ISSN: 2621-4709 E-ISSN: 2621-2528
Journal of Applied Agricultural Science and Technology
Vol. 9 No. 4 (2025): 516-527

Phenotypic Evaluation and Potential of Superior Varieties in Hybrid Watermelon (F1) from Single Cross

Anung Wahyudi [a,*], Yesika Tarigan [a], Ria Putri [a], Akbar Hidayatullah Zaini [a], Septiana [a], April Lia Sahidah [a]

[a] Department of Food Crop Cultivation, Seed Technology Study Program, Politeknik Negeri Lampung, Bandar Lampung, Indonesia

Abstract. *Superior hybrid watermelon seeds developed by university plant breeders are currently very limited, with most farmers relying on seeds from national seed companies. This research aims to identify the superior characteristics of watermelon plants, both qualitatively and quantitatively. This study employed a Randomized Block Design (RBD), with six F1 hybrid watermelon lines and four control varieties as factors. Data were analyzed using the F-test, and significant differences were further examined using the Least Significant Difference (LSD) test at the 5% level. Qualitative data were used to cluster analysis based on agronomic characteristics, calculated using NTSYS software. The results indicate significant variations in several morphological and agronomic traits among watermelon genotypes. Genotype WM 2210-1606 is superior in stem diameter, flowering time, and early harvest. Genotype WM 2210-1110 excels in vine and leaf length. GARNIS has the highest fruit weight, and WM 2210-1606 shows higher sugar content at the fruit's edge. Cluster analysis divides the genotypes into three main groups based on trait similarities. These variations highlight the potential for improving watermelon quality through breeding superior genotypes.*

Keywords: *characterization; plant breeding; production; seed.*

Type of the Paper: Regular Article.

1. Introduction

Watermelon (*Citrullus lanatus*) is a summer plant valued for its sweet and juicy flesh. It is rich in phytochemicals that confer health benefits, including reducing the risk of cancer, heart disease, diabetes, and eye disorders [1–3]. Due to its refreshing taste and popularity, the demand for watermelon is very high. Watermelon is an economically valuable plant commonly cultivated in tropical and subtropical regions. In Southeast Asia, Indonesia is the second-largest producer after Vietnam [4,5]. Currently, over 1,200 watermelon cultivars are available in various sizes, colors, and seed types [6].

Superior hybrid watermelon seeds developed by university plant breeders are currently very limited, with most farmers using seeds from national seed companies. One way to produce superior and stable seeds is through hybrid variety development. According to Patel et al. [7], high-yield seeds are economically important, motivating breeders to develop high-quality varieties or

https://doi.org/10.55043/jaast.v9i4.473.
Received June 23, 2025; Received in revised form September 2, 2025; Accepted November 24, 2025; Published November 30, 2025
* First corresponding author
Email: anung@polinela.ac.id

hybrids. Superior hybrid watermelon varieties are expected to generate certified, disease-resistant, and adaptable cultivars suitable for large-scale farming [4,8,9]. Plants are considered superior when they have high productivity and strong growth [10].

The production of superior melon seeds through artificial hybridization involves crossing two genetically different parents [11]. According to Mwangangi et al. [12], hybridization aims to create plant diversity, combine superior traits, and develop hybrid varieties. The process starts with hybridization to form an initial population, which is then purified into pure lines by self-pollination until the seventh generation or until a homozygous genotype is achieved [13]. Kayes [14] highlights that morphological characterization is a simple, reliable, and cost-effective method for assessing plant similarities and selecting superior parents. Research on watermelon breeding is limited, with only a few universities conducting such programs [15]. The Applied Seed Technology Program at Lampung State Polytechnic has been breeding watermelon since 2014, producing six hybrids (WM 2210-0806; WM 2210-0104; WM 2210-1110; WM 2210-0308; WM 2210-1204; and WM 2210-1606). This study aims to characterize these six hybrids (F1), identify their phenotypic traits, determine superior varieties, and compare them with four control varieties for varietal release.

2. Materials and Methods

2.1. Materials

This research was conducted from September to December 2023 at the Seed Teaching Farm (STEFA), Research and Hybrid Seed Production Center, Food Crop and Horticulture, Lampung State Polytechnic. The study materials included six F1 hybrid watermelon genotypes from single crosses between the following parents: WM 08-19-1 x WM 08-19-1 (WM 2210-0806), WM 01-3-3-4-1 x WM 04-12-11-1-1 (WM 2210-0104), WM 11-1-2-2-8 x WM 10-1-1-9-10 (WM 2210-1110), WM 03-27-21 x WM 08-6-14 (WM 2210-0308), WM 12-1-5 x WM 04-1-5-10 (WM 2210-1204), and WM 16-1-5-6-3 x WM 06-1-11-5 (WM 2210-1606), and four hybrid control varieties: F1 Garnis (PT. East West Seed Indonesia), Esteem (PT. Bisi International Tbk), Jamanis (PT. Prabu Agro Mandiri), and Mardy (PT. Benih Citra Asia).

