

Deciphering the Genetic Variability in Mangalore Melon Genotypes (*Cucumis melo* var. *acidulus*) for Growth, Flowering and Yield Traits

Sowmya H.M.*, Satish D., Ratnakar M. Shet, Amarananjundeshwara H., Raghavendra G. and Mahesh Y.S.

Department of Biotechnology and Crop improvement,
College of Horticulture, University of Horticultural Sciences, Bagalkot (Karnataka), India.

(Corresponding author: Sowmya H.M.*)

(Received: 25 February 2023; Revised: 15 April 2023; Accepted: 19 April 2023; Published: 20 May 2023)

(Published by Research Trend)

ABSTRACT: Mangalore melon is gaining much importance because of its earliness, high production potential with nutritive value and it is the most unique cucurbitaceous vegetable with respect to its keeping quality (8-10 months). Unfortunately, very little work has been done to maintain the genetic purity and development of superior hybrids in Mangalore melon. However, attempts have been made to collect and improve the local cultivars grown in different parts of India for many traits. Seventeen Mangalore melon genotypes (*Cucumis melo* var. *acidulous*) were evaluated to estimate the genetic variability for growth, flowering and yield parameters. Results revealed that significant genetic variability present among the genotypes for almost all traits. High estimates of GCV and PCV values were observed for number of fruits per vine, fruit width, fruit length, average fruit weight, fruit yield/vine, mesocarp thickness, seed cavity length and seed cavity width. High estimates of heritability coupled with high values of GAM were observed for the characters viz., Vine length, no. of primary branches, node at first male flower appears, days to first female flower appears, number of female flowers, sex ratio, number of fruits per vine, fruit width, fruit length, average fruit weight, fruit yield/vine, mesocarp thickness, seed cavity length, seed cavity width and test weight, it indicates less environmental influence, broader genetic base and also it depicts presence of additive gene action. MS 78 and MS 34 were found to be high yielding genotypes with the yield of about 9.29 and 5.30 kg/vine respectively.

Keywords: Mangalore melon, genetic variability, heritability, genetic advance.

INTRODUCTION

Mangalore melon or culinary melon (*Cucumis melo* var. *acidulus*) is one among the non-dessert melon group vegetable belongs to the family Cucurbitaceae and the genus cucumis with a diploid chromosome number of $2n = 2x = 24$ (Pitrat, 2008). It is considered to be the most ancient form of melon domesticated in China (Jeffrey, 1980) and also it is known that it is originated from wild melon (var. *agrestis*) in China. The family is represented by some 118 genera and 825 species (Jeffrey, 1980). In India, it is an all-time favourite vegetable crop grown in Malnad and coastal Karnataka especially Mangalore, Udupi, Uttara Kannada, Chikmanglore, Shivamogga, Hassan and Coorg districts: besides grown in Kerala, Tamil Nadu, Telangana and Andhra Pradesh.

In Karnataka, it is well known with many vernacular names such as sambarsouthe, Managalouthe, mogghekayi, doskayi (Swamy, 2017). These culinary melons are not actually group of cucumbers they are typically a group of acidulous under a species melo. They are having special features that the fruits of these plants can be stored up to 8-10 months without losing their freshness; they are stored upto

many weeks by hanging from ceiling with thin coconut fiber ropes.

Mangalore melons are used in an array of traditional dishes like curry, sambar, soup, daal, chutney and also in making dosa, aavakaaya (Indian pickle). Even its small and edible seeds are used for preparation of juice, which is known for treating dyspepsia and it is a good source of dietary fibre. Fruits are varying in size, colour, shape, pulp texture, with smooth tender skin, moisture rich, white flesh usually with little sweetness and odour (Gondi *et al.*, 2016). It possesses cooling properties and are used as skin moisturizer and digestive agent (Swamy, 2017). It is effective in reducing constipation and protection against colon cancers. Seeds also have medicinal values as juice from them can help to cure dyspepsia. (Suzanne, 2016).

The fruits are large, botanically known as pepo. The crop best thrives at warm weather with bright sunlight (Nerson *et al.*, 1988) and also in rainfed, irrigated and in rice fallows area during *kharif* as well as in summer seasons.

