

Original Research Article

<https://doi.org/10.20546/ijcmas.2018.703.210>

## Studies on Genetic Variability, Heritability and Genetic Advance in Bitter Gourd (*Momordica charantia* L.) for Yield and Yield Contributing Traits

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### ABSTRACT

Little information is available regarding genetic control and inheritance of economically important traits in bitter gourd (*Momordica charantia* L.). Previous genetic studies of this crop used a narrow range of germplasm and in different environmental conditions. Thirty one genotypes of bitter gourd were accessed concerning the variability, heritability and genetic advance for 12 quantitative traits. Analysis of variance showed significant differences among the genotypes for all the characters. The estimates of phenotypic coefficient of variation (PCV) were higher than corresponding genotypic coefficient of variation (GCV) which indicated that variation is not only due to genotypes, but, also due to the influence of environment. High PCV and GCV values were obtained for average fruit weight, fruit yield per plant, vine length and fruit length which suggest the presence of substantial variability for the traits thereby ensuring ample scope for improvement of these characters through selection. High heritability in broad sense coupled with high genetic advance as percent of mean was observed for fruit length (cm), number of nodes per vine, fruit diameter (cm), node number to anthesis of first staminate flower, fruit yield per plant, average fruit weight (g) indicating such characters were controlled by additive gene action. Selection on the basis of these characters could be more effective for the improvement of bitter gourd.

#### Keywords

*Momordica charantia* L., Variability, Heritability, Genetic advance

#### Article Info

##### Accepted:

16 February 2018

##### Available Online:

10 March 2018

### Introduction

Bitter gourd (*Momordica charantia* L.) is an important cucurbitaceous crop due to its potential to return profit, nutritional value, and production potential. It is also known as bitter melon, bitter gourd, bitter cucumber, bitter squash, balsam pear, karela, cassilla and maiden apple (Morton, 1967). It is adapted to a wide range of environments and can be grown tropical and sub tropical climate (Lim, 1998). The center of origin of this crop is

India, with a secondary center of diversity in China and South East Asia (Grubben, 1977). It is highly cross-pollinated and monoecious in nature, with separate yellow male and female flowers, and exhibits large variations for fruit and vegetative characters (Resmi and Sreelathakumary, 2012). It is a common cucurbit of wild flora of tropical Africa which offers great resources for breeding of cultivated bitter gourd for desirable qualitative traits, tolerance to biotic and abiotic factors etc. Fruits contain a reasonable amount of

different nutrients such as proteins, carbohydrates, fats, minerals and vitamins (A, B<sub>2</sub>, and C) (Raja *et al.*, 1984). It contains considerable amount of water (83-92%), carbohydrates (4.0-10.5%), protein (1.5-2.0%), fat (0.2-1.0%), minerals (0.5-1.0%) and fiber (0.8-1.7 %).

In India, *Momordica charantia* have relatively broad phenotypic species variation (i.e., sex expression, growth habit, maturity, and fruit shape, size, colour and surface texture (Behera *et al.*, 2006). Estimates of heritability have to be considered with conjunction with genetic advance and change in mean value among successive generation, alone it do not provide idea about expected gain in next generation (Shukla *et al.*, 2006). For a successful planning of breeding improvement program, the analysis of variability among the traits and their association of a particular character in relation to yield and yield attributing traits it would be great importance (Mary and Gopalan, 2006).

It also gives an estimate of genetic advance a breeder can expect from selection applied to a population and help in deciding on what breeding method to choose (Idahosa *et al.*, 2010). High heritability and high genetic advance for a given trait indicates that it is governed by additive gene action and, therefore, provides the most effective condition for selection (Hamdi *et al.*, 2003). It is possible to develop high-yielding open-pollinated varieties, or hybrids, by utilizing existing variability (Islam *et al.*, 2009) and this technique could be used in improvement of bitter gourd. Before aiming at an improvement of yield, it is necessary to have information on genetic variability and heritability, in respect of important characters associated with yield. Therefore, the present study was taken up to obtain information on the range of variability for different important economic traits.

