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Research Article

Morpho-Physiological and Phytochemical Profiling of Exotic Watermelon (*Citrullus lanatus*) Genotypes in Bangladesh

Md. Shohel Tanvir,[1] Khadijatul Kobra,[1] Pijush Kanti Jhan,[1] Md. Mostafijur Rahman,[2] Najmul Hossain,[1] Md. Mostofa Kamal,[3] Shimul Das,[3] and Mehede Hassan Rubel[1]

[1]*Department of Agriculture, Noakhali Science and Technology University, Noakhali 3814, Bangladesh*
[2]*Hybrid Rice Division, Bangladesh Rice Research Institute (BRRI), Joydebpur, Gazipur 1701, Bangladesh*
[3]*Agrotechnology Discipline, Khulna University, Sher-E-Bangla Road, Khulna 9208, Bangladesh*

Correspondence should be addressed to Mehede Hassan Rubel; mehede@nstu.edu.bd

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Watermelon exhibits a diverse range of morphological, physiological, and phytochemical variations all around the world, which can be strategically utilized in breeding programs for better and improved cultivars. In this study, 12 exotic watermelon germplasms (advanced F7 generation inbred lines) and one local cultivar were filed screened in a randomized complete block design (RCBD) layout with three replications to investigate and identify the most suitable genotypes based on morphological, yield-related, and phytochemical traits. Results revealed that variation was observed in fruit skin color and flesh color among the genotypes evaluated for qualitative traits using the International Union for the Protection of New Varieties of Plants (UPOV). Significant variations were also found among the genotypes in terms of the quantitative traits. Positive correlation was observed among total yield (TY), days of first flowering, time of ripening (TR), and fruit flesh width (FW) in Pearson's correlation coefficient (PCE) analysis. Principal component analysis (PCA) determined PC1 accounted for 22.7% of the total variation among genotypes with positive loadings associated with traits (viz., FW, fruit length [FL], fruit firmness [FF], pericarp thickness [PeT], fruit weight [FrW], TY, soluble solids content [SSC], vitamin C [Vit. C], and lycopene [Lyco.]), while PC2 explaining 16.4% of the total variation observed. Heat map hierarchical clustering analysis, using Euclidean distance as a metric and ward's squared cluster agglomeration method, grouped the genotypes into three distinct clusters based on their heterogeneity. Moreover, genetic variability demonstrated a higher percentage of genotypic coefficient of variation (GCV%), phenotypic coefficient of variation (PCV%), heritability (h^2_b%), and genetic advance (GA) of mean (%) for almost all the characters, which indicates more reliability for selection. However, the present study suggested that the genotypes of G3, G7, G8, G9, and G11 as superior in terms of higher yield and biochemical elements such as SSC, Lyco., total phenolic content (TPC), and total flavonoid content (TFC). Thus, these genotypes could be valuable materials for future watermelon breeding programs.

Keywords: cluster analysis; exotic watermelon genotypes; principal component analysis; qualitative traits; quantitative traits

1. Introduction

Watermelon (*Citrullus lanatus* L.) ([Thunb.] Matsum & Nakai) [1] is a native crop to Africa [2]. It is a globally important monoecious, vine, and juicy cucurbitaceous crop grown widely in China, Japan, Thailand, Vietnam, Brazil, India, Algeria, Turkey, Iran, Russia, Uzbekistan, Mexico, the United States, and other Middle East countries [3]. The worldwide production of watermelon has researched up to 100 million tons [4].

Bangladesh is located in the subtropical region between the Himalayan Mountains and the Bay of Bengal, with its unique agroclimatic conditions, rich river networks, and fertile plains making it ideal for cultivating various fruits, including the delicious watermelon. It is widely cultivated in different districts of Bangladesh, including Patuakhali, Bhola, Borguna, Noakhali,

Pirojpur, Khulna, Bagerhat, Jashore, Sunamganj, Pabna, Natore, Panchagarh, Gopalganj, Jhenaidah, and Feni [5]. Interestingly, it is now grown nearly year-round in Bangladesh, with both seasonal and off-season varieties available in the market. Therefore, consumers enjoy the taste of watermelon throughout the year. In Bangladesh, watermelons are cultivated on an average of 23,778 ha of land, with an average production of 23.38 metric ton/ha [6]. However, the price of watermelon remains very high during both season and off-season, the reason behind this is that the production in Bangladesh of watermelon is not up-to the mark, and it may increase up-to 30 ton/ha [7]. So, improving high-yielding watermelon varieties is a dire need to address this issue.

Alongside, watermelon contains about 91%–95% of water [8], which makes it more pleasant to the people during the summer season. Sweetness, one of the major qualities of watermelon, is connected to the soluble solids content (SSC) present in it, and its juice is acidic in nature (pH 5.18–6.7); as a perfect balance of SSC and acidity gives it the pleasant flavor [9]. Though the flesh of watermelons varies in colors because of the presence of naturally occurring carotenoids and polyphenols [10], which draws the attention of consumers, but we mostly witness red flesh colored watermelons. It is an excellent natural source of lycopene (Lyco.), flavonoids, and anthocyanins, which act as powerful antioxidants and have been shown to prevent various cancers and help against heart disease [11]. Those compounds not only provide fascinating colors to watermelons, but also significantly reduce the risk of various cardiovascular diseases (CVDs) [12]. Additionally, it contains polyphenols, which have the capacity of scavenging free radicals [13]. In Bangladesh, the watermelon consumption rate is tremendous, but growers rely mostly on commercial varieties for cultivation, and the cultivation of exotic genotypes of watermelon is limited in this location to make them adaptive in the local environment. Some watermelon cultivars with great yield potential sometimes produce very low-quality fruits under unfavorable edaphic and climatic conditions. Therefore, to identify the optimal varieties (which collectively exhibit high yield and beneficial phytochemical components) suitable for a specific agro-ecological zone, it is crucial to carry out performance trials with the standard varieties found in that region, alongside some additional varieties to evaluate for more desirable traits so as to introduce them as the more promising germplasm [14]. The morphological characters are importantly related to the yield of watermelon as they directly or indirectly affect the overall production. The agronomic and phytochemical elements of germplasm/genotypes may vary with the climate or location, or the cultivating process. Additionally, the high price of exotic variety seed demotivates farmers to cultivate the exotic varieties. By utilizing the diversity of plant genetic resources, plant breeders can produce new, enhanced cultivars with desired qualitative and quantitative features. A superior cultivar that directly affects the producer's commercial value can be obtained by selecting promising cultivars based on their high adaptability, profitability, and nutrition. These cultivars also have the potential to replace older ones. So, this study aimed at evaluating some exotic genotypes based on their morpho-physiology and phytochemical characters, as well as their yield attributing traits to satisfy both seasonal and off-seasonal demand.

2. Materials and Methods

2.1. Experimental Site and Climate. The field experiment was carried out at the Field Research Laboratory, Department of Agriculture (coordinates of the location are 22° 47′ 31″ North latitude; 91° 6′ 3″ East longitude) [15] Noakhali Science and Technology University, Sonapur, Noakhali-3814, Bangladesh (from November 2021 to March 2022). The agro-ecological zone of the research area was the Young Meghna Estuarine Floodplain (AEZ-18) [16]. According to the Bangladesh Meteorological Department [17], Noakhali station, the average temperature was 27.4°C and the relative humidity was 81%, in November 2021, and 28.75°C and 62 % relative humidity in March 2022. The annual rainfall was ~3302 mm. According to Roy et al. [18], the particle size composition of the soil at that site is Sand:Silt:Clay = 40%:40%:20%. The soil of the experimental site was slightly alkaline with pH 8.30 [19]. Amount of N was 0.04%, P was present at 27.79 μg/g soil, and K was present at 0.18 mEq/100 g soil. The soil had an EC of 1.3 dS/m, which means the soil was not saline. The organic matter content of soil was 0.64%, which was very low [20].

2.2. Experiment Design and Planting Materials. The experiment was conducted with maintaining a randomized complete block design (RCBD) with three replications in a polythene greenhouse. Each replication contains 13 plots of 2.5 m × 2 m size. Space was kept 2 m between replications. Row to row and plant to plant distances were 1 m and 1 m, respectively. A total of 12 exotic watermelon (advanced F7 generation inbred lines) genotypes (G1–G12) were obtained from the Department of Horticulture, Sunchon National University, South Korea (temperate climatic region), and one commercial variety (G13) of Bangladesh was used as experimental materials.

2.3. Land Preparation, Seedling Transplanting, and Plant Management. The land was prepared before 1 month of the seedling transplantation for better incorporation of the fertilizer with the soil. The experimental plots were plowed, harrowed, and leveled to pulverize the soil for having a good tilth. After removing all the weeds land was finally prepared with the addition of a basal dose of cow dung and neem cake. Recommended fertilizer dose: cow dung 8–10 ton /ha, neem cake 5–6 kg/ha, urea 60 kg/ha, muriate of potash (MoP) 60 kg/ha, Gypsum 20 kg/ha for fertilization were used as a basal dose. Borax (5 kg/ha) and *Trichoderma harzianum* (Bioderma 5 kg/ha) were applied during final land preparation before covering the plot with black plastic mulch. Sowing of seed was carried out on December 25, 2021, in seedling trays in the equal mixture of coco dust and vermicompost. Before sowing, the seeds were presoaked in fungicide (carbendazim; 5 g/L water) overnight. For each genotype, five seeds were sown for each replication as watermelon shows poor germination percentage, and after germination, 1-month-old seedlings were transplanted into the plot in a net house on January 25, 2022. Fertilization was done by following the fertilizer recommendation guide [21], and other intercultural operations were done as required.

