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Assessment of genetic variability among oriental pickling melon (*Cucumis melo* var. *conomon*) genotypes

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Abstract

Forty diverse genotypes of oriental pickling melon were used to study the genetic variability for growth and yield characters in oriental pickling melon in randomized block design with two replications during *Kharif* 2017-18. Analysis of variance had shown highly significant ($P=0.01$) difference among genotypes for all the twenty characters related to growth and yield traits except for number of primary branches. The estimate of PCV is higher than GCV in all the characters studied indicating the influence of environment towards expression of characters. Higher PCV and GCV were recorded for nodes at first female flower appears, number of male flowers, number of female flowers, average fruit weight, number of fruits per vine, fruit yield per vine and seed weight per fruit indicating the higher variability present for these characters. High heritability coupled with high GAM recorded for 16 characters indicating predominance of additive components and hence, these traits can be improved by following simple selection.

Keywords: oriental pickling melon, variability, heritability, genotypic coefficient of variance, phenotypic coefficient of variance

Introduction

Oriental pickling melon (*Cucumis melo* var. *conomon*) is one among the melon group vegetables belongs to Cucurbitaceae family with a diploid chromosome number $2n=2x=24$. It is also called as golden melon or culinary melon in English. In Karnataka it is called by local names as Sambar southe, Mogge kayi or Mangalore southe. It is an ideal summer vegetable crop mainly growing for fresh vegetable as well as for pickling and cooking purpose (Gondi *et al*, 2016) [4]. Oriental pickling melons are mainly grown in Japan and East Asia. It is a highly cross pollinated and usually andromonoecious in nature, preferring warm weather and bright sunlight for its better growth and development. Kerala, Coastal and Malnad region of Karnataka, Andhra Pradesh and Tamil Nadu are the major oriental pickling melon growing states in India.

In general, variability is the basic material and pre-requisite for any crop improvement programme. Therefore, knowledge about the existence of genetic variability is the useful adjunct to carry out effective selection for improving yield. Genetic variability study will help in estimating genetic parameters *viz.*, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2) and genetic advance as percent mean which are essential for effective selection of superior genotypes and partition the observed variability into heritable and non-heritable components. An estimate of phenotypic and genotypic variation quantifies the amount of variability present within a set of breeding material with regard to its essential characteristics. Heritability denotes the proportion of phenotypic variation due to genotypes and thus helps the breeders to select an elite variety for a character. Genetic advance denotes the improvement in the mean genotypic values of selected families over base population and thus helps the breeder to select the progenies in the earlier generation itself (Singh and Narayanan, 1993) [14]. Sufficient variability present in this crop for fruit color, size, shape fruit weight etc. with this information, the present investigation was undertaken to assess the genetic variability for growth and yield characters in oriental pickling melon genotypes.

Material and Methods

The present study carried out at College of Horticulture Sirsi, Karnataka during late *Kharif* 2017. The 40 genotypes were assessed in a field experiment under a randomized block design with two replications. Eight plants maintained in each treatment with spacing of 1 m X 0.6 m between rows and plants, respectively. The data were recorded on five randomly selected plants from each genotype for twenty growth and yield characters. Observations recorded for vine length at 30 and 60 DAS (cm), number of primary branches, number of nodes at 30 and 60 DAS, node at first male flower appearance, nodes at first female flower appearance, number of male flowers, number of female flowers, sex ratio, fruit length (cm), fruit width (cm), average fruit weight (g), number of fruits per vine, fruit yield per vine (Kg), flesh thickness (cm), seed cavity diameter (cm), seed weight per fruits (g), number of seeds per fruit and Total Soluble Sugar (TSS-°brix). The total variability of the forty genotypes for each of the quantitative trait was partitioned into sources attributable to genotype, replication and error using ANOVA technique (Panse and Sukhatme, 1967) [9]. Genetic variability

parameters like phenotypic and genotypic co-efficient of variation (PCV and GCV) were computed as per Burton and Devane (1953). The heritability in broad sense and genetic advance as percent mean (GAM) were determined by using the formula given by Johnson *et al.* (1955) [6]. The GCV, PCV and GAM were classified as low (0-10%), moderate (10-20%) and high (20-100%). Whereas, heritability is as low (0-30%), moderate (30-60%) and high (60-100%) The statistical analysis was carried out using software program windostat version 9.1.

