

A Comprehensive Analysis of the Phenotypic Diversity of Introduced Melon Germplasm Resources in High-altitude Agroecosystems

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Abstract. At high altitudes, low melon (*Cucumis melo* L.) yields are a common problem. This often results from a decrease in atmospheric temperature. Growing melons in greenhouses offers an option in this context, because one can optimize temperature along with other environmental variables. However, screening suitable varieties based on the logistics of the greenhouse is still important. We conducted a study in 2023 and 2024 that focused on comparing 21 melon germplasms in a greenhouse experiment for high yields of winter melons on the Yunnan–Guizhou Plateau. Results show that the growth period of the tested germplasms ranged between 105 and 123 d, with the shortest period observed for YTH-TG-13 and YTH-TG-21. The trait with the highest coefficient of variation was rind/peel thickness (41%), followed by yield (28%) and traits related to yield, such as flesh thickness (31%) and single fruit weight (28%). There was a strong positive correlation between fruit transverse diameter and flesh thickness. The yield-contributing parameters, such as single fruit weight, fruit transverse diameter, fruit longitudinal diameter, and flesh thickness, affected yield significantly ($P < 0.01$). Moreover, the first five principal components explained 80% of the cumulative variations in the original dataset. Fruit longitudinal diameter, fruit transverse diameter, flesh thickness, single fruit weight, and yield were identified as the main indexes for evaluating melon germplasm. Cluster analysis divided the 21 melon germplasm resources into three groups. Group I consisted of low-sugar, small-fruit varieties; group II consisted of large-fruit, high-yield, medium-sugar varieties; and group III consisted of medium-yield, medium-sugar varieties. Subgroup III-C consisted of high-yield, medium-sugar varieties. The top five varieties based on F values are YTH-TG-01 ($F = 13,462$), YTH-TG-18 ($F = 13,089$), YTH-TG-12 ($F = 11,160$), YTH-TG-16 ($F = 11,157$), and YTH-TG-03 ($F = 10,660$), with YTH-TG-21 having the lowest F value ($F = 2888$). Our results suggest these five varieties could grow successfully in high-altitude areas.

Melons (*Cucumis melo* L.) are cultivated as a high-value cash crop throughout the world. They are one of the top 10 most popular fruit worldwide (Andrade et al. 2021; Hu et al. 2013; Lija and Beevy 2021; McCreight et al. 2013; Torres et al. 2020). However, a shortened vegetation period at high altitude as a result of large differences in daytime and nighttime temperatures, and a continual decrease in temperature hamper crop yields and quality (Benavides et al. 2017; Poincelot 1980). This is particularly true for the cultivation of winter melons in mountainous climate such as that found on the Yunnan–Guizhou Plateau. The exact figures of crop yield decline are not available, but they are likely to be substantial.

To reduce inefficiencies of high-altitude agroecosystems, the development of suitable cultivation techniques are needed. In this context, mulching is adopted on a wide scale because it helps to increase the temperature and subsequently reduce the temperature difference between daytime and nighttime

(Bristow 1988; Ekinici and Atilla 2009; Reddy 2016). The efficacy of mulching has been tested on a wide range of crops, including melon. However, regulating temperature under plastic mulch can be challenging. It may become excessively hot, potentially causing injury to seedlings (Johnson and Ernest 2023), or may impair reproductive development in melons, ultimately leading to reduced yields (Sarkar et al. 2013). Alternatively, ventilated high and low plastic tunnels are also used for melon cultivation. The ventilation in tunnels can stabilize temperature, which could lead to greater crop productivity (Choudhary et al. 2021; Jayasurya et al. 2021). However, for this cultivation system, the development of suitable melon varieties is important.

Previous studies had investigated extensively the genetic diversity of melon germplasm resources (Mliki et al. 2001; Monforte et al. 2014; Wang et al. 2021). These studies revealed that phenotypic traits exhibit rich genetic diversity and complex interrelationships

(Pavan et al. 2017; Soltani et al. 2022). Most importantly, and most notably, Pitrat (2013) observed that cultivated melons exhibit a high degree of phenotypic polymorphism, in contrast to the relatively limited variation found in their wild counterparts—a pattern that is consistent with that documented in numerous other domesticated crops. Similarly, Luan et al. (2008) conducted a diversity analysis of melon varieties obtained from India, Africa, Greece, Japan, Europe, the United States, and China. Their study highlighted that the germplasm obtained from China has a high level of genetic diversity that can be used to improve yields. However, studies comparing the performance of Chinese germplasm particularly at high altitudes are limited.

In China, the selection of suitable winter varieties is very important to meet the rising production demand of local markets. Thus, our study compared 21 high-yielding varieties that are available at research institutes and private agricultural companies for high-altitude agroecosystems. We hypothesized that varieties with greater genetic diversity will outperform genetically uniform varieties in terms of crop yield across multiple environments. Our specific objectives included 1) to evaluate phenological manifestations of different germplasms, 2) to determine the distribution frequency of quality traits, and 3) to investigate key growth and yield traits. In addition, we planned to develop reasonable evaluation criteria for melon introduction by tracking the cultivation performance of different varieties. Our results could lay a foundation for the development of the winter melon industry in the Yungui Plateau.

Materials and Methods

Materials and experimental site. A total of 21 melon germplasm accessions were used in this study. YTH-TG-01 ‘Cuiwang 8’, YTH-TG-02 ‘Ruby-6’, YTH-TG-03 ‘Honey Sapphire1’, YTH-TG-04 ‘Honey Sapphire 2’, YTH-TG-05 ‘Honey Sapphire 3’, YTH-TG-06 ‘Sky Sapphire’, YTH-TG-07 ‘Jiaomei’, and YTH-TG-08 ‘Coarse Net 6’ were provided by Beijing Jiaoxue Seedling Technology Development Co Ltd (Beijing, China). Accessions YTH-TG-09 ‘Shuai Guo 580’, YTH-TG-10 ‘DM 101’, YTH-TG-11 ‘DM 104’, and YTH-TG-12 ‘DM 105’ were obtained from the Institute of Vegetables and Flowers, Chinese Academy of Agricultural Sciences (Beijing, China). YTH-TG-13 ‘Zhongtian Hong Xiaoxian’, YTH-TG-14 ‘Zhongtian Huili’, YTH-TG-15 ‘Zhongtian 9’, YTH-TG-16 ‘Zhongtian 51’, and YTH-TG-17 ‘Zhongtian 65’ were obtained from the Fruit Tree Research Institute, Chinese Academy of Agricultural Sciences (Zhengzhou, China). YTH-TG-18 ‘Shuai Guo 66’, YTH-TG-19 ‘Shuai Guo 88’, YTH-TG-20 ‘Snow Pear 1’, and YTH-TG-21 ‘Green Honey 58’ were provided by the Institute of Horticulture, Guangxi Academy of Agricultural Sciences (Nanning, China). Our research was conducted at farmer fields located at Donghui Town (lat. 22°24′6″N, long. 99°48′6″E), Lancang County, China. Ten soil samples (depth, 15 cm) were collected randomly