2.2. Experimental design and analysis

The research employed a one-factor Randomized Block Design (RBD) with F1 hybrid watermelon as the factor. Six F1 hybrid lines and four control varieties were tested with two repetitions, resulting in 20 experimental units. Three samples were taken from each unit, totaling 60 plant samples. Data were analyzed using the F test, and significant differences were further examined using the Least Significant Difference (LSD) test at the 5% significance level. Statistical analyses were performed using statistical product and service solutions (SPSS) version 16.0.

According to Pan et al. [16], the linear model for F-Test used is expressed as follows Eq. (1).

$$\mathbf{Yij} = \mu + \alpha\mathbf{i} + \boldsymbol{\beta}\mathbf{j} + \boldsymbol{\varepsilon}\mathbf{ij} \quad (1)$$

Explanation:

- Y_{ij} = Observation on the i-th treatment and j-th replication
- μ = General mean
- αi = Effect of the i-th line treatment
- βj = Effect of the j-th block
- εij = Experimental error effect from the i-th variety and the j-th block
- i=1,2,3,...,8
- j=1,2,3

2.3. Phenotypic Characterization and Cluster Analysis

Color observations based on the RHS mini chart. Cluster analysis (dendrogram) was conducted using agronomic characteristics in NTSYS software. Qualitative data were converted to binary, and the UPGMA method (Unweighted Pair-Group Method with Arithmetic Mean) was applied for the analysis.

3. Results and Discussion

3.1. Quantitative Characters on Vegetative Growth Parameters

Genotype tests showed variations due to the unique characteristics of each genotype, although overall growth, flowering, and harvest quality were good. Quantitative traits showing significant differences included stem diameter, internode length, tendril length, leaf length, and leaf width. The F-test showed significant differences in these traits, with variations ranging from 5.81% to 11.45%. Stem diameter (0.49-0.88 cm) and internode length were measured during the flowering phase. Genotype WM 2210-1606 had the largest stem diameter (0.88 cm), while WM 2210-1110 had the longest internodes and tendrils (330.83 cm) and leaf length (20.22 cm). WM 2210-1110 and WM 2210-0104 had the widest leaves (Table 1).

Table 1. Recapitulation of quantitative growth parameters

Genotype	Stem Diameter (cm)	Internode Length (cm)	Tendril Length (cm)	Leaf Stalk Length (cm)	Leaf Length (cm)	Leaf Width (cm)
WM 2210-0104	0.74 cd	8.29 d	266.83 bc	7.57 abc	18.24 bcd	18.16 cd
WM 2210-1204	0.67 bc	6.63 c	256.50 abc	7.14 ab	16.64 ab	15.19 ab
WM 2210-0806	0.76 cd	8.90 de	263.17 bc	9.43 cd	19.39 cd	17.39 bcd
WM 2210-1606	0.88 d	8.25 d	275.50 c	9.29 cd	16.68 ab	15.63 ab
WM 2210-0308	0.49 a	3.68 a	223.50 a	9.59 d	17.81 abc	17.55 bcd
WM 2210-1110	0.71 bc	9.65 e	330.83 d	8.68 bcd	20.22 d	18.47 d
ESTEEM	0.55 ab	5.53 b	275.00 c	5.68 a	16.36 ab	14.51 a
GARNIS	0.71 bc	6.38 bc	282.17 c	8.75 bcd	17.77 abc	16.21 abcd
JAMANIS	0.67 bc	8.80 de	235.17 ab	9.35 cd	15.68 a	15.81 abc
MARDY	0.54 ab	6.70 c	279.50 c	8.71 bcd	17.14 abc	15.46 ab
LSD 5%	0.17	1.01	35.33	2.00	3.64	3.31
CV%	11.45	6.11	5.81	10.51	5.91	6.41

Explanation: The numbers in each column and row followed by the same letter are not significantly different at the 5% level based on the LSD test.

A larger diameter allows the plant to better support branches and fruits [17,18]. Genotype WM 2210-1606 had the largest stem diameter (0.88 cm) among all genotypes. Differences in vine length among watermelon hybrids were influenced by genotype, environment, and plant vigor, similar to findings in cucumber studies [19,20]. WM 2210-1110 had the longest internodes, vines, and leaves, while WM 2210-0308 had the longest petioles. Leaf traits, which are important for photosynthesis and branch formation, include crown width, length, and width [21].

Quantitative traits observed include components of plant yields influenced by genetic and environmental factors [22,23]. Vegetative growth before the generative phase plays an important role in production and is controlled by many genes, requiring several generations to improve [24]. Agronomic traits can be improved through breeding, and genetic diversity can be studied using morphological and agronomic traits [25]. Genetic characterization is essential for identifying valuable resources, although environmental factors also affect traits and harvest time [26,27]. Significant differences in growth and yield between genotypes and environments have been observed, supporting the development of superior genetic material [28-30].

