RESEARCH ARTICLE

Genetic Diversity, Variability, and Correlation Studies in South Indian Culinary Melon (*Cucumis melo* ssp. *agrestis* var. *acidulus*) Accessions

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Abstract

Genetic diversity, parameters and correlation among 15 quantitative traits were studied in 80 diverse culinary melon accessions from South India during the summer 2019 and 2020 at the College of Horticulture, Sirsi. The ward's clustering revealed the presence of five clusters, which are differentiated based on geographical regions. The phenotypic coefficient of variance (PCV) estimate is higher than the genotypic coefficient of variance (GCV) in all the characters studied, indicating the influence of the environment on the expression of characters. Among the traits, except for vine length, seed cavity width, seed length and seed diameter, all other quantitative traits exhibited the highest estimate of PCV and GCV. High heritability and high genetic advance as percent mean were recorded for all the characters except vine length and seed cavity width. The correlation study revealed that peduncle length (0.524), average fruit weight (0.588), fruit length (0.551), seed cavity length (0.496), flesh thickness (0.415), and fruit number per vine (0.386) had a highly significant correlation with fruit yield per vine. The high genetic variability and nature of correlations among the fifteen traits in the collected accessions would serve as a basis for deploying specific accessions and formulating strategies for further improvement of culinary melon.

Keywords: Genetic diversity, Variability, Heritability, Correlation, Culinary melon and Mangalore melon.

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Introduction

Culinary melons (*Cucumis melo* subsp. *agrestis* var. *acidulus*) of South India, locally referred as Mangalore melon or Sambar Southe, belong to the family Cucurbitaceae with a somatic chromosome number 2n = 2x = 24 (Pitrat *et al.,* 2000). In Karnataka, it is called by local names as Mogge kayi or Mangalore southe. In Kerala, it is known as Vellari, Kanivellari and Dosakaya in Andhra Pradesh (Shet *et al.,* 2022). Previously, culinary melon/Mangalore melons were classified under var. *conomon* rather than under var. *acidulus* (Gondi *et al.,* 2016; Lakshmi *et al.,* 2017; Mukunda *et al.,* 2017; Swamy, 2017; Vinutha *et al.,* 2017). The majority of the morphological traits, including sex type (monoecious) of culinary melons, are similar to the traits of *C. melo* ssp. *agrestis* var. *acidulus* (Pitrat, *et al.,* 2000) and classified under var. *acidulus*. Culinary melon is a cross-pollinated crop that performs better in warm weather compared to rainy, humid conditions and is traditionally cultivated in paddy fallow using residual soil moisture mainly grown for fresh vegetables as well as for pickling and cooking purposes (Gondi *et al.,* 2016, Kamgaoud *et al.,* 2018, Shet *et al.,* 2022).

An improvement in yield and quality of cross-pollinated crops like culinary melon is affected mainly by selecting genotypes with desirable characters from the germplasm or by developing hybrids. The basic requirement for adopting a suitable breeding method is

sound knowledge of the genetic makeup of the characters and their expression in different genetic backgrounds. The assessment of diversity present among the collected genetic stock and further clustering will help the breeders for the selection of desirable genotypes for the trait-based hybridization program.

In general, genetic variability is the basic material and pre-requisite for any crop improvement program and knowledge of certain genetic parameters is essential for proper understanding followed by their manipulation during plant breeding. Genetic parameters such as genotypic coefficients of variation (GCV), phenotypic coefficient of variation (PCV), heritability and GA are useful biometric tools for the determination of genetic variability. Information on the nature and extent of genetic variability and the degree of character transmission is paramount in enhancing the efficiency of selection. The fruit yield is a complex quantitative trait, and an integrated function of a number of component characters. Therefore, selection for yield *per se* may not be very rewarding unless other yield-attributing traits are taken into consideration. A correlation study provides a measure of association between characters and helps identify important characters to be considered while selecting. The knowledge of correlations between various characters and their relative contribution to yield is useful for the selection of multiple characters and suitable plant type (Nayana and Fakrudin, 2020). The present study was aimed at understanding the magnitude of genetic variability and the nature of correlations among a set of 15 traits, including fruit yield.