Results and Discussion

Analysis of Variances

Analysis of variance had shown highly significant ($P=0.01$) difference among genotypes for all the twenty characters related to growth and yield parameters except for number of primary branches was presented in table.1. This indicates the existence of high degree of genetic variability among the genotypes and enough scope for bringing about improvement in the desirable direction.

Table 1: Analysis of variance (mean squares) for different growth and yield parameters in oriental pickling melon genotypes

Characters	Genotype	Replication	Error	C.D.@5%	C.D.@1%
Number of primary branches	0.318	0.936	0.157	0.803	1.075
Number of nodes at 30 DAS	15.92**	4.51	3.70	3.89	5.21
Number of nodes at 60 DAS	14.79**	9.13	4.19	4.14	5.54
Vine length at 30 DAS (cm)	360.02**	160.54	19.888	9.021	12.076
Vine length at 60 DAS (cm)	1105.39**	237.21	54.707	14.961	20.029
Nodes at first male flower appears	1.046**	0.320	0.198	0.900	1.205
Nodes at first female flower appears	1.6**	0.23	0.44	1.35	1.80
Number of male flowers	469**	37.32	31.89	11.42	15.29
Number of female flowers	2.515**	0.023	0.201	0.908	1.215
Sex ratio	4.63**	3.37	0.24	1.00	1.34
Fruit length (cm)	23.634**	10.361	4.076	4.083	5.467
Fruit width (cm)	15.182**	12.09	3.584	3.829	5.127
Average fruit weight (g)	0.279**	0.009	0.055	0.473	0.634
Number of fruits per vine	1.183**	0.152	0.376	1.247	1.662
Fruit yield per vine (kg)	0.427**	0.012	0.196	0.896	1.199
Flesh thickness (cm)	0.934**	0.023	0.187	0.871	1.17
Seed cavity diameter (cm)	1.476**	0.019	0.167	0.827	1.107
Seed weight per fruits (g)	1.476**	0.019	0.167	1.93	1.107
TSS (° brix)	11.299**	0.029	0.907	0.68	2.579
Number of seeds per fruit	13548.65**	3712.81	1252.56	71.59	95.84

Note: * and ** indicate significant at 5 and 1 per cent probability level, respectively. DAS – Days after sowing.

Analysis of variance by itself is not enough and conclusive to explain all the inherent genotypic divergence in the collections. This is revealed by determining the total genetic variability inherent in the genotypes obtained after due partitioning of the phenotypic variance. The phenotypic variation of traits is attributable to genotype and environment assuming absence of interaction between them. The variation due to genotype can only be managed to suit to end-user needs. To compare variation of the genotypes across twenty traits at phenotypic and genotypic levels, the phenotypic and genotypic variations were standardized to make them unit-free and expressed as phenotypic coefficient of variability (PCV) and genotypic coefficient of variability (GCV). The estimate of PCV is higher than GCV in all the characters studied (Table 2) and indicates the influence of environment on genotypes.

High GCV and PCV (>20%) were observed for nodes at first female flower appears, number of male flowers, number of female flowers, average fruit weight, number of fruits per vine, fruit yield per vine and seed weight per fruit. These

results are in conformity with the findings of earlier workers *viz.*, Lakshmi *et al.* (2017) [8] in oriental pickling melon for nodes at first female flower appears; Afangideh *et al.* (2007) in cucumber for number of male flowers; Afangideh *et al.* (2007) [7] in cucumber for number of female flowers; Reddy and Shanthi (2013) [13], Potedar *et al.* (2014), Janghel *et al.* (2018) [5] in musk melon for average fruit weight; Reddy and Shanthi. (2013) [13], Potedar *et al.* (2014), Janghel *et al.* (2018) [5], in musk melon for number of fruits per vine; Reddy and Shanthi (2013) [13], Potedar *et al.* (2014), in musk melon for fruit yield per vine and Karadi *et al.* (2016) [7] in wild melon for seed weight per fruit. This indicates presence of greater amount of genetic variability for these characters. Hence, there is ample scope for improving these characters.