3.2 Flowering and Harvest Age Parameters

Significant differences were also observed in generative traits, including female and male flowering age, harvest age, fruit weight, fruit diameter and length, fruit skin and flesh thickness, and sweetness at fruit's edge and center. Male and female flowering ages were recorded when 50% of the plants flowered, at 32-37 HST (female) and 20-26.5 HST (male). Genotypes WM 2210-1606 and GARNIS had the fastest female flowering (32 HST), followed by WM 2210-1204 and WM 2210-0308 (33 HST), while WM 2210-0104 and JAMANIS flowered latest (37 HST). The fastest male flowering occurred in WM 2210-1204 and GARNIS (20 DAP), followed by WM 2210-0308 and WM 2210-1110 (22 DAP), with JAMANIS flowering last (26 DAP). Harvest age ranged from 50-55.5 days, with WM 2210-1606 having the earliest harvest (Table 2).

Watermelon is a monoecious plant, producing both male and female flowers on the same plant, with male flowers appearing first on the lower nodes, followed by female flowers. Early emergence of female flowers on the lower nodes indicates earlier maturity [31,32]. Significant variation in flowering time was observed among genotypes: male flowers bloomed at 20-26 days after planting (DAP), and female flowers at 32-37 DAP. WM 2210-1606 had the earliest female flowers (32 DAP), and WM 2210-1204 had the earliest male flowers (22 DAP), affecting harvest time, with WM 2210-1606 reaching the earliest harvest at 50 DAP.

Differences in flowering time reflect genetic diversity and affect harvest duration, which is primarily genetically determined but also influenced by environmental factors. Harvest time is critical for developing varieties with different life cycles, providing farmers greater flexibility in planting [33].

Table 2. Data on female flowering age, male flowering age, and harvest age

Genotype	Female Flowering Age (DAP)	Male Flowering Age (DAP)	Harvest Age (DAP)
WM 2210-0104	37.50 e	23.00 abc	54.50 bc
WM 2210-1204	33.00 abc	20.00 a	54.51 bc
WM 2210-0806	35.50 cde	23.50 bcd	52.50 ab
WM 2210-1606	32.50 ab	24.00 cd	50.00 a
WM 2210-0308	33.50 abcd	22.00 abc	54.00 bc
WM 2210-1110	34.00 abcd	22.50 abc	55.01 bc
ESTEEM	36.00 de	25.00 cd	54.53 bc
GARNIS	32.00 a	20.50 ab	55.50 c
JAMANIS	37.00 e	26.50 d	55.02 bc
MARDY	35.00 bcde	24.50 cd	55
LSD 5%	4.1	3.06	2.63
CV%	3.83	5.84	2.15

Explanation: The numbers in each column and row followed by the same letter are not significantly different at the 5% level based on the LSD test.

3.3 Quality and Yield Parameters

Quantitative traits for fruit diameter, fruit length, number of seeds per fruit, and seed weight per fruit are shown in Table 3. Meanwhile, the fruit weight, skin thickness, flesh thickness, center sweetness, and edge sweetness are shown in Table 4.

Table 3. Follow-up quantitative variables on fruit diameter, fruit length, number of seeds per fruit, and seed weight per fruit

Genotype	Fruit Diameter (cm)	Fruit Length (cm)	Number of Seeds per Fruit	Seed Weight per Fruit (mg)
WM 2210-0104	14.07 bc	23.97 b	136.50 b	4.05 abc
WM 2210-1204	12.67 ab	19.32 a	156.83 b	5.58 bcd
WM 2210-0806	14.08 bc	24.18 b	191.67 cd	6.43 cd
WM 2210-1606	13.55 bc	25.93 bc	229.83 e	9.23 e
WM 2210-0308	13.28 bc	22.72 ab	160.17 bc	5.20 abcd
WM 2210-1110	13.03 bc	24.3 b	129.67 b	4.43 abc
ESTEEM	11.37 a	19.6 a	82.83 a	2.72 a
GARNIS	13.85 bc	24.78 bc	208.83 de	7.57 de
JAMANIS	13.07 bc	28.05 c	157.17 b	3.35 ab
MARDY	14.2 c	23.68 b	199.50 de	7.20 de
LSD 5%	3.31	5.52	34.07	2.52
CV%	5.01	6.62	9.11	19.99

Explanation: The numbers in each column and row followed by the same letter are not significantly different at the 5% level based on the LSD test.

Fruit diameters ranged from 11.37 cm to 14.2 cm, with MARDY, WM 2210-0104, and WM 2210-0806 having the largest. Fruit lengths varied significantly, with WM 2210-1204 and ESTEEM having the shortest (19 cm) and JAMANIS the longest (28.05 cm). Seed counts per fruit ranged from 82.83 to 229.83, all classified as "few" categories (under 400 seeds). ESTEEM had the fewest seeds and lowest seed weight, while WM 2210-1606, GARNIS, and MARDY had higher seed counts and heavier seed weight, suggesting better seed quality.