Mangalore melon is monoecious and highly cross-pollinated in nature, and such pollination mechanism can be exploited for the development of hybrid. The ultimate goal of any crop improvement programme is to improve the plant traits for agronomic and economic

superiority, which depends largely on the magnitude of genetic variability and the extent to which the desirable trait is heritable. The estimates of variability for yield and its contributing characters and their heritable components in the material are more important in plant breeding programmes. Therefore, the present investigation was carried out to estimate the genetic variability, heritability and genetic advance for various growth, flowering and yield traits among different Mangalore melon genotypes.

MATERIAL AND METHODS

Investigation on evaluation of Mangalore melon genotypes for productivity and quality traits was carried out at research block, Horticultural Research and Extension Centre, Hassan Karnataka, India. Seventeen genotypes were planted in RCBD design with the spacing of 2 m × 60cm and were replicated twice. The genotypes were evaluated for eighteen growth, yield and quality parameters *viz.*, vine length @ 60 DAS (cm), number of primary branches, node at first male flower appears, node at first female flower appears, days to first male flower appears, days to first female flower appears, number of male flowers, number of female flowers, sex ratio, number of fruits /vine, fruit width (cm), fruit length (cm), average fruit weight (g), fruit yield/vine (kg), mesocarp thickness (cm), seed cavity length (cm), seed cavity width (cm) and test weight(g) for the assessment of genetic variability parameters. The mean data were subjected to statistical analysis for Analysis of Variance (Cochran and Cox, 1957) and genetic variability analysis (Burton and De Vane 1953).

RESULTS AND DISCUSSION

The analysis of variance indicated significant variation among the genotypes for all the characters studied *viz.*, Vine length @ 60 DAS (cm), number of primary branches, node at first male flower appears, node at first female flower appears, days to first male flower appears, days to first female flower appears, number of male flowers, number of female flowers, sex ratio, number of fruits /vine, fruit width (cm), fruit length (cm), average fruit weight (kg), fruit yield/vine (kg), mesocarp thickness (cm), seed cavity length (cm), seed cavity width (cm), test weight (g) (Table 1). In the present investigation, totally 17 genotypes of Mangalore melon were subjected for the assessment of extent of genetic variability for growth, earliness and yield parameters. Mean performance of seventeen Mangalore melon genotypes for different parameters are presented in Table 2. Thus, it is implied that there was reasonably a sufficient variability in the material used for the study, which provides ample of scope for selecting superior and desired genotypes by the plant breeders for further improvement.

With a view to understand the extent of variability due to genetic factors *viz.*, the range, mean, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2), genetic advance (GA) and genetic advance as per cent mean (GAM) were worked and presented in Table 3. The data revealed the

existence of large amount of variability for most of the characters studied. PCV were generally higher than GCV for all the characters which indicated that substantial influence of environment in the expression of characters.

High estimates of GCV and PCV values were observed for number of fruits per vine (28.33 and 29.53 %), fruit width (28.67 and 28.85 %), fruit length (26.15 and 26.44 %), average fruit weight (31.93 and 32.39 %), fruit yield/vine (35.25 and 35.86 %), mesocarp thickness (21.67 and 21.93 %), seed cavity length (32.16 and 32.50 %) and seed cavity width (28.37 and 28.78 %). It indicates existence of broad genetic base, which would be amenable for further selection. The results are accordance with Ahmed *et al.* (2004); Ohashi *et al.* (2009); Babu (2013); Tyagaraj *et al.* (2014); Shah *et al.* (2018); Janghel *et al.* (2018); Silpa *et al.* (2020); Kalgudi *et al.* (2021). High GCV and PCV values with narrow difference is an indication of existence of broad genetic base among the population, suggesting the stable expression of genotypes for these traits which provides scope for the improvement of these characters through simple selection.

Moderate GCV and high value of PCV observed for node at first male flower appears (18.96 and 24.08 %). As it had moderate GCV with high PCV indicating more environmental influence on the characters. Moderate GCV and PCV was observed for the traits such as vine length (12.82 and 13.30 %), number of primary branches (14.42 and 17.27 %), node at first female flower appears (11.40 and 14.13 %), days to first female flower appears (10.44 and 10.90 %), number of female flowers (14.32 and 15.71 %), sex ratio (15.07 and 16.76 %) and test weight (12.20 and 12.69 %).