Materials and Methods

The experimental material for the study consisted of 80 diverse culinary melon germplasm accessions collected from South Indian states *viz.,* Karnataka, Kerala, Andhra Pradesh, Tamil Nadu, Telangana and Goa. These diverse lines were evaluated for different growth and yield parameters at the College of Horticulture, Sirsi, Karnataka, following the recommended package of practice of melon during March-May 2019 and 2020. The experiment was laid out in augmented block design with Mudicode Local and Soubhagya as check varieties. The seeds of 80 accessions and two checks were soaked in water for overnight. The next morning, soaked seeds were sown in the main field, laid out by mulch sheet and drip irrigation system. The spacing of 0.60 m between vine to vine and 2 m between rows was followed with a row containing 10 seedlings. After every ten accessions one check variety was repeated and each block consisted of 20 accessions. Four equal such blocks were maintained. Recommended cultural operations and plant protection measures were taken to ensure uniform and healthy crop stand per the package of practices. The observations were recorded for five plants in each accession

on 15 yield-related traits *viz.,* number of female flowers at peak flowering stage, vine length (cm), peduncle length (cm), average fruit weight (g), number of fruits per vine, fruit length (cm), fruit breadth (cm), seed cavity length (cm), seed cavity width (cm), flesh thickness (cm), 100 seed weight (g), seed diameter (mm), seed length (mm), total soluble sugar (TSS %brix) and fruit yield per vine (kg) and pooled mean values over two years data were used for analysis. The data obtained were subjected to analysis of variance (ANOVA) by using SAS software version 9.2 (SAS, 2008). The hierarchical cluster analysis of Ward's minimum variance method (Ward, 1963) was adopted. The phenotypic and genotypic coefficients of variability were computed using Burton and De Vane's (1953) methods. The method of (Johnson *et al.,* 1955) was followed to estimate broad sense heritability and record the genetic advance for all the traits. The correlation coefficient among all possible character combinations were estimated using SAS software employing Pearson's correlation coefficient formula.

Results and Discussion

The analysis of variance indicated significant differences among the accessions for all the studied traits (Table 1). The significant range observed among the accessions for sex ratio (7.7–20.0%), average fruit weight (196–2400 g), fruit length (10.4–29.4 cm), fruit width (4.5–14.8 cm), seed cavity length (6–26.2 cm), flesh thickness (0.50–4.40 cm), TSS (1.5–5.80% brix) and fruit yield per vine (0.60–8.10 Kg) indicating maximum variability present in these traits (Table 2). It showed the existence of high degree of genetic variability among the accessions and enough scope for bringing about improvement in the desirable direction (Kamgoud *et al.* 2018). Apart from these inherent traits, culinary melon fruits are attracted by its wide range of color, shape and size. Most of the Karnataka accession fruits are oblate to ovate in shape, with colors varying from light green to dark green and a combination of patchy green with white to yellow stripes. Whereas, the Kerala accessions produced oblate to elongated yellow color fruits on maturity with or without prominent stripes. However, the Andhra and Telangana accessions fruits were round or globular in shape and yellow color with plain or scattered patches on the skin (Figure 1). This indicated availability of wide in fruit shapes and colors for breeding consumer preferable size and color fruits varieties/hybrids in the future (Shet *et al.,* 2022).

The diversity among the accessions using cluster analysis revealed five distinct major clusters at the level of 14 Euclidean distances (Figure 2). Among these five clusters, four major clusters, namely cluster I, cluster II, cluster III and cluster V, constituted of 15, 28, 18 and 17 accessions, respectively. The accessions collected from Karnataka, Kerala and Andhra Pradesh states formed the major clusters and exhibited a reasonable level of locational grouping.

Table 1: Analysis of variance for quantitative traits in germplasm accessions of culinary melon