Table 4. Follow-up quantitative variables on fruit weight, skin thickness, flesh thickness, center sweetness, and edge sweetness

Genotype	Fruit Weight (kg)	Skin Thickness (cm)	Flesh Thickness (cm)	Center Sweetness (% Brix)	Edge Sweetness (% Brix)
WM 2210-0104	2.13 abc	1.28 bcd	11.18 bc	10.87 cd	9.08 cd
WM 2210-1204	1.90 a	1.52 d	9.77 b	10.69 bc	8.37 abc
WM 2210-0806	2.70 cd	1.47 cd	11.27 de	10.38 abc	8.65 bcd
WM 2210-1606	2.63 cd	1.32 bcd	11.00 de	10.57 abc	9.28 d
WM 2210-0308	2.23 bcd	1.27 bcd	10.78 bc	10.6 abc	9.18 cd
WM 2210-1110	2.37 bcd	1.43 bcd	9.85 cd	9.95 a	8.48 abcd
ESTEEM	1.50 a	0.9 a	9.55 a	11.45 d	8.88 bcd
GARNIS	2.93 d	1.18 b	11.30 e	10.13 ab	7.65 a
JAMANIS	2.65 cd	1.23 bc	10.38 de	10.67 bc	8.17 ab
MARDY	2.77 cd	1.38 bcd	11.73 e	10.88 cd	9.1 cd
LSD 5%	0.72	0.26	6.95	4.18	0.88
CV%	13.38	8.98	3.78	2.72	4.47

Explanation: The numbers in each column and row followed by the same letter are not significantly different at the 5% level based on the LSD test.

Analysis of ten watermelon genotypes showed fruit weights ranging from 1.50 kg to 2.93 kg. ESTEEM and WM 2210-0104 had the lowest weights (1.50-1.90 kg), while GARNIS had the highest. ESTEEM had the thinnest skin (0.9 cm), while GARNIS, MARDY, and others had thicker flesh than ESTEEM and WM 2210-0104. ESTEEM also had the thinnest flesh. Regarding sugar content, measured as total soluble solids (TSS), ESTEEM, WM 2210-0104, and MARDY were sweetest at the fruit center, while WM 2210-1606 was sweeter at the edge.

Watermelon fruit quality is determined by factors such as sugar content, appearance, flesh thickness, and taste, which affect consumer preferences [34]. The breeding program aims to develop superior varieties with short growth periods, high productivity, thick fruit skin, and high sugar content [5]. This aligns with Napolitano et al. [35] who stated that melon breeding focuses on increasing productivity, improving traits, fruit quality, and resistance to pests and diseases. Selecting appropriate parents is crucial for producing competitive hybrids with good quality and yield [36]. Among the genotypes studied, GARNIS had the heaviest fruit (2.93 kg), followed by WM 2210-0806 (2.70 kg) and WM 2210-1606 (2.63 kg). The smallest fruit weight was found in the ESTEEM and WM 2210-1204.

Fruit size and shape are influenced by length and circumference, which are positively correlated with fruit weight [31,32]. The largest fruit diameter was observed in the MARDY cultivar, and the longest fruit in the JAMANIS genotype. The thickest fruit skin occurred in WM 2210-1204, WM 2210-0806, and WM 2210-1110, increasing storage and transportation durability. Total soluble solids (TSS), measured at the fruit center and edge, are key indicators of sweetness, increasing as enzymes such as α- and β-amylases convert starch into sugars during ripening [31]. ESTEEM had the highest TSS in the center, WM 2210-1110 the lowest, and WM 2210-1606 the highest at the edge. Watermelon flesh contains approximately 8-10% solids and 20-25% sugars,

with sugar accumulation increasing as the fruit ripens due to changes in enzyme activity [37–39]. Morphological variations provide valuable genetic resources for improving agronomic traits through plant breeding programs, including those using mutagen treatments [40].

Seed production is an important economic factor, and breeders aim to develop varieties with few seeds. WM 2210-1606 produced the highest number of seeds and the heaviest seeds per fruit, while ESTEEM produced the fewest. Watermelon seeds are categorized as abundant (over 600 seeds per fruit), moderate (400-600), or few (below 400) [37]. Seeds store food reserves that affect viability, storage, germination, and vigor, thereby affecting overall seed quality [5].

3.4 Qualitative Variables

Plant characterization involves observing traits for grouping based on morphological characters, which are easily assessed and show clear variation. Cluster analysis using the UPGMA method was conducted based on characteristic similarities, producing a dendrogram of six genotypes and four control varieties (Fig. 1).

