gram of fresh flesh weight and estimated by this formula:

$$CAC\ (\mu g/g) = \frac{Absorbance\ reading\ x\ Total\ volume\ of\ juice\ (mL)\ x\ 10000}{\text{Carotene extension coefficient in methanol}\ x\ Fresh\ weight\ of\ flesh\ (g)}$$

Three replications have been used to calculate the average value of each genotype.

pH measurement

Juice was collected and homogenized from known weights of flesh melons, and a known volume of deionized water was added to each juice sample. The pH was obtained after calibrating the pH meter (Hanna Instruments, Romania) for pH 4 and 7 with standard solutions. Furthermore,

three readings were taken from each juice genotype, and such values from triplicate samples were used to calculate the mean.

Measurement of total soluble solids (TSS)

The TSS in the juice was determined using a handheld refractometer (Eltom et al. 2017). TSS was expressed as Brix unit. Three replications have been used to calculate the average value of each genotype.

Assessment of titratable acidity (TTA)

The titratable acidity of melon genotypes was evaluated using the method described previously by Ranganna (1986). The titratable acidity was then estimated by the formula of Nielsen (2017) and expressed as percentage unit.

Statistical data analysis

XLSTAT version 2020.1.3 (Addinsoft, 2020) was used to generate principal component analysis (PCA) and conduct the one-way-ANOVA-RCBD analysis of growth and fruit morpho-physicochemical parameters. The Least Significant Difference (LSD) test was performed to analyze the differences between the means ($p \leq 0.01$).

RESULTS

Assessment of growth characters in melon genotypes

The pairwise analysis (LSD test) of the phenotypic data revealed highly significant differences between genotypes in all tested parameters (Table 3). The tallest plant (MSL) was G46 (85.48 cm) followed by G36 (85.37 cm), and the shortest plants were G37 (20.49 cm) and G41 (20.95 cm). G51 had the highest lateral stem length (LSL) (92.63 cm), which was statistically equivalent to G36 (92.52 cm), G46 (91.15 cm), and G12 (88.79 cm), The genotype G7 produced the smallest LSL (29.45 cm). A pairwise study revealed that the main stem diameter (MSD) and lateral stem diameter (LSD) varied significantly between melon genotypes. Among the genotypes studied, G26 and G31 had the highest values of MSD (1.77 cm) and LSD (0.74 cm), respectively. On the other hand, G7 and G42 gave the minimum values of MSD (0.85 cm) and LSD (0.42 cm), respectively. The genotype G36 had the maximum number of lateral stems (NLS), while the genotypes G4 and G37 had the lowest. There were substantial differences in length (LL) and width (LW) of leaf among melon genotypes, according to the results of the pair-wise comparison. The maximum LL (9.15 cm) and LW (13.48 cm) were observed by G24. Different methods were employed to characterize genotypes, with multivariate analysis being the most appropriate. Data mining was a highly beneficial way of selecting, exploring, and modeling big datasets in order to uncover unique tendencies that would make the explanation more appealing and definitive. For genotypes clustering, multivariate analysis approaches such as agglomerative hierarchical clustering (AHC) and principal component analysis (PCA) were applied. The variance in melon genotypes was analyzed and described using principal component analysis. As a result, the plot formed by the first two components could distinguish the melon genotypes based on their major determining features. The two main components of PCA, F1 and F2, explained 62.75% of the total variation (Figure 1). Following the PCA result, the first principal component (F1) was positively linked with MSL and LSL; the second principal component (F2) was positively associated with LL and LW and negatively correlated with the MSD and LSD traits. Four groups of genotypes (Gr1-Gr4) were formed. Genotypes with low values of NLS, MSL, LSL, MSD, LSD, LL, AND LW were clustered to the left of the PCA plot (Gr1 and Gr3) by these components. Genotypes with high NLS, LL, and LW values were found in the scatter plot's top right (Gr2). Genotypes with high MSL, LSL, MSD, and LSD values were revealed in the bottom-right quadrant of the plot (Gr4).

Table (3): Means comparison (LSD) for growth traits collected from melon genotypes