	Mean square values				
Traits	Block	Genotype	check	che+ check vs var	error
	df = 3	df = 81	df = 1	df = 80	df = 3
No female flower	0.99	0.3421*	0.05	0.3458*	0.05
Sex ratio	14.68	6.63*	3.93	6.66*	3.97
Vine length (cm)	588.00	233.6**	343.2**	232.2**	42.40
Peduncle length (cm)	3.23	1.62*	3.72	7.66*	0.22
Fruit weight (g)	153259	55833*	180901**	54270*	2941
Number of fruits /vine	3.95	0.60*	0.32	0.60	0.20
Fruit width (cm)	2.56	3.425*	9.418*	3.351*	1.70
Fruit length (cm)	37.06	15.97*	11.04*	16.04*	1.81
Seed cavity length (cm)	24.04	13.18**	349.8***	8.97**	0.03
Seed cavity width (cm)	2.76	0.455**	0.165*	0.459**	0.01
Flesh thickness (cm)	3.64	0.624*	0.98*	0.62*	0.04
100 seed weight (g)	0.43	0.11*	0.00	0.11	0.03
Seed diameter (mm)	0.42	0.824**	1.638***	0.814**	0.01
Seed length (mm)	3.36	1.072*	2.916*	1.049*	0.11
TSS (%brix)	6.07	0.809**	0.361**	0.815**	0.01
Fruit yield/vine (kg)	0.29	0.3357*	0.6845**	0.3313*	0.01

*&** indicates significant at 5 and 1% probability level

Table 2: Estimates of mean, range and genetic parameters for 15 quantitative traits in culinary melon accessions

Traits	Mean $\pm$ SE	Range		PCV (%)	GCV (%)	h^2 (bs) (%)	GAM (%)
		Min	Max				
Number of female flower at peak flowering stage	3.75 $\pm$ 0.14	1.50	9.00	32.21	29.11	81.68	54.28
Vine length (cm)	152.59 $\pm$ 3.31	101.8	233.69	20.13	13.9	47.71	19.81
Peduncle length (cm)	3.12 $\pm$ 0.14	1.07	6.2	29.00	24.68	72.41	43.26
Average fruit weight (g)	810.61 $\pm$ 56.7	88.12	2209	55.03	49.79	87.29	59.37
Number of fruits/vine	3.37 $\pm$ 0.26	1.25	16.25	32.82	26.80	66.67	45.08
Fruit length (cm)	15.33 $\pm$ 0.47	6.31	25.12	29.19	26.06	79.14	48.00
Fruit breadth (cm)	10.09 $\pm$ 0.37	4.57	27.53	34.23	33.54	95.99	67.78
Seed cavity length (cm)	11.46 $\pm$ 0.40	4.50	22.00	31.40	29.81	90.11	58.39
Seed cavity width (cm)	4.81 $\pm$ 0.12	2.49	7.64	20.70	11.34	30.01	12.82
Flesh thickness (cm)	2.55 $\pm$ 0.098	0.50	4.50	35.14	29.97	72.73	52.73
100 seed weight (g)	2.25 $\pm$ 0.062	0.67	3.66	24.44	24.08	97.13	48.98
Seed diameter (mm)	3.39 $\pm$ 0.076	0.562	4.47	20.05	19.31	92.73	38.37
Seed length (mm)	8.18 $\pm$ 0.13	4.6	10.06	14.77	14.68	98.91	30.13
TSS (%brix)	2.72 $\pm$ 0.11	0.63	5.38	36.14	35.35	95.51	71.26
Fruit yield/vine (kg)	2.53 $\pm$ 0.17	0.57	8.83	57.18	45.46	63.22	74.58

GCV-Genotypic coefficient of variation, PCV- Phenotypic Coefficient of variation, h^2 (bs) –Heritability in broad sense, GAM- Genetic advance as mean
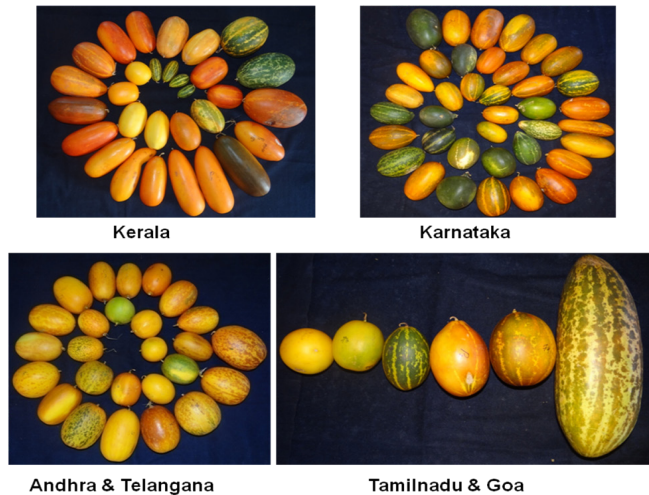
Figure 1: The diversity observed among accessions collected from different south Indian states for fruit color, size and shape