in a W pattern from the experimental field and then mixed to prepare a composite. The composite sample was used to test the physicochemical characteristics of the experimental soil. The soil was well drained, with a pH of 6.06, and included organic matter (27.4 g·kg⁻¹), hydrolyzable nitrogen (70.53 mg·kg⁻¹), and available phosphorus (21.4 mg·kg⁻¹), potassium (62.19 mg·kg⁻¹), iron (138 mg·kg⁻¹), manganese (29.1 mg·kg⁻¹), copper (3.07 mg·kg⁻¹), and zinc (2.74 mg·kg⁻¹).

Experimental design. All seed germplasms were sown in the nursery 25 Oct 2023. Sixteen-day-old seedlings were transplanted to the ridges in the field plastic greenhouse 1 Dec 2023. The height, width, and spacing of the ridges were 20 × 40 × 50 cm. A randomized block design was used, with three replicates per variety (treatment). Each treatment covered ~700 m², with a total cultivation area of 1.47 ha. One fruit was maintained on the 14th node of the main vine, where female flowers born, using the manual pruning method. All vines except the main vine were removed. Planting density was maintained at 22,500 plants/ha.

Determination of traits. According to Ma et al. (2019), 14 melon fruit traits were investigated (Table 1). The tape measure

(length, 0–5 m; accuracy, 0.1 cm; GOLDLAND® high accuracy measuring tape; Henan Jianghua Measure tools Co., Ltd., Henan, China) method was used to measure fruit retention height, maximum leaf length and width, and fruit longitudinal and transverse diameters. A Vernier caliper (155 mm; accuracy, 0.1 mm; Deli®, Deli Group Co., Ltd., Ningbo, China) was used to measure stem diameter, rind/peel thickness, inner cavity diameter and flesh thickness. A DiFluid refractometer (range, 0%–32%; accuracy, 0.1%; DiFluid® Shenzhen Digitizing Fluid technology Co., Ltd, Shenzhen, China) was used to measure the soluble solids content at the fruit center. A high-precision electronic scale (500 g to 3 kg; accuracy, 0.01 g; Haozhan® Electronic Scale; Kunshan Huake Electronic Technology Co., Ltd., Kunshan, China) was used to measure single fruit weight. Yield was calculated by multiplying average single fruit weight with planting density (22,500 plants/ha).

The physiological stages were also determined. The flowering stage was considered to have occurred when two thirds of the plants had open female flowers with fully expanded corollas and visible stigmas secreting. Fruit set was considered to have occurred when approximately two thirds of the plants had egg-size fruit, with completed shedding of surface hair and the formation of a separation layer at the base of the fruit stalk. The fruit enlargement stage was when two thirds of the plants exhibited a significant enlargement in fruit volume, a reduction in surface hair, an increase in glossiness, darkening of the peel color, and formation of ring-shaped cracks near the stalk. The harvest stage was based on fruit appearance, aroma, firmness, and sugar content. At this stage, the netting pattern on the fruit surface was fully developed and evenly distributed. The peel at the base of the fruit exhibited a color change to grayish white, milky white, bright yellow, or light yellow, and a distinct separation layer was visible at the fruit stem. In terms of aroma and firmness, the fruit emitted the characteristic scent of the variety, the calyx area had softened, and the fruit displayed slight elasticity when pressed gently.

Data processing. All data analyses were performed using SPSS v. 25.0 (SPSS Inc, Chicago, IL, USA) and Origin v. 2021 (OriginLab, Northampton, MA, USA). Genetic diversity was evaluated using the Shannon-Wiener diversity index (H'), by calculating the mean (μ) and standard deviation (σ). The test materials were then divided into seven levels for each trait: I, $X < \mu - 2.5\sigma$; II, $\mu - 2.5\sigma < X < \mu - 1.5\sigma$; III, $\mu - 1.5\sigma < X < \mu - 0.5\sigma$; IV, $\mu - 0.5\sigma < X < \mu + 0.5\sigma$; V, $\mu + 0.5\sigma < X < \mu + 1.5\sigma$; VI, $\mu + 1.5\sigma < X < \mu + 2.5\sigma$; and VII, $X > \mu + 2.5\sigma$; where X is the corresponding value of each trait indicator for each material (Niu et al. 2012). The distribution frequency was calculated as

$$P_{ij} = \frac{n_{ij}}{n},$$

where P_{ij} is the distribution frequency of

Table 1. Criteria to assess qualitative traits across melon varieties.