2.4. Data Recording. Data were collected on a total of seven prominent qualitative aspects, including leaf type and color, fruit shape, fruit skin and flesh color, and seed color. Leaf type and color were observed 45 days after transplantation (DAT), and the rest of the data were collected after harvesting fruits. Leaf color, fruit skin color, fruit flesh color, and seed color were compared to modify the International Union for the Protection of New Varieties of Plants (UPOV) descriptor list [22] at cotyledon, flowering, and mature fruit stages.

Data on hypocotyl length (HL) (cm), cotyledon width (CW) (cm), and cotyledon length (CL) (cm) were collected at seedling stage (20 DAT) with a centimeter scale and data on vine length (VL) (cm), leaf blade length (LBL) (cm), leaf blade width (LBW) (cm), petiole length (cm), and stem diameter (SD) (cm) were measured by a measuring tape after 45 days of transplantation. Furthermore, leaf chlorophyll was measured by hand held SPAD–502 Plus chlorophyll meter (Konika Minolta, Tokyo, Japan) [23] after 60 days of transplantation, and leaf number per plant, days to first flowering (DFF), were counted at the reproductive stage, and time of fruit ripening (DAT) was conducted during the stage of fruit ripening. Total yield (TY) (ton/ha) was estimated during harvesting. Harvested fruit samples were sent to the laboratory (Department of Agriculture, NSTU) for biochemical analyses. Fruit firmness (FF) (kg/cm^2), flesh width (FW) (cm), pericarp thickness (PeT) (mm), single fruit weight (FrW) (kg), fruit length (FL) (cm), seed width (SW) (cm), seed length (SL) (cm), and weight of 100 seed (g) were taken in the lab prior to the biochemical analyses.

SSC of fresh fruit juice was determined by a refractometer. A drop of fresh fruit juice was poured on the prism of the refractometer, and the reading was taken as (% Brix) [24] and fruit juice acidity by pH meter (Hanna Instruments, Woonsocket, RI, USA). Lyco. (mg/100 mL) and beta carotene (B. caro) (mg/100 mL) were estimated by the method given by Nagata and Yamashita [25]. According to the methodology, 1 g of watermelon fresh sample was placed in a test tube; acetone: hexane (4:6) was poured into the test tube for extraction, and the mixture was homogenized. At 663, 645, 505, and 453 nm, the optical density of the homogenized mixture was measured by a spectrophotometer. The values of Lyco. and B. caro were calculated by the following formula:

$$\text{Lycopene (mg/100 mL)} = 0.0458\,A_{663} + 0.204\,A_{645} + 0.372\,A_{505} - 0.0806\,A_{453},$$

$$\text{Beta carotene (mg/100 mL)} = 0.216\,A_{663} - 1.22\,A_{645} - 0.304\,A_{505} + 0.452\,A_{453},$$

where A is the absorbance at 663, 645, 505, and 453 nm.

The oxidation-reduction titration method was used to determine vitamin C (Vit. C) [26]. To prevent aerobic oxidation of the dye solution, the titration was carried out in the presence of glacial acetic acid and meta-phosphoric acid (2,6-dichlorophenol indophenol). The solution was dye-titrated; the mean of the observations gave the amount of dye required to oxidize a particular quantity of L-ascorbic acid solution of unknown concentration, using L-ascorbic acid as a known sample.

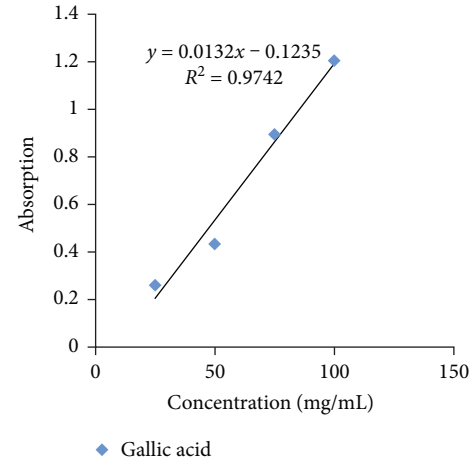


Figure 1: Calibration curve of total phenolic content of gallic acid (standard).

Total phenolic content (TPC) and total flavonoid content (TFC) determination was conducted by following the methods described by Ali et al. [27] and Phuyal et al. [28] with some modifications.

2.4.1. TPC

2.4.1.1. Standard Gallic Acid Preparation for Calibration Curve. For a standard Gallic acid solution, 10 mg of Gallic acid was diluted by 10 mL of methanol. The resulting solution (1 mg/1 mL) was mixed with 5 mL of 10% Folin–Ciocalteu reagent (FCR), and 4 mL of 7% Na_2CO_3 were added to bring the final volume to 10 mL. The mixture formed blue color, and then it was vortexed well for 20 s and incubated in a water bath at 40°C for 30 min. The solution turned into dark blue due to the oxidation of phenols in fruit extracts by the FCR reagent. From the stock solution, working samples of different concentrations were prepared (25, 50, 75, and 100 µg/mL). A blank value using methanol was taken against 765 nm absorbance with a UV–visible spectrophotometer. A standard gallic acid curve was prepared by plotting different concentration values (Figure 1), and the experiment was repeated for three times to avoid errors, and the average value was calculated. The standard curve showed a regression value, $R^2 = 0.97$.

2.4.1.2. Sample Preparation and TPC Estimation. Extract solutions (80% methanol extraction) of various concentrations (25, 50, 75, and 100 µg/mL) were prepared from the fruit samples and were covered with an aluminum foil to prevent evaporation. The procedure as described for standard gallic acid preparation was followed for sample preparation, and the average value of absorbance was used to plot the calibration curve to determine the level of phenolic compounds in the extracts. The TPCs in all the samples were calculated by the using the formula:

$$\text{TPC} = c \times (V/m),$$

where TPC = total phenolic content, c = concentration of gallic acid obtained from calibration curve in mg/mL, V = volume of

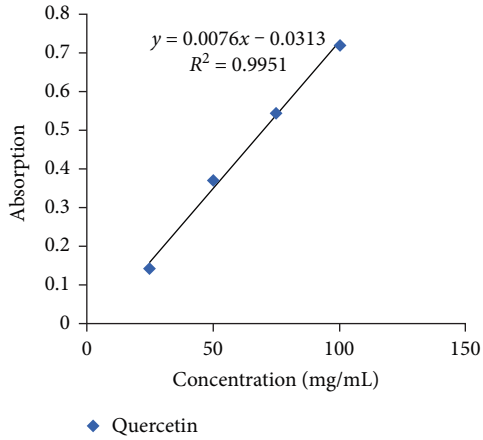


FIGURE 2: Calibration curve of total flavonoid content of quercetin (standard).

extract in mL, and m = mass of extract in kg. TPC of the extracts was expressed as mg Gallic acid equivalents (GAEs) per kg of sample in fresh weight (mg GAE/kg FW).

2.4.2. TFCs

2.4.2.1. Standard Quercetin Solution Preparation for Calibration Curve. TFCs in the extracts were determined by the aluminum chloride colorimetric assay. 4 mg of quercetin was dissolved in 1 mL of methanol. This standard solution (4 mg/mL) was diluted to make working samples of 0.25, 0.5, 0.75, and 1 mg/mL solutions. Then, 1 mL of quercetin in each concentration was added to the test tube containing 4 mL of distilled water. At the same time, 0.3 mL of 5% $NaNO_2$ was added to the test tube, and after 10 min, 0.3 mL of 10% $AlCl_3$ was added. Then, 2 mL of 1 M NaOH was added to the mixture after 12 min. The volume of the mixture was made 10 mL by immediately adding 4.4 mL of distilled water. The TFC was expressed as quercetin equivalents using the linear equation ($Y = mx + c$) based on the calibration curve (Figure 2) with the regression value, $R^2 = 0.99$.

2.4.2.2. Sample Preparation and TFC Estimation. Methanolic extracts of the samples were prepared at a concentration of 4 mg/mL, and they were diluted serially to make different concentrations (0.25, 0.5, 0.75, and 1 mg/mL) solutions. A similar procedure as described for quercetin was followed for the extracts also, and the absorbance was measured by a spectrophotometer at 510 nm. The experiment was repeated three times, and the average value of absorbance was used to calculate the TFC. The flavonoid content was expressed as quercetin equivalent in mg QE/kg fresh weight (mg QE/kg FW) using the linear equation based on the standard calibration curve.

2.4.3. Total Anthocyanin Quantification. Total anthocyanin content (TAC) was determined by photometric determination of anthocyanins according to the method given by Mehrtens et al. [29]. About 1 mL of acidic methanol (1% HCl, w/v) was added to 300 mg of fresh fruit flesh. Samples were incubated for 18 h at room temperature under moderate shaking. It was sedimented by centrifugation (14,000 rpm, room temperature, 1 min), and 400 μL of the supernatant was added to 600 μL of acidic methanol. Absorption of the extracts at 530 and 657 nm wavelength was determined photometrically (UVIKON 922, Bio-Tek Kontron). Quantification of anthocyanins was performed using the following equation:

$$Q_{(\text{Anthocyanin})} = (A_{530} - 0.25 \times A_{657}) \times M^{-1},$$

where $Q_{(\text{Anthocyanins})}$ is the amount of anthocyanins, A_{530} and A_{657} are the absorption at the indicated wavelengths (nm), and M is the weight of the plant material used for extraction (g). All samples were measured as triplicates, and the TAC was expressed as g/100 g fresh weight (mg/100 g FW).