Which indicates that there is moderate amount of variability was found for these traits. As this character had moderate PCV and GCV representing that the trait is controlled by both additive and non-additive gene actions hence, recurrent selection can be practiced for improvement. These results are same as the results of Babu *et al.* (2013); Lakshmi *et al.* (2017); Silpa *et al.* (2020). Low GCV and PCV was observed for the traits such as days to first male flower appears and number of male flowers. This indicated the narrow genetic base and variability has to be generated for these characters either through introduction or through hybridizing divergent genotypes to recover transgressive segregants. These, results are accordance with Gichimu *et al.* (2008); Babu *et al.* (2013); Singh *et al.* (2020); Kalgudi *et al.* (2021).

Very often, heritability in broad sense is not the true indicator of inheritance of traits. Since, only additive component of genetic variance is efficiently transferred from generation to generation. Therefore, heritability in broad sense may mislead in judging the effectiveness of selection for the trait. Considering heritability in broad sense along with genetic advance may reveal the prevalence of specific components (additive or non-additive) of genetic variance and thus helps in judging the effectiveness of selection for the trait more accurately.

High heritability accompanied with high genetic advance indicates the prevalence of additive gene

effects and hence, selection would be effective for such traits. High estimates of heritability coupled with high values of GAM were observed for the characters viz., Vine length, no. of primary branches, node at first male flower appears, days to first female flower appears, number of female flowers, sex ratio, number of fruits per vine, fruit width, fruit length, average fruit weight, fruit yield/vine, mesocarp thickness, seed cavity length, seed cavity width and test weight. This indicates predominance of additive components for these traits and lesser influence of environment hence direct

selection would be more effective in improving these traits. These results are accordance with Babu *et al.* (2013); Shah *et al.* (2018); Janghel *et al.* (2018); Silpa *et al.* (2020).

Node at first female flower appears, days to first male flower appears and number of male flowers had high heritability coupled with moderate GAM. Which, indicated that prevalence of non-additive components and there can be little response to selection and these traits can be exploited through heterosis breeding.

Table 1: Analysis of variance for growth and yield parameters in Mangalore melon genotypes.

Sr. No.	Characters	Replication	Genotypes	Error
	Degrees of freedom	2	16	32
1.	Vine length @ 60 DAS (cm)	116.49	1435.45**	101.43
2.	No. of primary branches	0.28	0.71**	0.22
3.	Node at first male flower appears	0.32	0.44**	0.17
4.	Node at first female flower appears	0.37	1.13**	0.39
5.	Days to first male flower appears	20.31	52.06**	6.98
6.	Days to first female flower appears	2.90	97.40**	8.17
7.	Number of male flowers	1.24	132.49**	16.51
8.	Number of female flowers	0.84	2.39**	0.41
9.	Sex ratio	1.19	15.77**	3.03
10.	Number of fruits per vine	0.08	5.41**	0.43
11.	Fruit width (cm)	0.05	22.49**	0.28
12.	Fruit length (cm)	0.30	69.75**	1.51
13.	Average fruit weight (g)	15.03	40.76**	11.54
14.	Fruit yield/vine (kg)	0.09	7.34**	0.25
15.	Rind thickness (cm)	0.01	1.13**	0.03
16.	Seed cavity length (cm)	0.43	37.95**	0.79
17.	Seed cavity width (cm)	0.03	2.39**	0.07
18.	Test weight (g)	0.01	0.15**	0.01

** Indicates significance at 1 per cent level; * Indicates significance at 5 per cent level

Table 2a: Per se performance of Mangalore melon genotypes for growth parameters.

