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Research Article

Characteristics and variability of melon genotypes under shade conditions in greenhouse

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ABSTRACT

The utilization of controlled greenhouses can be an alternative for melon (Cucumis melo L.) cultivation. Growing melon in greenhouses lowers the risk of pests and infections by diverse pathogens. Low solar irradiation during the rainy season and pollution in the greenhouse roof, may cause shade stress conditions for the plants inside. This study aimed to elucidate the plant and fruit characteristics of nine genotypes of melon grown under shade conditions in a greenhouse and the variability among them. The experiment was conducted in a greenhouse of Cikabayan Experimental Station, IPB University, Bogor, from November 2016 to January 2017. The genetic materials evaluated were nine melon genotypes from the Center for Tropical Fruit Studies at IPB University. A randomized complete block design with three replicates was followed. Shade intensity in the greenhouse was approximately 25%. The results showed that the genotype effect was significant for internode length, petiole length, plant height fruit, flesh thickness, fruit rind thickness, fruit weight, and total soluble solids. Genotype means for fruit weight were small in this experiment (< 300 g), whereas the total soluble solids were moderate to high (8.7-14.3 °Brix). Fruit diameter had a positive and significant correlation with leaf length, leaf width, and fruit length, whereas fruit weight had a positive and significant correlation with fruit diameter and fruit length.

Keywords: correlation, honeydew, melon breeding, melon group, traits

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INTRODUCTION

Melon (*Cucumis melo* L.) belongs to the *Cucurbitaceae* family and has high genetic diversity. It can be grouped into six groups, namely, *cantalupensis*, *inodorus*, *flexsuosus*, *conomon*, *dudaim*, and *momordica* (Robinson & Decker-Walters, 1999). Pitrat (2016), melons are classified into 19 groups based on sex expression, fruit shape, fruit size, skin color, flesh color, presence of gelatinous sheath around the seeds, and seed size. Cui et al. (2022) mentioned that *cantalupensis*, *inodorus*, and *ibericus* groups are economically important and largely consumed. Melons also have high levels of nutrients. USDA (2022) revealed that 100 g cantaloupe contains several minerals, including 157 mg potassium, 9 mg calcium, 0.38 mg Fe, 13 mg magnesium, 17 mg phosphorus, 30 mg sodium, and 0.44 mg zinc. The vitamin content in melons includes 10.9 mg of vitamin C, 232 µg vitamin A, 0.694 mg of niacin, 0.04 mg of vitamin B-6, 0.05 mg of vitamin E, and 2.7 µg vitamin K. The inodorus type has a lower content of vitamins C and A, which are 18 mg and 50 IU, respectively.

Melon has an economic importance in Indonesia. BPS (2022) revealed that from 2018 to 2021 melon production shows an increasing trend. In 2018 melon production reached 118,708 tons, in 2019 it was 122,105 tons, in 2020 it was 138,177 tons, and in 2021 it was 129,147 tons. The melon harvest area in 2021 is 7,336 ha. Melon cultivation in a greenhouse can optimally control some environmental factors compared to the open field, such as water requirements, temperature, humidity, light, nutrients, and soil pH. Mukarami et al. (2017) revealed that the use of a plastic net as shade is an effective approach for reducing greenhouse temperature in the mid-summer season.

In Indonesia, most of the melon cultivation is in the open field and only a small proportion is in greenhouses. One of the reasons is related to the high cost of making greenhouses. However, growing melon in greenhouses lowers the risk of pests and infections from various pathogens. Melons cultivated in greenhouses and the open field may show different characteristics, so experiments conducted in greenhouses are necessary. Furthermore, low solar irradiation during the rainy season and pollution in the greenhouse roof may cause shade stress conditions for the plants inside.

Information about diversity genetics based on morphology becomes a basis for breeding. Selection of superior genotypes requires a considerably large genetic variation and minimum environmental variation. One approach to better control microenvironmental effects is melon cultivation in greenhouses. The experiment carried out in a greenhouse provides information on fruit morphology characteristics, which may differ from those carried out in open fields. This study aimed to elucidate the plant and fruit characteristics of nine genotypes of melon grown under shade conditions in a greenhouse.