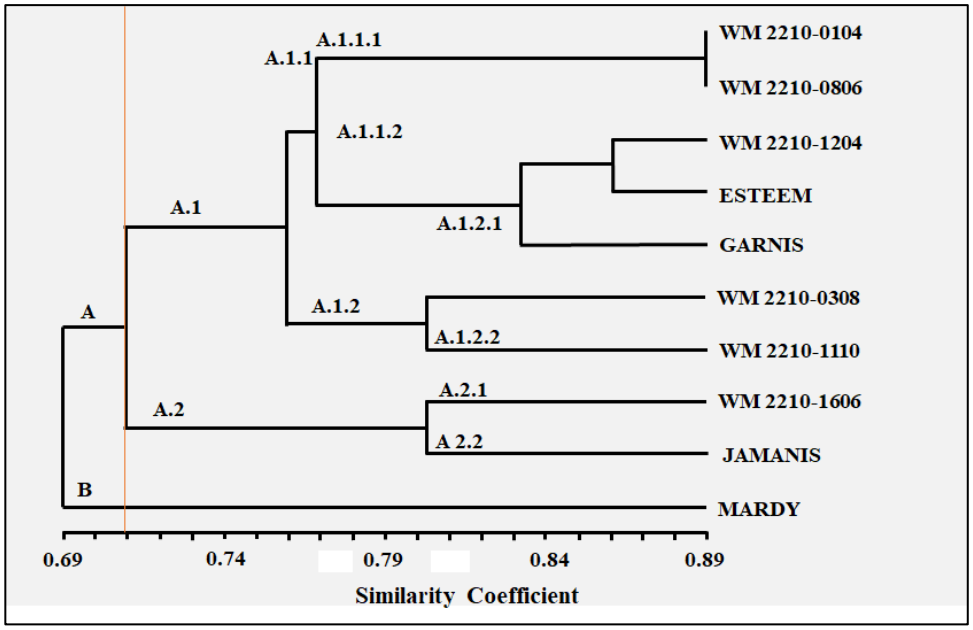

Fig. 1. Dendrogram analysis based on qualitative character observations. Kluster I (A1): WM 2210-0104, WM 2210-0806, WM 2210-1204, Esteem, Garnis, WM 2210-0308, WM 2210-1110. Kluster II (A2): WM 2210-1606, WM 2210-Jamanis. Kluster III (B): Mardy.

The cluster analysis/dendrogram results divide it into three clusters, with a similarity level of 69%. An index similarity below 0.60 indicates a distant relationship. Cluster I included seven genotypes with similar traits: WM 2210-0104, WM 2210-0806, WM 2210-1204, ESTEEM, and GARNIS. Cluster II included WM 2210-1606 and JAMANIS, with similarity in various characters. Cluster III only contained MARDY, exhibiting specific characteristics.

3.5 Qualitative Characteristic Data

The ten tested watermelon genotypes and the control had seeded fruit types with elongated shapes. The rind color was green, with varying RHS codes among genotypes. The fruit stripe types

ranged from thin to medium to thick. Most fruits had red flesh with differing RHS codes, although a few genotypes displayed red-orange flesh. At the post-harvest phase, most genotypes had a crunchy texture, except one with a sandy texture. All tested and controlled genotypes had sweet-tasting flesh (Table 5 and Table 6).

Table 5. Qualitative Characteristics of 10 Watermelon Genotypes

GENOTIP	Fruit shape	Fruit skin color	Fruit striations	Fruit flesh color	Fruit Flesh Texture	Fruit Type
WM 2210-0104	Oval	RHS N189A (Grayed Green Group)	Thin	RHS 43B (Red)	Crisp	Seeded
WM 2210-1204	Oval	RHS 138 (Green Group)	Medium	RHS 9A (Yellow)	Crisp	Seeded
WM 2210-0806	Oval	RHS N189A (Grayed Green Group	Thin	RHS 43B (Red)	Crisp	Seeded
WM 2210-1606	Oval	RHS 143A (Green Group)	Medium	RHS 42 (Red)	Crisp	Seeded
WM 2210-0308	Oval	RHS 143A (Green Group)	Medium	RHS 41B (Red)	Grainy	Seeded
WM 2210-1110	Oval	RHS N189A (Grayed Green Group	Medium	RHS 43B (Red)	Crisp	Seeded
ESTEEM	Oval	RHS NN 137 A (Green Group)	Medium	RHS 14A (Yellow-Orange)	Crisp	Seeded
GARNIS	Oval	RHS NN 137 A (Green Group)	Medium	RHS 6A (Yellow)	Crisp	Seeded
JAMANIS	Oval	RHS NN 137 A (Green Group)	Medium	RHS 45A (Red)	Crisp	Seeded
MARDY	Oval	RHS 139A (Green Group)	Thin	RHS 45B (Red)	Crisp	Seeded

Table 6. Data observation of qualitative characteristics of ten watermelon genotypes

Variable	Qualitative Character	Genotype
Fruit Type	Seeded (10 Genotype)	A1,A2,A3,A4,A5,A6,A7,A8,A9, and A10
Fruit Shape	Oval (10 Genotype)	A1,A2,A3,A4,A5,A6,A7,A8,A9, and A11
Fruit skin color	Grayed Green Group N189A (3 Genotype)	A1,A3, and A6
	Green Group 138 (1 Genotype)	A2
	Green Group 143A (2 Genotype)	A4 and A5
	NN 137 A (3 Genotype)	A7,A8, and A9
	Green Group 139A (1 Genotype)	A10
Fruit striations	Thin (3 Genotype)	A1,A3, and A10
	Medium (4 Genotype)	A2,A5,and A8
	Medium (3 Genotype)	A4,A6,A7, and A9
Fruit flesh color	RG 41b (1 Genotype)	A5
	RG 42A (1 Genotype)	A4
	RG 43B (3 Genotype)	A1,A3, and A6
	RG 45B (1 Genotype)	A10
	RG 45A (1 Genotype)	A9
	YG 9A (1 Genotype)	A2
	YDG 14 A (1 Genotype)	A7
	YG 6 A (1 Genotype)	A8
Fruit flesh texture	Crisp (9 Genotype)	A1,A2,A3,A4,A6,A7,A8,A9, and A10
	Grainy (1 Genotype)	A5
Seed shape	Broad Oval, Flat (10 Genotype)	A1,A2,A3,A4,A5,A6,A7,A8,A9, and A10
	Flat (4 Genotype)	A1,A7,A8, and A9
Seed size	Medium (3 Genotype)	A2,A4,and A5
	Long (3 Genotype)	A3,A6,and A10

