Vegetable Science (2025) 52(2): 220-236
doi: 10.61180/vegsci.2025.v52.i2.02
ISSN- 0970-6585 (Print), ISSN- 2455-7552 (Online)
www.isvsvegsci.in

RESEARCH ARTICLE

Assessment of stability for expression of monoecism in newly developed inbred lines of muskmelon (*Cucumis melo* L.) and their evaluation for horticultural traits

Nidhi[1*], Sat Pal Sharma[1], and Neena Chawla[1] and Navraj Kaur Sarao[2]

Abstract
In muskmelon, the development of F1 hybrids involving andromonoecious inbred lines as female parents is laborious, costly and time-consuming. Therefore, monoecious lines can potentially be exploited to replace maternal andromonoecious lines in hybrid production. However, in muskmelon, the linkage of the monoecious trait with oval fruit shape and sourness limited its extensive utilization in hybrid breeding. Thus, the present investigation was carried out to investigate a set of newly generated melon inbred lines for stability monoecious trait and their evaluation for morphological and biochemical characteristics, such as average fruit weight (g), flesh thickness (cm), rind thickness (mm), fruit shape index, total soluble solids (TSS), ascorbic acid, acidity, β-carotene and firmness (kg/cm2). Through assessment of the andromonoecy index (AI), eighteen stable monoecious lines have been identified. The monoecious line, Mono-1621/CTS, exhibited the highest β-carotene (2.73 mg/100g), while Mono1426/S-1 recorded the highest TSS (14.9 °Brix). Unlike earlier reports, AI showed no correlation with fruit shape index or sourness, suggesting these traits are independent of sex expression in muskmelon. This indicates that stable monoecious lines with low sourness, ideal TSS/TA ratio, and round fruits can be developed using improved genetics and modern breeding tools. Furthermore, identified lines with horticulturally desirable traits can further be utilized in heterosis breeding by selecting suitable parent combinations.
Keywords: Acidity, andromonoecy index, β-carotene, firmness, fruit shape index, monocious.

[1]Department of Vegetable Science, Punjab Agricultural University, Ludhiana-141004, Punjab, India

[2]School of Agricultural Biotechnology, Punjab Agricultural University, Ludhiana-141004, Punjab, India

[*]**Corresponding author;** Email: nidhi-vs@pau.edu

Citation: Nidhi, Sharma, S.P., Chawla, N., & Sarao, N.K. (2025). Assessment of stability for expression of monoecism in newly developed inbred lines of muskmelon (*Cucumis melo* L.) and their evaluation for horticultural traits. Vegetable Science 52(2), 220-236.

Source of support: Nil

Conflict of interest: None.

Received: 06/06/2025 **Revised:** 03/07/2025 **Accepted:** 04/07/2025

Introduction
Muskmelon (*Cucumis melo* L.) is an important member of the Cucurbitaceae family, which is relished for its unique flavour, texture, sweetness and fleshy fruits throughout the tropical and subtropical regions of the world Pitrat et al., 2000; Sharma et al., 2020. In 2021, muskmelon was cultivated in an area of 1.07 million ha with 28.61 million tonnes of production worldwide (FAOSTAT, 2021). China is the major producer of muskmelon, followed by Turkey, India, Iran, Egypt, the USA and Spain. In India, muskmelon is grown on 70 thousand ha, with an annual production of 1.5 million tonnes (NHB, 2022). Depending upon the geographical regions of cultivation and local preferences, muskmelon exhibits a substantial variability in fruit morphology and biochemical traits (Singh *et al* 2020). Key morphological and nutritional traits such as fruit shape, skin color, weight, flesh color, ascorbic acid, TSS, and β-carotene are important determinants of consumer preference and market acceptance, as documented by Monforte (2017) and Kaur et al. (2022). Several heritable patterns of floral sex expression in muskmelon have served as an important genetic source for hybrid breeding in

melons, according to Choudhary et al. (2018) and Ansari et al. (2020). Andromonoecious is the most prevalent sex pattern in muskmelon. Sex expression in muskmelon is governed by the interplay of at least three major genes, A, G, and M, which might interact to give rise to a range of sex types, as described by Kubicki (1969) and Kenigsbuch and Cohen (1990). Kenigsbuch and Cohen (1990) suggested the following phenotype-genotype relationships in muskmelon: monoecious, *AAGGMM*; andromonoecious, *aaGGMM*; trimonoecious or gynomonoecious, *AAggM-*; hemaphrodite, *aagg--*; and gynoecious, *AAggmm*. Monoecism has been reported to be dominant to andromonecism by Rosa (1928) and Kalgudi et al. (2021). Thus, the development of monoecious lines (A_G_) possessing desirable fruit traits can be accomplished by transferring the A allele either through traditional backcross and recurrent selection method for monoecious sex form or using marker-assisted selection (MAS) with ACS gene-based molecular markers associated with monoecy, as demonstrated by Kim et al. (2015).

Heterosis breeding is preferred in muskmelon since hybrids are uniform, stable, high-yielding, and early maturing, according to Kaur et al. (2022). The use of andromonoecious lines in the hybridization process requires emasculation, which increases the possibility of the damaged pistil and ultimately reduces the fruit set. Besides, the emasculation is a tedious and expensive process for quality hybrid seed production, as reported by Zhang and Luan (2016). Furthermore, gynoecious lines require stable genotypic conditions *AAggmm* and a combination of recessive alleles as indicated by Kenigsbuch and Cohen (1990). The use of genic male sterility is also constrained owing to certain problems, such as the maintenance of a single recessive gene because of heterozygous conditions and errors in identification and roguing of 50% fertile plants in a male sterile row, as noted by Singh et al. (2019). In contrast, monoecious lines eliminate the need for emasculation and the difficulties of male-sterile plant maintenance, thereby offering a reliable and efficient outbreeding mechanism for hybrid seed production, as emphasized by More (1980) and Rai and Rai (2006).

Monoecious lines developed through utilization of landraces and wild resources such as *momordica* exhibited oblong fruit shape, mealy texture and acidity, making these inbreds less acceptable, as documented by Kesavan and More (1991), Choudhary et al. (2018), Kalgudi et al. (2021), Ivanova and Velkov (2021), and Hiremata et al. (2023). However, the F_1hybrids based on these monoecious female parents produced fruits with desirable traits, such as earliness, high TSS, thick & firm flesh, small blossom end scar and larger fruit size, as demonstrated by Périn et al. (2002b), Kesavan and More (1991), and Choudhary et al. (2018). Several monocious inbred lines in muskmelon have been developed at the Punjab Agricultural University, Ludhiana, India, through classical breeding approaches, which need to be characterized for their suitability to be evaluated for hybrid breeding. Although the sex expression patterns in melons are genetically determined, their sex phenotypes can be influenced by environmental factors such as temperature, photoperiod, light intensity and quality, water and mechanical stress, making them unstable under certain environments, as reported by Lai et al. (2017) and Ikram et al. (2017). Stability of monoecism in female parents is critical for their use in F_1 hybrid seed production, as pointed out by Li et al. (2019). The fluctuations in temperature and photoperiod regimes have been attributed to several changes in the sex expression in melons*, for instance* change in the ratio of staminate to pistillate flowers, conversion of female flowers into bisexual ones, and the number of pistillate flowers with only primordial stamens, as noted by Martínez et al. (2014). In *C. pepo,* Manzano et al. (2014) assessed the stability of monoecism using the andromonoecy index (AI) based on their degree of stamen development.

Overall, this study aimed to identify stable monoecious muskmelon lines with a round shape and an ideal blend of sweet and sourness, along with high yield potential for utilization in F_1 hybrid breeding programmes. Furthermore, information about correlation, magnitude, type of genetic variability, and heritability is important for selecting superior genotypes for genetic improvement.

Materials and Methods

Plant material and experimental design

The experimental material comprised nineteen monoecious and five andromonoecious/ monoecious reference genotypes belonging to four horticultural groups of the species *C. melo* L., viz. *cantalupensis, reticulatus, inodorous,* and *momordica*. These accessions were used for morphological and biochemical characterization as well as to evaluate the stability of monoecism. The experiments were performed during three growing seasons (Table 1) (spring-summer 2020 and 2021 and under polyhouse during kharif 2020) at Punjab Agricultural University, Ludhiana, India (30.9◦ N and 75.85◦ E at 244 m above sea level). In the first experiment, monoecious lines were evaluated for stability of monoecism during the spring-summer and autumn seasons of 2020. In the second experiment, monoecious lines were evaluated for morphological and biochemical traits. In February 2020, seeds were sown in the pro-trays in a medium comprised of cocopeat, perlite, and vermiculite mixture (3:1:1) for nursery raising. The one-month-old seedlings were transplanted in March. For the monoecism stability experiment, direct sowing was performed under protected conditions in a naturally ventilated polyhouse. The experiments were conducted with ten plants for each genotype in a randomized complete block design with three replications at a spacing of 3.0 × 0.6 m, following

Table 1: Description of muskmelon inbred lines used for characterization

S. No.	*Genotypes*	*Source*	*Pedigree*	*Horticultural group*	*Descriptive traits*
1	Mono-970	PAU, Ludhiana	INT-9634// INT-4632/ F2-8-3-4-7	*Reticulatus*	Fruits are round, green fleshed and intensely netted with golden rind
2	Mono-916	PAU, Ludhiana	NS-916//Mono-2015-5/-2-15-4-7	*Reticulatus*	Fruits are round, orange fleshed, light brown rind and sparsely netted
3	Mono-916/ NTS	PAU, Ludhiana	NS-916//Mono-2015-5/-2-15-7-2	*Reticulatus*	Fruits are round, orange fleshed, light brown rind and intensely netted with sutures
4	Mono-916/ NT	PAU, Ludhiana	NS-916//Mono-2015-5/-5-10-8-4	*Reticulatus*	Fruits are oval round, orange fleshed, light brown rind and intensely netted
5	Mono-916/S	PAU, Ludhiana	NS-916//Mono-2015-5/-7-15-3-18	*Cantalupensis*	Fruits are oval round, orange fleshed, light brown rind and fruit surface with dark sutures
6	Mono-PAUS-15	PAU, Ludhiana	Non-descriptive market collection	*Reticulatus*	Fruits are oval, light orange flesh, thick rind and light brown fruit surface with netting
7	Mono-1032015	PAU, Ludhiana	Kashi Madhu//Mono-2015-5/5-15-4-7-6	*Cantalupensis*	Fruits are oval-round, creamy yellow ribbed background with light orange flesh
8	Mono-KP1520156	PAU, Ludhiana	KP4HM-15//Mono-2015-6/2-1-13-4	*Reticulatus*	Fruits are oval with orange fleshed, thick rind and fruit surface with dark sutures
9	Mono-610	PAU, Ludhiana	NS-610//Mono-2015-5/12-5-31-8	*Reticulatus*	Fruits are oval round, orange fleshed, greenish yellow rind
10	Mono-IC-0599709	NBPGR, New Delhi	IC-0599709	*Reticulatus*	Fruits are oblong, large cavity with white creamy mealyinsipid flesh
11	Mono-2015-5	Non-descriptive market collection	-	*Reticulatus*	Fruits are oval, light green fleshed, fruit surface with dark green sutures and yellow rind
12	Mono-1621/ CTS	Non-descriptive market collection	-	*Cantalupensis*	Fruits are flat round, thick orange fleshed, fruit surface with netting and sutures
13	Mono-1805	Non-descriptive market collection	-	*Reticulatus*	Fruits are round with small seed cavity, dark orange flesh and fruit surface with high netting.
14	Mono-CRBH-891	PAU, Ludhiana	Caribbean Heart F1/8-9-1-7	*Reticulatus*	Fruits are oval round weighing around 1.25-2.0 kg, orange fleshed and intensely netted
15	Mono-103916	PAU, Ludhiana	Kashi Madhu//Mono-916/5-3-8-3	*Cantalupensis*	Fruits are flat round, light orange fleshed with yellow reddish background
16	Mono-1424	PAU, Ludhiana	INT-9634// INT-4632/8-11-5-9	*Reticulatus*	Fruits are round weighing around 1-1.2 kg, orange fleshed and intensely netted
17	Mono-2015-5-S1	Non-descriptive market collection	-	*Reticulatus*	Fruits are oval-round, light orange fleshed and reddish-yellow rind
18	MM-1426/S-1	PAU, Ludhiana	INT-9634// INT-4632/1-4-2-9-5	*Reticulatus*	Fruits are oval round, goldenrind with high netting intensity, firm and green fleshed
19	MM10391603	PAU, Ludhiana	Kashi Madhu //Mono-916/BC1F2-4-2-3-7	*Cantalupensis*	Fruits are oval, white fleshed and fruit surface with sutures and light cream rind
20	Farmers' Glory	PAU, Ludhiana	-	Reticulatus	Fruits are oval round with dark orange flesh and intense netting
21	MS-1	PAU, Ludhiana	-	Reticulatus	Male sterile line having oval round, reddish brown, sutured, and netted fruits
22	Hara Madhu	PAU, Ludhiana	-	Cantalupensis	Fruits are round and fruit skin is light yellow with green sutures
23	Punjab Sunheri	PAU, Ludhiana	-	Reticulatus	Fruits are globular round with orange flesh and intensenetting with light brown rind
24	SM-2015-2	PAU, Ludhiana	-	Momordica	Fruits are oblong, creamy white flesh and plain cream fruit surface