The majority of the accessions collected from Karnataka were accommodated in clusters I and II, while accessions from Kerala were grouped in cluster V. However, cluster III accommodated the Andhra and Telangana accessions. This could be due to the fact that quantitative clustering obtained from each state is related to similarity in adaptation (Van Hintum 1995). Cluster IV has only four accessions and is characterized by more fruits per vine and small fruits, of which two accessions belong to agrestis, the progenitor for culinary melon. Similar results were obtained by Raja *et al.* (2009) in a bitter gourd diversity analysis study from tribal belts of India. A relationship between clusters and geographical region could exist due to the restricted movement of planting material from one state to another. The estimates of genetic parameters, *viz.,* genotypic and

phenotypic coefficients of variation, heritability in a broad sense, genetic advance, and mean and range of different characters, are presented in Table 2. A considerable range of variation was observed for all the characters under study. Generally, the PCV revealed relatively high values in comparison to the corresponding GCV for all the characters, indicating the effects of environment in the expression of traits. The range of PCV was observed from 14.77 to 57.18% for the traits under study, which provides a picture of the extent of phenotypic variability in the population. The PCV was noted high for characters like fruit yield per vine (57.18%), average fruit weight (55.03%), TSS (36.14%), flesh thickness (35.14%), fruit length (34.23%) number of fruit per vine (32.82%), number of female flowers at peak flowering stage (32.21%), fruit breadth (29.19%) and peduncle length (29%). The rest of the characters showed moderate values of PCV. The genotypic coefficient of variation, which expresses the picture of the extent of genetic variability in the population, ranged from 13.9 to 49.79%. The GCV was noted high for the characters like average fruit weight (49.79%), fruit yield per vine (45.46%), TSS (35.35%), fruit length (33.54%), flesh thickness (29.97%), number of female flowers at peak flowering stage (29.11%), number of fruit per vine (26.80%), fruit breadth (26.06%) and peduncle length (24.68%). Moderate GCV values were observed for seed diameter (19.31%) seed length (14.68%), vine length (13.90%) and seed cavity width (11.34%). These findings are in agreement with Rakhi and Rajamony (2005) and Silpa *et al.* (2020). Thus, these traits further provided an opportunity for genetic improvement. The phenotypic and genotypic coefficient of variation indicated that fruit yield per vine (kg), average fruit weight (g), flesh thickness (cm), fruit length (cm), number of fruit per vine, number of female flowers
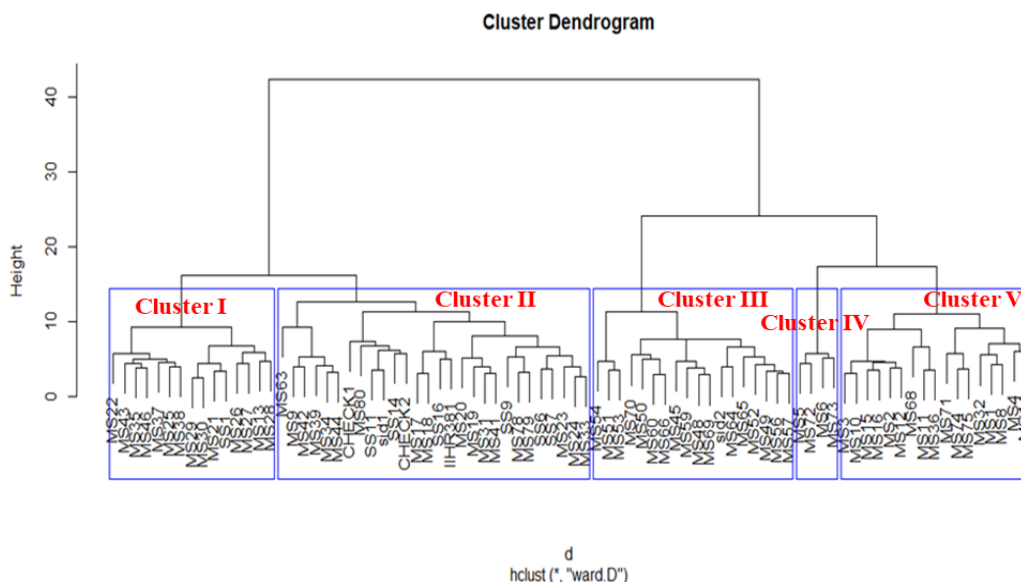