Qualitative traits in plants are controlled by major genes (simplegenic) and are minimally affected by the environment, making them key markers for plant varieties [41]. In watermelon,

these traits include fruit type, shape, skin color, line type, flesh color and texture, seed shape, and size. Table 5 shows that watermelon can have seeded, elongated fruit, green skin with various line thicknesses, red or yellow flesh, and a crisp texture. Seed lengths vary from short to long, and market-preferred shapes include round, oval, and elongated [5].

4. Conclusions

The study showed significant variations in several morphological and agronomic characteristics among watermelon genotypes. WM 2210-1606 was superior in stem diameter, had the fastest flowering time, and the earliest harvest. WM 2210-1110 excelled in vine and leaf length, while GARNIS produced the heaviest fruit, and WM 2210-1606 showed higher sugar content at the fruit edge. Cluster analysis grouped the genotypes into three main groups based on trait similarities. Overall, these variations indicate the potential for improving watermelon quality through the breeding of superior genotypes.

Abbreviations

WM	Watermelon
RBD	Randomized Block Design
LSD	Least Significant Difference
RHS	Royal Horticultural Society
NTSYS	Numerical Taxonomy and Multivariate Analysis System software
UPOV	The International Union for the Protection of New Varieties of Plants

Data availability statement

The data presented in this study will be made available upon reasonable request to the corresponding author.

Credit authorship contribution statement

Anung Wahyudi: Conceptualisation, Methodology, Validation, Writing-original draft, Visualisation, Validation. **Yesika Tarigan:** Data collection, Investigation. **Ria Putri**: Data curation, Formal analysis. **Akbar Hidayatullah Zaini**: Data curation, Formal analysis. **Septiana:** Project administration. **April Lia Sahidah:** Writing draft.

Declaration of Competing Interest

The authors of this manuscript declare no conflict of interest or competing interest.

Acknowledgement

This study was funded by the Applied Research Scheme Batch 1 (2024) from the Ministry of Education, Culture, Research, and Technology, in collaboration with the Directorate General of Vocational Education, under research grant contract number 56/SPK/D.D4/PPK.01.APTTV/III/2024.

References

[1] Naz A, Butt MS, Sultan MT, Qayyum MM, Niaz RS. Watermelon lycopene and allied health claims. EXCLI J 2014;3:650-660. https://pmc.ncbi.nlm.nih.gov/articles/PMC4464475/.

[2] Mohanta S, Mandal J. Evaluation of some watermelon hybrids and cultivars under lateritic belt of West Bengal. J Crop Weed 2019;15:78-82. https://www.cropandweed.com/archives/2019/vol15issue1/15-1-11.pdf.

[3] Kumar U, Prasad S, Tiwari RK, Sinha BM. Evaluation of high yielding varieties of watermelon for river bed cultivation under solar based boat operated gravitational drip irrigation. J. of Pharmacognosy and Phytochemistry 2020;9:214-217. https://l1nq.com/JmiGb.

[4] Rahmandhias DT, WA Wibowo, Sufi A, Daryono BS. Stability of watermelon phenotype characters (Citrullus lanatus (Thunb.) Matsum. & Nakai) from crossing ♀ 'Putri Delima' with ♂ 'Maduri'. Biogenesis: J Ilmiah Biol 2021;9:50–56. http://dx.doi.org/10.24252/bio.v9i1.17719.

[5] Wahyudi A, Sari MF, Rajamin I, Arsri M. Evaluation of proximate analysis and yield production of watermelon in Lampung, Indonesia. Biodiversitas J Biol Divers 2023;24:6017-6022. http://dx.doi.org/10.13057/biodiv/d241122.

[6] Burton-Freeman B, Freeman M, Zhang X, Sandhu A, Edirisinghe I. Watermelon and l-citrulline in cardio-metabolic health: review of the evidence 2000-2020, CurrAtherosclerosis Rep 2021;23:81. https://doi.org/10.1007/s11883-021-00978-5.

[7] Patel MK, Prajapati NN, Chaudhari BA, Patel AB. Heterosis analysis for seed yield and quality traits in karingada [Citrullus lanatus (Thumb) Mansf.]. The Pharma Innova J 2020;9: 186-194. https://doi.org/10.22271/tpi.2020.v9.i5d.4651.

