improvement for all the traits associated with yield would be difficult in the population.

Multivariate hierarchical analysis revealed total of six clusters. It was concluded that 32 genotypes were mainly divided at first node into two clusters with 24 and 8 genotypes. Cluster with 24 genotypes was further divided into 3 groups with 9,7 and 8 genotypes respectively.

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Studies on Genetic and Biochemical Parameters of Introduced and Indigenous Germplasm in Snap Melon (*Cucumis melo* L var. *momordica* Duth. and full.)

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Key Words: GCV, Genetic Advance, Heritability, PCV, Variability

Snap melon (*Cucumis melo* L. var. *momordica*) belongs to family cucurbitaceae and is grown in many parts of India. The tender fruits are used as a vegetable and ripe fruits are used as dessert. The fruits are rich in vitamins and minerals. Besides it has got enormous medicinal value. India, being a secondary centre of origin of snap melon, has accumulated a wide range of variability with respect to different quantitative and qualitative characters. The critical assessment of nature and magnitude of variability is a prerequisite for any efficient breeding programme and provides an opportunity to identify superior lines with desirable yield and quality characters. Heritability along with genetic advance will be helpful in assessing the reliability of a character for selection. Hence, the present investigation was undertaken to study variability, heritability and genetic advance for 19 important quantitative and biochemical characters in 30 genotypes of Snap melon.

The present investigation was carried out at the research farm of The Division of Vegetable Science, Indian Agricultural Research Institute, New Delhi, during the spring-summer season of 2003. The experimental materials consisted of 30 indigenous and exotic genotypes of snap melon collected from different sources. The experiment was laid out in a randomized block design with three replications. Each treatment comprised ten hills and two plants were allowed to grow per hill. The observations were recorded on five randomly selected plants per replication for each entry on nineteen quantitative and biochemical characters. The analysis of variance were carried out as suggested by Panse and Sukhatme (1967) and were used for calculating other genetic parameters. Genotypic and phenotypic coefficient of variation was calculated as per the formula suggested by Burton (1952). Heritability in broad sense and expected genetic advance were calculated as per the formula given by Allard (1960) and Johnson *et al.* (1955), respectively.

The extent of variability present in thirty genotypes of snap melon was measured in terms of phenotypic variance (Vp), phenotypic coefficient of variation (PCV), genotypic variance (Vg), genotypic coefficient of variation (GCV), heritability (broad sense) and genetic advance (GA). A perusal of data in Table 1 revealed that maximum

Table 1. Range, genotypic, phenotypic and environmental variances and coefficient of variation for 19 characters

S. No.	Characters	Range	Vg	Vp	Ve	GCV%	PCV%
1.	First male flower node	1.07-2.00	0.040	0.09	0.058	14.80	22.71
2.	First female flower node	3.20-4.40	0.046	0.20	0.16	5.91	12.58
3.	Days to first male flower appearance	31.40-39.40	3.96	6.34	2.38	5.81	7.36
4.	Days to first female flower appearance	36.47-48.40	6.28	11.29	5.01	5.93	7.95
5.	Days to fruit set from anthesis	2.0-3.20	0.10	0.16	0.063	14.58	18.46
6.	Number of fruits/plant	2.40-6.27	0.49	0.89	0.40	17.58	23.70
7.	Maturity period	18.93-27.97	5.52	7.87	2.35	10.25	12.24
8.	Fruit length (cm)	7.67-21.50	15.85	18.01	2.16	29.01	30.92
9.	Average fruit weight (g)	171.33-1303.33	64526.06	72432.62	7906.56	51.83	54.92
10.	Fruit diameter (cm)	5.23-12.0	2.76	3.33	0.57	20.84	22.91
11.	Flesh thickness (cm)	0.80-2.52	0.14	0.24	0.10	25.42	33.39
12.	Length of fruit cavity (cm)	3.37-8.07	1.26	1.57	0.31	22.41	25.04
13.	Yield/plant (kg)	0.72-5.23	0.81	0.97	0.16	47.93	52.73
14.	Vine length (m)	1.10-2.25	0.09	0.13	0.040	18.60	22.29
15.	Ascorbic acid (mg)	4.42-15.50	6.47	9.69	3.22	33.23	40.67
16.	Total carotenoids (µg)	43.07-1860.33	137788.34	143690.48	5902.15	65.55	66.93
17.	Reducing sugars (%)	0.93-2.75	0.17	0.19	0.022	24.00	25.54
18.	Non-reducing sugars (%)	0.85-3.05	0.17	0.18	0.012	25.90	26.78
19	T.S.S. (%)	4.67-9.0	0.90	1.07	0.17	15.83	17.25

Vg=Genotypic variance; Vp=Phenotypic variance; Ve=Environmental variance; GCV= Genotypic coefficient of variation; PCV= Phenotypic coefficient of variation

variation was exhibited by total carotenoids followed by average fruit weight at both genotypic and phenotypic levels. The variation was moderate for characters like fruit length and days to first female flower appearance both at genotypic and phenotypic levels. Rest all characters showed very low genotypic and phenotypic variance. Similar observations were reported by Kalloo *et al.* (1983) in musk melon and Rao *et al.* (1999) in cucumber for average fruit weight.