Trait and description	Code
Fruit shape	
Round	1
Ovate	2
Elliptical	3
Olive-shaped	4
Density of fruit surface reticulation	
None	1
Sparse	2
Moderate	3
Dense	4
Thickness of fruit surface reticulation	
None	1
Fine	2
Moderate	3
Coarse	4
Reticulation distribution on fruit surface	
None	1
Sparse	2
Half	3
Full	4
Cracks on fruit surface	
None	1
Sparse	2
Dense	3
Peel undertone	
Cream	1
Light yellow	2
Yellow	3
Dark yellow	4
Yellow-green	5
Dark green	6
Blackish green	7
Peel overlay color	
Cream	1
Grayish white	2
Patterns on fruit surface	
Spots	1
Band-shaped spots	2
Bands	3
Exocarp color	
White	1
Yellow-green	2
Green	3
Orange	4
Endocarp color	
White	1
Yellow	2
Yellow-green	3
Orange	4
Orange-red	5
Melon color	
White	1
Yellow	2
Orange	3
Flesh texture	
Soft	1
Mealy	2
Crisp	3
Cottony	4
Pulp aroma	
Fragrant	1
Uniquely fragrant	2
Pulp flavor	
Mild	1
Moderate	2
Strong	3

the j th variation of the i th trait, n_{ij} is the number of materials with the i th trait in the j th variation, and n is the total number of materials. The Shannon-Weaver index of genetic diversity was calculated as (Tian and Zheng 1994)

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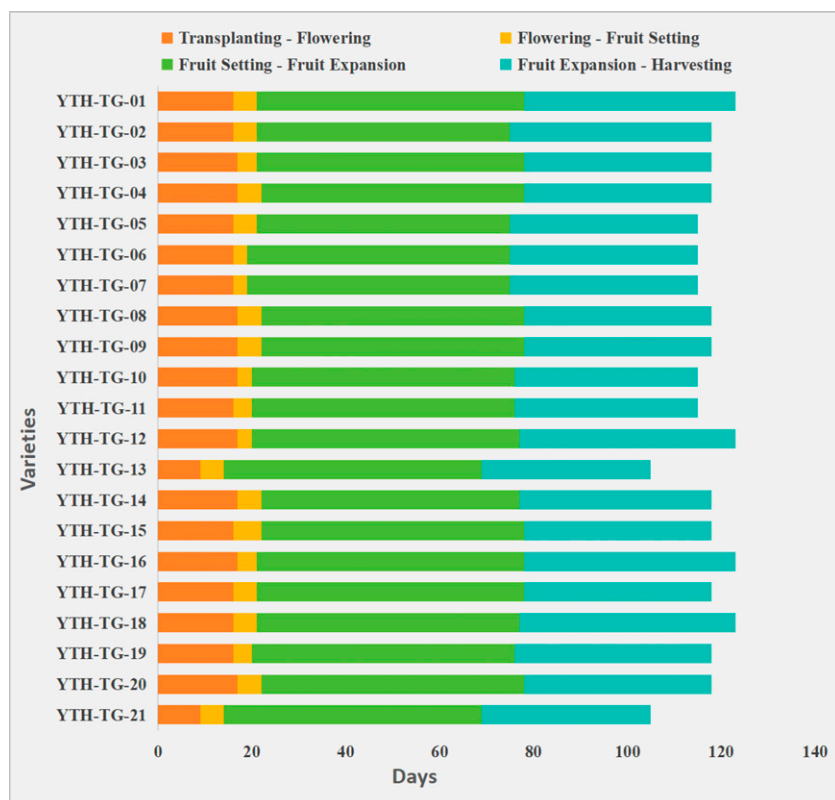


Fig. 1. Phenological manifestations of different melon varieties.

$$H' = \sum_{i=1}^k P_i \ln P_i,$$

where P_i is the percentage of samples at level i of a certain trait out of the total number of samples and $\ln$ is the natural logarithm (Shannon 2001).

For the principal component analysis, key principal components were determined based on the assumption that the eigenvector was > 1 . The composite model for each principal component was calculated using the obtained eigenvector. Then, the composite scores for each variety were calculated and ranked according to their scores.

Results

Phenological period. All varieties showed varying durations of phenological stages

(Fig. 1). Among the different varieties, YTH-TG-13 and YTH-TG-21 had the shortest total growth period (105 d). These varieties, exhibited a 9 d flowering period and a 36 d fruit enlargement period. However, YTH-TG-01, YTH-TG-12, YTH-TG-16, and YTH-TG-18 had the longest total growth period (123 d). In these varieties, the period of fruit enlargement was 45 to 46 d, with smaller differences in other stages compared with the other varieties. The total growth period of other varieties was 115 to 118 d.

Qualitative characteristics. Frequency distribution analysis revealed that the majority of varieties produced oval-shaped fruit, indicating moderate genetic diversity in fruit shape (Table 2). Dense reticulation was the most commonly observed fruit surface pattern. However, the reticulation was predominantly fine

and distributed across the entire fruit surface. Most of the cracks appearing on the fruit surface were dense. The peel undertone of most varieties exhibited a dark, greenish black color, accompanied by notably high genetic diversity indices. The peel overlay color was grayish white. The fruit surface was covered predominantly with band-shaped spots. The exocarp and endocarp colors also varied, with yellow-green outer flesh and yellow inner flesh being the most common. The melon color was predominantly white. All varieties exhibited an aromatic pulp with a unique fragrance, a soft texture, and a moderately strong flavor.

Quantitative characteristics. For all quantitative traits, coefficients of variation (CVs) ranged from 9% to 41% (Table 3). The highest CV was observed for rind/peel thickness (41%), followed by flesh thickness (32%), yield (28%), and single fruit weight (28%). However, the CVs for stem diameter (9%), seed cavity color (10%), and fruit transverse diameter (11%) were relatively less, indicating limited variation and stable inheritance of these traits.

Correlation analysis of the quantitative traits. The Pearson correlation coefficient analysis showed that there were varying degrees of association among quantitative melon traits (Fig. 2). Nine pairs of traits showed highly significant correlations ($P < 0.01$), whereas one pair demonstrated a significant correlation at the $P < 0.05$ level. Specifically, a strong correlation was observed between maximum leaf length and width ($r = 0.68$), fruit longitudinal diameter and single fruit weight ($r = 0.77$), fruit longitudinal diameter and yield ($r = 0.77$), fruit transverse diameter and flesh thickness ($r = 0.89$), fruit transverse diameter and single fruit weight ($r = 0.82$), fruit transverse diameter and yield ($r = 0.81$), flesh thickness and single fruit weight ($r = 0.79$), flesh thickness and yield ($r = 0.79$), and single fruit weight and yield ($r = 1$). A significant positive correlation ($r = 0.546$) was also observed between fruit retention height and rind/peel thickness. These results suggest that increasing single fruit weight, flesh thickness, fruit longitudinal diameter, and fruit transverse diameter affects melon

Table 2. Distribution frequency of quantitative traits across melon varieties.