Sr. No.	Genotypes	Vine length @ 60 DAS (cm)	No. of primary branches	Node at first male flower appears	Node at first female flower appears	Days to first male flower appears	Days to first female flower appears	Number of male flowers	Number of female flowers	Sex ratio
1.	MS- 2	181.00	2.67	1.67	4.33	41.67	41.00	73.00	5.33	14.92
2.	MS- 5	163.00	3.33	1.00	4.00	38.33	41.67	78.33	5.00	16.12
3.	MS- 6	142.00	2.33	2.00	5.33	44.33	51.33	72.67	4.33	18.17
4.	MS- 15	203.33	3.00	1.33	4.67	42.33	45.67	80.67	6.67	12.15
5.	MS- 17	151.67	2.33	2.00	3.67	48.67	52.00	84.67	6.00	13.91
6.	MS- 19	172.33	3.33	1.67	3.67	39.33	46.67	72.00	6.00	13.92
7.	MS- 28	141.67	2.67	1.00	3.33	49.33	55.00	78.33	5.33	14.87
8.	MS- 30	117.00	3.33	1.67	5.33	52.00	59.33	77.67	5.67	13.83
9.	MS- 31	157.00	2.67	1.00	4.00	47.33	59.33	80.00	5.33	15.08
10.	MS- 34	135.67	2.67	1.67	4.33	47.00	52.67	70.00	8.33	8.96
11.	MS- 36	185.67	3.00	2.00	4.67	49.33	55.33	80.00	6.33	14.22
12.	MS- 52	173.67	2.00	2.00	4.33	48.67	53.33	58.33	5.33	10.98
13.	MS- 74	185.67	2.33	2.00	4.67	53.33	57.33	70.33	6.00	12.60
14.	MS- 78	167.67	3.00	1.33	4.67	47.00	55.33	66.33	5.33	12.51
15.	SS- 17	186.00	4.00	2.00	3.33	48.67	54.67	83.67	5.33	16.20
16.	RNMS	164.33	2.67	1.33	5.00	46.00	49.33	78.00	5.67	13.84
17.	SOUBHAGYA	169.33	2.67	1.33	4.33	44.00	58.33	76.00	4.67	10.24
	S. Em±	5.81	0.27	0.24	0.36	1.53	1.65	2.35	0.37	1.00
	CD @ 5%	16.75	0.77	0.68	1.04	4.39	4.75	6.76	1.06	2.89
	CV %	6.12	16.44	5.70	14.47	5.70	5.47	5.40	11.20	12.72

Table 2b: Per se performance of Mangalore melon genotypes for yield parameters.

Sr. No.	Genotypes	Number of fruits per vine	Fruit width (cm)	Fruit length (cm)	Average fruit weight (g)	Fruit yield/vine (kg)	Mesocarp thickness (cm)	Seed cavity length (cm)	Seed cavity width (cm)	Test weight (g)
1.	MS- 2	3.00	7.55	23.95	1.14	5.13	2.54	17.67	2.63	1.76
2.	MS- 5	6.33	6.17	15.53	0.60	3.68	2.09	11.18	1.68	1.96
3.	MS- 6	3.33	5.84	15.18	1.25	4.09	3.11	9.05	1.32	1.49
4.	MS- 15	4.33	8.21	11.33	1.00	3.69	1.67	5.48	3.42	1.76
5.	MS- 17	5.33	8.67	18.25	1.70	5.19	2.38	13.85	3.00	1.80
6.	MS- 19	2.67	10.84	20.42	0.94	2.45	3.41	11.87	3.13	1.73
7.	MS- 28	4.67	9.47	20.25	1.06	4.47	3.59	11.88	2.53	2.12
8.	MS- 30	3.33	9.06	27.02	1.57	4.64	2.42	18.03	2.67	1.85
9.	MS- 31	4.00	10.82	22.00	1.05	3.53	2.68	14.59	4.23	1.36
10.	MS- 34	4.67	8.98	16.67	1.60	5.30	2.29	9.28	3.37	1.60
11.	MS- 36	2.67	10.30	14.91	0.74	1.98	3.07	8.08	3.05	1.33
12.	MS- 52	6.33	12.71	9.75	0.77	4.79	2.25	5.70	4.42	1.90
13.	MS- 74	4.33	7.12	15.75	0.98	4.04	2.65	8.95	2.48	1.94
14.	MS- 78	4.00	17.48	25.65	1.96	9.29	3.98	11.00	4.70	1.49
15.	SS- 17	3.67	11.16	20.22	0.89	3.23	3.24	11.00	3.92	1.80
16.	RNMS	5.33	8.13	13.50	1.09	4.31	2.63	8.30	3.10	1.63
17.	SOUBHAGYA	4.67	8.88	19.63	1.00	4.55	3.46	10.15	3.02	1.92
	S. Em±	0.38	0.31	0.71	0.62	0.29	0.09	0.51	0.15	0.06
	CD @ 5%	1.09	0.88	2.04	1.78	0.83	0.27	1.47	0.43	0.18
	CV %	14.46	5.58	6.74	9.44	11.41	5.76	8.10	8.41	6.08

Table 3: Estimation of components of genetic variability in Mangalore melon genotypes.