Whereas, moderate GCV and PCV (10-20%) were observed for number of nodes at 30 DAS, vine length at 30 and 60 DAS, Sex ratio, fruit length, fruit width and flesh thickness seed cavity diameter and TSS. These results are in conformity with the findings of earlier workers *viz.*, Lakshmi *et al.* (2017) [8] in oriental pickling melon; Shah *et al.* (2018) in cucumber

for number of nodes at 30 DAS; Reddy and Shanthi (2013)^[13], Potekar *et al.* (2014), Janghel *et al.* (2018)^[5] in muskmelon and Karadi *et al.* (2016)^[7], in wild melon for vine length at 30 and 60 DAS; Reddy *et al.* (2013), Janghel *et al.* (2018)^[5] in musk melon and Karadi *et al.* (2016)^[7] for fruit length; Reddy and Shanthi (2013)^[13] in musk melon for seed cavity diameter

and Reddy *et al.* (2013), in musk melon for TSS. This indicates presence of moderate amount of variability and environment also influencing expression for these characters. Other traits recorded low PCV and GCV indicating less variability and not useful for selection and further improvement of crop.

Table 2: Estimates of mean, range and genetic parameter for different growth and yield traits in oriental pickling melon genotypes

Character	Range		Mean \pm S. Em.	PCV (%)	GCV (%)	h ² bs (%)	GAM (%)
	Lowest	Highest					
Number of primary branches	2.50	4.18	3.37 \pm 0.28	14.44	8.39	33.74	10.34
Number of nodes at 30 DAS	12.50	24.33	17.96 \pm 1.36	17.44	13.76	62.24	22.36
Number of nodes at 60 DAS	21.67	36.17	27.25 \pm 1.45	11.30	8.35	55.83	13.00
Vine length at 30 DAS (cm)	83.50	153.99	111.83 \pm 3.15	12.32	11.66	89.34	22.73
Vine length at 60 DAS (cm)	129.00	240.16	165.60 \pm 5.23	14.54	13.84	90.57	27.13
Nodes at first male flower appears	2.63	4.66	3.74 \pm 0.22	12.54	9.48	57.11	14.75
Nodes at first female flower appearance	2.67	6.67	3.65 \pm 0.47	27.65	20.81	56.64	32.27
Number of male flowers	11.78	95.88	31.62 \pm 3.99	48.52	45.56	87.25	89.98
Number of female flowers	1.00	7.34	2.65 \pm 0.32	43.98	40.59	85.18	77.17
Sex ratio	10.12	15.21	11.77 \pm 0.44	13.26	12.58	90.02	24.58
Fruit length (cm)	14.42	29.82	21.56 \pm 1.43	17.27	13.86	70.58	25.12
Fruit width (cm)	6.62	20.51	15.23 \pm 1.34	20.12	15.82	97.13	25.61
Average fruit weight (g)	0.29	1.89	0.80 \pm 0.17	50.79	41.63	67.18	70.35
Number of fruits per vine	0.50	5.34	1.71 \pm 0.43	41.51	37.04	97.53	54.81
Fruit yield per vine (kg)	0.49	2.82	1.32 \pm 0.31	42.40	25.83	67.18	31.42
Flesh thickness (cm)	1.80	4.69	3.20 \pm 0.31	23.41	19.11	66.63	32.13
Seed cavity diameter (cm)	3.18	6.58	5.18 \pm 0.29	17.50	15.62	79.68	28.72
TSS ($^{\circ}$ brix)	3.83	5.90	4.84 \pm 0.24	13.77	11.88	74.52	21.13
Seed weight per fruit (g)	5.42	14.28	8.86 \pm 0.67	27.88	25.72	85.13	48.89
Number of seeds per fruit	132.5	660	245.43 \pm 25.03	35.05	31.95	83.07	59.98

Note: PCV: Genotypic coefficient of variance, GCV: Genotypic coefficient of variance h² bs: Heritability in broad sense, GAM: Genetic advance as percent mean S. Em: Standard error of mean