MATERIALS AND METHODS

Genetic material

The genetic materials evaluated were nine melon genotypes sourced from the Center for Tropical Fruit Studies at IPB University, namely G1, G30, G41, G59-A, G59-B, OMH-1, P27, P34×P27, and SMH. The trial was conducted from November 2016 to January 2017 in a greenhouse at the Cikabayan Experimental Station of IPB University, Bogor.

Experimental design and agronomic management practices

The trial was arranged in a single-factor randomized complete block design (RCBD) with three replicates. One experimental unit consisted of 15 plants. The trial was started with seed germination treatment. Seeds are soaked in warm water for 5 hours, then put in dampened papers for about 36 hours before sowing. The medium used is soil and manure with a ratio of 1:1. Seeding was carried out for eight days, then transplanting was carried out in polybags, one seedling per polybag. The size of the polybag used was 40 cm × 40 cm, while the planting medium used was soil, manure, and rice hulls with a ratio of 1:1:1. NPK fertilization is done every three days with a dose of 15 g L^{-1} as much as 200 ml per polybag. Fertilization using AB mix was also carried out once every three days at a dose of 5 ml L^{-1} as much as 200 ml per polybag. AB mix fertilizer provides macronutrients (N, P, K, Ca, Mg, and S) and micronutrients (Fe, Mn, Bo, Zn, Cu, and Mo). Pests and diseases are treated using fungicides, insecticides, and bactericides. Branch pruning was performed for branches 1 to 7, and branches 8 to 12 are left to produce fruit. Pollination of melon plants in the greenhouse was done manually. One fruit having a perfect shape was selected among the formed fruits in each plant, and the others were pruned. KNO_3 fertilizer was applied at a dose of 5 g L^{-1} as much as 200 ml per polybag starting 45 days after planting (DAP). Fertilization and pesticide application stopped just before harvest (50 DAP). All genotypes are inodorus types (without nets on the fruit rind), and fruit ready for harvest showed dark yellow or cream fruit rind color.

Observation and data analysis

The qualitative traits observed were stem color, leaf surface, leaf color, fruit shape, fruit rind color, and flesh color. The quantitative traits measured were internode length,

petiole length, leaf length, leaf width, plant height, fruit length, fruit diameter, fruit flesh thickness, fruit rind thickness, fruit weight, and total soluble solids. Morphological traits were observed based on Descriptor for Melon (IPGRI, 2003) with modifications.

Data analysis included analysis of variance followed by a post hoc test using the Tukey-Kramer method at a significance level of 0.05 using SAS. A fuzzy clustering analysis was conducted to understand the groping pattern of the genotypes, using PBSTAT-CL (www.pbstat.com).

RESULTS AND DISCUSSION

The greenhouse for this experiment is oriented in a North-South direction. This orientation should be suitable for melon cultivation based on a study by Pratama & Juniwati (2018). This condition will maximize the lighting sun from East to West of the building throughout the day so that the optimal length of irradiation obtained is supposed around 10 hours per day. However, the experiment was conducted during the rainy season, in which the duration of irradiation was far lower than that, as shown in Table 1 (BMKG, 2023).

Table 1. Approximate rainfall, irradiation condition, temperature average, and relative humidity average during the experiment.

Climate variables	November 2016	December 2016	January 2017
Rainfall (mm)	323.70	116.60	157.40
Avg. daily irradiance (hours)	4.08	3.81	3.67
Avg. temperature (°C)	26.01	26.09	25.81
Avg. relative humidity (%)	87.00	82.38	83.84

Hamidi (2014) the duration of irradiation is one of the climate factors and is defined as the strength of sunlight that exceeds 120 W m^{-2} that shines on earth in a period of one day (hours per day). The results of measuring the duration of irradiation can be related to many other elements of weather and climate, including air pollution and atmospheric turbidity. Based on Table 1, the irradiation duration during the planting season was relatively low, and relative humidity was relatively high which could influence plant growth and development.

In this experiment, the stem color of the genotypes was light green, green, and dark green. G30 and P34×P27 had a dull type (non-shiny) leaf surface and dark green leaf color, whereas other genotypes had intermediate leaf surface and green leaf color. The fruit shape of most genotypes was elliptical, while P34×P27 was flattened (Table 2).