Sr. No.	Characters	Mean ± SE	Range	PCV (%)	GCV (%)	h ² (bs)%	GAM (%)
1.	Vine length @ 60 DAS (cm)	164.53 ± 5.81	117 - 203.33	13.30	12.82	93	25.45
2.	Number of primary branches	2.82 ± 0.27	2 - 4	17.27	14.42	70	24.82
3.	Node at first male flower appears	1.59 ± 0.24	1 - 2	24.08	18.96	62	30.76
4.	Node at first female flower appears	4.33 ± 0.36	3.33 - 5.33	14.13	11.40	65	18.93
5.	Days to first male flower appears	46.31 ± 1.53	38.33 - 53.33	8.99	8.37	87	16.04
6.	Days to first female flower appears	52.26 ± 1.65	41 - 59.33	10.90	10.44	92	20.58
7.	Number of male flowers	75.29 ± 2.35	58.33 - 84.67	8.83	8.26	88	15.92
8.	Number of female flowers	5.69 ± 0.37	4.33 - 8.33	15.71	14.32	83	26.88
9.	Sex ratio	13.68 ± 1.01	8.96 - 18.17	16.76	15.07	81	27.91
10.	Number of fruits per vine	4.55 ± 0.38	2.67 - 6.33	29.53	28.33	92	55.97
11.	Fruit width (cm)	9.49 ± 0.31	5.84 - 17.48	28.85	28.67	99	58.69
12.	Fruit length (cm)	18.24 ± 0.71	9.75 - 27.02	26.44	26.15	98	53.29
13.	Average fruit weight (kg)	1138.16 ± 62.05	0.606 - 1.963	32.39	31.93	97	64.83
14.	Fruit yield/vine (kg)	4.36 ± 0.29	1.98 - 9.29	35.86	35.25	97	71.38
15.	Mesocarp thickness (cm)	2.79 ± 0.09	1.67 - 3.98	21.93	21.67	98	44.13
16.	Seed cavity length (cm)	10.95 ± 0.51	5.48 - 18.03	32.50	32.16	98	65.56
17.	Seed cavity width (cm)	3.09 ± 0.15	1.32 - 4.7	28.78	28.37	97	57.61
18.	Test weight (g)	1.73 ± 0.06	1.33 - 2.12	12.69	12.20	92	24.15

PCV= Phenotypic co-efficient of variation; GCV= Genotypic co-efficient of variation; h²= Heritability in broad sense; SE= Standard Error; GA= Genetic Advance; GAM= Genetic advance as percent of mean

CONCLUSIONS

India has been reported to be rich in melon genetic resources, as Mangalore melon is morphologically diverse, especially with regard to fruit traits because of cross pollination and monoecious nature. It can also show non-uniformity in fruit size, shape, color, quality and fruit yield. For attaining the uniformity in these traits, a good understanding of genetic stock of Mangalore melon and selection of superior genotypes is very important for any crop improvement programme that allows higher genetic gain. Collection of genotypes, evaluation and their maintenance could aid in genetic improvement of any crops, and for sustainable production. The results obtained from the study could be used to harness the improvement in genetic traits. The Analysis of variance revealed that there is variability present among the genotypes for all the characters under the study. The estimates of genetic parameters reveals that the characters namely number of fruits per vine, fruit width, fruit length, average fruit

weight, fruit yield/vine, mesocarp thickness, seed cavity length and seed cavity width recorded high GCV and PCV. Whereas the traits like vine length, no. of primary branches, node at first male flower appears, days to first female flower appears, number of female flowers, sex ratio, number of fruits per vine, fruit width, fruit length, average fruit weight, fruit yield/vine, mesocarp thickness, seed cavity length, seed cavity width and test weight showed high heritability with high genetic advancement. MS 78, MS 34 and MS 17 were found to be high yielding genotypes with the yield of about 9.29, 5.30 and 5.19 kg/vine respectively.

Acknowledgement. Authors special thanks to Department of Biotechnology and Crop Improvement. COH-Bagalkot, COH, Sirsi and Horticulture Research and Extension Centre, Hassan for their support.

Conflict of Interest. None.