Genotype	Main stem length (cm)	Lateral stem length (cm)	Main stem diameter (cm)	Lateral stem diameter (cm)	Lateral stem number	Leaf length (cm)	Leaf width (cm)
G1	60.11	70.33	1.54	0.61	3.33	7.51	12.04
G2	55.54	65.20	1.22	0.57	4.00	7.27	10.66
G3	45.47	53.55	1.29	0.54	4.33	7.46	10.45
G4	58.22	71.55	1.16	0.53	3.00	6.67	10.34
G5	75.44	75.26	1.43	0.66	4.67	7.93	11.86
G6	55.78	48.88	1.17	0.58	3.33	7.89	11.81
G7	24.88	29.45	1.05	0.42	4.67	6.81	10.92
G8	79.30	61.56	1.24	0.56	4.67	8.18	12.32
G9	55.20	56.64	1.34	0.67	4.00	6.61	9.67
G10	81.20	71.65	1.00	0.54	5.67	8.75	12.64
G11	44.49	50.06	1.03	0.73	4.33	6.67	9.83
G12	84.76	88.79	1.26	0.60	5.33	7.64	11.30
G13	65.62	62.48	1.06	0.55	5.33	7.10	10.86
G14	44.73	35.45	1.07	0.53	4.33	6.46	9.71
G15	40.95	39.09	1.23	0.62	5.67	6.52	9.37
G16	68.30	58.29	1.04	0.64	5.00	7.06	10.43
G17	41.84	43.59	1.17	0.57	5.67	7.48	11.73
G18	46.45	44.42	1.04	0.54	5.00	7.37	11.49
G19	40.52	35.66	1.36	0.53	4.67	6.67	10.22
G20	58.62	41.89	1.32	0.68	5.67	6.92	10.24
G21	53.72	58.06	1.47	0.64	4.67	6.74	10.09
G22	45.98	49.70	1.41	0.65	4.33	7.05	10.84
G23	53.30	58.71	1.44	0.58	5.33	6.64	10.00
G24	56.64	62.55	1.61	0.67	4.33	9.15	13.48
G25	63.48	63.47	1.53	0.73	5.67	8.10	11.48
G26	58.23	63.50	1.77	0.71	4.33	7.06	10.85
G27	24.51	40.49	1.13	0.57	5.00	6.14	9.14
G28	58.95	56.66	1.55	0.55	5.67	8.28	13.08
G29	50.42	47.33	1.14	0.54	5.00	6.46	8.43
G30	61.40	74.89	1.40	0.69	4.67	7.81	11.13
G31	64.01	81.25	1.07	0.74	4.00	8.28	11.57
G32	51.23	64.35	1.29	0.58	5.33	7.36	11.13
G33	58.74	54.93	1.68	0.66	5.33	7.18	10.76
G34	51.71	58.22	1.19	0.55	4.67	7.51	10.49
G35	48.46	55.66	1.25	0.55	3.67	6.93	10.19
G36	85.37	92.52	1.34	0.72	6.00	8.12	11.60
G37	20.49	31.34	1.02	0.45	3.00	6.21	8.32
G38	42.60	60.62	1.05	0.54	5.33	6.81	10.28
G39	73.03	78.91	1.43	0.63	3.33	8.19	12.47
G40	76.75	74.61	1.48	0.58	4.67	7.37	11.63
G41	20.95	33.67	1.03	0.54	4.67	6.43	9.03
G42	37.44	49.24	0.85	0.54	4.33	8.64	11.88
G43	40.88	64.33	1.14	0.54	4.33	7.52	10.41
G44	47.34	63.16	1.19	0.55	5.33	7.34	11.14
G45	35.86	41.76	1.23	0.47	5.33	6.85	10.77
G46	85.48	91.15	1.28	0.57	4.33	6.89	10.26
G47	54.61	67.97	1.29	0.55	4.67	6.58	10.36
G48	63.18	59.66	1.51	0.65	4.33	8.11	12.74
G49	54.31	45.95	1.26	0.54	5.33	6.12	9.65
G50	37.66	55.57	1.53	0.62	4.67	7.67	11.66
G51	80.10	92.63	1.51	0.61	4.67	8.19	12.63
G52	74.31	72.62	1.28	0.54	5.33	6.23	9.66
G53	47.01	62.12	1.60	0.67	3.67	6.59	10.07
G54	77.43	62.22	1.22	0.59	4.67	7.51	10.57
G55	63.60	81.33	1.45	0.65	5.00	7.66	12.06
G56	67.50	57.67	1.52	0.60	4.33	7.58	10.66
G57	23.18	40.26	1.26	0.47	5.33	8.80	11.89
LSD value	5.18	6.02	0.08	0.05	1.02	0.32	0.40