recommended standard agronomic practices for melon crop production, as described in detail in Singh *et al.* (2020) and Kaur *et al.* (2022). Meteorological data for various parameters such as temperature, relative humidity, and rainfall are presented in Figure 1. The soil properties of the experimental sites are detailed in Table 2.

Evaluation of morphological and quality traits

Morphological and biochemical characterization of available melon genotypes were performed with data recording for different characteristics such as average fruit weight (g), number of fruits per plant, yield per hectare (kg), polar diameter (cm), equatorial diameter (cm), fruit shape index, cavity area(cm^2), flesh thickness(cm), rind thickness(mm), fruit firmness(lb/inch^2), TSS (^{o}Brix), β-carotene (mg/100g), ascorbic acid (mg/100g), titratable acidity(g anhydrous citric acid/100ml of fruit juice), TSS/TA ratio and pH. Ascorbic acid was extracted using the method described by Heinze *et al.* (1944). Total soluble solids (TSS^{o}Brix) were determined by using a hand-held refractometer (ERMA, Japan) and β-carotene content (mg/100g) was estimated as described by McCollum (1955). The fruit firmness (kg/cm^2) was measured using a penetrometer fitted with an 11-mm plunger (T.R. TuroniSrl, Via NiccolòCopernico, 26, 47122 Forlì FC, Italy). Furthermore, fruit morphological and sensory evaluation of melon genotypes wascarried out with thirteen fruit characteristics *viz*.; fruit shape (1 ovate, 2 medium elliptic, 3 broad elliptic, 4 circular, 5 quadrangular, 6 oblate, 7 obovate, 8 elongated), fruit skin color (1 white, 2 light yellow, 3 cream, 4 pale green, 5 green, 6 dark green, 7 orange, 8 brown, 9 grey), fruit netting intensity (1 absent, 2 superficial, 3 intermediate, 4 pronounced), fruit sutures(present 1 and absent 2), flesh color (1 white, 2 yellow, 3 cream, 4 pale green, 5 green, 6 pale orange, 7 orange, 8 salmon) , flesh texture (1 firm, 2 grainy, 3 soft, 4 mealy, 5 ribs(1 absent, 2 superficial, 3 intermediate, 4 deep) fruit sourness of mature fruit (1 absent, 2 mild 3 high) bottom scar size (1 small, 2 medium,3 large, 4 pointed scar) UPOV (2006) Choudhary et al. (2015), Singh et al. (2020), Ivanova and Velkov (2019). All these characteristics were evaluated visually and organoleptically.

Evaluation of stability of monoecism

The second experiment was carried out with twenty-four muskmelon genotypes, where these genotypes were subjected to two distinct growing environments, i.e., in the open field (spring-summer 2020) and polyhouse cultivation (Kharif 2020) conditions for assessing the effect of environmental factors on the stability of expression of monoecious lines. An andromonoecy index (AI) was used to assess each flower, which was calculated from five plants with at least 15 pistillate flowers of the first 30 nodes along the main stem and lateral branches per plant. Pistillate flowers were categorized into three groups based on stamen development to assess the stability of monoecism. Female flowers were scored based on stamen development: AI=1 for no development, AI=3 for complete stamens with anthers that can produce pollen and AI=2 for primordial and medium-sized stamens. The AI of each plant was calculated from the average score of at least 15 flowers per genotype. Plants with an AI of 1 and 1.2 were considered monoecious, scores between 1.2 and 2.7 were unstable for monoecy or partially andromonoecious, and more than 2.7 were andromonoecious. The different flower phenotypes used for scoring the andromonoecy index are illustrated in Figure 2.

Statistical analysis

The data of all morphological and biochemical traits were analysed with the SAS program (SAS version 9.3, Cary, USA) for the analysis of variance using RCBD. For analysing the sensory and morphological fruit characteristics data frequency, correlation analysis, and PCA biplot were also processed by a statistical programme (SAS version 9.3, Cary, USA). Means were separated using Fisher's protected LSD method.

Results and Discussion

Morphological and quality trait characterization

Analysis of variance showed significant variation among the genotypes for fruit morphological traits such as polar diameter, equatorial diameter, FSI, cavity area, rind thickness, flesh thickness and fruit firmness (Table 4). The polar diameters of muskmelon genotypes ranged from 9.37cm (Mono- 103/916) to 17.5cm (916/NT), with both being monoecious genotypes from the *reticulatus* and *cantalupensis* groups. Among the *cantalupensis* group, the monoecious melon accession BGMEL42.2 (21.95 cm) had the longest fruit as reported by Dantas et al. (2015) and Barbosa et al. (2022). The momordica genotype SM-2012-2 had the highest equatorial diameter (15.84 cm), while the *reticulatus* genotype MS-1 had the lowest (8.38cm). Ivanova and Velkov (2021) and Kaligudi et al. (2021) found that monoecious accessions had a fruit length ranging from 7.01 to 21.2(cm) and a diameter from 13.53 to 17.53 cm. Polar and equatorial diameters are the determinants of the fruit shape index. Regarding the fruit shape index, genotypes varied from 0.78(Mono-103/916) to 1.44(IC0599709), indicating a range of fruit shapes from depressed, round, and oblong. Dantas et al. (2015) reported four accessions with round fruit shape that were andromonoecious, while 36 were monoecious with elongated, elliptical, oblate, and pyriform shapes, which is consistent with our present study. We found 15 monoecious genotypes with oval-round fruit shape with FSI >1. Likewise, Singh et al. 2020 and Barbosa et al. (2022) observed different shapes, ranging from round, elliptical, to elongate, in their collection of *Momordica* group and *cantalupensis* accessions.

The fruit cavity area of genotypes varied from 26.01(Mono-103/916) to 196.4 (SM-2012-2). Most monoecious

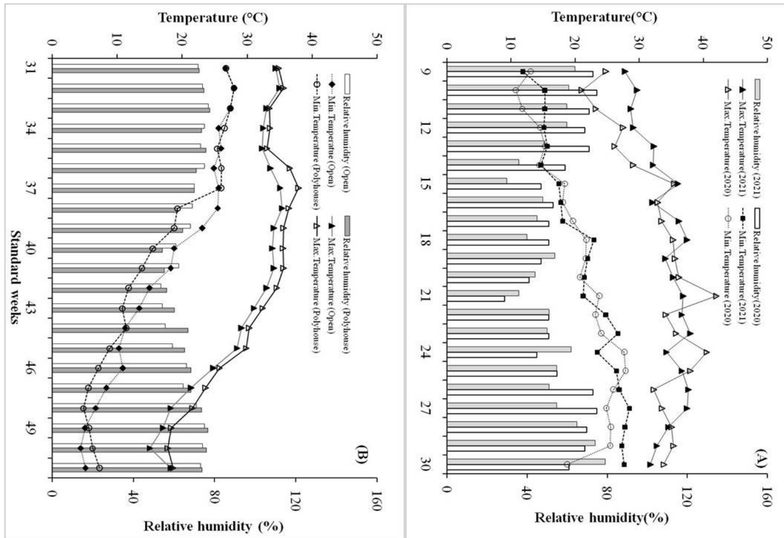

Figure 1: (A) Average weekly minimum temperature(°C), maximum temperature (°C) and relative humidity (%) at the open field conditions during 2020 and 2021 seasons, at PAU, Ludhiana **(B)** Average weekly minimum temperature (°C), maximum temperature (°C) and relative humidity (%) at the open (August-December) and inside polyhouse conditions (August-December) during 2020 at PAU, Ludhiana

Table 2: Physical and chemical characteristics of the experimental site

Soil measurements	2020(Open)	2020(Polyhouse)	2021(Open)
Soil texture	Sandy loam	Sandy loam	Sandy loam
Organic carbon (%)	0.27	0.24	0.29
Electrical conductivity (dS/m)	0.22	0.21	0.20
pH	8.03	7.67	7.79
N (mg kg-1)	24.5	24.1	23.9
P (kg ha-1)	17.2	17.6	18.1
K (kg ha-1)	225.4	219.2	223.5

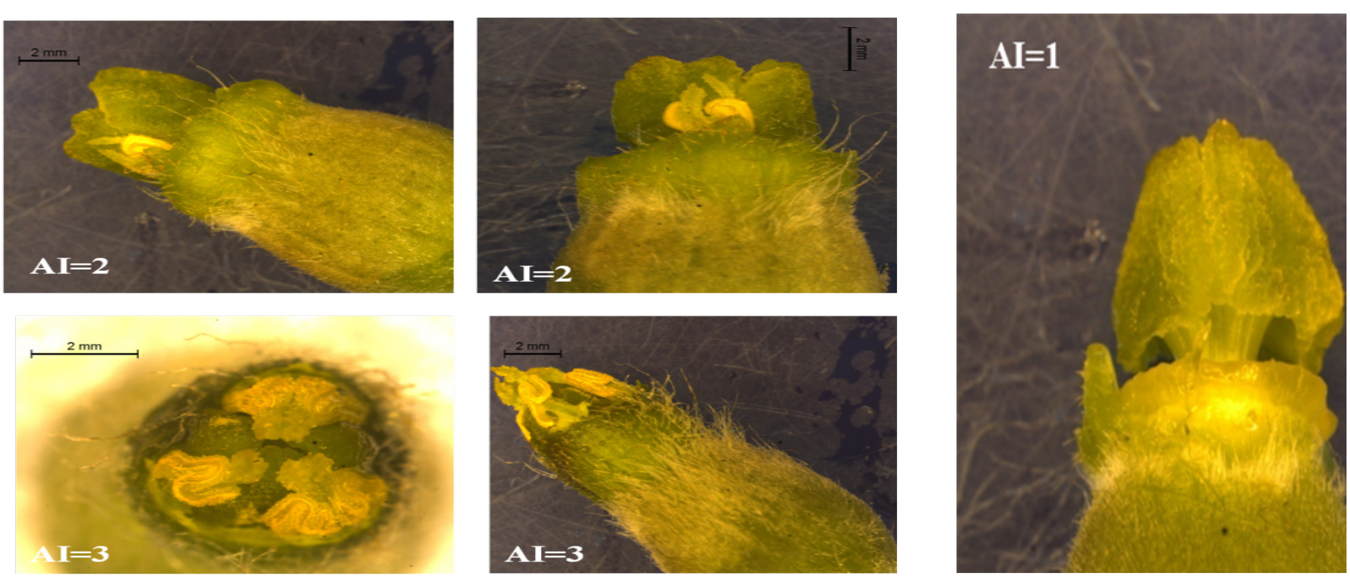

Figure 2: Phenotype of male, female, partial bisexual and bisexual flowers. The andromonoecious index is indicated for each female flower (AI=1, complete arrest of stamen development; AI=2 partial stamens; AI=3 complete stamens).