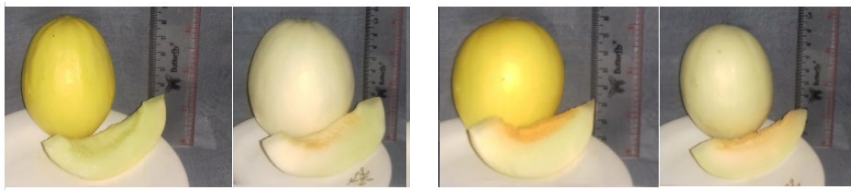
Table 2. Stem color, leaf surface, leaf color, leaf shape, rind color, and flesh color of nine melon genotypes.

Genotype	Stem color	Leaf surface	Leaf color	Fruit shape	Fruit rind color	Flesh color
G1	Green	Intermediate	Green	Globular	White; white with dark green spot	White
G30	Dark green	Dull	Dark green	Globular	Yellow-orange	Orange
G41	Dark green	Intermediate	Green	Globular	White; white with dark green spot	White
G59-A	Dark green	Intermediate	Green	Elliptical	Yellow	Orange
G59-B	Green	Intermediate	Green	Elliptical	Yellow; white	Orange
OMH-1	Light green	Intermediate	Green	Elliptical	Yellow; white	Light green; white
P27	Green	Intermediate	Green	Elliptical	Yellow	Orange
P34×P27	Dark green	Dull	Dark green	Flattened	Yellow	Orange
SMH	Green	Intermediate	Green	Elliptical	Yellow	Orange

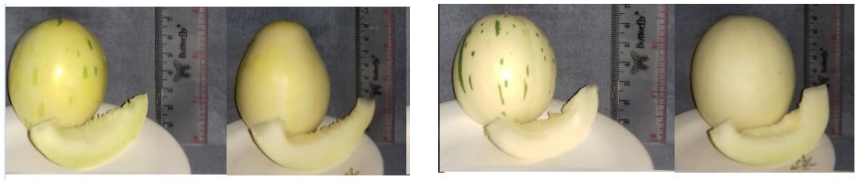
Five genotypes (G30, G59-A, P27, P34×P27, and SMH) showed uniformity of fruit rind color within the genotypes (Figure 1), while the other four genotypes (OMH-1, G59-B, G1, and G41) showed variation within genotypes. The OMH-1 genotype had a non-uniform flesh color, light green and white. G59-B showed yellow and white fruit rind color, and G1 and G41 showed white and white with dark green spot rind color (Figure 2). The flesh colors of the genotype are white, orange, and light green. Melons with these flesh colors are commonly found in the markets in Indonesia. However, when served as fruit slices, orange and green flesh colors may be more attractive than white.

The experiment by Saputra et al. (2022) using 15 melon genotypes from different variety groups showed that plant sex type and secondary skin color outside the groove were not varied among all tested genotypes. An experiment by Sudhakara and Manchali, (2016) using 30 local melons of Karnataka (India) showed that 23 genotypes had monoecious sex expression and seven genotypes had andromonoecious sex expression. Cui et al. (2022) mentioned that powdery mildew and downy mildew are common diseases in melon production. Another experiment by Rozikin & Daryono (2023) showed that powdery mildew infection causes breaks in the net, immature and rotten flesh, and a decrease in sweetness and aroma. Verzera et al. (2014) revealed that the grafting method in melon is an approach to increase disease resistance, and one of the appropriate rootstocks is pumpkin (C. *maxima* Duch. and C. *moschata* Duch.).

Figure 1. Melon genotypes with uniformity in fruit appearance



OMH-1 G59-B



G1 G41

Figure 2. Within-genotype variation in fruit appearance

The variability between genotypes was found in the traits of internode length, petiole length, and plant height, but not in the traits of leaf length and leaf width (Table 3). The coefficient of variation for internode length, petiole length, and plant height are 13.88%, 10.45%, and 12.75%, and for leaf length and width are 8.48% and 9.98%. The coefficient of variation indicates the level of accuracy in the experiment. If the coefficient of variation is high then the accuracy of the experiment is low, and vice versa.

The OMH-1 had the longest internode length (6.87 cm) and was significantly different from the G59-B (3.53 cm). The longest petiole length was shown by the G59-B (9.96 cm) and was significantly different from the G41 (7.15 cm). Based on this

experiment, the G59-B has the lowest internode length but the highest petiole length. P34 ×P27 had the highest plant height (227.00 cm), significantly different from genotype G59-B (104.47 cm).