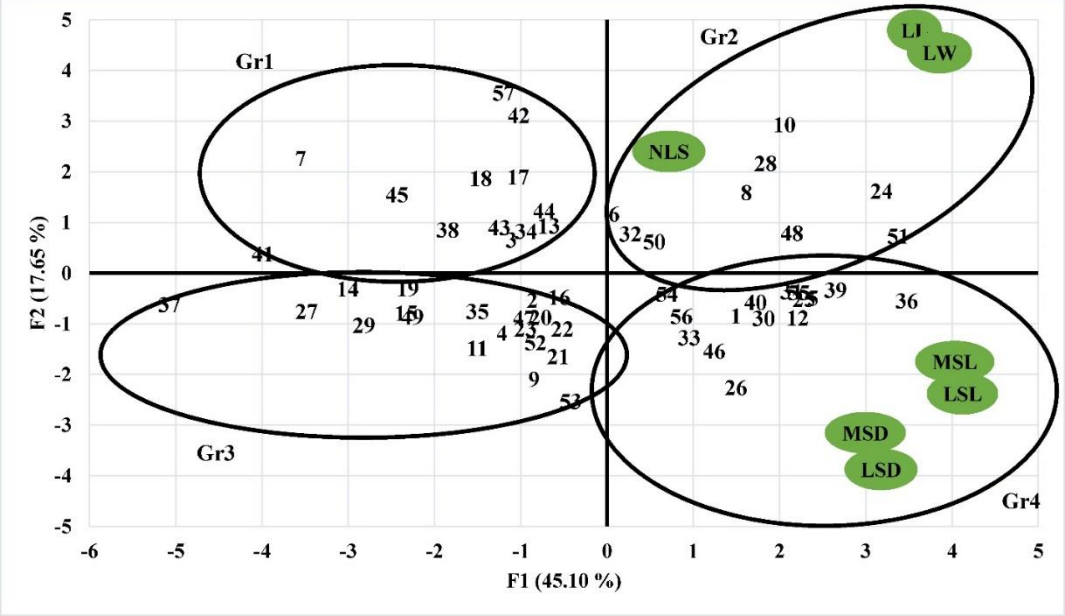

Figure (1): PCA plot displaying the distribution of growth traits and melon genotypes on the two PCA components (F1 and F2). Melon genotypes are represented by numbers (1-57). Growth characteristics are abbrivated by the letters MSL, LSL, MSD, LSD, NLS, LL, and LW. Gr1, Gr2, Gr3 and Gr4 represent the group 1, group 2, group 3, and group 4, respectively.

Variation in fruit morphological and physicochemical characteristics among melon genotypes

Table 4 shows that the difference between 57 melon genotypes was statistically significant ($p \leq 0.01$) for thirteen morphological characters. The largest number of fruits per plant (3.33) was observed in the G28 genotype, while the lowest number of fruits per plant was found in the G4, G9, G29, G36, and G37 genotypes (1). Fruit length (FL) differed significantly among melon genotypes. The G36 genotype had the lowest FL (8.92 cm) of the genotypes evaluated. On the other hand, G25 provided the greatest FL (17.27 cm). In terms of fruit width (FW), G34 had the greatest value of FW (8.38 cm) among the other genotypes, while G55 had the smallest value (15.97). The maximum and minimum fruit length/fruit width ratio (FL/FW) were registered by G9 and G13, respectively. The FWT produced by G34 was the smallest (285.51 g), while G11 achieved the highest FWT (1860.72 g). In respect of juice volume (FJA), G22 and G23 had the lowest FJA (44.78%). The G11 displayed the highest FJA (67.33%). G40 had the highest fruit moisture content (MC, 93.10%). Minimum flesh thickness (FT) was achieved by G37 (1.12 cm). G50 demonstrated the highest FT value (3.24 cm). The genotypes G14 and G29 had the maximum fruit rind thickness (RT) with a value of 0.77 cm, whereas G41 had the lowest value of RT. As demonstrated in Table 4, G50 had the highest placenta weight (PW) (176.06 g), while G29 had the lowest PW (11.28 g). As seen in Table 4, there was a large range of variation in seed number per fruit (NSF). G9 had the highest NSF (936.00). On the other hand, G49 received the lowest NSF (306.33). The length (SEL) and width (SEW) of the seeds ranged from 0.80 to 1.12 and 0.35 to 0.47 cm, respectively. G36 gave the maximum values of SEL and SEW. The pair-wise comparison results revealed significant differences between melon genotypes for all physicochemical variables (Table 5). The total phenol content (TPC) data ranged from 5.94 to 35.57 µg g^{-1}. The highest TPC was reported by G12, while the lowest TPC was displayed by G17. The overall flavonoid content (TFC) of the 57 melon genotypes varied substantially. TFC's mean ranged from 0.99 to 6.20 µg g^{-1}. TFC score was lowest in G53. The maximum TFC was denoted by G29. The antioxidant activity (AC) of G29 was the highest (79.00 µg g^{-1}). Significant genotypes effects for soluble sugar content (SSC) character were reported, as shown in Table 5. The SSC value ranged between 43.75 and 223.41 µg g^{-1}. G37 and G21 had the lowest and highest sugar levels, respectively. As stated in Table 5, G53 (65.11 µg g^{-1}) and G33 (3.63 µg g^{-1}), respectively, performed best in terms of ascorbic acid (ASC) and carotenoid content (CAC) characters. It was found that G45 and G17 genotypes performed poorly in terms of ASC and CAC characteristics. For the pH and total titratable acidity (TTA) characteristics, the

genotypes G22 and G20 surpassed all others. With an average of 10.10 Brix, the G12 had the highest physicochemical characteristic value for total soluble solids (TSS).

Table (4): Means comparison (LSD) of fruit morphological characters derived from melon genotypes