Table 3: Andromonoecy index of 24 muskmelon inbred lines evaluated under open field and polyhouse conditions

Genotypes	AI (Open-field)	Sex pression	AI(Polyhouse)	Sex expression
Mono-970	1.16	Monoecious	1.19	Monoecious
Mono-916	1.14	Monoecious	1.12	Monoecious
Mono-916/NTS	1.11	Monoecious	1.10	Monoecious
Mono-916/NT	1.09	Monoecious	1.12	Monoecious
Mono-916/S	1.02	Monoecious	1.00	Monoecious
Mono-PAUS-15	1.06	Monoecious	1.10	Monoecious
Mono-103/2015	1.02	Monoecious	1.00	Monoecious
MM-KP1520156	1.08	Monoecious	1.11	Monoecious
Mono-610	1.19	Monoecious	1.31	Partial Andromonoecious
IC0599709	1.12	Monoecious	1.15	Monoecious
Mono-2015-5	1.11	Monoecious	1.37	Monoecious
Mono-1621/ CTS	1.28	Monoecious	2.71	Partial Andromonoecious
Mono-1805	1.09	Monoecious	1.12	Monoecious
Mono-CRBH	1.01	Monoecious	1.00	Monoecious
Mono- 103/916	1.12	Monoecious	1.14	Monoecious
Mono-1424	1.16	Monoecious	1.18	Monoecious
Mono-2015-5-S1	1.12	Monoecious	1.17	Monoecious
MM-1426/S-1	1.02	Monoecious	1.00	Monoecious
MM10391603	1.09	Monoecious	1.00	Monoecious
Farmers' Glory	2.77	Andromonoecious	2.80	Andromonoecious
MS-1	2.91	Andromonoecious	3.00	Andromonoecious
Hara Madhu	2.84	Andromonoecious	3.00	Andromonoecious
Punjab Sunheri	2.67	Andromonoecious	2.80	Andromonoecious
SM-2015-2	1.17	Monoecious	1.19	Monoecious

genotypes displayed a cavity area ranging from 26.01 to 81.08 (cm^2), except a single *Momordica* genotype that measured 196.39 (cm^2) (Table 4). Dantas et al. (2015) found monoecious accessions with cavity area ranging from 19.63 to 211.13 (cm^2), where the majority of genotypes with large cavity area belonged to the *Momordica* and *flexuosus* groups. In contrast, Ivanova and Velkov (2021) found that monoecious genotypes had larger seed cavity diameters (5.83–8.67 cm) than andromonoecious genotypes (4.1–5.8 cm). However, our study revealed that monoecious and andromonoecious genotypes had comparable cavity diameters. Genotypes with smaller cavity areas maintain fruit integrity and nutritional quality, reduce the risk of disease and pests, and become more profitable according to Dantas et al. (2015). The fruit rind thickness is a crucial agro-morphic characteristic frequently used in morphological characterization studies. Rind thickness varies among the genotypes, ranging from 1.35 (SM-2012-2) to 3.42 (mm) (Mono-CRBH).

The present study found that monoecious genotypes had flesh thickness around 3.78 to 8.65 cm, while andromonoecious genotypes were around 4 to 5 cm. The highest flesh thickness was found in monoecious genotype MM-KP1520156 (8.65), followed by Mono-1424 (8.56) and MM10391603 (6.63). Similarly, Ivankova and Velkov (2021) evaluated fifty melon genotypes and found that monoecious genotypes had greater flesh thickness (3.17–4.50 cm) than andromonoecious genotypes (3–4.2 cm). In addition, Chikh-Rouhou and Sta-Baba R (2018) and Kaligudi et al. (2021) found that the flesh thickness of monoecious genotypes from the *flexuosus* and *acidulous* groups varies between 1.34 and 9.6 cm. These findings are significant as higher flesh thickness contributes to longer shelf life, better nutrient density, and enhanced consumer preference for melons. Among fruit morphological traits, fruit firmness is crucial for selecting genotypes with good texture, proper maturity, and longer shelf life. Monoecious genotypes MM-1426/S-1 (0.44 kg/cm^2) and Mono-970 (0.40

Table 4: Fruit morphological traits of monoecious inbred lines evaluated at PAU, Ludhiana during 2020 and 2021

Year	*Polar diameter(cm)*	*Equatorial diameter (cm)*	*Fruit shape index*	*Cavity area(cm2)*	*Rind thickness(mm)*	*Flesh thickness*	*Fruit firmness(kg/cm2)*
2020	12.48	11.12	1.12	54.40	2.53	4.67	0.30
2021	12.34	11.08	1.11	55.14	2.43	4.72	0.31
LSD(p≤0.05)	0.03	0.08	0.01	2.09	0.01	0.01	0.01
Genotypes							
Mono-970	10.3 ± 0.15	10.0 ± 0.23	1.03 ± 0.03	36.9 ± 0.58	2.42 ± 0.23	5.53 ± 0.21	0.40 ± 0.02
Mono-916	11.7 ± 0.09	11.3 ± 0.03	1.04 ± 0.01	44.6 ± 0.23	2.42 ± 0.20	4.26 ± 0.18	0.34 ± 0.01
Mono-916/NTS	13.5 ± 0.15	11.8 ± 0.30	1.14 ± 0.01	45.9 ± 1.48	2.75 ± 0.12	4.73 ± 0.12	0.33 ± 0.01
Mono-916/NT	17.5 ± 0.58	12.6 ± 0.12	1.39 ± 0.01	81.1 ± 0.73	3.18 ± 0.18	4.56 ± 0.27	0.36 ± 0.01
Mono-916/S	11.4 ± 0.09	12.0 ± 0.12	0.95 ± 0.01	49.5 ± 1.58	2.45 ± 0.06	5.73 ± 0.17	0.29 ± 0.01
Mono-PAUS-15	11.0 ± 0.19	10.2 ± 0.12	1.08 ± 0.01	53.2 ± 1.74	2.38 ± 0.18	4.73 ± 0.17	0.37 ± 0.01
Mono-103/2015	12.2 ± 0.23	10.6 ± 0.19	1.15 ± 0.02	40.1 ± 1.83	2.08 ± 0.09	3.76 ± 0.15	0.23 ± 0.01
MM-KP1520156	13.6 ± 0.09	9.98 ± 0.18	1.36 ± 0.02	62.0 ± 2.64	1.85 ± 0.12	8.63 ± 0.21	0.28 ± 0.03
Mono-610	10.9 ± 0.18	10.6 ± 0.15	1.03 ± 0.01	34.6 ± 1.38	2.48 ± 0.18	4.73 ± 0.17	0.29 ± 0.01
IC0599709	15.6 ± 0.39	10.9 ± 0.12	1.44 ± 0.04	81.7 ± 0.73	2.18 ± 0.15	3.56 ± 0.29	0.17 ± 0.01
Mono-2015-5	13.5 ± 0.12	11.5 ± 0.15	1.17 ± 0.02	51.0 ± 1.34	2.52 ± 0.18	2.36 ± 0.15	0.31 ± 0.01
Mono-1621/ CTS	9.91 ± 0.12	10.9 ± 0.20	0.9 ± 0.03	34.2 ± 0.45	2.65 ± 0.06	2.73 ± 0.12	0.34 ± 0.01
Mono-1805	10.1 ± 0.06	9.68 ± 0.15	1.05 ± 0.02	35.5 ± 1.24	2.48 ± 0.09	4.36 ± 0.22	0.37 ± 0.01
Mono-CRBH	15.4 ± 0.19	12.4 ± 0.18	1.24 ± 0.01	61.3 ± 2.81	3.42 ± 0.15	4.66 ± 0.20	0.34 ± 0.01
Mono- 103/916	9.37 ± 0.19	12.0 ± 0.49	0.78 ± 0.01	26.0 ± 0.53	2.72 ± 0.15	2.33 ± 0.23	0.29 ± 0.01
Mono-1424	14.1 ± 0.44	12.1 ± 0.49	1.17 ± 0.04	83.8 ± 1.75	3.32 ± 0.18	8.56 ± 0.20	0.34 ± 0.01
Mono-2015-5-S1	14.8 ± 0.15	11.4 ± 0.21	1.31 ± 0.02	57.1 ± 4.94	2.38 ± 0.20	4.69 ± 0.20	0.32 ± 0.01
MM-1426/S-1	12.6 ± 0.09	10.5 ± 0.55	1.2 ± 0.07	43.4 ± 1.72	3.02 ± 0.09	4.69 ± 0.20	0.44 ± 0.01
MM10391603	13.8 ± 0.21	12.0 ± 0.61	1.15 ± 0.04	47.6 ± 1.96	2.18 ± 0.12	6.63 ± 0.12	0.23 ± 0.02
Farmers'Glory	9.85 ± 0.03	9.72 ± 0.08	1.01 ± 0.01	49.7 ± 0.74	2.48 ± 0.12	5.21 ± 0.37	0.36 ± 0.01
MS-1	9.61 ± 0.10	8.38 ± 0.06	1.15 ± 0.02	38.1 ± 0.96	2.62 ± 0.30	4.96 ± 0.15	0.38 ± 0.01
Hara Madhu	9.44 ± 0.14	9.75 ± 0.06	0.97 ± 0.01	34.9 ± 1.16	1.82 ± 0.15	4.53 ± 0.12	0.20 ± 0.01
Punjab Sunheri	10.0 ± 0.06	9.75 ± 0.13	1.03 ± 0.01	26.0 ± 1.30	2.32 ± 0.18	5.59 ± 0.24	0.23 ± 0.01
SM-2015-2	17.4 ± 0.56	15.8 ± 0.91	1.1 ± 0.05	196.4 ± 11.81	1.35 ± 0.21	1.29 ± 0.18	0.09 ± 0.01
LSD (p≤0.05)	0.48	0.63	0.05	6.01	0.30	0.57	0.03

kg/cm^2) were significantly firmer than SM-2015-2 (0.09 kg/cm^2) (Table 4). According to Dantas et al. (2015), Brazilian melon accessions had lower fruit firmness, ranging from 1.05-3.4(kg/cm^2) compared to the *inodorous* accession with 4.57 kg/cm^2. Similarly, when monoecious genotypes were assessed for fruit firmness with fruit rind, a range of 2.57 to 12.7 kg/cm^2 was reported in melon Shajari et al. (2021) and Solatani *et al.* (2022). Our study supports previous studies indicating that MM-1426/S-1 of the inodorous group has the highest fruit firmness (0.44 kg/cm^2), as measured without the fruit skin.