## Materials and Methods

### Experimental site and layout

The experimental material consisted of thirty one genotypes including two check varieties (Pusa Vishes and Pusa Do Mausami), conducted during spring summer season of 2015 at the Main Experiment Station, Department of Vegetable Science, Narendra Deva University of Agriculture and Technology, Kumarganj, Faizabad, Uttar Pradesh, India. The experiment was laid out in RBD (Randomized Block Design) with three replications in individual plot size (3m × 2m). The distance maintained between row to row and plant to plant was 2m and 0.50 m, respectively. All recommended agronomic practices for the region were adopted to raise a healthy crop. Five plants were selected randomly from each plot to record observations on 12 characters. Data were recorded on various parameters, *viz.* node number to anthesis of first staminate flower, node number to anthesis of first pistillate flower, days to anthesis of first staminate flower, days to anthesis of first pistillate flower, days to first fruit harvest, vine length (m), number of nodes per vine, fruit length (cm), fruit diameter (cm), average fruit weight (g), number of fruits per plant and fruit yield per plant (kg).

### Statistical analysis

The analysis of variance for the design of experiment (RBD) was carried out according to the procedure outlined by Panse and Sukhatme (1967).

### Estimation of components of variances

#### Phenotypic variance ( $\sigma_P^2$ )

The phenotypic variance was calculated by following formula as suggested by Burton and

de Vane (1953). Phenotypic variance ( $\sigma_p^2$ ) =  $\sigma_g^2 + \sigma_e^2$

Where,

$\sigma_g^2$  = Genotypic variance  
 $\sigma_e^2$  = Error variance

### Genotypic variance ( $\sigma_g^2$ )

The mean squares due to errors were subtracted from the mean square due to genotypes and their difference was divided by replications for obtaining the genotypic variance, which was calculated according to the method suggested by Burton and de Vane (1953).

$$\text{Genotypic variance } (\sigma_g^2) = \frac{\text{MSg} - \text{MSe}}{r}$$

Where,

MSg = genotype mean square

MSe = error mean square

r = number of replications

### Estimation of genotypic and phenotypic coefficient of variation

The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were computed following Burton and de Vane (1953).

$$\text{GCV} = \frac{\text{Genotypic standard deviation}}{\text{Mean } (\bar{X})} \times 100$$

$$\text{PCV} = \frac{\text{Phenotypic standard deviation}}{\text{Mean } (\bar{X})} \times 100$$

### Estimation of heritability

Heritability in broad sense ( $h_{bs}^2$ ) was calculated using the formula suggested by Burton and de Vane (1953).

$$h_{(bs)}^2 = \frac{\sigma_g^2}{\sigma_g^2 + \sigma_e^2} \text{ or } \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Where,

$h_{bs}^2$  = Heritability in broad sense

$\sigma_g^2$  = Genotypic variance

$\sigma_p^2$  = Phenotypic variance

### Estimation of genetic advance

The expected genetic advance for different characters under selection was estimated using the formula suggested Johnson *et al.*, (1955).

$$\text{G.A.} = \frac{\sigma_g^2}{\sigma_{ph}^2} \cdot K \cdot \sigma_p$$

Or

$$\text{G.A.} = K \cdot h^2 \cdot \sigma_p$$

Where,

K = Selection intensity, the value which is 2.06 at 5% selection intensity

$h^2$  = Heritability in broad sense

$\sigma_g^2$  = Genotypic variance

$\sigma_{ph}^2$  = Phenotypic variance

### Estimation of genetic advance as percentage of mean

Genetic gain expressed as per cent ratio of genetic advance of population mean was

calculated by the method given by Johnson *et al.*, (1955).

$$\text{G.A. (\%)} = \frac{\text{Genetic advance}}{\bar{X}} \times 100$$

## Results and Discussion

### Analysis of variance

Analysis of variance for 12 characters (Table 1) of bitter gourd revealed that mean squares due to genotypes were highly significant for all traits under study, thereby suggesting existence of great amount of variation among the genotypes.

