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Genetic variability and correlation studies in intervarietal hybrids of Mangalore melon (*Cucumis melo* var. *acidulous*) for productivity traits

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Abstract
Sixteen intervarietal hybrids of Mangalore melon (*Cucumis melo* var. *acidulous*) were developed and evaluated at college of horticulture, Sirsi (Karnataka) to study the genetic variability and correlation present among the hybrids. Results revealed that significant genetic variability present among hybrids for almost all traits. A high range of variation, high PCV, GCV and high heritability observed for all the traits studied. However, high heritability coupled with high genetic advance was recorded for average fruit weight, vine length, days to first harvest, fruit diameter and fruit length it indicates less environmental influence, broader genetic base and also it depicts presence of additive gene action. Rest of the traits showed high heritability with low to moderate genetic advance indicates presence of dominant gene action. Further correlation study reveals that at genotypic level, fruit yield per plant had a highly significant and positive correlation with vine length, number of primary branches, number of fruits per plant, fruit length, fruit width, fruit diameter, average fruit weight, flesh thickness and seed cavity length and at phenotypic level, fruit yield per plant had a highly significant and positive correlation with vine length, number of primary branches, number of fruits per vine, fruit length, fruit diameter, average fruit weight, flesh thickness and seed cavity length.

Keywords: Inter varietal, Mangalore melon, genetic variability, heritability, correlation

Introduction

Mangalore melon (*Cucumis melo* var. *acidulous*) commonly called as Culinary melon is a distinct class of a cucurbitaceae family having the chromosome number 2n=24. It is very well adopted vegetable for tropical parts of southern India. This is called by different names in English as culinary melon, Indian yellow melon, Japanees pickling melon, round melon, lemon cucumber, yellow cucumber etc. In Karnataka, it is well known with many vernacular names such as sambarsouthe, Managalore southe, mogghekayi, doskayi (Swamy 2017) [13]. 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 up to many weeks by hanging from ceiling with thin coconut fibre ropes.

Mangalore melon/Culinary melon is all time grown vegetables in Kerala, Tamil Nadu, Malnad and coastal parts of Karnataka especially Mangalore, Udupi, Uttara Kannada, and Shivamogga districts. This vegetable is popular in every home of southern India. Now a days this vegetable gaining importance and we can see it on shelves of super markets, malls and it can be used for preparation of vegetable soups in restaurants. This is popular in Andhra Pradesh by the name like Budamkaya, dosekaya in Kerala it is popularly called as "Vellari" or "Kanivellari". With respect to its culinary utilization, this vegetable is consumed as raw or used after cooking. The fruits are just stirred and fried for many dishes like curries, also used to prepare sambar, palya and fruit pieces are ingredients in dhals (Swamy, 2017) [13].

In general existing of genetic variability is the key factor for selection for improving yield. However, the crop is highly cross pollinated due to moneocious nature of flowers and there is a wide range of variability exists in the germplasm and scope for developing hybrids utilizing diverse germplasm accessions for fruit traits. The different combination of hybrids may achieve the uniformity in fruits traits with higher productivity. An estimate of genetic parameters namely phenotypic and genotypic coefficient variation and heritability with genetic advance will helps to quantify the amount of variability present within a set of inter varietal

hybrids with regard to its essential productivity characteristics and also the selection of desirable traits for improvement of hybrids. Further yield is a complex trait and depended on other associated traits. Correlation studies helps for deciding which trait contribute towards productivity traits positively or negatively in developed hybrids. With this background present study is taken to assess the genetic variability and correlation present among the traits in newly developed intervarietal hybrids of Mangalore melon.

Material and Methods

The Mangalore melon hybrids required for assessment of genetic variability and correlation was developed at an experimental block of Department of Genetics and Plant breeding, College of Horticulture, Sirsi (Karnataka) during *kharif* 2019-20. The top performing 15 parents were selected from UHSB-PNASF project. The hybridization between selected parents was performed by synchronizing flowering days. Flower buds of female parents were selected on the previous evening prior to the day of anthesis and were covered with butter paper bags to avoid contamination. Next day morning between 7 to 8 am hybridization/crossing was carried out using male flowers from selected male parents. Finally pollinated female flowers were covered with butter paper bags and labelled it. The successful hybrids were harvested and seeds are used for evaluation.

The evaluation of developed 16 inter varietal hybrids were carried out in randomized complete block design (RCBD) with two replications along with parents during summer 2020-21 at College of Horticulture, Sirsi farm. The spacing 0.60m between vine to vine and 2 m between rows to row was maintained and each replication contains 10 seedlings. Drip irrigation and mulching system was adopted to conserve soil moisture and control weeds. Plant protection measures were taken to achieve healthy growth of vines. The observations were recorded on Vine length (cm), Number of primary branches, Days to first harvest, Number of fruits per plant, Fruit length (cm), Fruit width (cm), Fruit diameter (mm), Average fruit weight (g), Flesh thickness (cm), Seed cavity length (cm), Seed cavity width (cm), Fruit yield per plant. The mean data were subjected to statistical analysis for Analysis of Variance given by Cochran and Cox (1957) [4]. The phenotypic and genotypic coefficients of variability were computed as per the methods of Burton and De Vane (1953) [3]. The method of (Johnson *et al.,* 1955) [5] was followed for estimation of broad sense heritability and genetic advance for all the traits recorded. The correlation co-efficient among all possible character combinations were estimated employing formula of Al-Jibouri *et al.* (1958) [2].