Analysis of variance exhibited significant variation among the muskmelon genotypes for yield and yield-related traits such as fruit weight, number of fruits per plant and fruit yield (Table 5 and Figure 3). The average fruit weight is a crucial factor in determining the yield of melons. The current study has noted a significant variation in average fruit weight among monoecious genotypes (Table 5). Fruit weight ranged from 390–1537 g, where Mono 1424 (1537), Mono-CRBH (1368.8), and Mono 916 (966.8) genotypes recorded the highest fruit weight. Monforte et al. (2014) classified melons into four types based on fruit weight: very small (<400 g), small (100–400 g), medium (400 g–1 kg), and large (>4 kg). In the present study, most monoecious genotypes were medium to large (400-1000g), while andromonoecious genotypes were small to medium.

Table 5: Yield and its component traits of monoecious inbred lines evaluated at PAU, Ludhiana during 2020 and 2021

Year	*Average fruit weight(g)*	*Number of fruits per plant*	*Yield/ha(t)*
2020	738.6	3.3	21.9
2021	883.6	3.4	27.0
LSD(p≤0.05)	0.01	0.26	2.31
Genotypes			
Mono-970	679.2 ± 17.7	2.77 ± 0.26	17.8 ± 1.33
Mono-916	966.8 ± 9.49	2.8 ± 0.19	25.6 ± 1.99
Mono-916/NTS	813.8 ± 10.3	3.76 ± 0.25	28.8 ± 1.00
Mono-916/NT	959.2 ± 40.9	3 ± 0.19	27.2 ± 1.65
Mono-916/S	851.2 ± 21.9	3.07 ± 0.13	24.7 ± 1.31
Mono-PAUS-15	742.5 ± 67.7	4.24 ± 0.18	29.7 ± 3.39
Mono-103/2015	755.8 ± 42.1	3.37 ± 0.20	24.0 ± 0.63
MM-KP1520156	708.5 ± 35.9	3.74 ± 0.27	25.1 ± 2.00
Mono-610	837.8 ± 7.75	2.57 ± 0.15	20.3 ± 1.32
IC0599709	837.1 ± 54.2	3.21 ± 0.13	25.4 ± 2.58
Mono-2015-5	775.8 ± 31.7	3.44 ± 0.11	25.4 ± 2.90
Mono-1621/ CTS	861.5 ± 17.4	2.64 ± 0.30	21.4 ± 1.30
Mono-1805	745.8 ± 53.2	3.56 ± 0.16	25.0 ± 1.98
Mono-CRBH	1368.8 ± 48.3	2.57 ± 0.15	33.2 ± 2.85
Mono- 103/916	863.2 ± 29.3	2.74 ± 0.21	22.3 ± 1.38
Mono-1424	1537.8 ± 75.3	2.2 ± 0.14	31.9 ± 2.85
Mono-2015-5-S1	886.5 ± 11.9	2.18 ± 0.11	18.3 ± 0.91
MM-1426/S-1	928.2 ± 43.0	4.2 ± 0.14	36.9 ± 2.64
MM10391603	749.2 ± 70.4	4.2 ± 0.15	29.8 ± 2.76
Farmers'Glory	639.2 ± 28.0	1.92 ± 0.23	11.7 ± 1.10
MS-1	610.5 ± 20.7	2.82 ± 0.06	16.2 ± 0.32
Hara Madhu	555.5 ± 14.9	5.94 ± 0.17	31.1 ± 0.94
Punjab Sunheri	401.2 ± 11.3	5.01 ± 0.24	19.2 ± 1.15
SM-2015-2	390.2 ± 9.82	4.19 ± 0.19	15.6 ± 1.09
LSD (p≤0.05)	109.04	0.37	5.36

Fergany et al. (2010) examined fifty monoecious genotypes for average fruit weight and found that genotypes varied from 0.18 to 1.74 kg. Additionally, studies by Dantas et al. (2015), Ivankova and Velkov (2021), and Barbosa et al. (2022) demonstrated that the *cantalupensis* sub-*prescott* and *flexuosus* group's monoecious melon accessions had the highest fruit weight, ranging from 0.7 to 2.3 kg. Additionally, Kaligudi et al. (2021) reported that monoecious genotypes had fruit weight ranging from 236 to 905 g and were used as male parents in melon heterosis breeding.

The number of fruits per plant varied from 1.92(Farmer's Glory) to 5.94 (Hara Madhu). Landrace Hara Madhu is still popular among Punjab growers. It was used to develop two hybrids, Punjab Sunehri and Punjab Hybrid, due to its good horticultural traits, including the highest number of

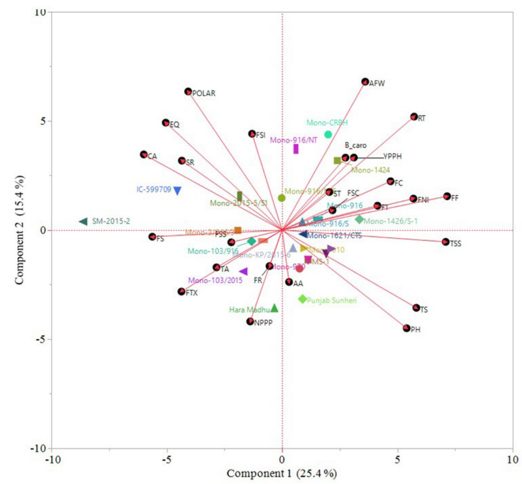

Figure 3: Principal component analysis (PCA) biplot of five quantitative, ten qualitative and fruit morphological traits of 24 muskmelon inbred lines

fruit per plant (Nandpuri et al., 1975; Nandpuri et al., 1982; Vashisht et al., 2019; Singh et al., 2020). Andromonoecious accessions of the *cantalupensis* and *inodrous* groups produced a higher number of fruits per plant 3-8 compared to monoecious accessions, which produced 2-5 fruits per plant. These findings are consistent with the results of our study. In the present study, it was found that the fruit weight has a significant influence on the fruit yield. Muskmelon genotypes differed significantly for yield, where MM-1426/S-1, Mono-1424 and Mono-CRBH recorded the highest yield. The monoecious genotypes had the highest yield, ranging from 17.8 to 36.8 t/ha, while andromonoecious genotypes recorded a yield of 11.7 to 31.14 t/ha. Recent studies conducted by Shajari et al. (2021), Barbosa et al. (2022), and Soltani et al. (2022) have found that the fruit yield of monoecious melon accessions varied from 11.1 to 53.6 kg/plant. The reason for the lower yield of andromonoecious genotypes was attributed to the lower average fruit weight.

Analysis of variance showed significant variation among the genotypes for biochemical traits such as ascorbic acid, β-carotene, pH, TSS, titratable acidity and TSS/TA ratio (Table 6). For ascorbic acid, Hara Madhu (19.02) and Punjab Sunheri (18.45) were found to be significantly higher than those of the Mono 1621/CTS (2.49), Mono-103916(2.69) and Mono-1424(3.62). The present study is consistent with Fergany et al. (2010) findings that monoecious accessions containing ascorbic acid ranged from 1.4 to 9.0 (mg/100 g). Similarly, according to Singh et al. (2020), Hara Madhu and Punjab Sunheri had the highest ascorbic acid, ranging from 14.5 to 46.3 (mg/100 g) with a mean value of 26.8 (mg/100 g). Moreover, Hiremata et al. (2023) reported that the levels of ascorbic acid in Mangalore melon accessions ranged from 20 to 33.75%. In the present study, orange-fleshed monoecious genotypes of the *cantalupensis* and *reticulatus* group had more β-carotene content than other flesh (green, cream)

Table 6: Biochemical fruit traits of muskmelon genotypes evaluated at PAU, Ludhiana during 2020 and 2021

Year	*Ascorbic Acid (mg/100 g)*	*β-carotene (mg/100g)*	*pH*	*TSS (o Brix)*	*Titratable acidity (g anhydrous citric acid/100ml of fruit juice)*	*TSS/TA ratio*
2020	11.73	1.73	3.70	9.02	0.19	50.5
2021	11.92	1.99	3.73	10.91	0.20	61.5
LSD(p≤0.05)	0.04	0.15	0.14	0.26	0.002	0.65
Genotypes						
Mono-970	7.45 ± 0.71	1.53 ± 0.12	3.76 ± 0.11	11.9 ± 0.12	0.15 ± 0.01	78.8 ± 0.86
Mono-916	15.83 ± 0.14	1.6 ± 0.13	3.33 ± 0.08	12.0 ± 0.14	0.15 ± 0.01	82.8 ± 0.53
Mono-916/NTS	14.79 ± 0.91	2.09 ± 0.08	3.26 ± 0.16	9.61 ± 0.29	0.15 ± 0.01	62.8 ± 0.64
Mono-916/NT	16.97 ± 0.95	2.64 ± 0.11	3.46 ± 0.16	10.5 ± 0.09	0.16 ± 0.02	64.4 ± 0.94
Mono-916/S	14.77 ± 0.65	2.65 ± 0.11	3.62 ± 0.15	11.6 ± 0.18	0.14 ± 0.01	83.7 ± 1.14
Mono-PAUS-15	13.87 ± 0.94	1.61 ± 0.12	4.52 ± 0.15	12.9 ± 0.12	0.26 ± 0.03	48.9 ± 0.35
Mono-103/2015	12.76 ± 0.70	1.88 ± 0.10	3.52 ± 0.16	10.7 ± 0.09	0.24 ± 0.03	45.2 ± 0.11
MM-KP1520156	11.54 ± 0.56	1.76 ± 0.11	3.92 ± 0.34	12.7 ± 0.18	0.17 ± 0.03	76.8 ± 1.33
Mono-610	15.73 ± 0.58	1.71 ± 0.14	3.27 ± 0.17	11.6 ± 0.17	0.22 ± 0.03	54.9 ± 0.61
IC0599709	4.16 ± 1.45	1.45 ± 0.16	2.06 ± 0.13	5.75 ± 0.12	0.32 ± 0.01	18.1 ± 0.32
Mono-2015-5	12.01 ± 0.42	1.36 ± 0.10	4.99 ± 0.13	8.91 ± 0.15	0.27 ± 0.04	33.4 ± 0.90
Mono-1621/ CTS	2.49 ± 0.24	2.73 ± 0.12	4.02 ± 0.07	11.6 ± 0.15	0.18 ± 0.01	63.9 ± 0.53
Mono-1805	10.24 ± 0.48	2.67 ± 0.15	4.46 ± 0.09	13.7 ± 0.12	0.17 ± 0.04	79.3 ± 0.73
Mono-CRBH	11.68 ± 0.85	1.87 ± 0.16	3.98 ± 0.15	9.61 ± 0.12	0.15 ± 0.03	63.2 ± 1.42
Mono- 103/916	2.69 ± 0.30	1.53 ± 0.16	1.86 ± 0.10	7.75 ± 0.24	0.26 ± 0.03	29.6 ± 0.70
Mono-1424	3.62 ± 0.56	2.6 ± 0.16	2.86 ± 0.16	9.71 ± 0.15	0.14 ± 0.01	72.1 ± 1.83
Mono-2015-5-S1	12.17 ± 0.75	1.57 ± 0.16	1.75 ± 0.15	8.05 ± 0.18	0.15 ± 0.02	55.6 ± 0.73
MM-1426/S-1	13.5 ± 0.39	1.62 ± 0.17	5.09 ± 0.08	14.9 ± 0.14	0.20 ± 0.02	74.3 ± 0.61
MM10391603	11.84 ± 0.10	1.72 ± 0.23	3.61 ± 0.15	8.61 ± 0.24	0.24 ± 0.01	27.9 ± 0.93
Farmers'Glory	18.45 ± 0.47	1.5 ± 0.19	4.12 ± 0.06	9.08 ± 0.12	0.17 ± 0.02	52.9 ± 0.17
MS-1	4.44 ± 0.08	1.66 ± 0.17	4.89 ± 0.08	7.85 ± 0.07	0.15 ± 0.01	52.8 ± 0.26
Hara Madhu	19.02 ± 0.35	1.67 ± 0.15	5.69 ± 0.08	8.07 ± 0.11	0.15 ± 0.01	56.1 ± 0.56
Punjab Sunheri	18.97 ± 0.66	1.73 ± 0.12	5.95 ± 0.05	8.25 ± 0.12	0.15 ± 0.01	55.6 ± 0.36
SM-2015-2	14.86 ± 0.28	1.59 ± 0.19	1.19 ± 0.05	4.03 ± 0.15	0.37 ± 0.02	10.9 ± 0.25
LSD (p≤0.05)	1.28	0.28	0.26	1.42	0.001	3.05