Genotype	NFP	FL (cm)	FW (cm)	FL/FW	FWT (g)	FJA (%)	MC (%)	FT (cm)	RT (cm)	PW (g)	NSF	SEL (cm)	SEW (cm)
G1	2.33	11.22	11.79	0.95	757.13	62.00	88.83	1.65	0.43	84.24	389.67	1.02	0.42
G2	1.33	13.10	14.20	0.92	1276.31	62.89	89.41	2.53	0.28	131.48	647.33	0.90	0.39
G3	1.67	13.49	11.91	1.13	1044.43	66.89	90.53	3.10	0.60	91.55	508.67	0.90	0.38
G4	1.00	9.24	10.16	0.91	474.87	45.33	90.35	1.43	0.28	108.23	472.00	1.09	0.40
G5	1.33	12.43	15.00	0.84	1322.69	56.44	90.78	1.88	0.64	130.29	565.67	1.01	0.43
G6	1.67	9.76	10.49	0.93	611.92	56.11	90.88	1.35	0.29	96.72	498.00	0.84	0.39
G7	1.33	9.22	9.49	0.97	403.46	48.22	91.20	2.30	0.42	58.86	463.33	0.81	0.35
G8	2.00	14.32	11.79	1.22	1056.28	59.11	91.78	2.10	0.41	120.67	648.33	0.94	0.39
G9	1.00	13.47	9.13	1.48	543.26	53.33	91.65	1.70	0.35	110.52	936.00	0.87	0.36
G10	2.00	11.23	13.92	0.81	962.20	56.56	92.15	1.87	0.38	125.44	667.67	0.95	0.43
G11	2.00	14.38	15.64	0.92	1860.72	67.33	90.49	2.42	0.73	171.46	844.67	0.94	0.43
G12	1.67	9.67	11.85	0.82	729.68	49.33	88.60	1.57	0.41	137.77	737.33	0.91	0.39
G13	1.67	11.03	14.49	0.76	1039.50	56.56	91.62	1.87	0.38	132.99	724.00	0.96	0.42
G14	1.67	15.56	12.51	1.24	1121.02	46.78	90.26	2.34	0.77	112.28	538.67	0.98	0.41
G15	2.67	9.13	9.17	1.00	391.36	65.22	91.93	1.62	0.26	64.72	356.67	0.92	0.36
G16	1.67	11.07	11.82	0.94	755.39	56.44	91.96	1.88	0.44	117.63	631.33	0.90	0.39
G17	1.33	9.81	10.40	0.95	586.75	56.22	91.06	1.56	0.36	113.31	629.67	0.83	0.38
G18	1.33	11.21	11.33	0.99	644.33	51.56	90.38	2.04	0.66	95.06	506.67	0.95	0.39
G19	2.00	16.73	12.46	1.34	1273.25	49.89	90.24	2.44	0.63	117.16	584.33	0.89	0.37
G20	2.00	10.80	13.36	0.81	700.32	56.33	90.34	1.63	0.43	78.77	346.00	1.08	0.42
G21	1.67	11.85	13.57	0.87	931.42	53.22	90.91	2.20	0.30	114.20	660.00	0.92	0.40
G22	1.33	10.54	11.47	0.92	648.95	44.78	90.24	1.77	0.28	93.51	523.00	0.90	0.39
G23	1.67	11.64	12.35	0.94	805.13	44.78	90.23	1.88	0.27	120.98	644.00	0.93	0.40
G24	1.67	16.04	13.86	1.16	1451.13	50.56	91.26	2.78	0.36	141.90	762.00	0.97	0.40
G25	1.67	17.27	12.70	1.36	1270.02	63.89	90.83	2.98	0.45	105.75	428.67	1.06	0.45
G26	1.33	11.71	13.26	0.88	877.56	50.44	91.17	1.61	0.51	113.95	708.67	0.91	0.39
G27	1.33	13.46	12.95	1.04	955.22	67.22	91.34	1.48	0.51	121.33	571.00	1.04	0.41
G28	3.33	9.70	10.63	0.92	614.44	60.33	92.38	1.98	0.42	101.10	310.45	1.04	0.43
G29	1.00	12.35	12.08	1.02	828.30	47.00	88.00	2.14	0.77	11.28	609.00	0.92	0.41
G30	1.67	10.94	12.62	0.87	895.94	58.89	89.86	1.63	0.52	146.26	730.33	0.94	0.41
G31	1.33	12.18	12.91	0.95	1002.12	61.44	92.21	1.67	0.55	104.67	698.00	0.96	0.40
G32	1.67	14.13	12.41	1.14	1157.78	53.33	91.16	2.69	0.42	152.94	675.33	0.97	0.42
G33	2.00	11.12	10.71	1.04	684.68	51.44	91.44	1.75	0.44	116.11	571.33	0.99	0.43
G34	1.67	9.32	8.38	1.11	285.51	45.89	89.00	1.46	0.40	55.95	326.00	0.98	0.42
G35	2.00	16.36	14.19	1.15	1699.91	53.89	89.43	2.82	0.53	143.12	704.33	0.99	0.42
G36	1.00	8.92	9.56	0.93	413.51	59.00	92.45	1.50	0.62	60.36	396.00	1.12	0.47
G37	1.00	9.73	10.61	0.92	430.27	48.33	90.77	1.12	0.41	114.62	833.00	0.80	0.35
G38	3.00	10.16	12.83	0.80	836.93	58.00	92.91	2.67	0.33	117.04	373.33	0.98	0.43
G39	2.00	10.02	10.27	0.98	483.43	50.33	89.76	1.71	0.45	74.79	406.67	0.98	0.39
G40	3.00	11.17	12.41	0.90	919.95	58.33	93.10	2.30	0.41	84.12	551.00	0.93	0.39
G41	2.33	11.82	9.71	1.22	572.86	57.56	91.53	2.10	0.14	95.84	700.67	1.04	0.43
G42	1.67	12.42	11.63	1.07	830.37	58.89	91.29	1.56	0.39	71.08	347.00	1.00	0.43
G43	2.00	11.40	9.79	1.16	533.60	55.89	92.98	2.05	0.31	87.77	485.67	1.08	0.43
G44	2.67	11.62	13.69	0.85	1127.80	53.44	90.84	2.72	0.48	130.85	464.67	0.97	0.42
G45	2.00	12.70	11.72	1.08	861.03	55.78	89.81	2.41	0.55	64.73	344.67	0.97	0.41
G46	1.67	15.13	13.50	1.12	1316.99	50.67	88.67	2.61	0.46	115.02	507.67	0.94	0.40
G47	1.33	14.57	12.61	1.16	1202.47	62.22	91.66	2.24	0.51	148.57	620.00	0.98	0.42
G48	1.33	11.46	13.06	0.89	934.47	56.44	91.07	1.86	0.66	130.29	565.67	1.01	0.44
G49	1.67	10.53	10.77	1.03	501.55	50.22	89.16	1.57	0.47	71.45	306.33	1.00	0.40
G50	2.33	13.19	13.92	0.95	1384.10	50.44	91.28	3.24	0.36	176.06	777.00	0.97	0.43
G51	1.67	10.70	10.88	0.98	483.46	52.22	89.12	1.73	0.52	77.77	355.33	0.97	0.39
G52	2.67	10.41	9.05	1.15	439.19	45.67	89.13	1.68	0.43	70.88	326.33	1.00	0.40
G53	1.67	11.40	14.40	0.79	1133.66	65.11	91.29	1.91	0.73	107.62	544.00	0.99	0.42
G54	2.00	11.93	11.54	1.05	766.25	58.22	92.20	1.67	0.48	81.21	444.67	0.92	0.38
G55	1.33	13.11	15.97	0.82	1525.15	59.33	90.58	1.84	0.60	173.69	902.67	0.98	0.43
G56	2.00	15.42	13.80	1.12	1450.58	58.22	91.48	1.87	0.38	124.15	641.67	0.91	0.40
G57	1.67	9.58	8.29	1.16	322.21	53.22	91.49	1.54	0.36	47.57	307.00	0.94	0.40
LSD value	1.15	1.37	1.46	0.14	231.34	4.33	0.95	0.43	0.18	30.79	146.71	0.09	0.03