2.4.4. Statistical Analyses. Analysis of variance (ANOVA) was accomplished to find out signification variation among the treatments (13 watermelon germplasms) on the various studied variables. Tukey's Honest Significant Difference test for pairwise comparison. In addition, the percentage of coefficient of variation (CV%) was studied to find out the existing variability among the studied traits, if there is any. Pearson's correlation coefficient (PCE) was constructed to evaluate the interrelationship between the variables; principal component analysis (PCA) was performed to determine, which variable mostly contributes to the total variation, positively focusing on the first two principle component, which has the eigenvalues greater than one and a PCA biplot was used to visualize the variation of variables by RStudio and R-statistics platform (software version 4.3.2 using the packages dobioresearch, RColorBrewer, factoextra and FactoMineR, respectively. Furthermore, cluster analysis was conducted to divide the genotypes based on their similarity and dissimilarity. Inter- and intracluster distances were calculated to quantify the similarity and dissimilarity. Average intercluster (Mahalanobis D^2) distances were calculated by the following formula [30]:

$$\text{Average intercluster, } D^2 = \frac{\sum D_{ij}^2}{ni \times nj},$$

where $\sum D_{ij}^2$ = sum of distances between all possible populations in cluster i and j, ni = number of populations in cluster i and Nj = number of populations in cluster j.

Average intracluster distances (D) were calculated by the following formula [30]:

$$\text{Average intracluster, } D = \frac{\sum D^2}{n},$$

where $\sum D^2$ = sum of distances between all possible combinations (n) genotypes included in a cluster, n = number of all possible combinations between the populations in a cluster. Silhouette coefficient was calculated to determine the optimal cluster (K) number following the formula of Dinh et al. [31]. The average distance to all other data points within the intracluster and the average distance to all data points in the nearest intercluster were calculated. Computation of the silhouette coefficient for each data point was done using the following formula:

$$\text{Silhouette coefficient} = (\text{intercluster distance} - \text{intracluster distance})/\max(\text{intercluster distance}, \text{intracluster distance}).$$

Calculation of the average silhouette coefficient was done across all data points to obtain the overall silhouette score for the clustering result. Heat map and hierarchical clustering for quantitative traits constructed using the pheatmap package by R. The dendrogram shows hierarchical clustering of watermelon genotypes based on the Euclidean as the measure of distance and Ward's squared cluster agglomeration method [32, 33].

2.4.5. Estimation of Genetic Parameters. Genotypic variance (σ^2_g), phenotypic variance (σ^2_p), and broad-sense heritability (h^2_b) were computed using the formulas described by Johnson et al. [34] $\sigma^2_g = \frac{GMS - EMS}{r}$ where, GMS = genotypic mean square, EMS = error means square (environmental variance), r = number of replications; $\sigma^2_p = \sigma^2_g + EMS$ and $h^2_b = \frac{\sigma^2_g}{\sigma^2_p} \times 100$. Heritability was grouped into three classes: 0%–30% = low, 31%–60% = medium and >60% = high [35]. Genotypic CV (GCV), phenotypic CV (PCV), and genetic advance (GA) as mean percentages estimated according to Burton [36] as: $GCV = \frac{\sqrt{\sigma^2_g}}{\mu} \times 100$ and $PCV = \frac{\sqrt{\sigma^2_p}}{\mu} \times 100$, where μ = grand mean of the trait. PCV levels greater than 20% were classified as high variability, whereas values less than 10% and between 10% and 20% represented relatively low and moderate variability, respectively. Expected GA at a 5% selection intensity was calculated using the formula given by Johnson et al. [34] and Allard [37] as $GA = k \times \sigma_p \times h^2_b$, where k = selection differential for 5% selection intensity ($k = 2.06$), σ_p = phenotypic standard deviation. GA as the percent of the population mean (GAM) was calculated as $GAM = \frac{GA}{\mu} \times 100$, where GA = genetic advance and μ = population mean Comstock and Robinson [38]. GA was characterized as: low (<10%), moderate (10%–20%), or high (>20%) [34].

3. Results and Discussion

3.1. Qualitative Characteristics. We assessed qualitative traits for 13 watermelon genotypes, including one commercial cultivar (Table 1 and Figure 3). The leaf type and fruit shape of all the genotypes were simple types and different shapes, respectively. However, variation was observed in the leaf color. It was found that 75% of the genotypes has green colored leaves where some genotypes (G1, G5, and G12) had leaves with dark green and yellow patches, which is an indication of genotypic differences due to particular genetic action as Gusmini et al. [39] detected Yl gene responsible for yellowish color of watermelon leaves and also concluded that YI gene is incompletely dominant over green leaf. In the present study, color variation was found in terms of fruit skin and flesh color (codified according to the UPOV Table 1) [21]. The color of fruit and skin of watermelon is controlled by several genetic actions suggested by Weetman [40]. Moreover, flesh color is controlled by several genes to produce red, orange, salmon yellow, canary yellow, or white revealed in different experiments noted by Shimatsuma [41] and Henderson et al. [42]. In terms of seed morphology, it has been found that the seeds were varied in color in our study. Finding breeding lines with different colors is a necessary first step in figuring out how genetic variations result in this minute, yet horticulturally significant, phenotypic variances [43].

3.2. Quantitative Characteristics. We observed significant variation ($p \leq 0.001$) among all the quantitative traits, viz. HL, CL, CW, petiole length of leaf (PeL), VL, number of leaves per plant (LPP), SD, LBL, and LBW (Table 2). These are some of the significant components since it has the greatest beneficial impact on fruit yield, indicating that the plant is vigorous and healthy, which means the potentiality of the seed embryo, suggested by previous studies [44, 45].

A considerable variance ($p \leq 0.001$) was seen in the mean performance of DFF across the watermelon genotypes, and the range was between 30 and 40 DAT. Early flowering provides yields early on because it signals the beginning of fruit production early. A similar result was also revealed in an experiment carried out in India by Choudhary et al. [46]. After transplantation, exotic watermelon fruit took an average of 65–82 days to ripen, whereas the average days taken by the commercial variety was 72 DAT. It means the days of maturity time is very close to the exotic genotypes, which indicates a possibility to develop a new cultivar by successive breeding and selection for earliness suggested by Gichimu et al. [47]. They reported that under optimum conditions (day temperature ranges 21–30°C) watermelon fruit matures in 80–110 days from the od sowing, which very closely aligns with the present study. The range of PeT was 0.31–0.80 cm. Nearly the same outcome was discovered by a previous researcher. One of the previous studies in Türkiye mentioned the range of fruit peel thickness 0.1–2.8 cm [48]. Regarding commercialization and the evaluation of organoleptic qualities, one of the most important aspects of internal fruit quality is fruit compactness, which is correlated with PeT. Genotype G10 demonstrated the highest FF (3.41 kg/cm^2), which distinguished it significantly from the other genotypes. Anees et al. [49] discovered almost similar range of FF in the ripening stage of watermelon fruit (highest 2.1 kg/cm^2). The weight and size of the fruits determine the overall production of fruits, and they have a strong correlation with one another, similarly found by De Souza et al. [50]. Fruit FW, FrW, and TY, three of the quantitative features under study, have a significant market value. In the research project, the FW ranged from 7.5 to 22 cm, and the weight of a single fruit ranged from 1.67 to 5.38 kg. The main objective of any breeding workshop is to introduce a genotype that yields more than the others in comparison. In line with the findings, the TY was 20–31 ton/ha, which is remarkable in the case of those parameters that showed a significant variation ($p \leq 0.001$) (Table 2), which is supported by Goreta et al. [51]. From a morphological perspective, the watermelon seeds under investigation also displayed notable variation. A 100 seed weight (HSW) between 2.30 and 6 g [52]. The seed measured 0.27–0.53 cm in width. Poole [53] suggested two different genes responsible for small and large size genes, which is an indication of genotypic differences.

Table 1: Variations of watermelon genotypes observed in the experiment, along with their qualitative traits (leaf type, fruit shape, leaf color, fruit color, fruit flesh color, and seed color) using UPOV descriptors.

Sn	Genotypes	Leaf type	Fruit shape	Leaf color	Fruit color	UPOV descriptor (SL. 20)	Fruit flesh color	UPOV descriptor (SL. 28)	Seed color	UPOV descriptor (SL. 33)
1	G1	Simple	Elongated elliptic	Yellow green	Dark yellow	1	Yellow	2	Dark brown	6
2	G2	Simple	Elliptic	Green	Medium green	4	Red	6	Dark brown	6
3	G3	Simple	Circular	Green	Dark green striped	5	Dark red	7	Light brown	5
4	G4	Simple	Circular	Green	Dark green striped	5	Yellow	2	Brown	6
5	G5	Simple	Circular	Yellow green	Dark green striped	5	Pinkish Red	5	Dark brown	6
6	G6	Simple	Circular	Green	Dark green striped	5	Orange	3	Brown	6
7	G7	Simple	Circular	Green	Dark green striped	5	Pinkish red	5	Dark brown	6
8	G8	Simple	Circular	Green	Dark green striped	5	Dark red	7	Brown	6
9	G9	Simple	Circular	Green	Dark green striped	5	Dark red	7	Brown	6
10	G10	Simple	Circular	Green	Light green	3	Yellow	2	Brown	6
11	G11	Simple	Circular	Green	Dark green striped	5	Dark red	7	Dark brown	6
12	G12	Simple	Circular	Yellow green	Very light green	2	Orange	3	Brown	6
13	G13 (commercial variety)	Simple	Elliptic	Green	Light green	3	Dark red	7	Light brown	5

Abbreviation: G, genotypes.