Trait	Distribution frequency (%)							Shannon H'
	1	2	3	4	5	6	7	
Fruit shape	19.05	4.76	52.38	23.81	—	—	—	1.14
Density of fruit surface reticulation	9.52	14.29	14.29	61.90	—	—	—	1.08
Thickness of fruit surface reticulation	4.76	47.62	9.52	38.10	—	—	—	1.09
Reticulation distribution on fruit surface	4.76	9.52	4.76	80.96	—	—	—	0.67
Cracks on fruit surface	19.0	19.05	61.90	—	—	—	—	0.93
Peel undertone	19.05	4.76	4.76	4.76	14.29	9.52	42.86	1.62
Peel overlay color	42.86	57.14	—	—	—	—	—	0.68
Patterns on fruit surface	4.76	42.86	52.38	—	—	—	—	0.85
Exocarp color	14.29	52.38	4.76	28.57	—	—	—	1.12
Endocarp color	23.81	28.57	14.28	19.05	14.29	—	—	1.43
Melon color	61.90	33.34	4.76	—	—	—	—	0.81
Flesh texture	52.38	4.76	38.10	4.76	—	—	—	0.99
Pulp aroma	90.48	9.52	—	—	—	—	—	0.31
Pulp flavor	9.52	47.62	42.86	—	—	—	—	0.94

Shannon H' = Shannon-Weaver index.

Table 3. Variation of quantitative traits across melon varieties.

Trait	Mean $\pm$ SD	Variation range	Range	CV (%)
Fruit retention height (cm)	70.2 $\pm$ 14.26	42.3–93.7	51.4	20.31
Maximum leaf length (cm)	19.8 $\pm$ 3.19	14.1–23.9	9.8	16.11
Maximum leaf width (cm)	25.3 $\pm$ 3.58	20.3–31.2	10.9	14.15
Stem diameter (mm)	10.5 $\pm$ 0.90	8.9–11.9	3.0	8.57
Fruit longitudinal diameter (cm)	16.2 $\pm$ 2.67	9.9–19.9	10.0	16.48
Fruit transverse diameter (cm)	13.9 $\pm$ 1.47	10.6–15.8	5.2	10.58
rind/peel thickness (cm)	0.64 $\pm$ 0.26	0.20–1.00	0.80	40.63
Seed cavity diameter (cm)	6.02 $\pm$ 0.63	4.80–7.22	2.42	10.47
Flesh thickness (cm)	4.30 $\pm$ 1.34	1.42–6.08	4.66	31.16
Soluble solids content (%)	14.18 $\pm$ 2.29	9.91–18.25	8.34	16.15
Single fruit weight (kg)	1.67 $\pm$ 0.46	0.52–2.44	1.92	27.54
Yield (kg·ha ⁻¹)	37,485 $\pm$ 10,414.92	54,855–11,700	43,155	27.78

CV = coefficient of variation; SD = standard deviation.

yield positively, whereas increasing fruit retention height may lead to a thicker melon peel.

Principal component analysis of agro-economic traits. The principal component analysis showed that the cumulative variance explained by the first five components was 80.35% (Table 4). Among them, the first principal component contributed the most, accounting for 29.30% of the total variance, with the main traits being fruit longitudinal diameter, fruit transverse diameter, flesh thickness, single fruit weight, and yield. However, the second through fifth principal components accounted for 9.19% to 17.4% of the total variance.

To understand more fully how quantitative traits are affected by the genetic diversity of melon, we performed principal component

analysis for 21 germplasms (Fig. 3). Overall, the first two dimensions explained 47% variability in our datasets, with stem diameter and fruit retention height contributing strongly in dimension 1, and flesh thickness, fruit transverse diameter, and single fruit weight contributing in dimension 2. There was multivariate divergence among germplasms and a distinct clustering of positively correlated traits. Notably, soluble solids content and maximum leaf length correlated positively with seed cavity diameter, stem diameter, and fruit retention height among YTH-TG-07, YTH-TG-10, YTH-TG-11, YTH-TG-02, and YTH-TG-19. Moreover, fruit longitudinal diameter correlated positively with fruit transverse diameter and single fruit weight in YTH-TG-18, YTH-TG-12, YTH-TG-03, YTH-TG-15, and YTH-TG-05.

Comprehensive evaluation of 21 melon germplasms. Based on the feature vectors of the 12 traits in different principal components (Table 5), the five corresponding principal component score formulas were obtained:

$$F1 = 0.24FRH + 0.34MLL + 0.24MLW + 0.4SDi + 0.78FFLD + 0.86FTD + 0.13RPT + 0.17SCD + 0.82FT + 0.16SSC + 0.97SFW + 0.97Yield,$$

$$F2 = -0.68FRH + 0.55MLL + 0.28MLW + 0.14SDi - 0.25FLD + 0.16FTD - 0.87RPT + 0.59SCD + 0.06FT + 0.25SSC - 0.09SFW - 0.09Yield,$$

$$F3 = 0.24FRH + 0.67MLL + 0.79MLW - 0.01SDi + 0.33FLD - 0.32FTD + 0.08RPT - 0.16SCD - 0.28FT - 0.5SSC - 0.07SFW - 0.07Yield,$$

$$F4 = 0.3FRH + 0.16MLL - 0.32MLW + 0.8SDi + 0.2FLD - 0.2FTD + 0.04RPT + 0.28SCD - 0.38FT + 0.23SSC - 0.07SFW - 0.07Yield, \text{ and}$$

$$F5 = 0.25FRH + 0.11MLL + 0.17MLW + 0.01SDi + 0.02FLD - 0.17FTD - 0.28RPT - 0.59SCD + 0.19FT + 0.71SSC - 0.07SFW - 0.07Yield,$$

where FLD is fruit longitudinal diameter, FRH is fruit retention height, FT is flesh thickness, FTD is fruit transverse diameter, MLL is maximum leaf length, MLW is maximum leaf width, RPT is rind/peel thickness; SCD is seed cavity diameter, SDi is stem diameter; SFW is single fruit weight, and SSC is soluble solids content.