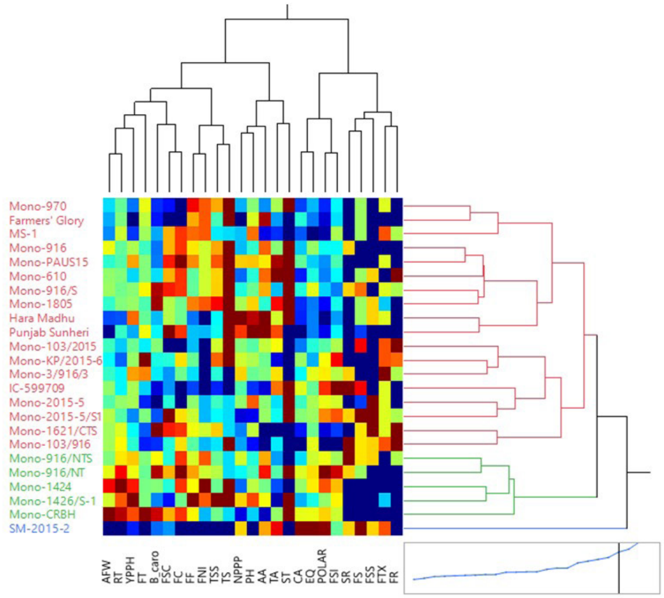

Figure 4: Heatmap and hierarchical clustering (double dendrogram) responses to morphological, biochemical and fruit morphological traits of 24 muskmelon inbred lines constructed using GGA biplot. The heatmap plot describes the relative abundance of each muskmelon inbred line (columns) within each feature (rows). The color code (blue to dark red) displays the row z-score: red color indicates high abundance, blue color low abundance.

Abb: used in Figures. 3,4 and 5- Average fruit weight (AFW), Rind thickness(RT), Yield per ha(YPPH), Flesh thickness(FT), β-carotene(B-caro), Fruit skin color (FSC), Flesh color (FC), Flesh firmness (FF), Fruit netting intensity (FNI),Total soluble solids (TSS), Fruit taste(TS), Number of fruits per plant (NPPP), pH (PH), Ascorbic acid (AA), Titratable acidity (TA), Fruit sutures (FS), Cavity area (CA), Equatorial diameter (EQ), Polar diameter (Polar), Fruit shape index (FSI), Fruit Sourness (SR), Fruit shape (FS), Fruit scar size (FSS), Fruit texture (FTX), Fruit ribs(FR)

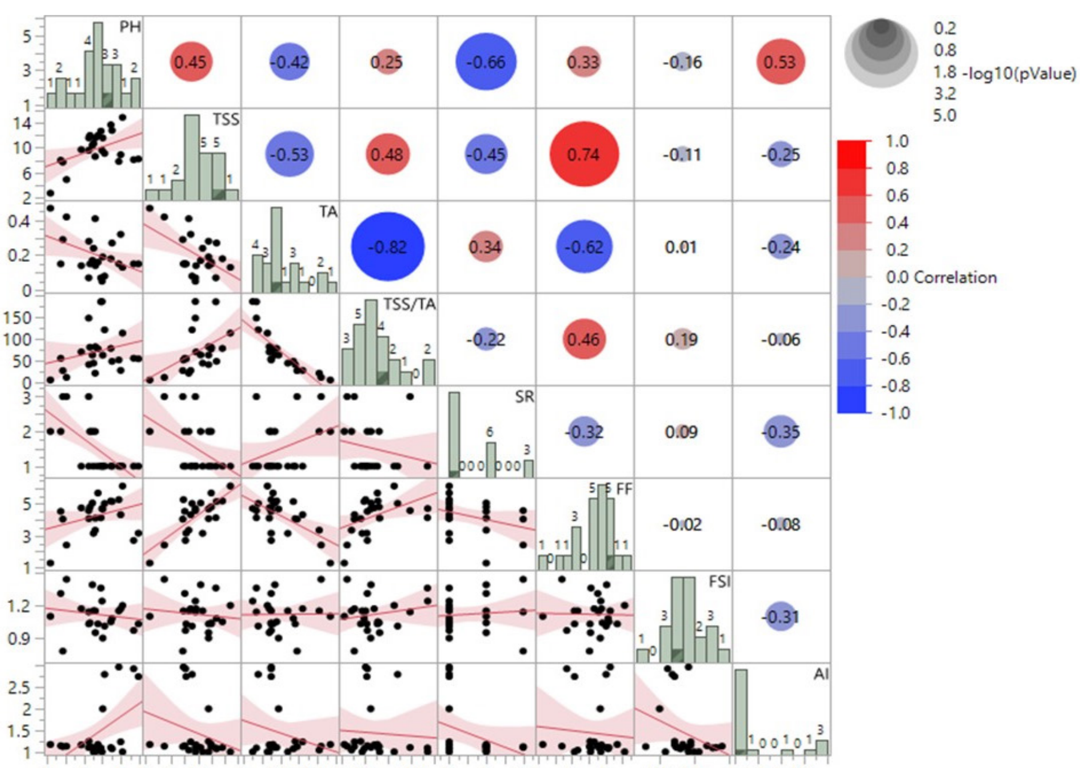

Figure 5: Correlation analysis of pH, TSS, titratable acidity, TSS/TA ratio, fruit sourness, fruit firmness, fruit shape index and andromonoecy index of monoecious lines; where correlation matrix shows the distribution of each genotype on the diagonal, the value of the correlation (on the top of the diagonal), and the bivariate scatter plots with a fitted line (on the bottom of the diagonal)

Table7: Sensory and fruit morphological evaluation of muskmelon inbred lines

Genotypes	*Fruit taste*	*Fruit skin color*	*Fruit netting intensity*	*Fruit suture*	*Flesh color*	*Flesh texture*	*Fruit shape*	*Fruit sourness (mature fruit)*	*Fruit ribs*	*Bottom scar size*
Mono-970	Sweet	Light yellow	Pronounced	Absent	White	Soft	Circular	Absent	Absent	Small
Mono-916	Sweet	Dark green	Intermediate	Absent	Orange	Firm	Ovate	Mild	Absent	Small
Mono-916/NTS	Intermediate	Pale green	Pronounced	Present	Orange	Firm	Quadrangular	High	Superficial	Medium
Mono-916/NT	Intermediate	Dark green	Intermediate	Absent	Salmon	Firm	Circular	Mild	Absent	Small
Mono-916/S	Sweet	Orange	Intermediate	Absent	Orange	Soft	Oblate	Mild	Superficial	Small
Mono-PAUS-15	Sweet	Orange	Intermediate	Absent	Salmon	Soft	Ovate	Absent	Absent	Small
Mono-103/2015	Sweet	White	Absent	Present	White	Mealy	Obovate	Absent	Deep	Small
MM-KP1520156	Sweet	Pale green	Absent	Present	Pale orange	Mealy	Ovate	Absent	Intermediate	Small
Mono-610	Sweet	Dark green	Intermediate	Absent	Orange	Firm	Circular	Absent	Deep	Medium
IC0599709	Insipid	Cream	Absent	Absent	White	Soft	Obovate	High	Absent	Small
Mono-2015-5	Intermediate	Pale green	Superficial	Absent	White	Soft	Medium elliptic	Absent	Absent	Large
Mono-1621/ CTS	Intermediate	Orange	Intermediate	Present	Orange	Soft	Quadrangular	Absent	Deep	Large
Mono-1805	Sweet	Green	Pronounced	Absent	Green	Grainy	Circular	Absent	Absent	Medium
Mono-CRBH	Sweet	Pale green	Pronounced	Present	Orange	Firm	Ovate	Absent	Absent	Small
Mono- 103/916	Intermediate	Pale green	Superficial	Present	Pale orange	Mealy	Quadrangular	High	Deep	Medium
Mono-1424	Sweet	Dark green	Superficial	Absent	Orange	Firm	Ovate	Absent	Absent	Small
Mono-2015-5-S1	Intermediate	Brown	Superficial	Absent	Pale orange	Soft	Elongated	Mild	Superficial	Large
MM-1426/S-1	Sweet	Light yellow	Pronounced	Absent	Green	Grainy	Ovate	Absent	Absent	Small
MM10391603	Insipid	Cream	Absent	Present	Green	Fibrous	Ovate	Mild	Superficial	Small
Farmers'Glory	Sweet	White	Pronounced	Present	White	Firm	Circular	Absent	Absent	Small
MS-1	Intermediate	Dark green	Pronounced	Present	Orange	Mealy	Circular	Absent	Absent	Small
Hara Madhu	Sweet	Green	Absent	Absent	Green	Soft	Circular	Absent	Superficial	Medium
Punjab Sunheri	Sweet	Brown	Superficial	Present	Orange	Firm	Medium elliptic	Absent	Absent	Small
SM-2015-2	Insipid	Cream	Absent	Present	White	Mealy	Elongated	Mild	Superficial	Medium

color fruit. The dark orange-fleshed Mono-1621/CTS had the highest value (2.73), followed by the orange-fleshed Mono-1805(2.67). The light green fleshed Mono-2015-5 (1.36) and cream-fleshed IC0599709 had low β-carotene values. Fergany et al. 2010 found that the *Momordica* group with orange flesh had a higher carotenoid content of 30.8 to 146.3 μg/100g than the white flesh acidulous group. Similarly, Singh et al. (2020) found that *reticulatus* accessions had the highest β-carotene content, ranging from 0.24 to 3.32 mg/100g, while wild melon accessions had the lowest. This aligns with Hiremata et al. (2023) findings, where Mangalore melon accessions with white-green flesh recorded a β-carotene content of 0.5 mg/100 g. Likewise, Kaur et al. 2022 reported that parents and hybrids from the *reticulatus* group with orange flesh had the highest β-carotene content, ranging from 0.52 to 2.5 and 0.21 to 3.4 (mg/100 g), respectively. Melon genotypes with high ascorbic acid and β-carotene levels contribute to improved nutritional value, extended shelf life, and enhanced flavour and aroma.

Titratable acidity and pH are indicators of a fruit's acidity, which affects its taste. The pH values of melon genotypes ranged from 1.19(SM-2012-2) to 5.95 (Punjab Sunehari). The titratable acidity of fruit pulp, which is also associated with pH, was in the range of 0.53 (Mono-1621/CTS) to 0.84 (Mono-610). Among different melon groups, *cantalupensis* (cantaloupe), *reticulatus* (muskmelon), and *inodorus* (honeydew) are sweet melons that have low levels of acid, whereas *momordica* (snap melon) and *agrestis* (wild melon) are acidic melons, as reported by Barreiro et al. (2001) and Pitrat (2016). In a similar study, Fergey et al. (2010) found that there was no significant difference in the titratable acidity of mature fruits between accessions of the *Momordica* and *acidulous* groups, which ranged from 0.12 to 0.57%. Dantas et al. (2015) reported that Brazilian monoecious accessions had fruits with low to medium sugar content, pH ranged from 3-7.2, and titratable acidity from 0.05 to 0.59%, making them quite acidic in taste. Likewise, Singh et al. 2020 found that *Momordica* accessions had the highest level of titratable acidity, with a value of 0.63. This finding is consistent with the current study, where the Momordica accession SM-2012-2 had a titratable acidity of 0.80 (Table 6). Another main factor affecting melon's sensory quality is sourness, mainly associated with pH and, to a lesser extent, with the degree of acid dissociation as reported by Furukawa et al. (1969). In this way, titratable acidity and pH are deciding factors for developing fruits with high sugar and less sourness, as reported by Burger et al. (2006).

