Plant Archives Vol. 20 Supplement 1, 2020 pp. 2221-2224 **e-ISSN:2581-6063 (online), ISSN:0972-5210**

STUDIES ON GENETIC VARIABILITY IN BITTER GOURD (*MOMORDICA CHARANTIA* L.) UNDER COASTAL ECOSYSTEMS

Waikhom Jupiter Singh* and R. Kandasamy

Department of Horticulture, Faculty of Agriculture, Annamalai University, Annamalainagar - 608 002 (Tamil Nadu), India.

Abstract

Forty genotypes of bitter gourd collected from different agro-climatic regions of India were evaluated to assess the variability, heritability, genetic advance. Quantitative and qualitative characters like days to first male flower, days to first female flower, node number of first male flower, node number of first female flower, sex ratio, vine length (m), number of primary branches per vine, days to first fruit harvest, fruit length (cm), fruit girth (cm), average fruit weight (g), number of fruits per vine, seeds per fruit, TSS (Brix°), ascorbic acid content (mg/100g) and fruit yield per plant (kg) were studied. Analysis of variance revealed that there were significant differences among the genotypes studied for all the characters. In variability studies, among 40 genotypes MC 13 was identified as the best genotypes as it recorded higher yield per vine followed by MC 1, MC 20 and MC 14. Maximum phenotypic and genotypic coefficient of variation (PCV and GCV) was found for fruit yield per vine followed by the number of fruits per plant and sex ratio. High heritability was observed for all the characters. Genetic gain was maximum for fruit yield per vine followed by number of fruits per vine. The characters like yield per vine, number of fruits per plant and sex ratio had high heritability along with high genetic gain which reveals the predominance of additive gene action of these characters.

Key words : Variability, heritability, genetic advance, bitter gourd.

Introduction

Bitter gourd is an important vegetable crop that has a distinct bitter taste and is cultivated for its immature tubercular fruit. The bitter principle present in the fruit is momordicin, a bitter glucoside, which decides the taste. Bitter gourd fruit is known to be a rich source of minerals and vitamins, with 88 mg per 100 g vitamin C. Bitter gourd fruit has medicinal value and is used to treat diabetes, asthma, diseases of the blood and rheumatic problems. Genetic diversity knowledge is an important factor in heritable improvement of any plants and the nature and extent of divergence information would be very important to choose desirable parents from the germplasm available for a successful breeding programme. The nature and magnitude of the genetic distance between genotypes serve as an indication that high levels of heterotic hybridization can occur. Genetic diversity is essential to applied plant breeding as it reduces the vulnerability to pests and helps to choose the most promising parental combinations. The aim of the present study is therefore to determine the nature and extent of genetic diversity in a set of forty bitter genotypes.

***Author for correspondence :** E-mail: jupiwai@gmail.com

Research Methods

The experiment was carried out at the Shivapuri, Cuddalore, Tamil Nadu, India. The geographical location of the research farm is having an altitude of 16 m above Mean Sea Level, latitude of 11°24'N and longitude of 79°41'E. The materials used for this study consisted of 40 genotypes of bitter gourd which were collected from different agro-climatic regions of India. The experimental plots were ploughed to fine tilth and pits of 30 cm × 30 cm × 30 cm size at 1.5 × 1.5 m spacing were dug and then basins were formed. The experiment was laid out in RBD design with three replications. Agronomic practices adopted were as per the package of practices recommendations of the Tamil Nadu Agricultural University for raising the crop. To evaluate genotypes,

five plants were selected at random per replication for each treatment and quantitative as well as qualitative traits like days to first male flower, days to first female flower, node number of first male flower, node number of first female flower, sex ratio, vine length (m), number of primary branches per vine, days to first fruit harvest, fruit length (cm), fruit girth (cm), average fruit weight (g), number of fruits per vine, seeds per fruit, Total soluble solids (TSS) (Brix°), ascorbic acid content (mg/100g) and fruit yield per vine (kg) were recorded. The data were analyzed in accordance with the Panse and Sukhatme (1985) protocol for the variance. The coefficient of phenotypic and genotypic variations was determined according to Burton and De Vane (1953). Heritability and genetic advance were computed using the Johnson *et al*. (1955) formula.

Results and Discussion

Significant difference between genotypes was noticed for all the characters examined (table 1). There has been a wide range of variations on all characters, which suggests high genetic variability. The mean range, phenotypic co-efficient of variation (PCV), genotypic co-efficient of variation (GCV), genetic advance and genetic advance as per cent of mean are given in table 2. Average fruit weight exhibited the highest phenotypic variance (405.82) followed by ascorbic acid content (196.32). Among the sixteen traits studied, the phenotypic variance ranged from as low as 0.24 fruit yield per vine to 405.82 in average fruit weight.

The characters such as fruit yield per vine, TSS and vine length exhibited relatively lesser phenotypic value. The phenotypic coefficient of variation (PCV) ranged (9.84 per cent for days to first female flower to 41.82 per cent for fruit yield per vine. The genotypic coefficient of variation (GCV) was also higher on respect of average fruit weight (397.73) followed by ascorbic acid content (195.09) and sex ratio (87.11). The GCV ranged from 9.80 per cent for days to first female flower to 40.74 per cent for fruit yield per vine. The highest GCV was exhibited by fruit yield per vine and number of fruits per vine. Similar reports were also made on Maurya *et al*. (2018) and Alekar *et al*. (2019). In general, phenotypic values were higher than genotypic values, but the differences were less fruit yield per vine, node number of first male flower, node number of first female flower, sex ratio, vine length, number of primary branches per vine, days to first fruit harvest, fruit length, fruit girth, number of fruits per vine, seeds per fruit and TSS suggesting that these characters were less influenced by the environmental factors and for these characters

Table 1 : General analysis of variance for various characters of bitter gourd genotypes.