Table 3. Means of internode length, petiole length, leaf length, leaf width, and plant height.

Genotype	Internode length (cm)	Petiole length (cm)	Leaf length (cm)	Leaf width (cm)	Plant height (cm)
G1	6.49abc	7.77abc	9.39a	9.80a	153.47bcd
G30	6.70ab	9.78ab	10.16a	12.29a	179.87ab
G41	5.67a-e	7.15c	9.30a	10.81a	137.33bcd
G59-A	5.50a-e	8.21abc	10.34a	13.09a	114.20cd
G59-B	3.53e	9.96a	9.55a	12.93a	104.47d
OMH-1	6.87a	8.33abc	10.71a	12.66a	144.13bcd
P27	4.97a-e	8.58abc	9.67a	11.24a	125.60bcd
P34×P27	6.21a-d	8.62abc	10.02a	12.55a	227.00a
SMH	5.78a-e	9.71abc	10.27a	12.75a	168.27bc
p-value	0.003	0.018	0.487	0.044	<.0001
CV (%)	13.88	10.45	8.48	9.98	12.75

Note: Numbers followed by the same letter in the same column are not significantly different based on the Tukey-Kramer test at the 5% level; CV: coefficient of variation.

Table 4. Means of fruit length, fruit diameter, flesh thickness, skin thickness, fruit weight, and total soluble solids.

Genotype	Fruit length (cm)	Fruit diameter (cm)	Flesh thickness (cm)	Skin thickness (cm)	Fruit weight (g)	Total soluble solids (°Brix)
G1	6.50a	5.31a	0.79b	0.56abc	111.8c	12.4ab
G30	6.08a	6.06a	1.11ab	0.49abc	125.9c	12.1ab
G41	6.21a	5.86a	0.90b	0.58bc	115.9c	11.2ab
G59-A	8.33a	6.83a	1.03ab	0.79a	–	10.7ab
G59-B	6.94a	5.63a	1.25a	0.70ab	126.9c	10.7ab
OMH-1	7.41a	6.17a	1.08ab	0.51abc	152.7bc	8.7b
P27	7.25a	6.05a	0.96ab	0.39c	131.5bc	10.0ab
P34×P27	8.75a	6.26a	1.14ab	0.59abc	226.8ab	11.1ab
SMH	7.66a	6.69a	0.96ab	0.54abc	267.8a	14.3a
p-value	0.077	0.093	0.008	0.012	0.007	0.031
CV (%)	9.14	6.62	8.36	11.06	11.38	9.93

Note: Numbers followed by the same letter in the same column are not significantly different based on the Tukey-Kramer test at the 5% level; CV: coefficient of variation.

One of the obstacles encountered in growing melons in greenhouses is the absence of insects (bees) that assist the pollination process, so manual pollination is necessary. In the field, natural pollination of melon plants was assisted by bees. The experiment by Tschoekea et al. (2015) revealed a moderate correlation between the intensity of bee visitation and the fruit weight of C. *melo*.

The effect of genotype was not significant on fruit length and diameter, but significant on fruit skin thickness and total soluble solids, and highly significant on flesh thickness and fruit weight (Table 4). The highest average flesh thickness was found in the G59-B (1.25 cm) and was significantly different from the G41 (0.90 cm). Genotype G59-A had the highest average rind thickness (0.79 cm) and was significantly different from genotype P27 (0.39 cm). The SMH had the highest fruit weight (267.8 g) but was not significantly different from the P34 ×P27 (226.8 g). G1, G30, G41, G59-B, OMH-1, and P27 had similar fruit weights, ranging from 111.8 to 131.5 g. The low fruit weight of the genotypes (< 300 g) is thought to be caused by the relatively low duration irradiation and shade conditions in this experiment. An experiment by Ong & Khandaker (2021) revealed that melon fruit weight in dry season cultivation was significantly greater than in wet-season cultivation. The low solar radiation in the wet season may reduce the rate of photosynthesis and cause low fruit weight. The reduced transpiration in the wet season may be caused by high

relative humidity. Table 1 shows that the relative humidity average during the experiment was at a high rate (>80%).