So, there is a scope for considerable improvement in the crop through the characters studies such as node number to anthesis of first staminate flower, node number to anthesis of first pistillate flower, days to anthesis of first staminate flower, days to anthesis of first pistillate flower, days to first fruit harvest, vine length (m), number of nodes per vine, fruit length (cm), fruit diameter (cm), average fruit weight (g), number of fruits per plant and fruit yield per plant (kg). Similar to the present findings, significant differences for various characters was reported by Islam *et al.*, (2009), Gupta *et al.*, (2013), Yadav *et al.*, (2013), Pathak *et al.*, (2014) and Singh *et al.*, (2017) in bitter gourd.

### Genotypic and phenotypic co-efficient of variation

The coefficient of genotypic and phenotypic variability is helpful to measure the extent of variability present in particular trait. They also provide a measure to compare the variability present among various quantitative traits. The estimates of coefficient of variability revealed that in general magnitude of phenotypic coefficient of variation for all the traits were

higher than the magnitude of genotypic coefficient of variation (Table 2). The estimates of phenotypic as well as genotypic coefficient of variation were observed higher for average fruit weight (28.70%) followed by fruit yield per plant (23.10%), vine length (22.56%) and fruit length (21.80%) whereas, node number to anthesis of first staminate flower, number of fruits per plant, node number to anthesis of first pistillate flower, number of nodes per vine and fruit diameter showed moderate coefficient of variability while, days to anthesis of first staminate flower, days anthesis of first pistillate flower and days to first fruit harvest showed the lowest coefficients of variation. Narayan *et al.*, (2006), Raja *et al.*, (2007), Yadav *et al.*, (2013), Pathak *et al.*, (2014), Singh *et al.*, (2017) and Yadagiri *et al.*, (2017) in bitter gourd reported similar trend of variation for genotypic coefficient of variation and phenotypic coefficient of variation of various characters studied which is in conformity with the present findings.

### Heritability and genetic advance as per cent of mean

High heritability accompanied by high genetic advance is more useful than heritability alone and considerable importance could be made in these characters by predicting the result and selecting the best individual (Johnson *et al.*, 1955). Estimates of heritability in broad sense ( $h^2_{bs}$ ) and genetic advance as per cent of mean for twelve characters in bitter gourd genotypes are shown in Table 2.

The estimates of heritability in broad sense ( $h^2_{bs}$ ) ranged from 31.21 percent (vine length) to 92.41 per cent (fruit length). Highest estimates of heritability were observed for all the characters fruit length (92.14), number of nodes per vine (89.27), fruit diameter (82.30), node number to anthesis of first staminate flower (76.3), fruit yield per plant (72.67).

**Table.1** Analysis of variance for twelve metric traits in bitter gourd

Characters	Source of variation		
	Replications	Treatments	Error
d.f.	(2)	(30)	(60)
Node number to anthesis of first staminate flower	1.623	8.663**	0.812
Node number to anthesis of first pistillate flower	2.236	10.265**	1.758
Days to anthesis of first staminate flower	8.301	56.399**	14.345
Days to anthesis of first pistillate flower	2.032	61.777**	17.887
Days to first fruit harvest	3.333	65.277**	21.368
Number of nodes per vine	13.752	183.068**	7.052
Vine length (m)	0.032	0.861**	0.027
Fruit length (cm)	1.898	33.029**	0.879
Fruit diameter (cm)	0.142	0.686**	0.045
Number of fruits per plant	1.306	44.388**	10.930
Average fruit weight (g)	0.558	1533.561**	172.610
Fruit yield per plant (kg)	0.004	0.457**	0.050