Source	Df	Mean sum of square (MSS)															
		Days to first male flower	Days to first female flower	Node number of first female flower	Node number of first male flower	Sex ratio	Vine length	Number of primary branches per vine	Days to first fruit harvest	Fruit length	Fruit girth	Average fruit weight	Number of fruits per vine	Seeds per fruit	TSS	Ascorbic acid content	Fruit yield per vine
Replication	2	0.095	0.197	0.892	0.535	0.373	0.810	0.059	0.21[illegible]	0.787	0.015	6.169	0.998	0.338	0.054	8.650	0.128
Genotype	39	35.739**	7[illegible].031**	73.88[illegible]**	55.285**	261.609**	2.336**	19.225**	16.931**	24.865**	19.564**	1201.274**	86.489**	45.794**	2.340**	58[illegible].5032**	0.7013**
Error	78	0.190	0.170	0.216	0.252	0.2682	0.212	0.343	0.305	0.246	0.316	8.088	0.278	0.137	0.035	1.227	0.012

** Significant at 1%.

Table 2 : Mean range, phenotypic variance (Vp), genotypic variance (Vg), phenotypic co-efficient of variance (PCV), genotypic coefficient of variance (GCV), heritability, genetic advance and genetic advance as per cent of mean.

Characters	Mean range	Phenotypic variance (Vp)	Penotypic variance (Vg)	Phenotypic co-efficient of variance PCV (%)	Genotypic coefficient of variance GCV (%)	Heritability (h^2)	Genetic advance	Genetic advance as per cent of mean (Genetic gain)
Days to first male flower	32.45-48.43	19.04	18.85	10.77	10.72	99.00	8.90	21.96
Days to first female flower	40.24-57.23	24.13	23.96	9.84	9.80	99.31	10.05	20.12
Node number of first male flower	5.18-11.23	2.61	2.39	19.26	18.44	91.71	3.05	36.38
Node number of first female flower	12.51-20.47	5.26	5.01	14.17	13.82	95.22	4.50	27.78
Sex ratio	10.49-48.35	87.38	87.11	34.16	34.11	99.69	19.20	70.15
Vine length (m)	1.64-5.35	0.89	0.67	27.39	23.90	76.12	1.48	42.95
No. of primary branches per vine	7.65-16.50	6.87	6.53	22.24	21.68	95.01	5.13	43.53
Days to first fruit harvest	56.58-79.33	54.85	54.54	10.90	10.87	99.45	15.17	22.33
Fruit length (cm)	6.61-19.14	8.45	8.21	20.76	20.46	97.09	5.81	41.52
Fruit girth (cm)	5.53-16.56	6.73	6.42	23.45	22.89	95.31	5.09	46.04
Average fruit weight (g)	30.52-120.23	405.82	397.73	25.97	25.71	98.01	40.67	52.44
Number of fruits per vine	6.29-25.53	29.00	28.73	37.52	37.34	99.04	10.99	76.54
Seeds per fruit	4.40-20.23	15.33	15.18	28.83	28.69	99.00	7.99	58.80
TSS (Brix^o)	3.15-6.31	0.80	0.77	17.90	17.50	95.64	1.77	35.26
Ascorbic acid content (mg/100g)	46.06-98.25	196.32	195.09	20.76	20.70	99.37	28.68	42.50
Fruit yield per vine (kg)	0.41-2.38	0.24	0.23	41.82	40.74	94.87	0.96	81.73

indicates presence of high degree of variability and better scope of improvement through straight selection. Such findings are closely consistent with the results of Kumar *et al*. (2018) and Kumari *et al*. (2018).

The estimation of GCV alone is not enough to calculate the amount of heritable variation. Heritable variation can be discovered with more prominent level of exactness when heritability is contemplated related to genetic advance. The broad-sense heritability was highest for sex ratio while it was least for vine length. High values of heritability was reported for days to first fruit harvest, ascorbic acid content, days to first female flower, number of fruits per vine, days to first male flower, seeds per fruit, average fruit weight, fruit length, TSS, fruit girth, node number of first female flower, number of primary branches per vine, fruit yield per vine, node number of first male flower, vine length. This is in conformity with the results of Tiwari *et al*. (2018) and Alekar *et al*. (2019). The character average fruit weight (40.67) exhibited the highest genetic advance while lowest genetic advance exhibited by fruit yield per plant (0.96).

High values of genetic advance as per cent of mean were recorded for all the characters except days to first female flower, days to first male flower, days to first fruit harvest, node number of first female flower, total soluble solids (TSS) and node number of male flower. High heritability coupled with high genetic advance per cent of mean was reported for fruit yield per vine, number of fruits per vine and sex ratio indicated that the presence of additive gene action effects could be effectively used in phenotypic selection. This is in conformity with the results of Radha Rani *et al*. (2015) and Kumari *et al*. (2018). Other characters like days to first female flower, days to first male flower, days to first fruit harvest exhibited low to moderate genetic gain. The high heritability and moderate genetic gain were observed in days to first female flower, days to first male flower, days to first fruit harvest indicated that expression of these characters was govern by non additive gene action and can be exploited for heterosis breeding.

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