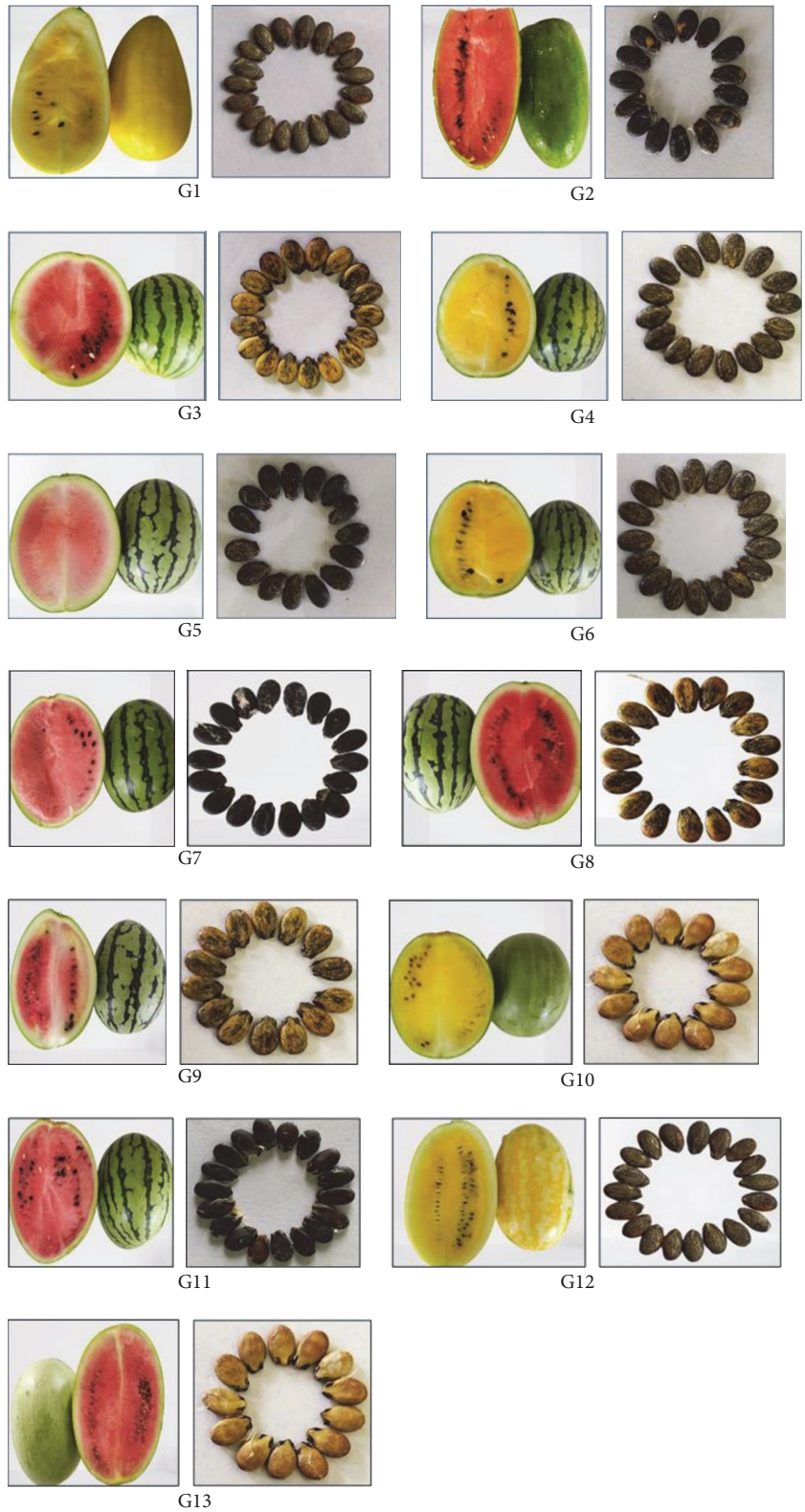


Figure 3: Categorization of 13 watermelon genotypes based on fruit flesh and skin color (left side) and seed morphology (right side) (where G1 to G12 represent the exotic genotypes and G13 represents the commercial variety; green diamond-13).

The green pigment found in plants, called chlorophyll, is necessary for photosynthesis. The range of the leaf's chlorophyll content (Chlo.) in the experiment was (44.67–55.29 SPAD value), which was moderate to high. It denotes healthy, green, and active photosynthesizing leaves, which ultimately produce more sugar suggested by Jaskani et al. [54], and they

Table 2: Characterization of watermelon genotypes based on quantitative traits.

Genotypes	HL	CL	CW	VL	LPP	LBL	LBW	PeL	SD	DFF	TR	FF	FW	PeT
G1	8.33^{a}	2.93^{a}	0.9^{d}	450.5$^{b–d}$	207$^{b–e}$	17^{e}	25^{a}	10.9$^{c–e}$	0.32^{c}	33.3^{e}	65.7^{f}	2.97^{bc}	12.3^{h}	0.47^{e}
G2	5.43^{d}	1.1^{e}	0.92^{d}	425.5$^{d–f}$	211.7$^{b–e}$	18$^{c–e}$	23^{ab}	12.1^{c}	0.35^{c}	38.3^{ab}	71$^{b–d}$	3.00^{bc}	13^{g}	0.31^{g}
G3	5.47^{d}	2.53^{bc}	1.67^{c}	389.17^{f}	193.3^{de}	19$^{a–c}$	24^{ab}	11.8^{cd}	0.32^{c}	35$^{c–e}$	74.3^{b}	3.41^{a}	17.5^{d}	0.68^{bc}
G4	5.47^{d}	2.2^{c}	1.06^{d}	396.24^{ef}	163.3^{f}	14^{f}	17.7^{f}	11$^{c–e}$	0.49^{a}	33.3^{e}	67$^{e–f}$	1.37^{f}	15^{f}	0.72^{b}
G5	5.1^{d}	1.6^{d}	1.02^{d}	342.24^{g}	163.7^{f}	15.2^{f}	18.7$^{d–f}$	11.3^{cd}	0.32^{c}	36.3^{c}	80^{a}	2.64^{d}	17^{d}	0.71^{bc}
G6	7.53^{b}	1.73^{d}	1.71^{c}	438.8$^{c–e}$	200$^{c–e}$	14.5^{f}	22^{bc}	14.8^{b}	0.31^{c}	35$^{c–e}$	71.3^{bc}	2.00^{e}	15^{f}	0.67^{c}
G7	6.63^{c}	2.2^{c}	0.92^{d}	380.5^{fg}	188.3^{e}	17.8$^{c–e}$	15.3^{g}	9.5^{f}	0.25^{d}	39^{a}	81^{a}	3.10^{b}	22^{a}	0.80^{a}
G8	7.6^{b}	2.6^{ab}	2.07^{b}	473.8$^{a–c}$	215$^{b–d}$	19.7^{ab}	20$^{c–e}$	10.7$^{d–f}$	0.4^{b}	35.7^{cd}	71$^{b–d}$	3.00^{bc}	20.7^{b}	0.58^{d}
G9	5.53^{d}	1.57^{d}	0.95^{d}	487.8^{ab}	206.7^{b-e}	18.5$^{b–d}$	23.3^{ab}	17.8^{a}	0.42^{b}	36^{c}	82.3^{a}	2.95^{c}	18.2^{c}	0.51^{e}
G10	5.43^{d}	1.67^{d}	1.04^{d}	482$^{a–c}$	246.7^{a}	20.2^{a}	20.7^{cd}	11.5^{cd}	0.31^{c}	36.7^{bc}	70.3$^{c–e}$	3.02^{bc}	17^{d}	0.40^{f}
G11	5.57^{d}	1.67^{d}	1.67^{c}	502.17^{a}	228.3^{ab}	17.4^{de}	23^{ab}	17.4^{a}	0.49^{a}	38.3^{ab}	67.7$^{d–f}$	2.97^{bc}	16.3^{e}	0.59^{d}
G12	8.23^{ab}	1.69^{d}	2.67^{a}	487.8^{ab}	245^{a}	16.6^{e}	20$^{c–e}$	9.6^{f}	0.49^{a}	34de	65^{f}	3.02^{bc}	7.5^{i}	0.49^{e}
G13	8.23^{ab}	1.60^{d}	2.5^{a}	508.17^{a}	220^{bc}	15^{f}	18^{ef}	10^{ef}	0.42^{b}	40^{a}	72.7^{bc}	3.01^{bc}	16^{e}	0.80^{b}
Min	5.10	1.10	0.90	342.30	163.33	14.00	15.33	9.53	0.25	33.33	65	1.37	7.5	0.31
Max	8.33	2.93	2.67	508.20	246.67	20.20	25.00	17.83	0.49	40	82.33	3.41	22	0.8
CV%	6.38	10.67	7.83	6.07	6.83	4.85	6.58	5.81	6.65	2.92	14.87	67.38	16.35	36.56
F value	28.71***	19.07***	89.60***	11.64***	10.13***	17.32***	13.13***	45.12***	30.75***	12.47***	23.16***	13.59***	38.37***	8.11***

