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Variability and heritability studies for yield and yield component traits in bitter gourd (*Momordica charantia* L.)

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Abstract

A field experiment was conducted using 24 genotypes of bitter gourd including varieties, local collections from different regions of Karnataka during summer 2017-18. The experiment was carried out at experimental block, department of Crop improvement and Biotechnology, College of Horticulture, Mudigere, University of Agricultural and Horticultural Sciences, Shivmogga for yield and its attributing traits and analyzed for Genotypic Coefficient of Variation, Phenotypic Coefficient of Variation, heritability and genetic advance as per cent mean. High estimates of PCV (%), GCV (%), heritability coupled with high genetic advance as per cent mean were observed for node at which first male flower appears, node at which first female flower appears, sex ratio, number of fruits per vine, fruit weight (g), fruit length (cm), fruit width (mm), rind thickness (mm), flesh thickness (mm), fruit yield per vine (kg), fruit yield per plot (kg) and vitamin C (mg/100g). Hence, these characters were highly influenced by the additive gene action and could be used in genetic improvement through direct selection.

Keywords: Bitter gourd, GCV, PCV, Genetic advance, Heritability

Introduction

Bitter gourd (*Momordica charantia* L.) (2n=22) is tropical and subtropical vine crop belongs to Cucurbitaceae family. It is a popular vegetable in India having economic, nutritional and medicinal uses. It is grown extensively in India, Indonesia, Malaysia, Singapore, Thailand, Japan, Tropical Africa and South America. In India, it is grown widely in Uttar Pradesh, Orissa, West Bengal, Maharashtra, Gujarat, Andhra Pradesh, Tamil Nadu and Kerala. It has the high export potential to South-East Asia, Gulf and also European countries. Concerning the nutrition value, bitter gourd fruits are rich in iron (2.0mg/100g), vitamin A, B, C and are the good source of proteins (2%) and minerals. Concerning about the medicinal importance the fruits are antidotal, antipyretic, appetizing, stomachic and control diabetes (Meir and Yaniv, 1985)^[4].

Bitter gourd 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 study the presence of genetic variability, heritability and genetic advance for seven quantitative traits among different bitter gourd genotypes.

Materials and Methods

Twenty four bitter gourd genotypes were collected from farmer's field and some released varieties were also evaluated at experimental plot, College of Horticulture, Mudigere during 2017-18. The genotypes were assessed in the field experiment under randomized block design with three replications and were planted with the spacing of 2×1.2 m. The crop was raised as per the package of practices of horticultural crops of University of Horticultural Sciences, Bagalkot (Anon, 2014) ^[1]. Observations were recorded on vine length (m), number of branches/vine, internodal length (cm), node at which first male and female flower appears, days to first male and female flower, sex ratio, number of fruits per vine, fruit weight (g), fruit length (cm), fruit width (mm), rind thickness (mm), flesh thickness (mm), fruit yield per plant

Corresponding Author: Sowmya HM College of Horticulture, Mudigere University of Agricultural and Horticultural Sciences, Shivamogga, Karnataka, India (kg), fruit yield per plot (kg), vitamin c (mg/100mg) and chlorophyll content (mg/g).

Results and Discussion

The extent of variability present among the genotypes was estimated in terms of range, mean, standard error, phenotypic and genotypic coefficient of variation, heritability and genetic advance as per cent mean. The analysis of variance showed significant differences among the genotypes for all the characters studied (Table 1). The extent of variability present in the germplasm provides scope for the crop improvement programme and also depends on the extent of heritability for a trait. Range of variation observed for all the traits indicated the presence of sufficient amount of variation among the genotypes for all the characters studied (Table 2).