Results and Discussion

The analysis of variance for yield and its related traits revealed significant differences for all the traits studied (Table 1). This suggested that there is an inherent genetic difference among the genotypes. The results of Phenotypic Coefficient of Variability (PCV), Genotypic Coefficient of Variability (GCV), heritability and genetic advance were presented in Table 2. PCV were generally higher than GCV for all the characters which indicated that substantial influence of environment in the expression of characters. The productivity traits namely fruit yield per plant, average fruit weight, flesh thickness, fruit width, vine length, seed cavity length, number of primary branches showed high phenotypic and genotypic coefficient of variation. This reflects greater genetic variability present among the hybrids for these traits. The narrow difference between PCV and GCV values for these characters may be expected that the influence of environment on the expression of these traits were negligible simple selection would be highly effective for further improvement. (Veena *et al.* 2012 [14]; Kamagoud *et al.* 2018 [7] in oriental pickling melon; Ahirwar and Singh, 2018 [1] in cucumber).

Table 1: Analysis of variance for growth, yield and parameters of hybrids in Mangalore melon

Sl. No.	Source of variation/character	Replication	Treatment	Error	CD at 5%
	Degrees of freedom	**1**	**15**	**15**	
2	Vine length (cm)	108.78	2138.12*	306.09	37.29
3	Number of primary branches	0.00	0.64*	0.12	0.74
10	Days to first harvest	1.38	9.46*	0.71	1.80
11	Number of fruits per plant	0.03	1.13*	0.08	0.61
12	Fruit length (cm)	0.32	11.73*	3.04	3.72
13	Fruit width (cm)	9.35	7.77*	1.15	2.29
14	Fruit diameter (cm)	4.10	27.53*	8.81	6.33
15	Average fruit weight (g)	3166.75	86896.84*	18064.94	286.48
16	Flesh thickness (cm)	0.08	0.82*	0.02	0.30
18	Seed cavity length (cm)	0.04	7.23*	0.06	0.53
19	Seed cavity width (cm)	0.00	0.76*	0.03	0.39
23	Yield per plant (kg)	0.04	4.10*	0.59	1.64

Table 2: Estimates of mean range and genetic parameters for growth and yield traits in the Mangalore melon hybrids

Characters	Mean ± SEM	Range		PCV (%)	GCV (%)	H2bs (%)	GA as % mean
		Lowest	**Highest**				
Vine length (cm)	180.00 ± 0.09	128.33	271.67	52.37	51.98	99.21	206.38
Number of primary branches	3.48 ± 0.22	2.50	5.00	52.13	51.71	98.66	3.95
Days to First harvest	58.84 ± 0.70	53.33	60.83	50.88	50.87	98.28	59.43
Number of fruits per plant	4.72 ± 0.21	4.67	6.83	51.80	51.67	99.67	5.78
Fruit length (cm)	18.91 ± 1.08	16.53	23.05	51.73	51.35	99.43	20.64
Fruit width (cm)	9.67 ± 0.87	7.39	13.91	52.96	52.28	97.34	10.80
Fruit Diameter (cm)	28.70 ± 1.85	22.47	35.42	51.79	51.31	98.21	31.32

Average fruit weight (g)	735.98 ± 84.58	387.17	1259.00	54.69	53.37	95.33	58.99
Flesh Thickness (cm)	3.18 ± 0.08	2.58	4.89	52.40	52.32	98.52	3.86
Seed cavity length (cm)	12.41 ± 0.15	10.39	16.32	51.84	51.82	98.76	13.97
Seed cavity width (cm)	4.62 ± 0.11	3.53	5.74	51.71	51.63	99.45	4.92
Yield per plant (kg)	3.45 ± 0.45	1.82	8.43	56.83	55.37	95.87	4.73

*PCV: Phenotypic coefficient of variability, GCV: Genotypic coefficient of variability, H^{2}bs: Heritability in broad sense, GA: Genetic advance