Based on these five formulas, the scores for each variety in the five principal components were obtained. Then, based on the contribution weights of the five principal components (29.3%, 17.4%, 14.3%, 10.3%, and 9.2%), the comprehensive scoring formula for each variety was obtained:

$$F = 0.293F1 + 0.174F2 + 0.143F3 + 0.103F4 + 0.092F5.$$

The 21 germplasm resources were ranked based on their final comprehensive scores, with higher F values indicating greater overall performance (Table 5). The F values of the 21 melon germplasm resources ranged from 2888 to 13,462. The highest F value was observed for YTH-TG-01 ($F = 13,462$), whereas the lowest was recorded for YTH-TG-21 ($F = 2888$). The top five varieties in terms of performance were TH-TG-01, TH-TG-18, TH-TG-12, TH-TG-16, and TH-TG-03.

Phenotypic trait cluster analysis. Cluster analysis was performed using five core indicators: fruit longitudinal diameter, fruit transverse diameter, flesh thickness, soluble solids content, single fruit weight, and yield (Fig. 4). The melon germplasms were divided into three major groups (groups I, II, and III) at a Euclidean distance of 10.0, with the third group subdivided further into three subgroups. Group I include the varieties YTH-TG-13 and YTH-TG-21. The values of the five indicators for these two varieties were less than those of the other two groups. These varieties have smaller

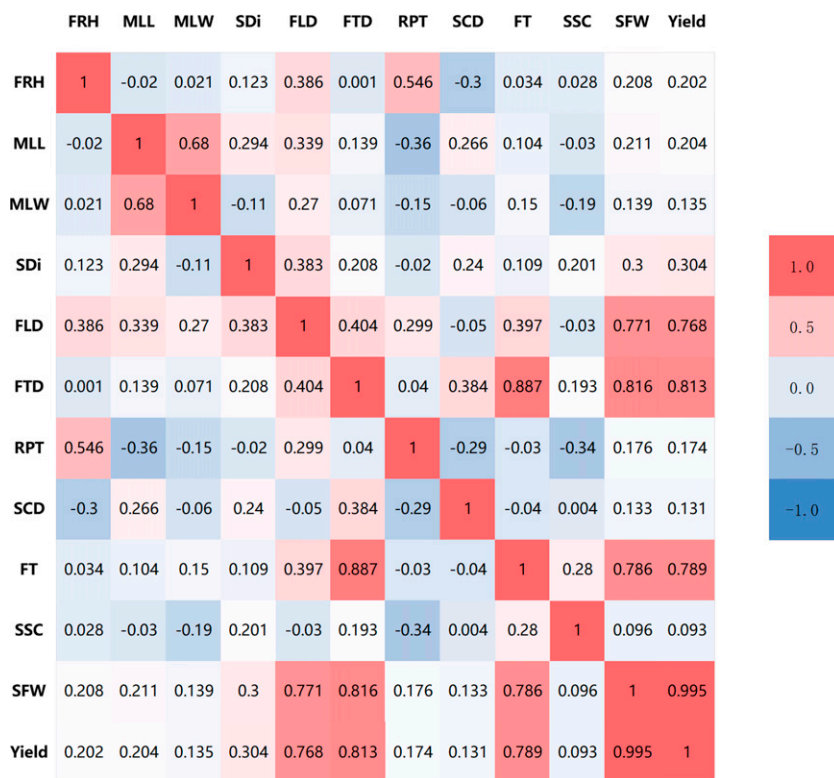


Fig. 2. Pearson correlation analysis of quantitative traits of melon varieties. FLD = fruit longitudinal diameter; FRH = fruit retention height; FT = flesh thickness; FTD = fruit transverse diameter; MLL = maximum leaf length; MLW = maximum leaf width; RPT = rind/peel thickness; SCD = seed cavity diameter; SDi = stem diameter; SFW = single fruit weight; SSC = soluble solids content.

Table 4. Principal component (PC) analysis of quantitative traits across melon varieties.

Index	PC1	PC2	PC3	PC4	PC5
Fruit retention height (cm)	0.24	-0.68	0.24	0.30	0.25
Maximum leaf length (cm)	0.34	0.55	0.67	0.16	0.11
Maximum leaf width (cm)	0.24	0.28	0.79	-0.32	0.17
Stem diameter (mm)	0.40	0.14	-0.01	0.80	0.01
Fruit longitudinal diameter (cm)	0.78	-0.25	0.33	0.20	0.02
Fruit transverse diameter (cm)	0.86	0.16	-0.32	-0.20	-0.17
rind/peel thickness (cm)	0.13	-0.87	0.08	0.04	-0.28
Seed cavity diameter (cm)	0.17	0.59	-0.16	0.28	-0.59
Flesh thickness (cm)	0.82	0.06	-0.28	-0.38	0.19
Soluble solids content (%)	0.16	0.25	-0.50	0.23	0.71
Single fruit weight (kg)	0.97	-0.09	-0.07	-0.07	-0.07
Yield (kg·ha ⁻¹)	0.97	-0.09	-0.07	-0.07	-0.07
Eigenvalue	4.35	2.12	1.71	1.23	1.10
Contribution rate (%)	29.30	17.40	14.26	10.25	9.19
Cumulative contribution rate (%)	29.30	46.70	60.96	71.16	80.35

fruit and lower yields (22,725 and 11,700 kg·ha⁻¹, respectively) (Table 6). Group II contained two varieties: YTH-TG-01 (54,855 kg·ha⁻¹) and YTH-TG-18 (53,325 kg·ha⁻¹). These varieties have large fruit and higher yields, with a greater longitudinal and transverse fruit diameter, flesh thickness, single fruit weight. Group III was comprised of 17 varieties, exhibiting moderate single fruit weight (1.69 kg) and yield (37,916 kg·ha⁻¹). They were divided further into three subclusters at a Euclidean distance of ~2. In particular, group IIIC included nine varieties (YTH-TG-02, YTH-TG-03, YTH-TG-12, YTH-TG-14, YTH-TG-15, YTH-TG-16, YTH-TG-17, YTH-TG-19, and YTH-TG-20) and displayed the second-

highest single fruit weight (1.86 kg), and a yield of 41,905 kg·ha⁻¹.