REFERENCES

Ahmed, M., Hamid, A. and Akbar, Z. (2004). Growth and

- yield performance of six cucumber (*Cucumis sativus* L.) cultivars under agro-climatic conditions of Rawalakot, Azad Jammu and Kashmir. *International Journal of Agriculture and Biology*, 6(2), 396–399.
- Babu, R. R. (2013). Genetic divergence studies in oriental pickling melon (*Cucumis melo* L. var. *conomon*) germplasm. *M. Sc. Thesis*. Dr. Y. S. R. Horticultural University, Rajendranagar, Hyderabad.
- Burton, G. W. and De Vane, E. M. (1953). Estimating heritability in tall Fescue (*Festuca arundinacea*) from replicated clonal material. *Agronomy Journal*, 51, 515-518.
- Cochran, W. G. and Cox, G. M. (1957). *Experimental Designs*. John Wiley and Sons, Inc., New York, 611.
- Gichimu, B. M., Owuor, B. O. and Dida, M. M. (2008). Agronomic performance of three most popular commercial watermelon cultivars in Kenya as compared to one newly introduced cultivar and one local landrace grown on dystrophic soils under sub-humid tropical conditions. *Journal of agriculture & biological sciences*, 3, 5-6.
- Gondi, S. P., Ganiger, V. M., Bhuvaneshwari, G., Madalageri, M. B., Kotikal, Y. K. and Manjunatha, G. (2016). Evaluation of Oriental Pickling Melon (*Cucumis melo* L. Var. *conomon*) Genotypes for Pest and Disease Reaction under Northern Dry Zone of Karnataka. *Journal of Environment and Ecology*, 7(1), 29-36.
- Janghel, A., Trivedi, J., Sharma, D., Lodhi, Y. and Kumar, L. (2018). Genetic variability in muskmelon (*Cucumis melo* L.) under protected condition. *International journal of current microbiology and applied sciences*, 6, 211-217.
- Jeffrey, C. (1980). A review of the Cucurbitaceae. *Botanical Journal of the Linnean Society*, 81, 233–247.
- Kalgudi, A., Shet, R. M., Shantappa, T., Lakshmidheevamma, T. N., Hongal, S. and Rathod, V. (2021). Assessment of heterosis in intra-specific 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), 423-428.
- Lakshmi, L. M., Lingaiah, H. B., Rao, A. M., Raju, T. B. P., Pitchaimuthu M. and Gowda, D. M. (2017). Variability and genetic divergence studies for economic traits in indigenous oriental pickling melon (*Cucumis melo* var. *conomon*) genotypes. *Electronic Journal of Plant Breeding*, 8(1), 365-370.
- Nerson, H., Harry, S. P., Edelstein, M., Burger, Y. and Karchi, Z. (1988). Breeding pickling melons for a concentrated yield. *Horticultural Science*, 23(1), 136-138.
- Ohashi, A., Al-Said, F. A. and Khan, I. A. (2009). Evaluation of different muskmelon (*Cucumis melo*) cultivars and production systems in Oman. *International. Journal of Agriculture and Biology*, 11, 596–600.
- Pitrat, M. (2008). Melon. In: Prohens, J. and Nuez, F. (Eds.), *Vegetables I: Asteraceae, Brassicaceae, Chenopodiaceae and Cucurbitaceae*. Springer Science + Business Media, LLC, New York, 283-315.
- Shah, K. N., Rana, D. K. and Singh, V. (2018). Evaluation of genetic variability, heritability and genetic advance in cucumber (*Cucumis sativus* L.) for various quantitative, qualitative and seed characters. *International journal of current microbiology and applied sciences*, 7, 3296-3303.
- Silpa, R., George, S. T., Anitha, P., Pradeepkumar, T., Bastian, D. and Pathrose, B. (2020). Genetic divergence analysis in oriental pickling melon (*Cucumis melo* var. *conomon* Mak.). *Research Journal of Agricultural Sciences*, 11(1), 115-119.
- Suzanne, F. (2016). Growing field marrow/Madras cucumber/Sambar cucumber in a pot in India. 9 October 2016. Available from <http://suespottedterracegarden.blogspot.in/2016/10/growing-field-marrowmadras-cumcucumber.html>.
- Swamy, K. R. M. (2017). Origin, distribution and systematics of culinary cucumber (*Cucumis melo* subsp. *Agrestis* var. *conomon*). *Journal of Horticultural Science*, 12(1), 1-22.
- Tyagaraj, G. N., Puttaraju, T. B., Santosh, N., Padmaraja, S. R. and Prakash. (2014). Evaluation of F₁ hybrids in oriental pickling melon for yield and quality attributes. *Trends in Biosciences*, 7(17), 2518-2523.

How to cite this article: Sowmya H.M., Satish D., Ratnakar M. Shet, Amarananjundeshwara H., Raghavendra G. and Mahesh Y.S. (2023). Deciphering the Genetic Variability in Mangalore Melon Genotypes (*Cucumis melo* var. *acidulus*) for Growth, Flowering and Yield Traits. *Biological Forum – An International Journal*, 15(5): 377-381.