	FL	FrW	TY	SL	SW	HSW	Chlo.	SSC	pH	Vit. C	B. Caro	Lyco	TAC	TPC	TFC
G1	26.3$^{c–e}$	3.35^{d}	22.8^{cd}	0.62^{e}	0.37^{c}	4.3^{e}	48.50^{de}	7.33^{g}	5.33^{cd}	1.03^{gh}	0.13^{e}	0.01^{g}	0.07^{a}	105.4^{c}	115.85^{h}
G2	25.3^{de}	2.33^{f}	22.2^{de}	0.76^{bc}	0.47^{ab}	4.1^{f}	54.97^{a}	9.33^{e}	5.21^{e}	1.61^{cd}	0.19^{c}	0.74^{b}	0.06^{a}	104.4^{cd}	162.72^{d}
G3	26.1$^{c–e}$	3.75^{c}	23.2^{cd}	0.72^{c}	0.43^{bc}	5.1^{c}	45.12^{g}	11.4^{b}	5.51^{b}	1.34^{f}	0.19^{c}	1.18^{a}	0.02$^{e–g}$	105.6^{c}	147.57^{e}
G4	24.9^{ef}	2.30^{f}	20.8^{ef}	0.57^{f}	0.47^{ab}	5.27^{b}	49.12^{d}	8.83^{f}	5.19^{e}	1.05^{gh}	0.87^{a}	0.004^{g}	0.012$^{g–i}$	102.2$^{c–f}$	188.48^{a}
G5	27.2^{c}	3.52^{cd}	24.2^{c}	0.55^{f}	0.37^{c}	5.07^{c}	50.83^{c}	6.33^{h}	5.2^{e}	1.90^{ab}	0.09^{f}	0.52^{cd}	0.008^{hi}	110.8^{b}	124.62^{g}
G6	27.3^{c}	3.20^{d}	23.3^{cd}	0.67^{d}	0.53^{a}	5.07^{c}	52.87^{b}	10.1^{d}	5.29^{d}	1.39^{ef}	0.15^{d}	0.0003^{g}	0.02$^{e–g}$	100.3$^{d–f}$	182.73^{b}
G7	34.7^{a}	4.95^{b}	27.5^{b}	0.78^{b}	0.53^{a}	4.53^{d}	44.67^{g}	10.2^{d}	5.30^{cd}	1.57^{de}	0.07^{g}	0.47^{de}	0.04^{c}	104.2^{cd}	149.02^{e}
G8	34.8^{a}	5.38^{a}	29^{a}	0.75^{bc}	0.47^{ab}	4.27^{e}	45.97^{fg}	11.5^{b}	5.54^{b}	1.70^{bd}	0.16^{d}	0.6^{c}	0.014$^{f–h}$	99.8^{ef}	142.16^{f}
G9	26.8^{cd}	2.73^{e}	20.8^{ef}	0.41^{g}	0.37^{c}	4.23^{ef}	49.03^{d}	10.93^{c}	5.31^{cd}	1.97^{a}	0.06^{g}	0.54^{cd}	0.013$^{f–i}$	134.8^{a}	188.76^{a}
G10	23.3^{f}	1.67^{g}	20^{f}	0.83^{a}	0.27^{d}	3.5^{g}	55.23^{a}	7.33^{g}	5.07^{f}	0.90^{h}	0.27^{b}	0.22^{f}	0.03^{d}	104.2$^{c–e}$	167.38^{c}
G11	25.8^{a}	5.33^{a}	30^{a}	0.65^{de}	0.52^{ab}	2.3^{g}	49.90^{cd}	9.03^{f}	5.36^{c}	1.79^{ac}	0.05^{g}	0.47^{d}	0.023^{e}	102.4$^{c–e}$	179.99^{b}
G12	27^{cd}	3.35^{d}	22.5^{d}	0.65^{de}	0.47^{ab}	4.27^{e}	47.33^{ef}	11.83^{a}	5.58^{b}	1.09^{g}	0.13^{e}	0.35^{e}	0.01^{i}	104.6^{cd}	160.25^{d}
G13	29.7^{b}	3.33^{d}	23.3^{cd}	0.72^{c}	0.53^{a}	6^{a}	44.67^{g}	11.03^{c}	5.7^{a}	1.67^{cd}	0.02^{h}	0.85^{b}	0.05^{b}	97.8^{f}	162.44^{d}
Min	23.27	1.67	20.00	0.42	0.27	2.3	44.67	6.33	5.07	0.9	0.02	0.00	0.001	97.8	115.85
Max	34.8	5.38	30.00	0.83	0.53	6	55.23	11.83	5.7	1.97	0.87	1.81	0.07	134.8	188.76
CV%	18.02	20.53	24.39	37.09	13.28	6.59	16.86	14.84	11.3	71.35	26.41	45.45	15.57	2.48	1.05
F value	38.23***	10.16***	38.70***	50.03***	7.4***	35.18***	41.51***	57.41***	51.27***	26.38***	14.21***	73.56***	69.19***	37.03***	57.55***

Note: *** = Significant at $p \leq 0.1\%$ level of significance, CV(%)—percentage of coefficient of variation, HL—hypocotyl length (cm), CL—cotyledon length (cm), CW—cotyledon width (cm), VL—vine length (cm), LBL—leaf blade length (cm), LBW—leaf blade width (cm), PeL—petiole length (cm), SD—stem diameter (cm), DFF—days to first flowering (days after transplantation), TR—time of ripening (days after transplantation), FF—fruit firmness (kg/cm^2), FW—flesh width (cm), PeT—pericarp thickness (mm), FL—fruit length (cm), FrW—fruit weight (kg), TY—total yield (ton/ha), SL—seed length (cm), SW—seed width (cm), HSW—weight of 100 seed (g), SSC—soluble solids content (% Brix), pH—fruit juice acidity, Chlo.—chlorophyll content (SPAD), Lyco—lycopene (mg/100 mL), B. caro—beta carotene (mg/100 mL), Vit.C—vitamin C (mg/100 g), TPC—total phenolic content (mg GAE/kg FW), TFC—total flavonoid content (mg QE/kg FW), TAC—total anthocyanin content (mg/100 g FW). Similar letter indicates the genotypes belong to the same group and vice versa.

Abbreviations: LPP, leaf per plant; Max, maximum; Min, minimum.

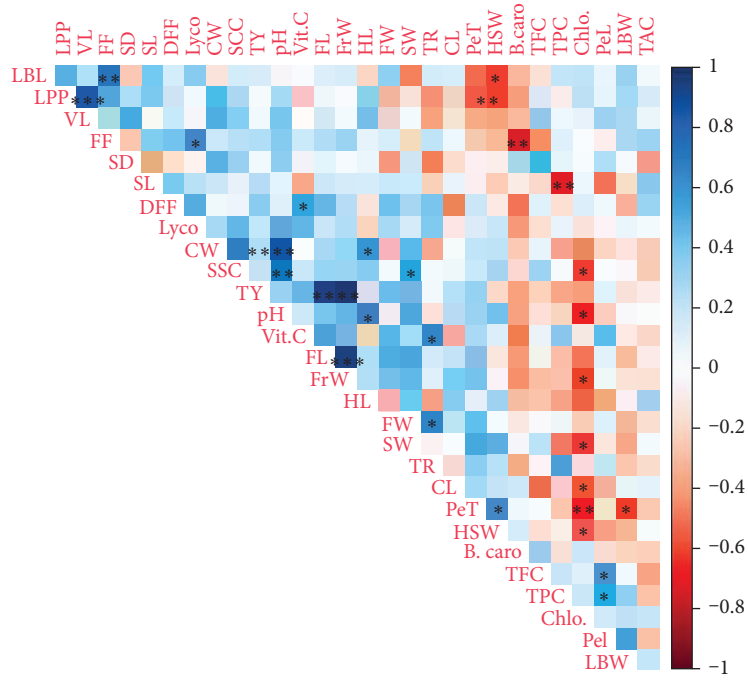


FIGURE 4: Pearson's correlation matrix between morphological, biochemical, and yield attributing traits. $^{*}p \leq 0.05$; $^{**}p \leq 0.01$; $^{***}p < 0.001$; HL—hypocotyl length (cm), CL—cotyledon length (cm), CW—cotyledon width (cm), VL—vine length (cm), LPP—leaf per plant, LBL—leaf blade length (cm), LBW—leaf blade width (cm), PeL—petiole length (cm), SD—stem diameter (cm), DFF—days to first flowering (days after transplantation), TR—time of ripening (days after transplantation), FF—fruit firmness (kg/cm^2), FW—flesh width (cm), PeT—pericarp thickness (mm), FL—fruit length (cm), FrW—fruit weight (kg), TY—total yield (ton/ha), SL—seed length (cm), SW—seed width (cm), HSW—weight of 100 seed (g), SSC—soluble solids content (% Brix), pH—fruit juice acidity, Chlo.—chlorophyll content (SPAD), Lyco—lycopene (mg/100 mL), B. caro—beta carotene (mg/100 mL), Vit. C—vitamin C (mg/100 g), TPC—total phenolic content (mg GAE/kg FW), TFC—total flavonoid content (mg QE/kg FW), TAC—total anthocyanin content (mg/100 g FW).

also reported a similar result. Besides, a refractometry indicator called SSC indicates the percentage (%) of dissolved solids in a solution. The watermelon fruit juice is composed of sugars (sucrose and hexoses; 65%), acids (citrate and malate; 13%), and other trace elements (phenols, amino acids, soluble pectin, ascorbic acid, and minerals). The range of SSC (% Brix) for the 13 watermelon genotypes was 6.33–11.83. The result was almost similar to the study of Kimball [55]. The greater the percentage, the sweeter the fruits will be. Additionally, fruit juices naturally have a slight acidity. According to the results, the pH content varied from 5.07 to 5.7. The range is almost ideal for maintaining the fruit taste quality suggested by Alam et al. [56].