Source of variation/characters	Replication	Genotypes	Error	S. Em ±	CD @ 5%	
Degrees of freedom	2	23	46	5. Em ±	CD @ 5%	
Vine length (m)	0.02	0.60**	0.04	0.11	0.31	
Number of branches/vine	0.05	3.31**	0.20	0.26	0.74	
Internodal length (cm)	0.29	5.08**	0.17	0.24	0.68	
Node at which first male flower appears	1.11	15.79**	0.69	0.48	1.37	
Node at which first female flower appears	0.32	40.16**	0.58	0.44	1.25	
Days to first male flower	20.36	59.13**	3.34	1.06	3.01	
Days to first female flower	2.20	61.89**	3.83	1.13	3.22	
Sex ratio	0.43	13.24**	0.25	0.29	0.32	
Number of fruits per vine	0.46	76.66**	1.47	0.69	1.99	
Fruit weight (g)	8.41	3035.63**	10.51	1.87	5.39	
Fruit length (cm)	0.74	40.67**	1.13	0.61	1.75	
Fruit width (mm)	3.04	290.17**	6.34	1.45	4.14	
Rind thickness (mm)	0.12	25.72**	0.25	0.29	0.32	
Flesh thickness (mm)	0.84	101.39**	0.95	0.56	1.60	
Fruit yield per plant (kg)	0.03	0.50**	0.04	0.11	0.32	
Fruit yield per plot (kg)	0.84	21.50**	1.14	0.62	1.76	
Vitamin C (mg/100mg)	3.14	1629.12**	3.98	1.15	3.28	
Chlorophyll content (mg/g)	0.00	0.17**	0.01	0.02	0.08	

Phenotypic expression of any traits largely depends on genotype of the plant and influence environmental variation but generally, higher environmental influence suppresses the complete expression of genes. Phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all the characters studied (Table 2). In the present investigation, high estimates of GCV and PCV values were observed for node at which first male flower appears (22.84% and 24.36%), node at which first female flower appears (25.81% and 26.37%), sex ratio (26.28% and 27.02%), number of fruits per vine (29.99% and 30.85%), fruit weight (48.97% and 49.23%), fruit length (21.52% and 22.43%), fruit width (27.53% and 28.44%), rind thickness (37.37% and 37.91%), flesh thickness (23.87% and 24.21%), fruit yield per vine (25.66% and 28.65%), fruit yield per plot (24.39% and 26.36%) and vitamin C content (23.66% and 23.74%). The similar results were also observed by Srikanth *et al.* (2017) ^[8] for number of branches per vine, sex ratio, number of fruits per vine,

Table 2: Estimates of mean, range, genetic components of variance, heritability and genetic advance for different parameters in bitter gourd

Characters	Mean ± S. Em	Range	GCV (%)	PCV (%)	h ² (%)	GA	GAM (%)
Vine length (m)	2.37 ± 0.11	1.86 - 3.23	18.34	20.03	83.87	0.82	34.60
Number of branches per vine	6.41 ± 0.26	4.73 - 9.43	15.89	17.36	83.79	1.92	29.97
Internodal length (cm)	7.47 ± 0.24	4.67 - 9.97	17.12	18.10	90.50	2.51	33.56
Node at which first male flower appears	9.82 ± 0.48	5.67 - 13.47	22.84	24.36	88.00	4.34	44.13
Node at which first female flower appears	14.08 ± 0.44	8.00 - 21.07	25.81	26.37	95.80	7.33	52.04
Days to first male flower	29.28 ± 1.06	22.60 - 36.20	14.73	16.00	84.80	8.18	27.94
Days to first female flower	36.08 ± 1.13	28.00 - 44.00	12.19	13.34	83.50	8.28	22.95
Sex ratio	7.92 ± 0.29	4.41 - 12.80	26.28	27.02	94.60	4.17	52.64
Number of fruits per vine	16.69 ± 0.70	9.28 - 25.21	29.99	30.85	94.50	10.03	60.04
Fruit weight (g)	64.84 ± 1.87	35.55 - 167.93	48.97	49.23	99.00	65.08	100.36
Fruit length (cm)	16.87 ± 0.61	11.17 - 26.17	21.52	22.43	92.10	7.18	42.54
Fruit width (mm)	35.33 ± 1.45	9.88 - 53.90	27.53	28.44	93.70	19.40	54.91
Rind thickness (mm)	7.80 ± 0.29	4.07 - 18.41	37.37	37.91	97.20	5.92	75.89
Flesh thickness (mm)	24.24 ± 0.56	15.97 - 41.87	23.87	24.21	97.24	11.75	48.49
Fruit yield per vine (kg)	1.52 ± 0.11	0.96 - 2.86	25.66	28.65	80.20	0.72	47.36
Fruit yield per plot (kg)	10.68 ± 0.62	6.92 - 18.89	24.39	26.36	85.60	4.96	46.47
Vitamin C (mg/100g)	98.39 ± 1.15	62.08 - 145.08	23.66	23.74	99.30	47.77	48.55
Chlorophyll content (mg/g)	1.93 ± 0.03	1.52 - 2.36	12.15	12.44	95.50	0.47	24.46