Total soluble solids (TSS) is a crucial biochemical trait in determining the quality of melons, and a range of 9 to 15 °Brix is considered excellent. Similarly, muskmelon genotypes differed significantly for total soluble solids and ranged from 4.03-14.9°Brix. The monoecious genotypes Mono1426/S-1(14.9), Mono-1805(13.7) and Mono PAUS15 (12.8) recorded the highest TSS than the snapmelon genotype SM-2015-2(4.03). Similarly, Sakata et al. (2013) and Choudhary et al. (2018) reported high TSS (11.6%) in their monoecious lines used for hybrid development. The level of TSS in monoecious genotypes belonging to the *cantalupensis*, *inodorus*, and *flexuosus* groups ranged from 5 to 14% (Shajari et al., 2021; Ivanova and Velkov, 2021; Soltani et al., 2022). The TSS/TA ratio is a key biochemical trait in determining the maturity and ripeness of melons. It helps to achieve a desirable balance between sweetness and acidity, improving sensory evaluation as reported by Albuquerque et al. (2006). The TSS/TA ratio varied greatly among muskmelon genotypes, with the monoecious genotype Mono 916/S showing the highest ratio at 83.7, followed by Mono916 and Mono-970 at 82.8 and 78.8, respectively. A higher TSS/TA ratio indicates a sweeter and more desirable flavor in the fruit. In contrast, the snap melon genotype and IC0599709 exhibited a TSS/TA ratio of 10.9 and 18.1, suggesting that higher acidity levels and lower sweetness characterize these genotypes. Similarly, a TSS/TA ratio of 85 to 119 was found in cantaloupes and Honey Dew melons as reported by Munira et al. (2012) and Supapvanich et al. (2011).

Stability of monoecism in *C. melo*: Identification of stable monoecious genotypes

Environmental factors such as light intensity, photoperiod, and temperature affect the sex expression of melons. According to Penaranda et al. (2007), high temperatures stimulate a partial or complete change of female flowers into bisexual flowers, while low temperatures hinder the development of male flowers in *C. pepo*. Moreover, frequent changes in photoperiod and temperature regimes alter the flower sex phenotype of melons and squashes, resulting in four types of female flowers: complete female without stamens, complete hermaphrodite flowers, female flower with complete carpels and partially developed stamens, and complete male flowers without carpels (Martinez et al. 2014 and Manzano et al. 2016). Some female flowers become bisexual under high temperatures, with partially or fully developed stamens. This condition is referred as unstable moneocy or partial andromonecy, as reported by Anguado et al. (2018).

In the current study, based on AI scores of pistillate and staminate flowers, melon inbred lines were classified into three phenotypic classes (Figure 2). Under open field conditions, the inbred lines Mono-610 (1.19) and Mono-1621/CTS (1.28) were observed to be monoecious. However, under polyhouse conditions, the same genotypes were partially andromonoecious with an AI score of 1.31 and 2.71, respectively. Temperatures ranging from 27 to 32°C and low humidity (Table 3) during flowering (5–9th week) promote the stability of monoecism in muskmelon genotypes grown in open field conditions. Conversely, high temperatures and low relative humidity (32–36°C, 55–62%) during flowering (5–9th week) in polyhouse conditions cause the development of partial stamens in female flowers of monoecious genotypes (Fig.1A, Table 3). Similarly, Martinez et al. (2014) identified three commercial hybrids and 26 partially andromonoecious cultivars of *C. pepo* under greenhouse spring-summer conditions.

Temperature plays a crucial role in sex conversion of monoecious to andromonoecious, with day temperatures exceeding 25 to 35°C. Additionally, high day temperature reduces the production and level of ethylene in floral buds and results in monoecy instability (Manzano et al., 2011; Zhang et al., 2017). Ethylene controls individual floral buds and sex expression within plants, where a decrease in ethylene biosynthesis reduces the number of female flowers in *C. melo*, *C. sativus*, and *C. pepo*. Likewise, two monoecious watermelon lines, P85 and P86, had predominantly female flowers and produced bisexual flowers, with an AI score of 1.2. Moreover, crossing the two lines with andromonoecious line P87 yielded an F_1 population with a partially andromonoecious phenotype, indicating that the monoecious alleles in watermelon lines P85 and P86 exhibit a semi-dominant trait in relation to andromonoecious (Manzano et al., 2016; Anguado et al., 2018). Moreover, day length and temperature variations in cucumber and melon alter ethylene production and formation of male or female flowers, linked to mediated sugar signalling as reported by Yamasaki et al. 2003. Therefore, temperature, humidity and day length are interrelated and control plants' ethylene levels, frequently changing the sex phenotype of muskmelon genotypes.

Out of a total of 24 melon genotypes, all genotypes were found stable for monoecy in both environments, with an AI score ranging from 1 to 1.2. The stability of monoecism was also affected by temperature in a genotype-dependent manner, where 29 out of 67 studied cultivars in *C. pepo were affected, suggesting* that genetics also impacts the monoecious trait. Similarly, two inbred lines, Bog and Veg, and their F_1 generations showed a stable monoecious phenotype under high temperatures as described by Martinez et al., 2014). Andromonoecious genotypes Farmers' Glory, MS-1, Hara Madhu, and Punjab Sunheri remain stable for andromonoecy under both environments, which were used as reference genotypes for assessing the stability of monoecism of monoecious genotypes. Likewise, a stable watermelon inbred P87 was found under greenhouse spring-summer conditions with an AI score of 3, which produced only staminate and hermaphrodite flowers with complete stamens, as reported by Manzano *et al.* (2016) and Anguado *et al.* (2018). After assessing the stability of monoecism in both environments, 18 stable monoecious, two partial andromonoecious, and four andromonoecious genotypes were identified (Table 3). Similarly, a diversity study of around 200 watermelon accessions was conducted to investigate sex morphotypes, revealing that 43% were andromonoecious, 18% were monoecious, and 39% were partially andromonoecious in both open field and greenhouse environments, as demonstrated by Anguado et al. (2020).

Biplot analysis

The Inbred line-by-trait PCA biplot analysis visually represents relationships among the morphological and qualitative fruit traits across muskmelon inbred lines Kaur et al., 2022. A combined analysis provided additional insight into their interrelationships with various fruit morphological traits after comparing quantitative and qualitative traits individually. The average fruit weight positively correlated with β-carotene, fruit netting intensity, fruit sutures, and fruit skin color. Similarly, a positive correlation was found between β-carotene and yield, fruit skin color, flesh color, and fruit netting intensity. The TSS was positively correlated with fruit netting intensity, fruit sutures, taste, and pH. Likewise, flesh thickness was positively correlated with fruit netting intensity and firmness and found a negative correlation with cavity area and fruit equatorial diameter. According to Naroui Rad et al. (2017), the first component accounts for 26.98% of the variations in morphology, with fruit weight, fruit length, cavity diameter, and single plant yield being the most significant variables in PC1. These findings highlight the importance of yield-related traits while evaluating melon genotypes. The monoecious genotypes, namely Mono-1426/S-1, Mono 916/S, Mono1424, and Mono916/ST, exhibited strong performance for different traits on PC1. However, other traits such as fruit ribs, number of fruits per plant, fruit texture, and fruit scar size had a negative association with both PC1 and PC2. On the other hand, genotypes such as Mono-103/916, Mono-KP2015-6, Mono-103/2015, SM-2012-2, and Hara Madhu were found to be inferior to different evaluated genotypes. Similarly, Trimech *et al.* 2013 evaluated fruit morphological, quantitative and qualitative traits together and found a positive correlation between fruit shape, fruit skin color, and fruit ribs. Additionally, a positive correlation was found between fruit sourness and titratable acidity, while a negative correlation was found between pH and fruit taste. According to Bibani and Pakniyat (2008), a single gene or genes that are closely linked can affect multiple traits within the same principal component (Figure 4). The first principal component shows strong correlations and links between traits that have the most variation, while the second and third principal components have traits that are located far apart in the genome. PCA-analyzed data is essential for developing a breeding program to combine particular fruit characteristics.

Cluster analysis

The heatmap analysis of morphological and biochemical traits showed a chromatic evaluation of 24 muskmelon genotypes (Figure 4). This analysis involved constructing two dendrograms, the first showing an arrangement of muskmelon genotypes in the vertical direction and the second dendrogram representing the studied traits that influenced the diffusion, which was on the horizontal direction. The first dendrogram showed two major groups; the first main group had two subgroups, where the first subgroup had a total of five genotypes from four *reticulatus* and one *inodrous* group, while the second subgroup had eighteen genotypes from 13 *reticulatus* and five *cantalupensis* groups. The second main-group of dendrogram-one only one genotype from the *Momordica* group.

The second dendrogram also displayed two major groups. The first main group was linked to traits AFW, RT, YPPH, FT, β-carotene, FSC, FC, FF, FNI, TSS, TS, NPPP, pH, AA, TA, and ST, whereas the other nine traits belonged to the second main group. In the first subgroup of dendrogram-one, the monoecious genotypes, Mono-CRBH, Mono 1424, and Mono-1426/S- had higher values of fruit yield, average fruit weight, rind thickness, and flesh thickness. Meanwhile, lower values were recorded for fruit sourness, fruit ribs and fruit scar size, which ultimately separate these four genotypes from other melon genotypes. Conversely, the second main group, genotype SM-2012-2, had lower values of all traits evaluated except for fruit cavity area, equatorial diameter, and polar diameter of fruit. The highest values were recorded for genotype Mono-1805(β-carotene, TS, ST, TSS), Mono PAUS-15(ST, TS, FC, TA), Punjab Sunheri (NPPP, PH, AA, FSC).

All other traits showed lower values and were responsible for making different groups among genotypes. Subgroup 1 of dendrogram one included the monoecious genotypes Mono-10391603, IC-599709, and Mono 2015-5, which exhibited lower values of most studied traits and higher values of other fruit traits such as sourness, fruit scar size, and the highest fruit shape index (Figure 5). Similarly, Dantas et al. (2015) assessed 40 types of Brazilian melon and grouped them into three clusters according to their flowering, fruit, and yield traits. Likewise, Amorim et al. (2016) evaluated 41 accessions and sub-accessions and separated them into two clusters based on fruit morphology and sex expression. In 2022, both Solatani et al. and Saputra et al. divided various genotypes into three and four clusters, respectively, demonstrating a heatmap of both quantitative and qualitative characteristics. Ultimately, a visual representation and clustering of genotypes using heat maps helps select superior improved monoecious genotypes with better qualitative and morphological traits.