The highest total soluble solids was shown by the SMH (14.3 °Brix), significantly different from OMH-1 (8.7 °Brix) but not significantly different from the other genotypes (Table 4). An experiment conducted by Andrade et al. (2021) evaluating 46 melon accessions resulted in a high estimate of heritability (0.92) of total soluble solids. The total soluble solids ranged from 3.39% to 7.45% for traditional accessions and 9.26%–11.12% for the commercial cultivar. An experiment by Anggara et al. (2020) showed that total soluble solids had broad-sense heritability greater than 50%. The experiment by Huda et al. (2018b) on open-field melon cultivation showed that the interaction of genotype and potassium nitrate (KNO_3) treatment had a significant effect on total soluble solids. Besides total soluble solids, texture trait is also one of consumer preferences. An experiment by Farcuh et al. (2020) showed that juiciness and firmness-related sensory and instrumental parameters were associated with shelf-life capacities.

Table 5. Correlation coefficients between melon traits.

Trait	Leaf length	Leaf width	Fruit length	Fruit diameter	Fruit thickness
Leaf width	0.72*				
Fruit length	0.50	0.56			
Fruit diameter	0.73*	0.69*	0.66*		
Flesh thickness	0.36	0.80	0.29	0.18	
Fruit weight	0.52	0.54	0.77*	0.82**	0.15

Note: ** significant at p<0.01; * significant at p<0.05

The correlation coefficient between melon traits is shown in Table 5. The leaf length had significant positive correlations with leaf width (r=0.72, p<0.05) and fruit diameter (r= 0.73, p<0.05). Leaf width was significantly correlated with leaf diameter (r=0.69, p<0.05). It indicates that the genotypes with large leaves tend to have a large fruit diameter. Fruit length had a significant positive correlation with fruit diameter (r=0.66, p<0.05). The correlation of fruit weight was stronger with fruit diameter (r=0.82, p<0.01) than with fruit length (r=0.77, p<0.05).

The correlation and path analysis showed that plant traits (stem diameter, stem length, and leaf chlorophyll) were considered in melon breeding programs for fruit weight improvement (Khomphet et al. 2022). A study by Huda et al. (2018a) showed that fruit weight also significantly correlated with fruit length (r = 0.53), fruit diameter (r = 0.85), rind thickness (r = 0.33), and flesh thickness (r = 0.63). Another experiment by Iskandar et al. (2019) using 10 honeydew genotypes showed that fruit weight had a significant correlation with fruit length (r=0.744, p<0.01). A study by Weng et al. (2021) on high temperature and humidity (HTH) stress at the seedling stage, through correlation analysis, determined that melon leaf length, leaf width, plant height, and stem diameter can be used as the identification indexes of early tolerance to high temperature and humidity.

A cluster analysis performed on nine melon genotypes based on 11 quantitative and 6 qualitative traits indicated apparent variability among the genotypes (Figure 3). The nine genotypes could be clustered into three groups. The first group comprising genotypes G41 and G1 showed similarity in fruit phenotype. Both of them showed similar fruit rind color (white or white with green spots) and flesh color (white). The second group consists of genotypes P34×P27 and G30. The phenotypes of plants and fruit at P34×P27 and G30 showed similarity in some plant traits observed (stem color, leaf surface, leaf color, and flesh color), though their fruit shapes were different. The third group consists of SMH, G59-A, OMH-1, P27, and G59-B. The similarities between them are in fruit shape (elliptical shape) and orange flesh color. A cluster analysis could be used to visualize genetic distance among genotypes as a consideration for crossing between them in a breeding program.

The cluster analysis showed that the diversity of *Cucumis melo* var. *flexuosus* in Palestine based on morphology clustering in three main groups, in line with the method

of seed saving by local farmers who maintain crop cultivars according to their local environment (Ali-Shtayeh et al., 2015). A study by Wang et al. (2018) with the SSR genotype data from 163 melon accessions showed two main groups, mainly represented by Indian and Chinese subsp. *agrestis* accessions, respectively. Indian and Chinese subsp. *agrestis* accessions have a distant relationship with each other and probably undergo different domestication pathways in their domestication history. The experiment by Maleki et al. (2018) using 27 Iran melon landraces resulted in the *ameri* group being close to the *inodorus* group and *reticulatus* being close to the *cantalupensis* group. Another experiment by Ning et al. (2014) using 43 Xinjiang Hami melon accessions was analyzed using 36 SSR markers elucidated that the accessions clustered into two major groups (thick and thin-skinned melons).