Heritability and genetic advance of a character is considered as essential genetic parameter to study of hybrids and segregating generations. Heritability accompanied with Genetic advance provides the information on nature of gene action (additive and dominance) among the hybrids as well as segregating generation for trait under selection. In the present study showed high heritability coupled with high genetic advance was estimated in the traits like vine length (99.21%:206.38%), days to first harvest (98.28%:59.43%), fruit length (99.43%:20.64%), fruit diameter (98.21%:31.32%) and average fruit weight (95.33%:58.99%). This indicates presence of additive gene effects to control these traits. However, other traits showed high heritability with low to moderate genetic advance (Table 2) indicating presence of dominant gene action. The dominant gene action is the characteristic features of hybrids. The heterozygous nature of such traits will be segregate in segregating generations and selection is ineffective. The characters with high genotypic variance and high heritability coupled with high genetic gain would be effective for selection of desirable hybrid and further improvement of crop (Yadav *et al.,* 2012) [15]. Yield being a complex quantitative character, 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 reveals that, at phenotypic level, Fruit yield per plant had a highly significant and positive correlation with vine length, number of primary branches, and number of fruits per vine, fruit length, fruit diameter, average fruit weight, flesh thickness and seed cavity length. However, fruit yield had non-significant positive correlation with seed cavity width fruit width which indicate lesser contribution to increase yield and had significant negative correlation with days to first harvest (Table 3).Similar results were also reported by Karthik *et al*. (2019) [8], Kumar *et al*. (2011) [9] and in cucumber. At genotypic level, fruit yield per plant had a highly significant and positive correlation with vine length, number of primary branches, number of fruits per plant, fruit length, fruit width, fruit diameter, average fruit weight, flesh thickness and seed cavity length while it had significant positive correlation with seed cavity width and had significant negative correlation with days to first harvest (Table 4).These results are in line with the findings of Panigrahi *et al.* (2018) [11] in bottle gourd and Shivaprasad *et al.* (2017) [12] in muskmelon and Janaranjani and Kantaswami (2015) [10] in bottle gourd.

Table 3: Phenotypic correlation coefficient among growth and yield parameters in Mangalore melon hybrids

Phenotypic correlations matrix	1	2	3	4	5	6	7	8	9	10	11	12
1	1.00	0.431**	-0.432**	0.531**	0.107	0.079	0.081	0.284*	0.469**	0.298*	0.038	0.506**
2		1.00	-0.180	0.531**	0.297*	-0.068	0.173	0.356**	0.372**	0.285*	0.002	0.503**
3			1.00	-0.520**	-0.144	-0.128	-0.298*	-0.303*	-0.628**	-0.318*	0.061	-0.482**
4				1.00	0.190	0.078	0.072	0.259*	0.506**	0.356**	-0.066	0.625**
5					1.00	0.161	0.445**	0.691**	0.336**	0.693**	0.084	0.620**
6						1.00	0.226	0.136	0.283*	0.073	0.204	0.206
7							1.00	0.556**	0.289*	0.210	0.253*	0.483**
8								1.00	0.457**	0.609**	0.257*	0.861**
9									1.00	0.341**	0.205	0.603**
10										1.00	0.059	0.605**
11											1.00	0.242
12												1.00

*Significant at p = 0.05   **Significant at p = 0.01
1. Vine length (cm)   2. Number of primary branches   3. Days to first harvest
4. Number of fruits per plant   5. Fruit length (cm)   6. Fruit width (cm)
7. Fruit diameter (mm)   8. Average fruit weight (g)   9. Flesh thickness (cm)
10. Seed cavity length (cm)   11. Seed cavity width (cm)   12. Fruit yield per plant (kg)

Table 4: Genotypic correlation coefficient among growth and yield parameters in Mangalore melon hybrids

Genotypic correlations matrix	1	2	3	4	5	6	7	8	9	10	11	12
1	1.00	0.533**	-0.484**	0.613**	0.095	0.221	0.127	0.290*	0.491**	0.325**	0.024	0.556**
2		1.00	-0.238	0.662**	0.318*	-0.015	0.250	0.440**	0.434**	0.336**	0.026	0.633**
3			1.00	-0.586**	-0.204	-0.298*	-0.481**	-0.386**	-0.667**	-0.336**	0.059	-0.571**
4				1.00	0.223	0.267*	0.088	0.312*	0.544**	0.364**	-0.058	0.685**
5					1.00	0.427**	0.526**	0.761**	0.384**	0.784**	0.131	0.656**
6						1.00	0.817**	0.358**	0.688**	0.156	0.534**	0.553**
7							1.00	0.517**	0.397**	0.276*	0.327**	0.482**
8								1.00	0.532**	0.714**	0.320*	0.858**
9									1.00	0.349**	0.204	0.664**

10									1.00	0.059	0.667**
11										1.00	0.287*
12											1.00

*Significant at p = 0.05   **Significant at p = 0.01

1. Vine length (cm)   2. Number of primary branches   3. Days to first harvest
4. Number of fruits per plant   5. Fruit length (cm)   6. Fruit width (cm)
7. Fruit diameter (mm)   8. Average fruit weight (g)   9. Flesh thickness (cm)
10. Seed cavity length (cm)   11.Seed cavity width (cm)   12. Fruit yield per plant (kg)

Conclusion
The Analysis of variance revealed that there is variability present among the newly developed intervarietal hybrids. Since hybrids are controlled by additive as well as dominance gene interaction. Additive gene action preferably found in homozygous condition, but heterozygous hybrids can be controlled by both additive and dominance gene action, the estimates of genetic parameters reveals that the characters namely vine length, days to first harvest, fruit diameter and average fruit weight showed higher heritability coupled with high genetic advance. The correlation study at phenotypic and genotypic level; Fruit yield per vine had a highly significant and positive correlation with vine length based on these traits results are helps in selection of better hybrid from the evaluation.

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