Besides, data from investigated watermelon genotypes revealed that the range of Vit. C levels were 0.9–2 mg/100 g, which was close to another study [57]. In addition, the enzyme Lyco.–β-cyclase converts Lyco. into B. caro. The range of B. caro was (0.02–0.86 mg/100 mL) and Lyco. was (0.0003–0.84 mg/100 mL), which is consistent with the results noted by Tamburini et al. [58] and Malviya [59] respectively. TAC, TFC, and TPC were measured in this investigation. TAC ranged from 0.006 to 0.06 mg/100 mg FW. The result was similar to the result found by Perkins-Veazie et al. [60], TFC from 115.85 to 188.76 mg QE/kg FW and TPC from 97.8 to 134.8 mg GAE/kg FW. Similar data were found by Dari et al. [61]. The presence of Vit. C and other phenolic compounds in the investigated genotypes are the indication of their potentiality to restore health-beneficial compounds, which may be helpful to prevent CVDs. Furthermore, the CV% was found to be quite higher (Table 2) for all the studied attributes except for LBL, DFF after transplanting, TPC, and TFC. The CV typically compares the relative amount of variability present between characters of plants [62]. Higher CV% implies that there are chances to exploit genetic variability among the studies traits of watermelon. Further statistical analyses were employed to identify genotypes retaining most of the evaluated traits.

3.3. Correlation Analysis Among Different Quantitative Characteristics. Correlation analysis visualized (Figure 4) the linear relationship between different quantitative traits of the genotypes. Direct selection of yield-related traits is very difficult as yield is a complex polygenic trait [63]. Therefore, it is crucial to identify interrelated traits that will ultimately affect the yield directly or indirectly. Additionally, interrelated phytochemical traits selection for better quality fruit juice is also necessary. Hence, PCE analysis is one of the best ways to investigate the correlation between the quantitative traits. In terms of TY of all the genotypes found to be positively correlated with FL, single FrW, HL, CL, CW, fruit FW, FF, PeT. A similar result was suggested by Correa et al. [64]. There was a significant relationship between TY and single FrW. As yield is controlled by many genes due to polygenic inheritance, so these interrelated characters can be taken into account for improving superior genotypes. DFF showed a positive correlation with time of

ripening (TR), which means early maturity can be obtained by utilizing this trait. On the contrary, leaf Chlo. has been found in negative correlation with SSC, which may be due to the source-sink relationship of energy, whereas SSC shared a positive interrelationship with fruit juice pH and Vit. C. which ensures its good flavor and quality of fruit juice. A similar outcome was reported by Candir et al. [65].

3.4. PCA. PCA reduces the dimensionality of data sets and also limits the multicollinearity of large data sets by changing a large set of variables into a smaller one that still contains most of the information in the large set. PCA tries to put maximum possible information in the first components and then maximum remaining information in the second components, and so on [66]. It helps to identify the most relevant characteristics, explaining the maximum proportion of the genetic variation. To find out the variation among the variables, PCA was employed, where the Eigenvalues of the first seven principal components were greater than one. The first two principal components collectively explained 39.1% of total variations among the accessions, whereas PC1, PC2 explained 22.7%, 16.4%, respectively (Table 3). The traits (12) correlated positively in PC1 except LBW, Chlo., PeL, B. caro, TAC, TPC, TFC, and in PC2 except CL, TR, FW, PeT, SW, weight of 100 seed (HSW), and B. caro; the rest of the traits correlated positively, which indicates significance of these traits during selection as affect the yield. Both PCs showed positive correlation in terms of HL, CW, VL, LPP, LBL, SD, DFF, FL, FF, FrW, TY, SL, SSC, fruit juice acidity (pH), Vit. C, and Lyco. Hence, breeders should use positive selection for those traits with a positive contribution to yield and phytochemical elements. The loadings of different variables based on the first two principal components are represented in the Biplot (Figure 5B). The sharp angles between the vectors in the biplot indicate positive and close correlation, while the unsharpened angle implies a negative correlation. Variables that showed remarkable variation are G4, G7, G10, and G11, which have been displayed in the Biplot (Figure 5). This variation facilitates breeders to conduct the selection of the genotypes more precisely on the basis of crucial traits.

3.5. Cluster Analysis of All Morphological, Biochemical, and Yield Attributing Characters. The intracluster average D values ranged from 6.49 to 7.92. The intracluster degree of diversity was observed at the highest in cluster III and the lowest in cluster I. Regarding the intercluster distances, the average D^2 value ranged from 7.82 to 8.06 (Table 4). The intercluster distances were greater than intracluster distances. The maximum intercluster distance was found between cluster II and cluster III, whereas the minimum distance was found between cluster I and cluster II. Intercluster distance showed more divergent among all the cluster pairs, and their genotypes are also more important for heterotic breeding than other pairs of cluster genotypes, indicating that more diversity between the genotypes is present in these clusters and hybridization between members of these clusters might be beneficial to produce a heterotic response with wide variability in segregating generations [67].

Table 3: Contributions of different watermelon traits towards the major PCs.

Traits	PC1	PC2
HL	0.19	0.01
CL	0.11	−0.11
CW	0.24	0.06
VL	0.05	0.30
LPP	0.02	0.38
LBL	0.01	0.33
LBW	−0.12	0.24
Chlo.	−0.29	0.17
PeL	−0.07	0.13
SD	0.01	0.03
DFF	0.16	0.15
TR	0.06	−0.06
FW	0.14	−0.05
FL	0.32	0.04
FF	0.14	0.34
PeT	0.22	−0.32
FrW	0.32	0.03
TY	0.29	0.05
SW	0.27	−0.16
SL	0.11	0.14
HSW	0.12	−0.33
SSC	0.24	0.05
pH	0.31	0.05
B. caro	−0.19	−0.26
Vit. C	0.17	0.02
Lyco	0.19	0.13
TAC	−0.02	0.11
TPC	−0.15	0.08
TFC	−0.07	0.01
Eigenvalues	6.57	4.74
% Variation	22.7	16.4
Cumulative variance (%)	22.7	39.1

Generally, genotypes from the same cluster show similarity in their performance but are highly divergent from other cluster groups. The optimal number of clusters (K-means) has been determined from the Silhouette graph. The score ranges from −1 to 1, where a high value indicates good clustering. The silhouette graph indicates that Clusters III have a high silhouette score, suggesting strong separation from other clusters. That is why cluster groups of 13 genotypes were divided into 3 clusters (Figure 6) depending upon the range of diversity by the silhouette method [68]. Genotypes with minimum intercluster distances might also be used in breeding programs for bi-parental crosses between the most diverse and the closest groups to break the unpleasant linkages between yield and its associated traits, but they are not effective for direct parental selection.

A grouped data heat-map analysis of the quantitative trait showed a color assessment of the different accessions. A heat map is a graphical representation of data where the individual values contained in a matrix are represented as colors. The heat