Table (5): Means comparison (LSD) of fruit physicochemical characters obtained from melon genotypes

Genotype	TPC (µg g^{-1} FW)	TFC (µg g^{-1} FW)	AC (µg g^{-1} FW)	SSC (µg g^{-1} FW)	ASC (µg g^{-1} FW)	CAC (µg g^{-1} FW)	pH	TTA (%)	TSS (Brix)
G1	16.38	2.43	48.36	193.17	19.08	1.69	5.37	1.10	9.33
G2	14.71	2.09	41.99	91.28	10.22	0.93	5.19	0.53	9.17
G3	11.78	2.47	23.39	134.40	23.91	0.67	5.05	0.84	7.73
G4	7.85	1.44	25.55	76.76	22.39	1.19	5.64	0.82	8.50
G5	11.36	1.75	36.04	81.77	18.32	1.47	5.06	0.91	7.23
G6	11.94	2.00	25.72	80.91	23.15	0.46	5.46	0.48	8.17
G7	9.87	1.72	21.24	92.31	20.60	0.98	4.88	0.91	8.00
G8	10.21	3.14	13.00	121.35	26.30	0.54	5.11	0.82	7.13
G9	10.19	2.49	16.12	70.62	16.52	1.57	5.81	0.72	7.20
G10	10.40	2.76	24.64	188.76	11.90	1.75	5.26	0.53	6.97
G11	21.36	5.45	61.40	123.77	22.66	0.67	5.30	0.77	7.63
G12	35.57	3.29	68.21	99.49	32.93	0.99	5.10	1.01	10.10
G13	11.86	1.67	40.49	67.51	26.20	1.05	5.66	0.72	6.70
G14	12.03	2.09	35.73	111.93	18.75	0.67	5.26	0.72	8.53
G15	10.86	2.44	26.48	77.80	12.83	0.76	5.19	0.72	6.93
G16	9.02	2.95	12.86	74.60	22.72	0.51	5.23	0.82	6.53
G17	5.94	1.21	5.71	145.89	25.43	0.40	5.30	0.62	8.77
G18	8.65	1.65	26.94	94.99	10.54	0.70	4.54	0.82	8.47
G19	18.54	2.21	68.13	164.13	26.30	0.96	4.94	0.96	8.83
G20	15.27	3.23	44.41	126.02	49.84	0.71	4.99	1.01	8.67
G21	17.35	1.70	61.80	223.41	30.43	0.59	5.50	0.53	7.67
G22	13.14	1.81	35.97	127.14	18.59	0.70	5.89	0.43	7.93
G23	9.04	1.34	14.72	92.92	20.38	1.56	5.34	0.58	7.43
G24	15.11	3.23	48.64	67.08	12.88	0.53	5.02	0.62	7.80
G25	10.90	1.75	28.61	110.89	32.93	1.28	5.25	0.58	8.43
G26	21.25	2.63	61.38	95.17	15.16	1.40	5.21	0.62	7.30
G27	20.33	2.81	69.29	89.20	41.09	0.47	4.72	0.91	7.47
G28	10.81	2.30	32.68	153.84	31.30	0.72	5.12	0.53	7.07
G29	32.07	6.20	79.00	79.00	19.62	1.27	5.15	0.72	9.80
G30	20.48	2.52	66.59	107.44	29.84	1.12	5.01	0.82	8.77
G31	13.24	3.00	26.36	74.94	24.78	0.59	5.26	0.29	6.50
G32	11.22	4.13	25.04	78.23	19.73	0.40	5.02	0.62	7.20
G33	16.44	3.34	39.90	85.92	40.00	3.63	5.30	0.48	7.00
G34	18.18	2.62	65.33	119.45	38.15	1.71	5.26	0.86	9.77
G35	14.17	3.08	38.43	124.55	44.62	1.36	5.11	0.53	8.97
G36	12.06	5.29	19.69	93.61	43.80	0.76	5.88	0.34	5.80
G37	9.31	2.00	19.85	43.75	24.84	0.92	4.64	0.62	8.30
G38	9.53	4.65	17.58	77.71	12.45	0.67	5.33	0.43	6.43
G39	13.50	2.57	31.04	109.77	52.12	1.19	5.25	0.53	9.10
G40	14.97	3.30	41.39	114.96	12.50	0.72	5.84	0.38	6.23
G41	11.91	3.59	22.61	105.45	54.24	0.46	5.13	0.53	7.27
G42	6.40	3.12	14.79	136.04	34.46	0.57	5.08	0.62	7.67
G43	8.09	2.92	24.28	58.87	14.40	0.68	4.57	0.62	6.07
G44	21.57	5.39	56.52	99.40	24.08	0.73	5.35	0.53	8.30
G45	10.43	2.90	23.08	117.63	9.78	0.64	5.30	0.62	9.50
G46	23.33	4.28	69.52	125.93	12.39	1.27	5.12	0.77	9.33
G47	13.46	2.38	21.58	143.82	49.29	0.40	5.07	0.43	7.57
G48	10.29	2.02	18.76	84.45	48.10	1.04	5.17	0.53	7.43
G49	18.25	4.82	53.94	79.87	55.33	1.21	5.50	0.62	9.97
G50	16.69	3.10	38.74	88.68	18.42	0.54	5.42	0.53	8.07
G51	14.36	3.11	30.54	73.91	18.04	1.36	5.28	0.58	9.53
G52	14.35	2.64	34.97	80.47	10.00	0.96	5.10	0.72	9.33
G53	8.52	0.99	18.35	77.54	65.11	0.62	5.35	0.53	7.53
G54	14.04	1.86	46.26	83.67	63.64	0.72	5.07	0.48	6.37
G55	12.68	1.54	29.09	79.00	13.91	0.75	5.27	0.58	8.17
G56	12.71	1.82	27.66	86.96	36.96	1.46	5.12	0.62	7.10
G57	13.33	2.37	26.38	92.23	10.87	0.61	5.16	0.43	7.53
LSD value	0.14	0.03	0.29	1.98	0.37	0.64	0.24	0.07	0.78