Figure 2: Dendrogram generated by ward's method of cluster analysis of morphological data of culinary melon accessions

Table 3: Pearson's correlation coefficients among 15 quantitative traits for accessions of culinary melon (N = 82, Prob > |r| under H0: Rho = 0)

Traits	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15
X1	1.000	0.118 / 0.292	-0.301 / 0.006	-0.283 / 0.010	0.437 / <.0001	-0.331 / 0.002	-0.327 / 0.003	-0.278 / 0.012	-0.163 / 0.144	-0.379 / 0.001	-0.182 / 0.102	-0.042 / 0.708	-0.337 / 0.002	0.032 / 0.772	-0.048 / 0.670
X2		1.000	-0.133 / 0.233	0.002 / 0.989	0.206 / 0.063	-0.170 / 0.128	0.130 / 0.245	-0.171 / 0.125	0.026 / 0.819	-0.317 / 0.004	-0.214 / 0.054	0.063 / 0.571	-0.250 / 0.023	-0.071 / 0.525	0.097 / 0.384
X3			1.000	0.685 / <.0001	-0.132 / 0.238	0.630 / <.0001	0.424 / <.0001	0.487 / <.0001	0.295 / 0.007	0.416 / <.0001	0.338 / 0.002	0.182 / 0.101	0.632 / <.0001	0.177 / 0.112	0.524 / <.0001
X4				1.000	-0.311 / 0.005	0.832 / <.0001	0.727 / <.0001	0.616 / <.0001	0.410 / 0.000	0.410 / 0.000	0.380 / 0.000	0.219 / 0.048	0.751 / <.0001	0.169 / 0.130	0.588 / <.0001
X5					1.000	-0.278 / 0.011	-0.291 / 0.008	-0.142 / 0.202	-0.129 / 0.250	-0.206 / 0.064	-0.127 / 0.254	-0.080 / 0.477	-0.377 / 0.001	0.210 / 0.058	0.386 / 0.000
X6						1.000	0.478 / <.0001	0.693 / <.0001	0.303 / 0.006	0.401 / 0.000	0.357 / 0.001	0.062 / 0.579	0.687 / <.0001	0.239 / 0.030	0.551 / <.0001
X7							1.000	0.439 / <.0001	0.379 / 0.001	0.339 / 0.002	0.287 / 0.009	0.214 / 0.054	0.485 / <.0001	0.095 / 0.394	0.329 / 0.003
X8								1.000	0.463 / <.0001	0.513 / <.0001	0.361 / 0.001	0.080 / 0.474	0.697 / <.0001	0.262 / 0.017	0.496 / <.0001
X9									1.000	0.303 / 0.006	0.238 / 0.031	0.248 / 0.025	0.411 / 0.000	-0.095 / 0.396	0.386 / 0.000
X10										1.000	0.572 / <.0001	0.444 / <.0001	0.503 / <.0001	0.118 / 0.292	0.270 / 0.014
X11											1.000	0.697 / <.0001	0.314 / 0.004	0.117 / 0.293	0.333 / 0.002
X12												1.000	0.123 / 0.271	-0.049 / 0.662	0.176 / 0.113
X13													1.000	0.256 / 0.020	0.415 / 0.000
X14														1.000	0.157 / 0.159

X1- Number of female flowers at peak flowering, X2- vine length(cm), X3- Peduncle length(cm), X4- Avg fruit wt (g)X5- Number of fruits /plant, X6- fruit length(cm), X7- fruit width (cm)X8- seed cavity length (cm), X9- seed cavity width (cm), X10-100 seed wt (g), X11- Seed length (mm), X12- Seed width (mm), X13- Flesh Thickness (cm), X14-TSS % brix, X15- Fruit yield per plant (Kg)

at peak flowering stage, fruit breadth (cm) and peduncle length (cm) were found to be important characters. The difference between PCV and GCV values was low for most of the characters studied, suggesting minimal influence of environment on the expression of the character.