Correlation analysis of fruit quality and sensory attributes with andromonoecy index

The correlation matrices of muskmelon genotypes depicting the relationships among fruit quality and sensory attributes, including pH, TSS, titratable acidity, TSS/TA ratio, fruit firmness, sourness, and fruit shape index with andromonoecy index, are shown in Figure 5. The present study found a significant (p <0.001) positive correlation between fruit pH and andromonoecy index (0.53) and a negative correlation with sourness (-0.63). Similarly, a significant (p <0.001) strong positive correlation was found between TSS and fruit firmness (0.74) for muskmelon genotypes. Additionally, titratable acidity showed a negative correlation with TSS/TA ratio (-0.82) and fruit firmness (-0.62) with statistical significance at p <0.001. The fruit shape index did not exhibit any correlation with any of the other traits studied. A diagonal distribution of genotypes provides a better understanding of the clustering patterns of genotypes for a specific trait. Similarly, bivariate scatter plots with trend lines at the bottom of the diagonal represent the relationship between traits and a distribution range. Similarly, Albuquerque *et al.* (2006) studied the correlation between fruit firmness, flavour, sourness, titratable acidity, TSS/TA, and pH of melon cultivars. They found a strong positive correlation between TSS, firmness, and flavour and a negative correlation between titratable acidity and sourness. A positive correlation was also found between sourness, pH and titratable acidity. Moreover, Burger *et al.* (2003) reported that *reticulatus*, *inodrous*, and *canatalupensis* genotypes had lower levels of organic acids than *momordica* and *acidulous*, dominated by citric acid and malic acid. Similarly, the present studied monoecious genotypes belonged to sweet melon groups and exhibited less acidity and sourness. In conclusion, the correlation between fruit quality traits and sensory attributes showed a negative relation between sourness, titratable acidity, and oblong fruit shape with monoecy. Moreover, the monoecious inbred lines had found a balance between acidity, sourness, and TSS, producing highly flavored fruits, increasing the market demand and consumer preference. Contrarily, Kesavan and More (1991) and Sandha and Lal (1999) had reported that monoecy traits are strongly associated with sourness and FSI (tendency towards oblong shape) and negatively associated with fruit weight and TSS. In the current study, we observed that it is possible to develop stable monoecious inbred lines with low sourness, an ideal TSS/TA ratio and round fruit shape (Chaudhary et al.*,* 2018).

Conclusion

Monoecious and andromonoecious inbred lines belonging to diverse horticultural groups were evaluated for stability for monoecious sex expression under varying environments, along with revisiting the association of various fruit morphological, yield and biochemical attributes with monoecism. In this study, we were able to identify stable monoecious inbred lines of muskmelon along with desirable fruit traits. MM-1426/S-1, Mono-1805, Mono-916and Mono-PAUS-15exhibited stability in expression of monoecism under both the environments varying in temperature and humidity. While two inbred lines, Mono-610 and Mono-1621/CTS, exhibited variable sex types in response to varying environments. Thus, studying the stability of monoecious plants. Based on the historical reports, there is an established notion that the monoecious trait in muskmelon is associated with sourness and oblong fruit shape, besides high fruit yield and improved TSS. However, the set of monoecious lines evaluated in this study indicated that there is a probability to development stable monoecious lines possessing a round to oval-round shape, very low sourness, a nice blend of TSS/TA, along with improved yield through improved fruit size. Thus, the findings of this study will be helpful to select monecious inbred lines for hybrid seed production and to design genetic improvement programmes to under mechanisms governing this trait.

References

Abdi, H., & Williams, L. J. (2010). Principal component analysis. Wiley Interdisciplinary Reviews: Computational Statistics, 2(4), 433–459. https://doi.org/10.1002/wics.101

Aguado, E., García, A., Iglesias-Moya, J., et al. (2020). Mapping a partial andromonoecy locus in Citrullus lanatus using BSA-Seq and GWAS approaches. Frontiers in Plant Science, 11, 1243. https://doi.org/10.3389/fpls.2020.01243

Aguado, E., García, A., Manzano, S., et al. (2018). The sex-determining gene CitACS4 is a pleiotropic regulator of flower and fruit development in watermelon (Citrullus lanatus). Plant Reproduction, 31, 411–426. https://doi.org/10.1007/s00497-018-0346-7

Albuquerque, B., Lidon, F., & Barreiro, M. (2006). A case study on the flavor properties of melon (Cucumis melo L.) cultivars. Fruits, 61(5), 333–339. https://doi.org/10.1051/fruits:2006033

Amorim, C. C., et al. (2016). Morphological diversity and identification of accessions of melon. African Journal of Agricultural Research, 11(38), 3622–3632. https://doi.org/10.5897/AJAR2016.11326

Andrade, I. S., Melo, C. A., Nunes, G. H., Holanda, I. S., Grangeiro, L., & Corrêa, R. X. (2019). Morphoagronomic genetic diversity of Brazilian melon accessions based on fruit traits. Scientia Horticulturae, 256, 108572. https://doi.org/10.1016/j.scienta.2019.108572

Ansari, W. A., Atri, N., Yang, L., Singh, B., & Pandey, S. (2020). Genetic diversity in muskmelon based on SSR markers and morphological traits under well-watered and water-deficit condition. Biocatalysis and Agricultural Biotechnology, 26, 101633. https://doi.org/10.1016/j.bcab.2020.101633

Barbosa, B. L. R., Queiróz, M. A. D., Amorim, C. C. D., Barbosa, G. D. S., & Oliveira, R. S. D. (2022). Morpho-agronomic diversity and botanical identification of melon accessions from northeastern Brazil. Revista Caatinga, 36(2), 251–261. https://doi.org/10.47468/caatinga.a2022.v35n02a04

Barreiro, M. G., Lidon, F. C., & Pinto, M. (2001). Physicochemical characterization of the postharvest senescence of the winter melon Tendral. Fruits, 56, 51–58. https://doi.org/10.1051/fruits:2001100

Burger, Y., Sa'ar, U., Distelfeld, A., et al. (2003). Developing of sweet melon (Cucumis melo) genotypes combining high sucrose and organic acid content. Journal of the American Society for Horticultural Science, 128(4), 537–540.

Burger, Y., Sa'ar, U., Paris, H. S., Lewinsohn, E., Katzir, N., Tadmor, Y., & Schaffer, A. A. (2006). Genetic variability for valuable fruit quality traits in Cucumis melo. Israel Journal of Plant Sciences, 54(3), 233–242. https://doi.org/10.1560/IJPS.54.3.233

Chikh-Rouhou, H., & Sta-Baba, R. (2018). Morphological and phytochemical characterization of Tunisian melon (*Cucumis melo* L.) landraces. In Proceedings of the 5th International Conference on Sustainable Agriculture and Environment (5th ICSAE) (pp. 329–332). Hammamet, Tunisia.

Chikh-Rouhou, H., Mezghani, N., Mnasri, S., & Garcés-Claver, A. (2021). Assessing the genetic diversity and population structure of a Tunisian melon (Cucumis melo L.) collection using phenotypic traits and SSR molecular markers. Agronomy, 11(6), 1121. https://doi.org/10.3390/agronomy11061121

Choudhary, B. R., Haldhar, S. M., & Maheshwari, S. K. (2018). Identification and possibility of monoecious inbred of muskmelon (*Cucumis melo* L.) for heterosis breeding. Vegetable Science, 45(1), 118–120.

Choudhary, B. R., Pandey, S., Rao, E. S., & Sharma, S. K. (2015). DUS characterization of muskmelon (Cucumis melo) varieties. Indian Journal of Agricultural Sciences, 85(12), 1597–1601.

Dantas, A. C. A., Holanda, I. S. A., Esteras, C., Nunes, G. H. S., & Picó, M. B. (2015). Diversity of melon accessions from Northeastern Brazil and their relationships with germplasms of diverse origins. Journal of the American Society for Horticultural Science, 140(5), 504–517. https://doi.org/10.21273/JASHS.140.5.504

Fergany, M., Kaur, B., Monforte, A. J., Pitrat, M., Rys, C., Lecoq, H., Dhillon, N. P. S., & Dhaliwal, S. S. (2010). Variation in melon (Cucumis melo) landraces adapted to the humid tropics of southern India. Genetic Resources and Crop Evolution, 58, 225–243. https://doi.org/10.1007/s10722-010-9562-1

Food and Agriculture Organization (FAO). (2021). FAOSTAT. http://faostat.fao.org

Furukawa, H., Saso, H., Maeda, S., & Ninomiya, T. (1969). Taste test of organic acids. Part I: Measurements of point of subjective equalities (PSE) on sourness of nine organic acids accepted as food additives. Journal of the Japanese Society for Food Industry, 16, 63–68.

Heinze, P. H., Kanapaux, M. S., Wade, B. L., Grimball, P. C., & Foster, R. L. A. A. (1944). Ascorbic acid content of 39 varieties of snap beans. Food Research, 9, 19–26. https://doi.org/10.1002/j.1532-6119.1944.tb16080.x

Hiremata, V., Shet, R. M., Gunnaiah, R., Kalgudi, A., Shantappa, T., & Rathod, V. (2023). Mangalore melon (*Cucumis melo* ssp. *agrestis* var. *acidulus*): A neglected and underutilized vegetable of the Western Ghats of India. Genetic Resources and Crop Evolution, 70, 1895–1902. https://doi.org/10.1007/s10722-023-01520-0

Ikram, M., Esyanti, R. R., & Dwivany, F. M. (2017). Gene expression analysis related to ethylene-induced female flowers of cucumber (*Cucumis sativus* L.) at different photoperiod. Journal of Plant Biotechnology, 44, 229–234. https://doi.org/10.5010/JPB.2017.44.4.229

Ivanova, Z. H., Velkov, N., & Grozeva, S. (2019). A survey of preferences to melon fruit characteristics among Bulgarian consumers. Scientific Works of Union of Scientists in Bulgaria – Plovdiv, 27, 235–241.

Ivanova, Z., & Velkov, N. (2021). Genetic variability in Bulgarian melon collection – flowering types and fruit quantitative traits. Genetika, 53(2), 545–558. https://doi.org/10.2298/GENSR2102545I

Kalgudi, A., Shet, R. M., Shantappa, T., Lakshmidevamma, T. N., Hongal, S., & Rathod, V. (2021). Assessment of heterosis in intraspecific hybrids derived from muskmelon (*Cucumis melo* L.) and Mangalore melon (*Cucumis melo* var. *acidulous*) for yield and quality traits including shelf life. Biological Forum – An International Journal, 13(3), Article ID not available.

Kaur, S., Sharma, S. P., Sarao, N. K., Deol, J. K., Gill, R., Abd-Elsalam, K. A., Alghuthaymi, M. A., Hassan, M. M., & Chawla, N. (2022). Heterosis and combining ability for fruit yield, sweetness, β-carotene, ascorbic acid, firmness and Fusarium wilt resistance in *Cucumis melo* L. involving genetic male sterile lines. Horticulturae, 8(1), 82. https://doi.org/10.3390/horticulturae8010082

Kenigsbuch, D., & Cohen, Y. (1990). The inheritance of gynoecy in muskmelon. Genome, 33(2), 317–320. https://doi.org/10.1139/g90-047

Kesavan, P. K., & More, T. A. (1991). Use of monoecious lines in heterosis breeding of muskmelon (*Cucumis melo* L.). Vegetable Science, 18, 59–64.

Kim, N., Oh, J., Kim, B., Choi, E. K., Hwang, U. S., Staub, J. E., Chung, S. M., & Park, Y. (2015). The CmACS-7 gene provides sequence variation for development of DNA markers associated with monoecious sex expression in melon (*Cucumis melo* L.). Horticulture, Environment, and Biotechnology, 56(4), 535–545. https://doi.org/10.1007/s13580-015-0135-5

Kubicki, B. (1969). Sex determination in muskmelon (Cucumis melo L.). Genetica Polonica, 10, 145–165.