The two main components of PCA, F1 and F2, explained 35.78% of the original variation (Figure 2). In terms of genotypes distribution on the PCA plot, genotypes that were dwelled away from the center of the plot in the positive trends of separate characteristics performed well, whereas genotypes that were subsisted away from the center of the plot in the negative direction of traits performed poorly. Following the PCA result, the first principal component (F1) explained 19.44% of the overall variation; it was positively linked with FT, FW, FL, PW, and FWT; the second

principal component (F2) clarified 16.34% of the total variability, and was positively associated with MC and FJA and negatively correlated with the TPC, AC, TTA, and TSS. The PCA plot divided 57 genotypes into 4 clusters. Cluster-1 had high values of MC, pH, and ASC, while cluster-2 had high values of RT, FT, FW, FL, PW, NSF, and FWT. Genotypes in cluster-3 had the highest value of CAC, whereas, the genotypes in cluster-4 had the maximum values of TPC, TFC, AC, SSC, TTA, TSS, and RT.

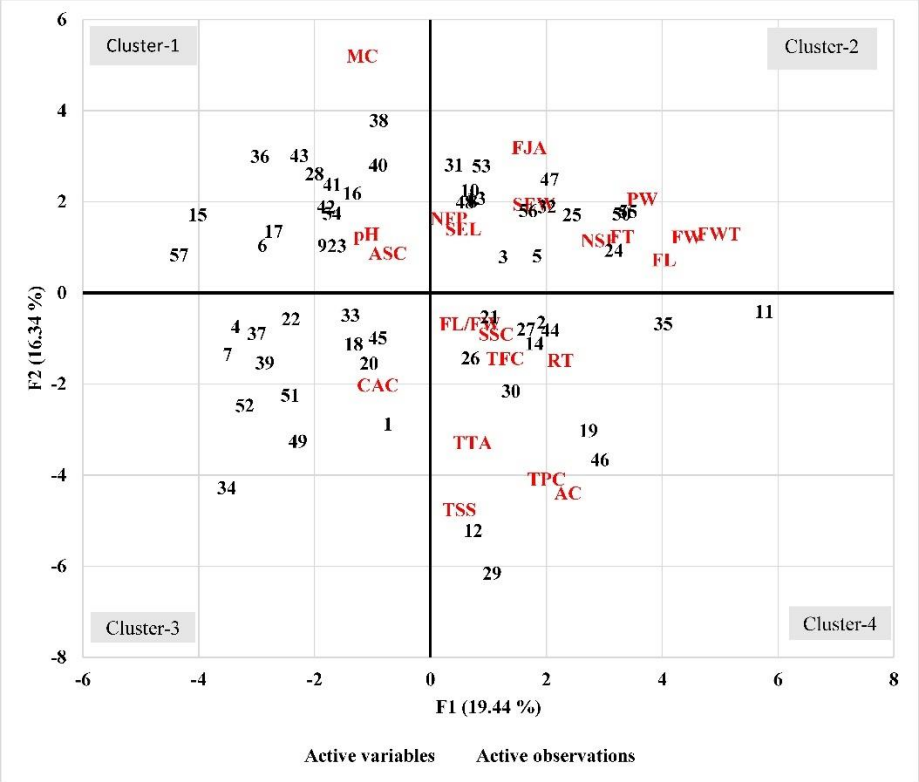

Figure (2): A biplot of principal component analysis (PCA) obtained from fruit morphological and physicochemical data from melon genotypes. Melon genotypes are represented by numbers (1-57). Fruit phenotypic characteristics are denoted by the letters NFP, FJA, MC, SEL, SEW, FL, FT, FW, FWT, PW, NSF, FL/FW, and RT. The letters TPC, AC, TFC, SSC, TTA, TSS, ASC, CAC, and pH represent fruit physicochemical traits.

DISCUSSION

Domestication, plant breeding, and genetic drift have most probably reduced melon phenotypic variation. Consequently, it is vital to preserve the melon germplasm in order to add a new variety to our gene pool and create breeding strategies for more resilient melon plants. The analysis of variance revealed substantial differences between genotypes for all traits, indicating that the Iraqi melon genotypes studied in this study have a high level of growth, fruit phenotypic, and physicochemical diversity. We identified the critical components that contribute the most to the diversity of previously uncharacterized Iraqi melon genotypes based on these features. The growth findings were comparable with those of Akhoundnejad and Sevgin (2019), who detected a distribution of main stem lengths (MSL) ranging from 40.51 to 68.42 cm across melon genotypes. Our main stem diameter (MSD) finding was larger than that of Yusuf et al. (2020), who reported a stem diameter range of 0.84 to 0.92 cm among three melon genotypes, Akhoundnejad and Sevgin (2019), who reported a range of 0.6 to 1 cm MSD, and Saputro et al. (2020), who reported an MSD of 0.8 cm. Our study's leaf length (LL) and leaf width (LW) were lower than those reported by Yusuf et al. (2020), which varied from 12 to 16 cm and 18 to 22 cm, respectively, and Zhang et al. (2012), who observed an average of 13.12 and 15.06 cm for LL and LW, respectively, across nine melon genotypes. The number of lateral stems (NLS) results agreed with those of Saputro et al. (2020), who measured four lateral branches per plant, but were lower than those of Zhang et al. (2012). These differences could be related to genetic differences as well as climate factors.

Furthermore, the fruit morpho-physicochemical characteristics utilized in this study were quite effective at differentiating the melon genotypes and disclosing the underpinning phenotypic variability. Fruit thickness (FT), fruit length (FL), fruit width (FW), placenta weight (PW), fruit weight (FWT), seed length (SEL), seed width (SEW), total phenolic content (TPC), total flavonoid content (TFC), antioxidant activity (AC), pH, and total titratable acidity (TTA) were the significant determinants of genetic diversity in the genotypes investigated. Based on the dispersion of fruit phenotypic traits on the PCA plot, significant relationships were found in a wide range of