\*\* significant at P<0.01 level

**Table.2** Estimates of genetic parameters of twelve characters of bitter gourd genotypes

Characters	Range	*PCV (%)	*GCV (%)	Heritability broad sense ( $h^2_{bs}$ ) (%)	Genetic advance	Genetic Advance in per cent of mean
Node number to anthesis of first staminate flower	6.33-13.00	20.17	17.61	76.3	2.91	31.70
Node number to anthesis of first pistillate flower	9.66-16.33	16.89	13.27	61.72	2.72	21.47
Days to anthesis of first staminate flower	35.00-50.66	12.91	9.07	49.24	5.42	13.14
Days to anthesis of first pistillate flower	40.66-60.66	12.24	8.21	44.99	5.28	11.34
Days to first fruit harvest	53.33-76.00	9.93	6.33	40.65	5.02	8.31
Number of nodes per vine	37.00-67.66	15.50	14.65	89.27	14.90	28.51
Vine length (m)	1.60-3.60	22.56	21.55	31.21	1.03	42.39
Fruit length (cm)	8.10-20.80	21.80	20.95	92.41	6.48	41.50
Fruit diameter (cm)	2.36-4.06	14.73	13.36	82.30	0.86	24.97
Number of fruits per plant	17.96-33.80	19.36	13.76	50.50	4.88	20.14
Average fruit weight (g)	42.43-129.46	28.70	24.42	72.44	37.34	42.82
Fruit yield per plant (kg)	0.85-2.61	23.10	19.69	72.67	0.64	34.58

\*GCV = Genotypic coefficient of variation; \*PCV = Phenotypic coefficient of variation



However, node number to anthesis of first staminate flower (61.72%) and number of fruit per plant (50.50%) which indicated moderate heritability, while days to anthesis of first staminate flower (49.24%), days to anthesis of first pistillate flower (44.99%), days to first fruit harvest (40.65%) and vine length (31.21%) indicated lower heritability. Results obtained here in agreement with the findings of Islam *et al.*, (2009), Dalamu and Behera (2013), Chakraborty *et al.*, (2013), Pathak *et al.*, (2014) and Yadagiri *et al.*, (2017). Highest estimates of genetic advance in per cent of mean was recorded for average fruit weight (42.82%), vine length (42.39) fruit length (41.50%), fruit yield per plant (34.58%), node number to anthesis of first staminate flower (31.70%), while number of nodes per vine (28.51%), fruit diameter (24.97%), node number to anthesis of first pistillate flower (21.47%), and number of fruits per plant (20.14%) showed moderate genetic advance in per cent of mean, whereas, days to anthesis of first staminate flower (13.14%), days to anthesis of first pistillate flower (11.34%), and days to first fruit harvest (8.31%) recorded the lower genetic advance in per cent of mean.

Fruit length (cm), number of nodes per vine, fruit diameter (cm), node number to anthesis of first staminate flower, average fruit weight (g) and fruit yield per plant (kg) had high estimates of heritability coupled with high genetic advance as percent of mean. Hence, these characters need to be given more emphasis in selection as these are expected to be controlled by additive genes.

The breeder should adopt suitable breeding methodology to utilize both additive and non-additive gene effects simultaneously, since varietal and hybrid development will go a long way in the breeding programmes especially in case of bitter melon. Similar kind of results in bitter melon was also reported by

several researchers (Raja *et al.*, 2007, Chakraborty *et al.*, 2013; Gupta *et al.*, 2013; Pathak *et al.*, 2014 and Yadagiri *et al.*, 2017).

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#### How to cite this article:

Nidhi Tyagi, V.B. Singh and Praveen Kumar Maurya. 2018. Studies on Genetic Variability, Heritability and Genetic Advance in Bitter Gourd (*Momordica charantia* L.) for Yield and Yield Contributing Traits. *Int.J.Curr.Microbiol.App.Sci*. 7(03): 1788-1794.

doi: <https://doi.org/10.20546/ijcmas.2018.703.210>