[8] Wahyudi A, Nazirwan, Kartahadimaja J, Setyawan AB, Mustakim NA, Askhary FA, Katfar BJ. Evaluation of yields on new varieties of hybrid watermelon. IOP Conf Ser Earth Environ Sci 2022;1012:012070. https://doi.org/10.1088/1755-1315/1012/1/012070.

[9] Adiredjo AL, Roviq M, Ardiarini NR, Leorentina AB. Performance of melon (Cucumis melo L.) hybrids across diverse environmental conditions. SABRAO J Breed Genet 2024;56:211–223. https://doi.org/10.54910/sabrao2024.56.1.19.

[10] Wahyudi A, Dewi R. Quality and fruit production improvement using the cultivation technology system "ToPAS" in 12 varieties of hybrid watermelons. J Penelitian Pertanian Terapan 2017;17:17–25. http://dx.doi.org/10.25181/jppt.v17i1.4 .

[11] Acquaah G. Breeding selected crops. In: Principles of plant genetics and breeding. 2nd ed. Chichester: John Wiley & Sons; 2012, p. 575. https://doi.org/10.1002/9781118313718.part9.

[12] Mwangangi I, Muli J, Neondo J. Plant hybridization as an alternative technique in plant breeding improvement. Asian J Res Crop Sci 2019;4:1-10. https://doi.org/10.9734/ajrcs/2019/v4i130059.

[13] Suwarno WB, Sobir, Gunawan E. Melon breeding: past experiences and future challenges. In: Proceedings of the International Seminar on Tropical Horticulture 2016: The Future of Tropical Horticulture; 2016 Nov 28–29; Bogor, Indonesia. Bogor: International Seminar on Tropical Horticulture; 2016. http://repository.ipb.ac.id/handle/123456789/88442.

[14] Kayes E. Morphological and molecular characterization of watermelon genotypes using RAPD markers. Fundam. Appl. Agric 2018;3:573–578. https://www.f2ffoundation.org/faa/index.php/home/article/view/241.

[15] Wahyudi A, Mutaqin Z, Dulbari. Evaluasi galur semangka berbiji tipe lonjong dan non biji tipe bulat. J Planta Simbiosa 2019;1:1-9. https://dx.doi.org/10.25181/jplantasimbiosa.v1i1.1258.

[16] Pan R, Wan Z, Wu M, Lu S, Tang L**.** Biomechanical analysis of Camellia oleifera branches for optimized vibratory harvesting. Agriculture 2024;14:2220. https://doi.org/10.3390/agriculture14122220.

[17] Triyanti VR. The Effect of Bokashi Fertilizer on the Growth and Yield of Watermelon (*Citrullus vulgaris* Schard) Variety Tafuma F1: Faculty of Agribusiness and Agricultural Engineering, Subang University. Agrorektan Journal 2018;5. https://ejournal.unsub.ac.id/index.php/agrorektan/article/view/992

[18] Ahmadi M, Souri MK. Growth characteristics and fruit quality of chili pepper under higher electrical conductivity of nutrient solution induced by various salts. Agrivita J Agric Sci 2020;42:143–152. https://doi.org/10.17503/agrivita.v42i1.2225.

[19] Gondi SP, Ganiger VM, Bhuvaneshwari G, Madalageri MB. Evaluation of oriental pickling melon (*Cucumis melo* L. var. conomon) genotypes for pest and disease reaction under northern dry zone of Karnataka. J Environ Ecol 2016;7:29–36. http://dx.doi.org/10.5296/jee.v7i1.9630.

[20] Kamagoud S, Shet RM, Nishani S, Hongal S, Hanchinmani CN, Prashanta A. Assessment of genetic variability among oriental pickling melon (*Cucumis melo* var. conomon) genotypes. IJCS. 2018;6:2630-2633. https://www.chemijournal.com/archives/?year=2018&vol=6&issue=4&ArticleId=3394&si=false.

[21] Singh SP. Broadening the genetic base of common bean cultivars: A review. Crop Science 2001;41:1659-1675. https://doi.org/10.2135/cropsci2001.1659.

[22] Dalimunthe MB, EL Azwana, Panggabean. Pertumbuhan Dan Produksi Tanaman Cabai Merah (*Capsicum annum* L.) Terhadap Pemberian Pupuk Organik Pada Berbagai Media Tanam. Agrotekma 2016;1:1-11. https://doi.org/10.31289/agr.v2i1.1101.

[23] Fitria E, Kesumawaty E, Basyah B. Peran Trichoderma harzianum sebagai Penghasil Zat Pengatur Tumbuh terhadap Pertumbuhan dan Produktivitas Varietas Cabai (*Capsicum annuum* L.). J Agron Indones 2021;49:45–52. https://dx.doi.org/10.24831/jai.v49i1.34341.

[24] Stoilova T, Pereira G, de Sousa M. Morphological characterization of a small common bean (Phaseolus vulgaris L.) collection under different environments. J Cent Eur Agric 2013;14. http://dx.doi.org/10.5513/JCEA01/14.3.1277.