variables investigated, including a substantial positive correlation between FWT with fruit juice amount (FJA), FL, FW, FT, rind thickness (RT), and number of seeds per fruit (NSF). The mean of fruit per plant (NFP) (1.77) and FWT (0.88 kg) in our study was similar to that described by Dantas et al. (2015). The average FWT in this study was consistent with the FWT reported by Singh et al. (2020) and Zhang et al. (2012). However, the averages of NFP and FT in this study were lower than those published by Singh et al. (2020). In this investigation, the mean value of FWT (0.88 kg) was lower than that found by Maleki et al. (2018) (1.78 kg), Bagheriyan et al. (2015) (1.17 kg) and Jianbin et al. (2013) (1.60 kg). The average flesh thickness of the fruit (FT) (2.00 cm) in this study was lower than that reported by Dantas et al. (2015), Bagheriyan et al. (2015) (2.68 cm) and Jianbin et al. (2013) (2.39 cm). The FL mean (28.97 cm) reported by Zhang et al. (2012) and Bagheriyan et al. (2015) (18.76 cm) were both greater than the FL observed in this study (11.98 cm). In this study, the average FW (12.02 cm) was larger than that obtained by Bagheriyan et al. (2015) (11.26 cm). The FL/FW ratio range (0.76-1.48 cm) obtained in this study was lower than that found by Merheb et al. (2020) (3.13-18.52 cm). The mean values of FL, FW, FT, SEL, and SEW in the studies reported by Guliyev et al. (2018) and Seungbum et al. (2020), were greater than those observed in this investigation. Twenty-three genotypes in this study have more than 100 mg g^{-1} FW of total sugar and can be used to breed sweeter cultivars in the breeding program. The melon genotype G37 had the lowest sugar content (43.75 µg g^{-1} FW), indicating that it could be a useful source for producing less sweeter melon varieties. Furthermore, moisture has a huge impact on the shelf life of fruit, normally high sugar content makes the moisture inaccessible for the growth of microbes. Our findings showed that among 57 genotypes, 26 samples had TSS values greater than 8.00 Brix, with one having a TSS of 10.10 Brix, which can be regarded as sweetness. Moreover, a rise in TSS indicates a reduction in the moisture content of melon genotypes, implying an elevation in the nutritious component of the samples. Likewise, DPPH activity was increased in samples with higher levels of polyphenols, TTA, and TSS, showing that these are important antioxidants in melons. Melon genotypes assessed for TPC in this study had substantially higher values than values reported in previous studies by Manchali et al. (2021) and Pandey et al. (2021) that studied several Indian types of melon. The TFC and CAC values in the present study were lower than those reported by Benmeziane et al. (2018) for melon jam. Manchali et al. (2021) revealed that the SSC of melon genotypes ranged from 20 to 61%, which was lower than the current analysis. The TSS and ASC in Indian melon were observed by Pandey et al. (2021), which were lower than the findings obtained in this study. In this investigation, the TSS and TTA values were higher than those obtained by Manchali et al. (2021). Our findings demonstrated a negative association between melon moisture content (MC) and TPC, AC, ASC, TTA, and TSS, which might be used in breeding to develop a novel melon variety with high amounts of bioactive chemicals and functional qualities. Because of high values in PWT, FW, FL, TPC, TFC, and AC, the genotype G11 was rated the highest performing genotype based on fruit morpho-physicochemical features. The PCA data may assist parents in developing an effective segregating population for discovering specific quantitative trait locus. These discrepancies in fruit phenotypic and phytochemical traits between our study and previous research are attributable to differences in the genetic makeup of genotypes, and methods of cultivation of genotypes, including rainfed or rainfed melons.