Further, GCV was less compared to that of PCV for all the characters indicating a considerable influence of environment on the expression of these characters. The GCV which gives a picture of the extent of genetic variability in the population, ranged from 5.81 percent (days to first male flower appearance) to 65.55 percent (total carotenoids). The GCV was considerably high for characters such as total carotenoids (65.55 percent) followed by average fruit weight (51.83%) and yield per plant (47.93 percent). Except for total carotenoids, this is in confirmation with the findings of Swamy *et al.* (1985) in musk melon, Rao *et al.* (1999) in cucumber, Jeeva and Pappiah (2002) and Pandey *et al.* (2003) in snap melon. The above mentioned characters having higher range of variation have a better scope of improvement through selection. Characters like ascorbic acid, fruit length, non-reducing sugars, flesh thickness, reducing sugars, length of fruit cavity and fruit diameter exhibited moderate values of GCV, which is also considered sufficient to make an effective selection. Characters such as total carotenoids, non-reducing sugars, reducing sugars and fruit length had very narrow difference in PCV and GCV values which indicated least influence of the environment on their expression. In such a situation, selection can be effective on the basis of phenotypic alone with equal probability of success. With the help of GCV alone, it is not possible to determine the amount of variation that is heritable. Heritable variation can be found out with greater degree of accuracy when heritability in conjunction with genetic advance is studied (Dudley and Moll, 1969). The heritability estimates ranged from 22.10 per cent for first female flower node number to 95.90 per cent for total carotenoids (Table 2). Very high heritability estimate were observed for total carotenoids, non-reducing sugars, average fruit weight, reducing sugars, fruit length, total soluble solids, fruit diameter, yield per plant and length of fruit cavity indicating least influence of environment on these traits. High heritability estimate for length of fruit cavity, fruit length and average fruit weight were also reported by Kalloo *et al.* (1983) in muskmelon and high heritability estimates for characters like average fruit weight, yield per plant and fruit length were also reported by Jeeva and Pappaiah (2002) in snap melon.

The heritability estimate was moderate for maturity period, vine length, ascorbic acid, days to first male flower appearance, days to fruit set from anthesis, flesh thickness, days to first female flower appearance and number of fruits per plant suggesting that environmental effects constitute a major portion of total phenotypic variation and hence direct selection for the characters will be less

Table 2. Heritability and genetic advance for different characters

	Character	Broad sense Heritability (%)	Expected genetic advance	
			5% intensity of selection	As percentage of mean
1	First male flower node number	42.50	0.28	20.00
2	First female flower node number	22.10	0.21	5.73
3	Days to first male flower appearance	62.40	3.24	9.46
4	Days to first female flower appearance	55.60	3.85	9.10
5	Days to fruit set from anthesis	62.40	0.53	23.87
6	Number of fruits per plant	55.10	1.07	26.81
7	Maturity period	70.10	4.05	17.67
8	Fruit length	88.00	7.70	56.12
9	Average fruit weight	89.10	493.90	100.78
10	Fruit diameter	82.70	3.11	39.02
11	Flesh thickness	58.00	0.60	40.00
12	Length of fruit cavity	80.10	2.07	41.40
13	Yield per plant	82.60	1.68	89.83
14	Vine length	69.70	0.53	32.31
15	Ascorbic acid	66.80	4.28	55.94
16	Total carotenoids	95.90	748.80	132.22
17	Reducing sugars	88.30	0.80	46.24
18	Non-reducing sugars	93.60	0.85	51.82
19	T.S.S.	84.20	1.80	29.95

effective. It can be further inferred that such traits are governed mostly by non-additive gene action and can be exploited effectively through heterosis breeding.

Expected genetic advance and its estimate as percentage of mean for various characters (Table 2) revealed that total carotenoids, average fruit weight and yield per plant exhibited the highest genetic advance. Though characters such as non-reducing sugars, reducing sugars, fruit length total soluble solids, fruit diameter and length of fruit cavity had high heritability estimates, their GCV was comparatively less, resulting in less genetic advance. First male flower node number and first female flower node number possessed low heritability values along with low GCV resulting in low genetic advance. This confirms the findings of Burton (1952) that GCV together with heritability estimates would give a better picture of genetic advance to be expected from selection. It is clear from Table 1 and 2 that total carotenoids, average fruit weight and yield per plant possess high GCV, heritability and genetic advance. These characters could be effectively improved through selection as it has been suggested that characters with higher heritability coupled with high genetic advance would respond to selection better than those with high heritability and low genetic advance (Johnson *et al.*, 1955).

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