fruit weight. Khan *et al.* (2015) ^[3] for branch per vine, vine length, days to first male and female flower. Rani *et al.* (2015) ^[5] for fruit yield per vine. High GCV and PCV values with

narrow differences is an indication of existence of broad genetic base among the population, suggesting stable expression of genotypes for these traits which provides scope for the improvement of these characters through simple selection.

Moderate GCV and PCV were observed for number of branches per vine (15.89% and 17.36%), internodal length (17.12% and 18.10%), days to first appearance of male flower (14.73% and 16.00%), days to first female flower (12.19% and 13.34%) and chlorophyll content (12.15% and 12.44%), which indicates presence of moderate amount of variability for these traits and little influence of environment on these traits. These observations are in line with the findings of Srikanth *et al.* (2017) ^[8] for vine length, fruit length and yield per vine, Khan *et al.* (2015) ^[5] number of laterals per vine, number of fruits per vine, average fruit weight and fruit length.

Vine length recorded moderate GCV (18.34%) and high PCV (20.03%), which indicates the considerable amount of genetic variability and less influence of non-genetic factors. The results obtained are in conformity with the findings of Devmore *et al.* (2010) ^[2] for vine length, days to fruit development, 100 seed weight and fruit yield per vine.

High heritability coupled with high genetic advance as per cent mean was observed for vine length (83.87% and 34.60%), number of branches per vine (83.79% and 29.97%), internodal length (90.50% and 33.56%), node at which first male appear (88.00% and 44.13%), node at which first female appear (95.80% and 52.04%), days to first male flower (84.80% and 27.94%), days to first female flower (83.50% and 22.95%), sex ratio (94.60% and 52.64%), number of fruits per vine (94.50% and 60.04%), fruit weight (99.00% and 100.36%), fruit length (92.10% and 42.54%), fruit width (93.70% and 54.91%), rind thickness (97.20% and 75.89%), flesh thickness (97.24% and 48.49%), fruit yield per vine (80.20% and 47.36%), fruit yield per plot (85.60% and 46.47%), vitamin C (99.30% and 48.55%) and chlorophyll content (95.50% and 24.46%) which indicates the prevalence of additive gene actions and lesser influence of environment in the expression of these traits, hence these characters are amenable for selection. The similar results were also observed by Rani *et al.* (2015)^[5] for vine length, number of laterals per vine, number of fruits per vine, fruit length and yield per vine, Singh et al. (2014)^[7] for number of branches per vine, fruit weight and fruit width and Rathod (2007)^[6] for vine length, days to first female flower and number of fruits per vine in bitter gourd.

Conclusion

In the present investigation, high GCV and PCV for the characters *viz.*, node at which first male flower appear, node at which first female flower appear, sex ratio, number of fruits per vine, fruit weight, fruit length, fruit width, rind thickness, flesh thickness, fruit yield per vine, fruit yield per plot and vitamin C. Hence, these attributes can be improved through direct selection from the existing genotypes, as these characters have high degree of additive components of genetic variance.

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