Discussion

We conducted a systematic investigation of the phenological stages of 21 melon varieties under wintering plastic film greenhouse cultivation conditions in high-altitude regions of China. The results indicated there were significant differences in the time from transplant to harvest among different varieties, with a time range of 105 to 123 d. Specifically, 10% of the varieties required 105 d, 24% required 115 d, 47% required 118 d, and 19% required 123 d. These findings differ slightly from the

Table 5. *F* statistics and performance ranking of different varieties

Variety	<i>F</i> value	Rank
YTH-TG-01	13,462	1
YTH-TG-02	9,903	8
YTH-TG-03	10,660	5
YTH-TG-04	8,719	14
YTH-TG-05	9,008	12
YTH-TG-06	7,016	19
YTH-TG-07	8,182	16
YTH-TG-08	7,519	18
YTH-TG-09	7,941	17
YTH-TG-10	8,788	13
YTH-TG-11	8,512	15
YTH-TG-12	11,160	3
YTH-TG-13	5,592	20
YTH-TG-14	9,723	10
YTH-TG-15	9,893	9
YTH-TG-16	11,157	4
YTH-TG-17	9,561	11
YTH-TG-18	13,089	2
YTH-TG-19	10,608	6
YTH-TG-20	9,947	7
YTH-TG-21	2,888	21

findings of Lotti et al. (2008) who compared 153 melon germplasms in summer and found that the average harvest time for all genotypes was 107 d. They further found that ~8% of genotypes exhibited longer growth cycles (121–130 d), whereas 60% of genotypes had harvest times concentrated between 101 and 110 d, and 32% of genotypes completed their growth cycles between 111 and 120 d. This variation may stem from differences

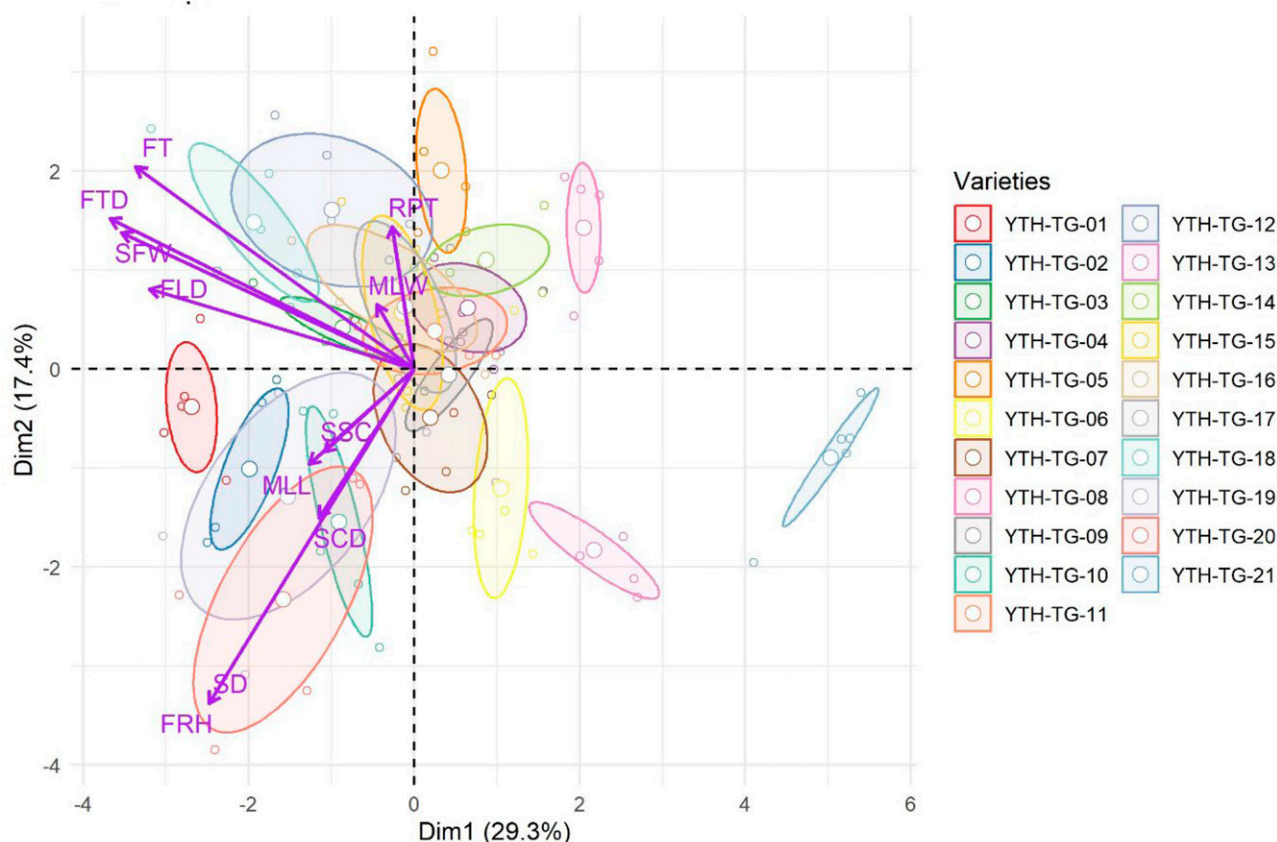


Fig. 3. Principal component analysis based on quantitative traits of melon varieties. Dim = dimension; FLD = fruit longitudinal diameter; FRH = fruit retention height; FT = flesh thickness; FTD = fruit transverse diameter; MLL = maximum leaf length; MLW = maximum leaf width; RPT = rind/peel thickness; SCD = seed cavity diameter; SD = stem diameter; SFW = single fruit weight; SSC = soluble solids content.