CONCLUSIONS

In essence, combining field results based on growth and fruit morpho-physicochemical features may be more useful in defining genetic variation among melon genotypes. The melon genotypes used revealed a wide range of variability in fruit morpho-physicochemical markers that

might be used for genetic investigations and breeding plans. According to the findings of the current study, fruit melon genotypes offer strong nutritional qualities that may enhance human health, allowing us to address chronic diseases through diet and nutrition. The genotype G11 was rated the highest performing genotype based on fruit morpho- physicochemical features. The melon genotype G37 had the lowest sugar content, indicating that it could be a useful source for producing less sweeter melon varieties. These findings imply that these genotypes can also be used to improve commercial melons by breeding for desirable attributes like appearance, organoleptic properties, and health advantages. Given the scarcity of detailed reports on secondary metabolites in this crop, identifying additional secondary metabolites in these samples may provide a fuller view of their potential advantages. Within the expanding consideration of agrobiodiversity and its important relevance in feeding communities, attention should be paid to the protection and sustainable usage of melon genetic resources.

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تقييم تنوع النمو والنوعية لثمرة البطيخ المحلي

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الخلاصة

تم تقييم التنوع الوراثي للأنماط الجينية للبطيخ التي تم الحصول عليها من إقليم كردستان العراق في عام 2021 في مديرية الحدائق في قلياسان التابعة لجامعة السليمانية باستخدام تصميم القطاعات العشوائية الكاملة بثلاث قطاعات، باستخدام الصفات النمو والنوعية. تم توصيف 57 طرزا وراثيا مظهريا وفسيوكيميائيا، ووجدت فروق معنوية كبيرة فيما بينهم. حيث تراوحت قيم طول الساق الرئيسي، طول الساق الجانبي، قطر الساق الرئيسي، وقطر الساق الجانبي من 20.49 إلى 85.84 سم و 29.45 إلى 92.52 سم و 0.85 إلى 1.77 سم و 0.42 إلى 0.74 سم على التوالي. ارتفعت نشاط مضادات الأكسدة في الانماط الوراثية ذات الكميات العالية من البوليفينول والحموضة القابلة للمعايرة والمواد الصلبة الذائبة الكلية. حقق وزن الثمرة المنتج بواسطة G11 أعلى قيمة (1860.72 غم). اظهر تحليل المكون الرئيسي (PCA) عن أربع مجموعات متميزة من الأنماط الجينية بناءً على الصفات المدروسة. أظهر مخطط PCA أن سمك الثمرة، طول الثمرة، عرض الثمرة، وزن المشيمة، وزن الثمرة، طول البذور، عرض البذور، إجمالي محتوى الفينول، إجمالي محتوى الفلافونويد، النشاط المضاد للأكسدة، الاس الهيدروجيني، وحمض المعايرة كانت صفات مهمة للتنوع الجيني في البطيخ. بناءً على غالبية الصفات المظهري والنوعية للثمرة، تم اعتبار النمط الجيني G11 هو الأفضل أداءً. تشير نتائج هذه الدراسة إلى وجود درجة كبيرة من التباين في الأصول الوراثية للبطيخ العراقي، والتي يجب الحفاظ عليها ودمجها في مشاريع التنمية المستقبلية.

الكلمات المفتاحية:
البطيخ ، صفات النمو ، صفات المظهرية والنوعية للثمرة ، اختلاف الوراثى ، تجميع الانماط الوراثية