1. Siddapur-1, 2.Local-1, 3.Local-5, 4-Local-2, 5.Man4, 6.Local-3. 7. SS-10, 8.SS-6, 9.manabi-1 10.M-3, 11.Local-1, 12. SS-11, 13-SS-13, 14-Ss-7, 15Soubhagya, 16.SS-2, 17.SS-14, 18.Mudicode, 19.IIHR381, 20.Local6 21Sidpur2, 22.SS-1, 23.Soubhagya, 24.SS-2, 25.Manabagii3, 26.Man-2, 27.Salkani2, 28.Salkani1, 29.SS-16, 30.M-2, 31.Slo-3 32.SS-3, 33.SS-5, 34.SS-15, 35.SS-12, 36.M-4, 37.IIHR386, 38. L-4, 39. SS-9, 40.SS-4

Plate 1: Variability in the fruit shape, size and color of 40 oriental pickling melon genotypes

The co-efficient of variation at genotypic and phenotypic levels explain only the extent of variability in different traits, but this variation fails to explain the amount of heritable portion. In this situation, heritability in broad sense has an important role in the determining the heritable portion of variation. Knowledge of heritability of a trait is an essential measure to breeder in choosing suitable genotypes to employ in improving the trait under specified situation. The results in the experiment revealed higher heritability estimate for most of the characters except for number of branches, number of nodes at 60 DAS, node at first male flower appears, number of nodes at 60 DAS and node at first female flower appears found low to moderate heritability. In a comparable study, Reddy and Shanthi (2013) ^[13] also reported low to moderate heritability for number of branches in muskmelon. High heritability indicates less influence of environment and is governed by additive gene effects. For the character with low heritability, selection may be considerably difficult or virtually impractical due to the masking effect of environment on genotypic effect.

Higher broad-sense heritability suggested effectiveness of selection for the traits under study as is also indicated by higher predicted genetic advance. Higher predicted genetic advance could be realized as the genetic variation among the germplasm accessions is solely attributable to genes acting additively, which cause greater resemblance between selected parents and their progeny. Present study high heritability (>60%) coupled with high GAM (>20%) were observed for maximum traits like number of nodes at 30 DAS, vine length at 30 and 60 DAS, number of male flowers, number of female flowers, sex ratio, fruit length, fruit width, average fruit weight, number of fruits per vine, fruit yield per vine, Vitamin-C content, flesh thickness, seed cavity diameter, seed weight per fruit, number of seeds per fruit and TSS (Table 2). In comparable study of earlier workers viz., Lakshmi *et al.* (2017) ^[8] in oriental pickling melon for number of nodes at 30 DAS; Reddy and Shanthi, (2013) ^[13] musk melon and Lakshmi *et al.* (2017) ^[8] in oriental pickling melon for vine length at 30 and 60 DAS; Afangideh *et al.* (2007) in cucumber for number of male flowers; Arunkumar *et al.* (2011) in cucumber for number of female flowers; Rakhi and Rajamony (2005) in culinary melons for sex ratio; Reddy *et al.* (2013), Janghel *et al.* (2018) ^[5] in musk melons for fruit length; Rakhi and Rajamony (2005) in culinary melon for fruit width; Reddy and Shanthi (2013) ^[13], Janghel *et al.* (2018) ^[5] in musk melon and Lakshmi *et al.* (2017a) ^[8] in oriental pickling melon for average fruit weight; Reddy and Shanthi (2013) ^[13], Janghel *et al.* (2018) ^[5] in musk melon for number of fruits per vine; Reddy and Shanthi (2013) ^[13], Potedar *et al.* (2014); in musk melon for fruit yield per vine; Lakshmi *et al.* (2017) ^[8] in oriental pickling melon for flesh thickness; Karadi *et al.* (2016) ^[7] in wild melon for Vitamin-C content; Karadi *et al.* (2016) ^[7], in wild melon for seed cavity diameter, seed weight per fruit and TSS; Karadi *et al.* (2016) ^[7], in wild melon for number of seeds per fruit. Even though the cross pollinated nature of crop attributable to dominance and dominance-additive based epistatic interaction of genes controlling different traits. The predominance of additive component indicates for above traits would be more effective for direct selection in improvement of oriental pickling melon.

From this study concluded that, the characters like number of nodes at 30 DAS, vine length at 30 and 60 DAS, number of male flowers, number of female flowers, sex ratio, fruit length, fruit width, average fruit weight, number of fruits per

vine, fruit yield per vine, flesh thickness, seed cavity diameter, seed weight per fruit, number of seeds per fruit and TSS are genetically variable and direct selection would be more effective in improving these traits in oriental pickling melon.

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