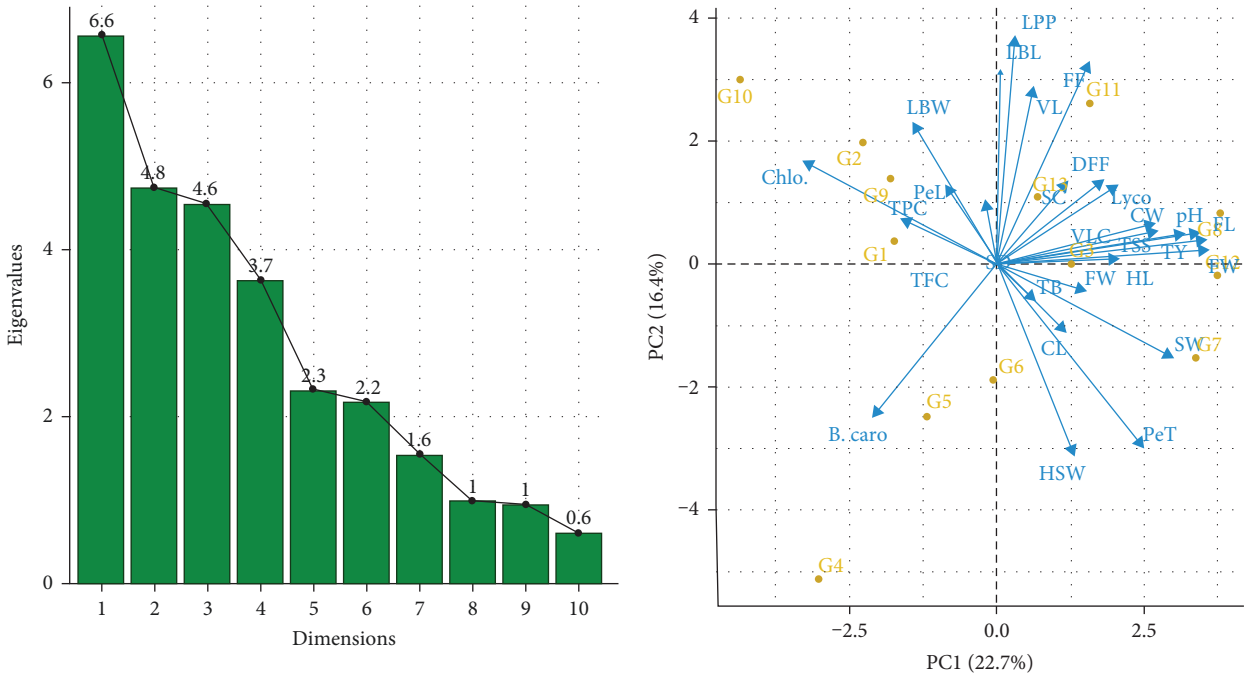


Figure 5: (A) Scree plot of PCA and (B) PCA Biplot of 13 watermelon genotypes based upon the first two major components for quantitative traits: HL—hypocotyl length(cm), CL—cotyledon length(cm), CW—cotyledon width (cm), VL—vine length (cm), LPP—leaf per plant, LBL—leaf blade length (cm), LBW—leaf blade width (cm), PeL—petiole length (cm), SD—stem diameter (cm), DFF—days to first flowering (days after transplantation), TR—time of ripening (days after transplantation), FF—fruit firmness (kg/cm^2), FW—flesh width (cm), PeT—pericarp thickness (mm), FL—fruit length (cm), FrW—fruit weight (kg), TY—total yield (ton/ha), SL—seed length (cm), SW—seed width (cm), HSW—weight of 100 seed (g), SSC—soluble solids content (%Brix), pH—fruit juice acidity, Chlo.—chlorophyll content (SPAD), Lyco—lycopene (mg/100 mL), B. caro—Beta carotene (mg/100 mL), Vit. C—vitamin C (mg/100 g), TPC—total phenolic content (mg GAE/kg FW), TFC—total flavonoid content (mg QE/kg FW), TAC—total anthocyanin content (mg/100 g FW).

Table 4: Average intercluster (D^2) and intracluster (D) distances present among the 13 watermelon genotypes.

Cluster no.	Genotypes	I	II	III
I	G3, G6, G7, G8, G11, G12, G13	**6.49**	7.82	8.1
II	G1, G2, G10	—	**6.55**	8.06
III	G4, G5, G9	—	—	**7.92**

Note: Diagonally bold values represent intracluster distance.

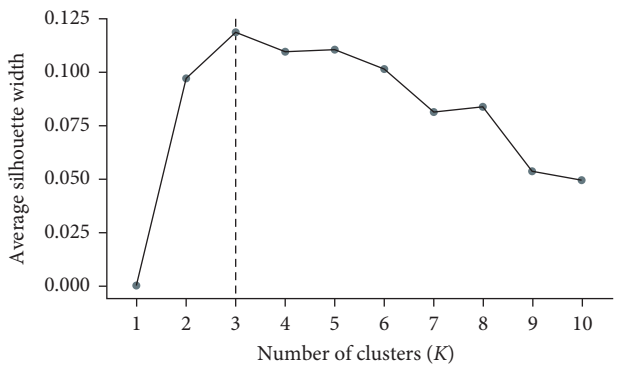


Figure 6: The silhouette coefficient obtained by the silhouette function in *R* for evaluating optimal cluster number.

map analysis showed two dendrograms; the vertical one represents the arrangement that corresponds to the watermelon accessions, and the horizontal one represents the trait distribution (Figure 7). Vertical one displayed three clusters. A color dissimilarity from dark to light indicates how the genotypes are grouped or how the values vary over space, thus making it easier to understand. No or white color in the matrix implies no relationship between the trait and genotypes. It also reveals the comparative form of highly abundant features against a background of mostly low-abundance features [69]. Higher color intensity was observed in Cluster I (G3, G6, G7, G8, G11, G12, and G13), Cluster II (G1, G2, and G10), and Cluster III (G4, G5, and G9) (Table 4). Higher color intensity responding to the traits TY, FL, single FrW, FF, and SSC, which significantly distinguish the group from the other (Figure 4). These

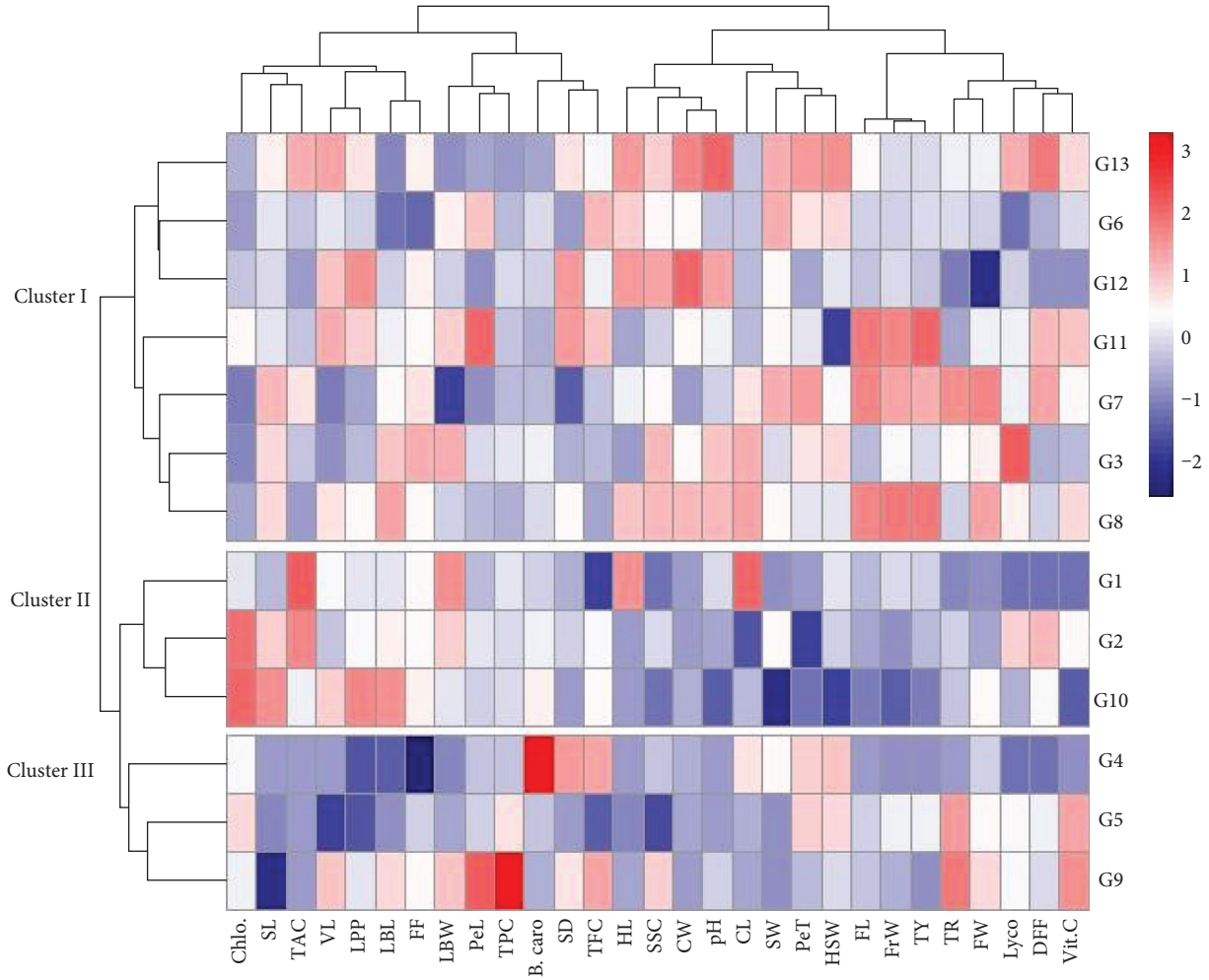


FIGURE 7: Heat map and hierarchical clustering for morphological traits constructed using the complex heat map package. The heat map plot describes the relative abundance of each watermelon genotype (columns) within each feature (rows). The color code (blue to dark red) displays the row *z*-score: red color indicates high abundance, blue color indicates low abundance. The dendrogram shows hierarchical clustering of watermelon genotypes based on the Euclidian as the measure of distance and Ward's squared cluster agglomeration method. Heatmap showing the clustering pattern of 13 watermelon genotypes with 20 quantitative traits. Heatmap also displays the relationship matrix among watermelon genotypes: HL—hypocotyl length (cm), CL—cotyledon length (cm), CW—cotyledon width (cm), VL—vine length (cm), LPP—leaf per plant, LBL—leaf blade length (cm), LBW—leaf blade width (cm), PeL—petiole length (cm), SD—stem diameter (cm), DFF—days to first flowering (days after transplantation), TR—time of ripening (days after transplantation), FF—fruit firmness (kg/cm^2), FW—flesh width (cm), PeT—pericarp thickness (mm), FL—fruit length (cm), FrW—fruit weight (kg), TY—total yield (ton/ha), SL—seed length (cm), SW—seed width(cm), HSW—weight of 100 seed (g), SSC—soluble solids content (%Brix), pH—fruit juice acidity, Chlo.—chlorophyll content (SPAD), Lyco—lycopene (mg/100 mL), B. caro— beta carotene (mg/100 mL), Vit. C—vitamin C (mg/100 g), TPC—total phenol content (mg GAE/kg FW), TFC—total flavonoid content (mg QE/kg FW), TAC—total anthocyanin content (mg/100 g).

traits are mostly expected in a watermelon genotype, and a selection can be carried out regarding the study, such as for SSC and other field-attributing traits. Cluster I is more divergent, whereas Cluster III is more divergent for phytochemical traits such as B. caro, Vit. C, TFC, and TPC. These two clusters are more important for heterosis breeding. A similar result was also stated by Zhao et al. [70] and Wilkinson and Friendly [71].