Genetic coefficient of variation, along with heritability estimates, would provide a clear picture on the efficiency of the selection (Burton, 1952). The estimate of broad sense heritability was the highest for all the characters studied except vine length (47.71%) and seed cavity width (30.01%) (Table 2). The values were especially high for seed length (98.91%), 100 seed weight (97.13%), fruit breadth (95.99%), TSS (95.51%), seed diameter (92.73%), seed cavity length (90.11%) and average fruit weight (87.29%). Similarly, high heritability values for average fruit weight, TSS, fruit yield/vine, fruit breadth and flesh thickness was reported by Kamgoud *et al.* (2018). In the present investigation, almost all the traits under the study showed a high magnitude of heritability in broad sense (>60%), suggesting that the highly heritable characters were least affected by environmental variations and selection for these characters based on phenotypic performance may be more effective for culinary melon improvement.

Heritability alone does not provide clues for genetic gain from the best-selected individuals. Burton (1952) suggested that heritability, in combination with genetic advance (GA), was more reliable in predicting the effect of selection. The estimates of genetic advance (as percent of mean) ranged from 12.82 for seed cavity width to 74.58 for fruit yield/vine (Table 2). The estimates of GA (as percent mean) were high (>20%) for all the traits studied except for seed cavity width (12.82%) and vine length (19.81%), which showed moderate estimates of GA (Table 2).

The results in the experiment revealed that higher heritability (>60%) estimates coupled with high genetic advance (>20%) for all the characters except vine length and seed cavity width. High heritability with high genetic advance indicated additive gene action in the control of making these characters to respond better for selection (Johnson *et al.*, 1955). The characters with high genotypic variance and high heritability coupled with high genetic gain would be effective for selection in the improvement of the crop. The traits namely number of female flower at peak flowering stage (81.68; 54.28%), peduncle length (72.41; 43.26%), average fruit weight (87.29; 59.37%), fruit length (79.14; 48.00%), fruit breadth (95.99; 67.78%), seed cavity length (90.11; 58.39%), flesh thickness (72.73; 52.73%), number of fruits per vine (66.67; 45.08%) and fruit yield/vine (63.22; 74.58%) showed high heritability coupled with high genetic advance as percent mean, respectively. Similar findings were also reported by Shivadatt *et al.* (2021), Kamgoud *et al.* (2018), Shet *et al.* (2019), Ramesh Babu and Hariprasad Rao (2018) in oriental pickling melon.

The present findings corroborated that the existing variability among the genotypes with respect to these traits is mainly due to additive types of genes (Panse 1957). However, the vine length and seed cavity breadth reported moderate to low heritability with moderate genetic advance, indicating the role of non-additive gene action, which can be exploited for heterosis breeding (Bhimappa and Choudhary, 2017). Thus, the traits with high heritability coupled with high genetic advance can be considered for the improvement of culinary melon accessions.

Yield is a complex quantitative character, and direct selection for yield may not result in successful improvement. Correlation coefficient analysis measures the mutual relationship between various plant characters and determines the component characters on which selection can be based for improvement of an associated complex quantitative character like yield. The correlation study revealed that peduncle length (0.524), average fruit weight (0.588), fruit length (0.551), seed cavity length (0.496), flesh thickness (0.415), and fruit number per vine (0.386) had highly significant positive correlation with fruit yield per vine (Table 3). It indicates that the selection in any of these yield-attributing traits will increase the other traits, thereby enhancing the fruit yield. Similar results were reported by Shivadatt *et al.* (2021), Shet *et al.* (2018), and Hossain *et al.* (2010) in cucumber. However, the number of female flowers at the peak flowering stage showed a significant positive association with the number of fruits per vine (0.437) but a negative correlation with other traits, including fruit yield per vine (-0.048), indicating that all the female flowers at peak flowering stage may not be contributes to the fruit yield. In conclusion, high genetic variability and the nature of correlations among the fifteen traits in the collected accessions would serve as a basis in deploying specific accessions and formulation of strategies for further improvement of culinary melon. The selection for average fruit weight, fruit length, fruit breadth, flesh thickness, seed cavity length, number of fruits per vine and peduncle length can enhance the productivity of culinary melon.

Conclusion

Evaluation of collected accessions is an important aspect of the breeding program. The grouping and further classification of accessions into different clusters help to select diverse accessions as a parent in a trait-based hybrid development program. The high genetic variability and nature of correlations among the 15 traits in the collected accessions would serve as a basis for deploying specific accessions and formulating strategies for further improvement of culinary melon. Molecular characterization and further molecular diversity study of collected accessions will provide the precise grouping of accessions for further improvement of culinary melon.

Acknowledgment

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