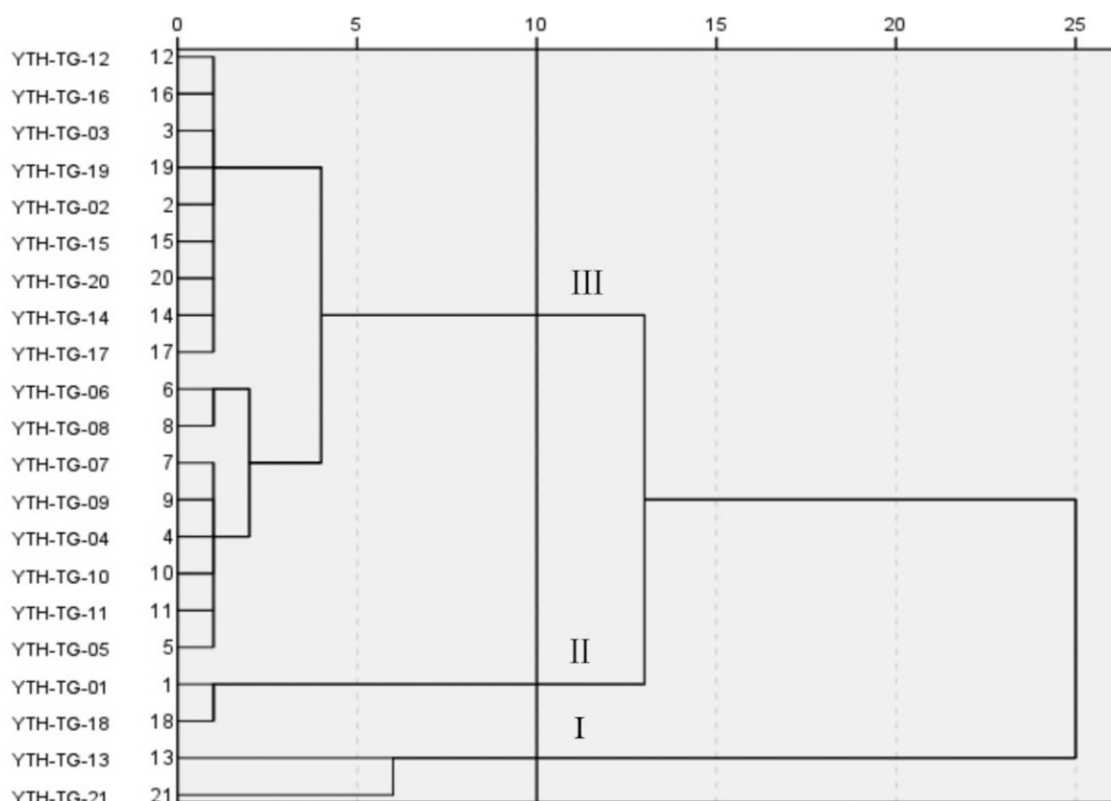


Fig. 4. Cluster analysis of melon varieties based on their key parameters.

in planting environments (high-altitude overwintering cultivation vs. summer conventional planting) and germplasm sources.

Crop phenotypic traits are the result of the interaction between the genetic characteristics of the variety itself and environmental factors (Sadras et al. 2013). The phylogenetic relationships among germplasm resources can be represented by genetic diversity indices and *CV* (Liu et al. 2007; Zhu et al. 2022). Genetic diversity serves as the foundation for studying biological evolution and breeding new varieties in germplasm resource research (de Carvalho et al. 2013; Salgotra and Chauhan 2023). Related studies have found that the higher the genetic diversity index, the stronger the resource's adaptability to the environment (Hawtin et al. 1996). The *CV* reflects the variation produced by a species during the process of adapting to the environment. A larger *CV* indicates a greater likelihood of obtaining superior resources (Carter et al. 1983). Therefore, by exploring the genetic diversity of biological traits, one can understand comprehensively the extent of the resources at hand (Booy et al. 2000; Lande and Shannon 1996). We conducted a

diversity analysis of 14 fruit quality traits in 21 melon germplasm resources. The results showed that the Shannon diversity index ($H' = 1.62$) for rind/peel color was significantly greater than that of other traits, indicating the richest phenotypic variation. This result is consistent with the findings of Karim (2024), which indicated that rind/peel color is the most widely variable trait in melon germplasm resources (Pitrat 2017). Hu et al. (2013) investigated 250 germplasm resources originating from South Asia, northeastern Europe, western Europe, North America, and East Asia. Their study revealed that, among qualitative traits, fruit shape exhibited the greatest diversity index ($H' = 1.47$), followed by the vein pattern on the fruit skin ($H' = 1.45$). This observed variation may be attributed to differences in the geographic origins of the accessions or inconsistencies in trait evaluation criteria. These findings underscore the importance of considering the heterogeneity of germplasm resources and methodological discrepancies when comparing results across different studies.

An analysis of the *CV*s for 12 melon plants, leaves, and fruit-related quality traits showed

that fruit-related traits exhibited more significant genetic variation. Among these, traits such as rind/peel thickness (41%), flesh thickness (32%), yield (28%), and single fruit weight (28%) showed particularly high levels of variation. This result is consistent with the findings of Lotti et al. (2008) and Burger et al. (2010). These data further confirm that fruit traits are the primary source of phenotypic variation in melon germplasm resources, which may be attributed to the relatively low artificial selection pressure on fruit traits during domestication, thereby preserving richer genetic diversity.

The correlation between phenotypic traits serves as the ultimate phenotypic expression of gene linkage or interaction, playing a crucial guiding role in crop genetic improvement and germplasm resource selection. By elucidating the association patterns between target traits and other easily observable traits, an efficient indirect selection system can be established, reducing breeding costs significantly and enhancing selection efficiency (Cobb et al. 2013; Messina et al. 2009; Rebetzke et al. 2019). In our study, the multitrait phenotypic correlation analysis of melons revealed a highly significant positive correlation ($P < 0.01$) between yield and individual fruit weight, fruit diameter, fruit length, and flesh thickness. This finding is consistent with the results reported by Taha et al. (2003) and Ibrahim and Ramadan (2013). This result confirms, from a phenotypic perspective, the core driving factors of yield composition. Increased single fruit weight enhances fruit weight accumulation per plant directly, whereas the synergistic increase in fruit diameter and length expands fruit volume. Increased flesh

Table 6. Data on average values of various groups.

Index	I	II	III			Mean
			III-A	III-B	III-C	
Fruit longitudinal diameter (cm)	12.01	18.29	15.05	13.99	17.99	15.68
Fruit transverse diameter (cm)	10.99	15.38	14.18	13.30	14.26	13.91
Flesh thickness (cm)	1.74	5.91	4.61	3.85	4.41	4.29
Soluble solids content (%)	12.20	14.71	14.88	15.78	13.69	14.78
Single fruit weight (kg)	0.77	2.40	1.54	1.31	1.86	1.57
Yield (kg·ha ⁻¹)	17,212.50	54,090	34,710	29,587.50	41,905.05	35,400.90

thickness further increases the proportion of edible parts in the fruit. These four factors interact through a multidimensional synergistic effect of quantity–volume–texture, driving increases in yield levels collectively.