3.6. Estimation of Genetic Parameter. According to Arslanoglu et al. [72], greater variability ensures better changes of producing new desirable forms. So, existing variation among the genotypes is very important to select a superior genotype for breeding purposes. In the present study, the variation that existed among the genotypes was estimated as CV. Medium to high estimates for both GCV percentage (GCV%) and PCV percentage (PCV%) were obtained in the case of quantitative traits that were registered for the traits (Table 5), viz. VL (11.44% and 12.95%), leaf number per plant (11.92% and 13.74 %), days of first flowering (16.58% and 17.12%), time of fruit ripening (24.15% and 25.54%), FF (16.82% and 20.41%), FW (117.88% and 118%), PeT (75.99% and 77.51 %), TY (18.48% and 18.53%, respectively), SSC (33.03.68% and 33.5%), B. caro (25.45 and 25.89), TAC (24.41% and 24.51%), TPC (12.99% and 13.43%), which suggest greater

Table 5: Estimations of statistical and genetic parameters for morphological and phytochemical traits of 13 watermelon genotypes.

Traits	Phenotypic variance (σ^2_P)	Genotypic variance (σ^2_g)	GCV (%)	PCV (%)	Heritability (%h^2_b)	GA	GA (%)
HL	1.60	1.77	19.42	20.44	90.2	2.47	38.00
CL	0.26	0.30	26.21	28.31	85.8	0.97	50.01
CW	0.39	0.40	42.59	43.30	96.7	1.27	86.29
VL	2571.73	3296.45	11.44	12.95	78	92.27	20.81
LPP	608.09	807.80	11.92	13.74	75.3	44.07	21.31
LBL	3.78	4.47	11.33	12.33	84.5	3.68	21.46
LBW	7.61	9.49	13.25	14.79	80.2	5.09	24.44
PeL	7.39	7.89	22.30	23.04	93.6	5.42	44.44
SD	0.01	0.01	20.99	21.98	91.2	0.15	41.29
DFF	0.01	0.01	16.58	17.12	93.9	0.22	33.11
TR	0.12	0.14	24.15	25.54	89.4	0.69	47.03
FF	0.01	0.01	16.82	20.41	67.8	0.13	28.55
FW	0.05	0.05	117.88	118.00	99.7	0.45	242.58
PeT	0.12	0.13	75.99	77.51	96.1	0.70	153.47
FL	0.03	0.03	3.34	3.43	94.3	0.36	6.68
FrW	12.85	13.80	7.30	7.57	93.1	7.12	14.51
TY	3.17	3.18	18.48	18.53	99.4	3.66	37.97
SL	83.46	90.41	8.62	8.98	92.3	18.08	17.07
SW	533.46	536.27	14.49	14.53	99.4	47.45	29.77
HSW	0.00	0.00	69.03	69.03	99.1	0.04	142.19
Chlo.	13.63	13.74	23.14	23.23	99.2	7.58	47.48
SSC	1.32	1.36	33.03	33.50	97.2	2.33	67.08
pH	0.29	0.29	19.11	19.32	97.8	1.09	38.95
Vit.C	15.77	17.04	14.00	14.56	92.5	7.87	27.75
B. caro	0.02	0.02	25.45	25.89	96.62	0.31	51.53
Lyco	4.30	5.42	5.72	6.43	79.28	3.80	10.50
TAC	1.14	1.15	24.41	24.51	99.1	2.19	50.06
TPC	9.57	10.23	12.99	13.43	93.6	6.17	25.89
TFC	31.49	35.75	7.77	8.28	88.08	10.85	15.01

Note: o^2_g = genotypic variance, o^2_P = phenotypic variance, GCV (%) = genotypic coefficient of variation, PCV (%) = phenotypic coefficient of variation, h^2_b (%) = broad sense heritability, GA (%) = genetic advance in the percentage of the mean. HL—hypocotyl length (cm), CL—cotyledon length (cm), CW—cotyledon width (cm), VL—vine length (cm), LBL—leaf blade length (cm), LBW—leaf blade width (cm), PeL—petiole length (cm), SD—stem diameter (cm), DFF—days to first flowering (days after transplantation), TR—time of ripening (days after transplantation), FF—fruit firmness (kg/cm^2), FW—flesh width (cm), PeT—pericarp thickness (mm), FL—fruit length (cm), FrW—fruit weight (kg), TY—total yield (ton/ha), SL—seed length (cm), SW—seed width (cm), HSW—weight of 100 seed (g), SSC—soluble solids content (% Brix), pH—fruit juice acidity Chlo.—chlorophyll content (SPAD), Lyco—lycopene (mg/100 mL), B. caro—beta carotene (mg/100 mL), Vit. C—vitamin C (mg/100 g), TPC—total phenol content (mg GAE/kg FW), TFC—total flavonoid content (mg QE/kg FW), TAC—total anthocyanin content (mg/100 g FW).
Abbreviations: GA, genetic advance; LPP, Leaf per plant.

phenotypic and genotypic variability among the accession and responsiveness of the attributes for making further improvement by selection. Moreover, PCV has been found to be higher than GCV for all the traits, which implies the environmental influence on the expression of that trait is higher than the genetic influence. But interestingly, the differences were very negligible, which indicates the minimal environmental influence, and those characters are mainly governed by genetic action. The small differences also imply that both environmental and genetic factors jointly influence the expression of these traits, yet the genetic actions are stronger [73].

High value of heritability suggests the major role of the genetic constitution in the expression of the character, and such traits are considered to be dependable from a breeding point of view [74]. In the present study, all the characters exhibited high heritability values, which ranged from 67.9% to 99.48%. The amount of phenotypic diversity that can be attributed to the average effects of genes is expressed by heritability, which, in turns, establishes the degree of similarity between relatives. Thus, heritability studies the connection between genotypic variance and phenotypic variance as well as their corresponding true genotypic values. High heritability ($\geq$60) values obtained for most of the traits in the present study suggest that these traits may generally be governed by additive gene action, and hence the phenotype would provide a fairly reliable measure of the genotype, which provides scope for selection based on the phenotypic performance [75].

In addition, for better and efficient selection of superior genotypes, high heritability coupled with high GA can give the best result, as heritability anticipates only the chances of

expressing themselves in the future, whereas genetic advancement in breeding progenies refers to the degree to which a character improves in response to a given selection intensity. Moreover, genetic advancement as a percentage of mean gives more accurate outcomes compared to the GA as a percent of mean indicates the expected genetic progress for a particular trait under a suitable selection system. Except FL, FrW, SL, Lyco., TFC; higher values (≥20) of GA as percent of mean coupled with heritability were recorded for almost all the quantitative traits, which indicates these characters are governed by additive gene effects. It may also be concluded that selection on the basis of these characters will be more useful for the improvement of this crop [76].

4. Conclusion

Although the identification of promising watermelon genotypes derived from exotic germplasm exhibiting desirable morphological characteristics, yield-associated traits, and phytochemical attributes poses significant challenges as these characteristics vary with the ecological condition, our research has successfully isolated five genotypes, specifically G3, for high Lyco. content, G4 for lower time for first initiation of flower and high in B. caro content; G9 has been found to have higher TPC, and G7, G8, and G11 were promising in terms of TY and single FrW, which have been recognized as superior. Notably, most of our genotypes (G3, G6, G7, G8, G11, and G12) showed similarity with the commercial variety (G13) as they belong to the same cluster. However, genetic variability and correlation analyses among the desirable traits of tested watermelon genotypes have provided insights for further breeding activities to develop an elite line/variety. Overall, the findings demonstrated that the exotic watermelon genetic resources G3, G4, G7, G8, G9, and G11 carry great value for genetic improvement through breeding techniques. In addition, multilocation trials of these genotypes are necessary for evaluating the broader adaptability and stable performance under varying environmental conditions.

Data Availability Statement

The data generated or analyzed in this study are available from the corresponding author upon request.

Disclosure

After the final revision, all the authors agreed to submit this manuscript.

Conflicts of Interest

The authors declare no conflicts of interest.

Author Contributions

The research was a combined effort of all the authors. The original idea of this study and the methodologies, such as designing the experiment and study framework, were developed by Mehede Hassan Rubel and Pijush Kanti Jhan, while the experiment was executed by Md. Shohel Tanvir and Khadijatul Kobra. Md. Shohel Tanvir, Khadijatul Kobra, and Md. Mostafijur Rahman worked collaboratively in gathering and managing data from the field and laboratory. Data analysis and visualization were performed by Khadijatul Kobra with the help of Najmul Hossain, while the interpretation and initial draft of this manuscript were framed by both Md. Shohel Tanvir and Khadijatul Kobra; Md. Mostofa Kamal and Shimul Das reviewed and edited the manuscript. Md. Shohel Tanvir and Khadijatul Kobra contributed equally to this work.

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