Lai, Y. S., Shen, D., Zhang, W., Jiang, J., Song, X., Wang, Z., & Lin, T. (2018). Temperature and photoperiod changes affect cucumber sex expression by different epigenetic regulations. BMC Plant Biology, 18, 268. https://doi.org/10.1186/s12870-018-1505-7

Li, D., Sheng, Y., Niu, H., & Li, Z. (2019). Gene interactions regulating sex determination in cucurbits. Frontiers in Plant Science, 10, 1231. https://doi.org/10.3389/fpls.2019.01231

Manzano, S., Aguado, E., Martínez, C., et al. (2016). The ethylene biosynthesis gene CitACS4 regulates monoecy/andromonoecy in watermelon (Citrullus lanatus). PLoS ONE, 11(4), e0154362. https://doi.org/10.1371/journal.pone.0154362

Manzano, S., Martínez, C., García, J. M., Megías, Z., & Jamilena, M. (2014). Involvement of ethylene in sex expression and female flower development in watermelon (*Citrullus lanatus*). Plant Physiology and Biochemistry, 85, 96–104. https://doi.org/10.1016/j.plaphy.2014.01.013

Manzano, S., Martínez, C., Megías, Z., Gómez, P., Garrido, D., & Jamilena, M. (2011). The role of ethylene and brassinosteroids in the control of sex expression and flower development in Cucurbita pepo. Plant Growth Regulation, 65, 213–221. https://doi.org/10.1007/s10725-011-9583-1

Martínez, C., Manzano, S., Megías, Z., Barrera, A., Boualem, A., Garrido, D., & Jamilena, M. (2014). Molecular and functional characterization of CpACS27A gene reveals its involvement in monoecy instability and other associated traits in squash (*Cucurbita pepo* L.). Planta, 239, 1201–1215. https://doi.org/10.1007/s00425-014-2042-2

McCollum, J. P. (1953). A rapid method for determining total carotenoids and carotene in tomatoes. Proceedings of the American Society for Horticultural Science, 61, 431–433.

Monforte, A. J. (2017). The genetic control of fruit morphology in Cucumis melo L. In V International Symposium on Cucurbits (pp. 1–3). Leuven, Belgium.

Monforte, A. J., Diaz, A., Caño-Delgado, A., & van der Knaap, E. (2014). The genetic basis of fruit morphology in horticultural crops: Lessons from tomato and melon. Journal of Experimental Botany, 65(16), 4625–4637. https://doi.org/10.1093/jxb/eru017

More, T. A., Seshadri, V. S., & Sharma, J. C. (1980). Monoecious sex expression in muskmelon Cucumis melo L. Cucurbit Genetics Cooperative Report, 3, 32–33.

Munira, Z. A., Rosnah, S., Zaulia, O., & Russly, A. R. (2013). Effect of postharvest storage of whole fruit on physicochemical and microbial changes of fresh-cut cantaloupe (Cucumis melo L. reticulatus cv. Glamour). International Food Research Journal, 20, 501–508.

Nandpuri, K. S., Singh, S., & Lal, T. (1975). Punjab Sunehri: A new variety of muskmelon. Progressive Farming, 11, 21–23.

Nandpuri, K. S., Singh, S., & Lal, T. (1982). Punjab Hybrid-A new variety of muskmelon. Progressive Farming, 18, 3–4.

Naroui Rad, M. R., Fanaei, H. R., & Ghalandarzehi, A. (2017). Integrated selection criteria in melon breeding. International Journal of Vegetable Science, 23, 125–134. https://doi.org/10.1080/19315260.2015.1131188

Naroui Rad, M. R., Fanaei, H. R., & Ghalandarzehi, A. (2017). Integrated selection criteria in melon breeding. International Journal of Vegetable Science, 23, 125–134. https://doi.org/10.1080/19315260.2015.1131188

National Horticulture Board (NHB). (2022). Indian horticulture database. Ministry of Agriculture, Government of India. http://www.nhb.gov.in

Peñaranda, A., Payán, M. C., Garrido, D., Gómez, P., & Jamilena, M. (2007). Production of fruits with attached flowers in zucchini squash is correlated with the arrest of maturation of female flowers. Journal of Horticultural Science and Biotechnology, 82, 579–584.

Périn, C., Hagen, L. S., Giovinazzo, N., Besombes, D., Dogimont, C., & Pitrat, M. (2002). Genetic control of fruit shape acts prior to anthesis in melon (*Cucumis melo* L.). Molecular Genetics and Genomics, 266, 933–941. https://doi.org/10.1007/s00438-001-0604-1

Pitrat, M. (2016). Melon genetic resources: Phenotypic diversity and horticultural taxonomy. In R. Grumet, N. Katzir, & J. Garcia-Mas (Eds.), Genetics and Genomics of Cucurbitaceae (pp. 25–60). Springer. https://doi.org/10.1007/978-3-319-24942-6_2

Pitrat, M., Hanlet, P., & Hammer, K. (2000). Some comments on intraspecific classification of cultivars of Cucumis melo. Acta Horticulturae, 510, 29–36. https://doi.org/10.17660/ActaHortic.2000.510.2

Rai, N., & Rai, M. (2006). Heterosis breeding in vegetable crops (p. 531). New Delhi: New India Publishing.

Rosa, J. T. (1928). The inheritance of flower types in Cucumis and Citrullus. Hilgardia, 3(11), 233–250. https://doi.org/10.3733/hilg.v03n11p233

Sakata, Y., Fukino, N., Ohara, T., Sugiyama, M., & Yoshioka, Y. (2013). Effect of monoecious trait on fruit shape and total soluble solid contents of melon. Horticultural Research (Japan), 12(1), 15–22.

Saputra, H. E., Syukur, M., Suwarno, W. B., & Sobir. (2022). Diversity and similarity of melon (Cucumis melo L.) groups and determination of distinguishing morphological characters. Biodiversitas, 23(12), 6254–6261. https://doi.org/10.13057/biodiv/d231206

Shajari, M., Soltani, F., Reza Bihamta, M., & Alabboud, I. (2021). Genetic analysis and inheritance of floral and fruit traits in melon (*Cucumis melo* L.) in the full diallel cross. Plant Breeding, 140, 486–496. https://doi.org/10.1111/pbr.12931

Sharma, S. P., Leskovar, D. I., Crosby, K. M., & Ibrahim, A. M. H. (2020). GGE biplot analysis of genotype-by-environment interactions for melon fruit yield and quality traits. HortScience, 55(4), 533–542. https://doi.org/10.21273/HORTSCI14706-19

Singh, D., Leskovar, D. I., Sharma, S. P., Sarao, N. K., & Vashisht, V. K. (2020). Genetic diversity and interrelationship among Indian and exotic melons based on fruit morphology, quality components, and microsatellite markers. Physiology and Molecular Biology of Plants, 26, 985–1002. https://doi.org/10.1007/s12298-020-00790-4

Singh, M., Sharma, S. P., Sarao, N. K., Kaur, S., & Chhuneja, P. (2019). Molecular mapping of nuclear male-sterility gene ms-1 in muskmelon (*Cucumis melo* L.). Journal of Horticultural Science & Biotechnology, 94(1), 1–7. https://doi.org/10.1080/14620316.2018.1537193

Soltani, F., Shajari, M., Mirbehbahani, G. S., & Bihamta, M. R. (2022). Assessment of melon genetic diversity based on fruit phenotypic traits and flowering habits. Journal of Horticultural Science, 9, 97–116.

Supapvanich, S., Boon-Lha, K., & Mhernmee, N. (2011). Quality attribute changes in intact and fresh-cut honeydew melon (Cucumis melo var. inodorus) cv. 'Honey World' during storage. Kasetsart Journal: Natural Science, 45, 874–882.

Trimech, R., Zaouali, Y., Boulila, A., et al. (2013). Genetic variation in Tunisian melon (Cucumis melo L.) germplasm as assessed by morphological traits. Genetic Resources and Crop Evolution, 60, 1621–1628. https://doi.org/10.1007/s10722-013-9953-z

UPOV.(2006) International Union for the Protection of New Varieties of Plants (UPOV). Guidelines for the conduct of tests for distinctness, uniformity and stability: Melon (Cucumis melo L.) (TG/104/5-Add.). Geneva, Switzerland: UPOV

Vashisht, V. K., Lal, T., Sharma, S. P., & Thind, T. S. (2019). KP4HM-15: An inbred line of muskmelon resistant to Fusarium wilt. Acta Horticulturae. https://doi.org/10.17660/ActaHortic.2019.1234

Yamasaki, S., Fujii, N., & Takahashi, H. (2003). Characterization of ethylene effects on sex determination in cucumber plants. Sexual Plant Reproduction, 16, 103–111. https://doi.org/10.1007/s00497-003-0180-3

Zhang, H. J., & Luan, F. S. (2016). Transformation of the CmACS-7 gene into melon (Cucumis melo L.) using the pollen-tube pathway. Genetics and Molecular Research, 15(3). https://doi.org/10.4238/gmr.15038067

Zhang, J., Shi, J., Ji, G., et al. (2017). Modulation of sex expression in four forms of watermelon by gibberellin, ethephon, and silver nitrate. Horticulture Plant Journal, 3(3), 91–100. https://doi.org/10.1016/j.hpj.2017.03.005

सारांश

खरबूजे में मादा माता-पिता के रूप में एंड्रोमोनोशियस इनब्रेड लाइनों को शामिल करते हुए 1 संकर का विकास श्रमसाध्य महंगा और समय लेने वाला है। इसलिए संकर उत्पादन में मातृ एंड्रोमोनोशियस लाइनों को बदलने के लिए एकलिंगी लाइनों का संभावित रूप से दोहन किया जा सकता है। हालांकि खरबूजे में अंडाकार फल के आकार और खट्टेपन के साथ एकलिंगी विशेषता के संबंध ने संकर प्रजनन में इसके व्यापक उपयोग को सीमित कर दिया। इस प्रकार वर्तमान जांच स्थिरता एकलिंगी विशेषता के लिए नव निर्मित खरबूजे की इनब्रेड लाइनों के एक सेट की जांच करने और रूपात्मक और जैव रासायनिक विशेषताओं जैसे कि औसत फल वजन (जी) की मोटाई (सेमी) छिलके की मोटाई (मिमी) फल आकार सूचकांक कुल घुलनशील ठोस (टीएसएस) एस्कॉर्बिक एसिड अम्लता बीटा -कैरोटीन और दृढ़ता (किग्रा/सेमी ^{2}) के लिए उनके मूल्यांकन के लिए की गई थी। एंड्रोमोनोसी इंडेक्स (एआई) के आकलन के माध्यम से अठारह स्थिर एकलिंगी लाइनों की पहचान की गई है। मोनो-1621 नामक एकलिंगी वंश में सबसे अधिक बीटा-कैरोटीन (2.73 पाया गया जबकि मोनो1426/S-1 में सबसे अधिक(14.9 पाया गया। पिछली रिपोर्टों के विपरीत ने फलों के आकार सूचकांक या खट्टेपन के साथ कोई सहसंबंध नहीं दिखाया जिससे पता चलता है कि ये लक्षण खरबूजे में लिंग अभिव्यक्ति से स्वतंत्र हैं। यह दर्शाता है कि कम खट्टेपन आदर्श अनुपात और गोल फलों वाली स्थिर एकलिंगी वंश की वंशावली को बेहतर आनुवंशिकी और आधुनिक प्रजनन उपकरणों का उपयोग करके विकसित किया जा सकता है। इसके अलावा बागवानी के लिए वांछनीय लक्षणों वाली पहचानी गई वंशों को उपयुक्त मूल संयोजनों का चयन करके हेटेरोसिस प्रजनन में आगे उपयोग किया जा सकता है।