Notably, this correlation pattern aligns with the findings of studies by Bagheriyan et al. (2015) and Rad et al. (2010) on the phenotypic diversity of Iranian melons, suggesting that this association may have broad applicability across melon crops. In the practice of germplasm resource breeding, these findings provide a scientific basis for screening high-yielding varieties based on easily measurable traits. Compared with yield traits that require multiyear, multilocation verification, phenotypic indicators such as single fruit weight, fruit diameter, and flesh thickness can be obtained through rapid field measurements. Breeders can prioritize these as “proxy traits” for early screening, thereby achieving early identification of high-yield potential. In addition, based on the positive interactive relationships between traits, a multitrait aggregation improvement strategy can be designed, such as using molecular marker-assisted selection to enhance single fruit weight and flesh thickness simultaneously, leveraging their synergistic effects to boost overall yield more efficiently.

Through principal component analysis, the original dataset containing numerous correlated variables is simplified into a smaller dataset derived from the original observations, thereby streamlining the analysis process significantly (Greenacre et al. 2022; Jolliffe and Cadima 2016). Ivanova and Velkov (2021) conducted principal component analysis on the genetic variation of Bulgarian melon varieties, and the results showed that the first three components accounted for 69.47% of the total phenotypic variation of the studied traits. The first principal component had the highest proportion (38.74%) and was associated primarily with yield-related traits such as single fruit weight, fruit length, fruit width, flesh thickness, and seed cavity diameter. In our study, principal component analysis was used to extract five principal components, with a cumulative contribution rate of 80.35%. In our study, the first principal component was dominated by key yield-related traits, namely fruit length, fruit width, flesh thickness, single fruit weight, and yield itself.

With the continuous growth in demand for off-season melons among Chinese consumers, the selection of melon varieties suitable for winter cultivation in high-altitude regions has become particularly important. Because of the unique climatic conditions in high-altitude regions and the technical limitations of winter cultivation, greater requirements are placed on stress tolerance, phenological stage, quality, and yield characteristics of melon varieties. Therefore, selecting high-quality melon varieties suitable for winter cultivation is of great significance for ensuring the supply of off-season melons in the market and improving planting efficiency. In our study, comprehensive scores (F values) were calculated for each germplasm based on principal component analysis results; five melon germplasm lines—

TH-TG-01, TH-TG-18, TH-TG-12, TH-TG-16, and TH-TG-03—with excellent comprehensive performance were selected. These findings provide a basis for germplasm selection and efficient use of germplasm resources under winter greenhouse cultivation conditions in high-altitude regions.

Cluster analysis has been widely applied in studies of genetic diversity in melon germplasm resources. Through cluster relationship diagrams, it is possible to distinguish clearly the genetic clustering relationships among different germplasm types, providing a reliable reference for selecting parental lines in melon hybrid breeding (Garcia et al. 1998; Pavan et al. 2017; Rad 2018). Yang et al. (2024) performed clustering on six texture-related chemical indicators of thick-skin melons, dividing 278 melon germplasms into three types: crisp and hard with little juice, sandy and soft with abundant juice, and crisp and hard with abundant juice. This provides a scientific basis for the breeding of different texture varieties of thick-skin melons. Shao et al. (2021) performed a cluster analysis of quality indicators for eight melon varieties, dividing them into four categories: sweet and sour flavor, high variety, high hardness, and high single fruit weight with low vitamin C content. Among these, high-quality varieties with high vitamin C content, high soluble solids content, and high glucose content accounted for 50%, providing foundational data support for the breeding of melons with different flavors and varieties. In our experiment, cluster analysis was conducted on five core indicators of the test melons: fruit diameter, fruit length, flesh thickness, soluble solids content, and single fruit weight and yield. The 21 melon germplasm resources were divided into three groups, or clusters. Group I consisted of small-fruit, low-sugar types, with smaller fruit size, lower yield, and lower sugar content. Group II melons were large, high-yielding, and medium-sugar varieties suitable for large-scale cultivation in production bases. Group III was comprised of medium-yielding, medium-sugar varieties. The III-C subgroup consisted of high-yielding, medium-sugar varieties. This suggests that the breeding of high-yielding, medium-sugar melons may be one of the current mainstream trends, consistent with the findings of Shao et al. (2021) and Chen et al. (2015).

With the advancement of artificial intelligence technology and breakthroughs in intelligent phenotyping analysis, Xu et al. (2024a) developed a deep learning–based melon phenotyping analysis system that uses computer vision technology to extract fruit morphology (transverse diameter, longitudinal diameter) and flesh thickness with millimeter-level precision, improving germplasm screening efficiency significantly. Similarly, the improved CSW-YOLO model achieved a 98.7% recognition accuracy in bitter melon phenotyping, providing a general technical framework for Cucurbitaceae crops (Xu et al. 2024b). Paczos-Grzęda et al. (2023) developed a multidimensional evaluation system for salt-alkali tolerance phenotypes in melons, combining

high-resolution images with ionomics data. They found a significant positive correlation between flesh cell wall thickness and Na^+/K^+ balance capacity ($r = 0.62$), providing a phenotypic anchor for marker-assisted breeding. Through interdisciplinary collaboration, it is hoped that key technical bottlenecks in the melon industry, with regard to quality improvement and sustainable cultivation, can be overcome.

Conclusion

Our results show that winter varieties of melons required 105 to 123 d to complete their life cycle, from transplant to harvest. Among 21 tested varieties, five (TH-TG-01, TH-TG-18, TH-TG-12, TH-TG-16, and TH-TG-03) demonstrated greater fruit quality in terms of fruit length, fruit width, flesh thickness, and single fruit weight as well as yield. A high CV (9%–41%) suggests that the observed variation in these traits is likely attributable to genetic diversity among the genotypes. Our research results provide a reference for future variety selection for winter cultivation of melons in high-altitude areas, and lay a theoretical foundation for melon germplasm innovation, genetic improvement, and efficient use of resources.

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