[25] Singh DP. Studies on extraction, degradation and utilization of lycopene from watermelon. Doctor of Philosophy in Food Technology. The Faculty of Sciences Guru Nanak Dev University: Amritsar; 2016. https://www.semanticscholar.org/paper/Studies-on-Extraction-Degradation-and-Utilization-Singh/57215b47d1e1ab9895099c1dedd71d5233fd7aa7.

[26] Pimenta S, Menezes D, Neder DG, Melo R, Araujo ALR, Maranhão EAA. Adaptability and stability of pepper hybrids under conventional and organic production systems. Hort. Brasileira 2016;34:168-174. http://dx.doi.org/10.1590/S0102-053620160000200004.

[27] Kandel M, Ghimire SK, Ojha BR, Shrestha J. Analysis of genetic diversity among the maize inbred lines (Zea mays L.) under heat stress conditions. J. of Maize Res and Development 2017;3:86-97. https://www.nmrp.gov.np/wp-content/uploads/2015/06/Article-08-2017.pdf.

[28] Sharma VK, Senwal CS, Uniyal SP. Genetic variability and character association analysis in bell pepper (Capsicum annuum L.). J of Hort and Forest 2010;2:58-65. https://doi.org/10.5897/JHF.9000056.

[29] Thul ST, Lal RK, Shasany AK, Darokar MP, Gupta AK, Gupta MM, et al. Estimation of phenotypic divergence in a collection of Capsicum species for yield-related traits. Euphytica 2009;168:189–196. https://link.springer.com/article/10.1007/s10681-009-9882-y.

[30] Syukur M, Sobir, Yulistyan A, Fajriah N, Widodo WD, Maharijaya A. Short communication: Morpho-agronomic performances of bird pepper (Capsicum annuum) lines under varying agro-ecological locations in Indonesia. Biodiversitas 2022;23:4838–4843. https://doi.org/10.13057/biodiv/d230952.

[31] Mohanta S, Mandal J. Performance of watermelon (Citrullus lanatus) in red and laterite zone of West Bengal. J Crop Weed 2016;12:175–177. https://www.researchgate.net/publication/334587739.

[32] Bhagyalekshmi TR, Gasti VD, Evoor S, Gopali JB, Mastiholi AB, Kamble CS. Studies on correlation and path-coefficient analysis for yield and its contributing characters in

watermelon (Citrullus lanatus (Thunb.) Mansf.). J Pharmacogn Phytochem 2020;9:1909-1912. https://www.phytojournal.com/archives?year=2020&vol=9&issue=3&ArticleId=11595.

[33] Padilha HKM, Sigales CV, Villela JCB, Valgas RA, Barbieri, RL. Agronomic evaluation and morphological characterization of chili peppers (Capsicum annuum, Solanaceae) from Brazil. Australian Journal of Basic and Applied Sciences 2016;10:63-70. https://www.alice.cnptia.embrapa.br/alice/handle/doc/1060263.

[34] Monge-Pérez JE. Evaluation of 70 melon (Cucumis melo L.) genotypes grown under greenhouse conditions in Costa Rica. InterSedes 2016;17:73–112. http://dx.doi.org/10.15517/isucr.v17i36.26944.

[35] Napolitano M, Terzaroli N, Kashyap S, Russi L, Jones-Evans E, Albertini E. Exploring heterosis in melon (Cucumis melo L.). Plants 2020;9:282. https://doi.org/10.3390/plants9020282.

[36] da Silva MJ, Carneiro PCS, de Souza CJE, Damasceno CMB, Parrella NNLD, Pastina MM, et al. Evaluation of the potential of lines and hybrids of biomass sorghum. Ind Crops Prod 2018;125:379-385. https://doi.org/10.1016/j.indcrop.2018.08.022.

[37] Syukur M, Sujiprihati S, Yunianti R. Teknik Pemuliaan Tanaman. Revised edition. Jakarta: Penebar Swadaya; 2010. https://books.google.com/books/about/Teknik_Pemuliaan_Tanaman.html?id=icNUCgAAQBAJ.

[38] Soumya V, TV Ramana Rao. Nutritional quality evaluation of four icebox cultivars of watermelon fruit during their development and ripening. Int Food Res J 2014;21: 631-639. http://www.ifrj.upm.edu.my/21%20(02)%202014/29%20IFRJ%2021%20(02)%202014%20Ramano%20Rao%20344.pdf.

[39] Oberoi DPS, Sogi DS. Utilization of watermelon pulp for lycopene extraction by response surface methodology. Food Chem 2017;232:316–321. https://doi.org/10.1016/j.foodchem.2017.04.038.

[40] Hasan N, Choudhry S, Laskar RA. Studies on qualitative and quantitative characters of mutagenized chili populations induced through MMS and EMS. Vegetos 2020;33:793-799. https://link.springer.com/article/10.1007/s42535-020-00164-z.

[41] Carrizo GC, Barfuss MH, Sehr EM, Barboza GE, Samuel R, Moscone EA, et al. Phylogenetic relationships, diversification, and expansion of chili peppers (Capsicum, Solanaceae). Annals of Botany 2016;118:35-51. https://doi.org/10.1093/aob/mcw079.