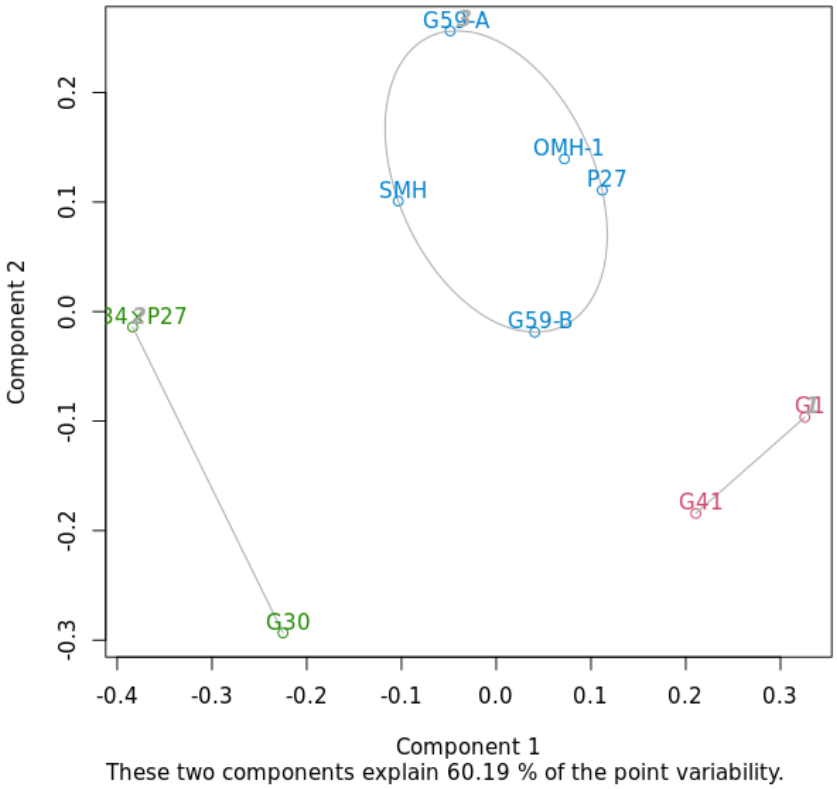


Figure 3. Fuzzy clustering of nine melon genotypes based on 11 quantitative and 6 qualitative traits.

Table 6. Membership coefficient of each genotype in each cluster.

Genotype	Cluster 1	Cluster 2	Cluster 3	Inferred number of clusters
G1	0.64	0.15	0.21	1
G30	0.20	0.58	0.22	2
G41	0.63	0.17	0.20	1
G59-A	0.22	0.25	0.54	3
G59-B	0.30	0.29	0.41	3
OMH-1	0.29	0.25	0.47	3
P27	0.31	0.20	0.49	3
P34×P27	0.17	0.60	0.23	2
SMH	0.24	0.33	0.44	3

Table 6 shows the membership coefficient of each genotype in each of the three clusters. The cluster with the highest coefficient may be fit for a particular genotype. As an example, G1 fit better in Cluster 1 (0.64), compared with Cluster 2 (0.15) and Cluster 3 (0.21).

Andrade et al. (2019) revealed that the total soluble solids were the most contributing trait for multivariate clustering formation and influenced the differentiation of Brazilian melon genotypes. The experiment by Huda et al. (2017) showed that the grouping of 17 melon genotypes based on morpho-agronomic traits (9 quantitative and 15 qualitative) separated the *reticulatus* and inodorus groups at a dissimilarity coefficient of around 0.52.

CONCLUSIONS

The melon genotypes evaluated showed variability based on several morphological and agronomic traits. The vegetative traits that varied among genotypes were internode length, petiole length, and plant height. The fruit traits that showed variability were flesh thickness, skin thickness, fruit weight, and total soluble solids. In this experiment, the genotypes had a low fruit weight (less than 300 g), but moderate to high total soluble solids (8.7–14.3 °Brix). Fruit diameter had a significant and positive correlation with leaf length, leaf width, and fruit length, while fruit weight had a significant and positive correlation with fruit diameter and fruit length. The genotypes could be grouped into three clusters, and the genotypes in the same clusters generally shared similar fruit and plant traits.

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