DOI : 10.5958/0974-0112.2020.00107.3

Indian J. Hort. 77(4), December 2020: 736-739

Short communication

Diversity and variability for yield and horticultural traits in bitter gourd

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ABSTRACT

Genetic divergence alongwith variability parameters of sixteen horticultural traits were studied in eighteen bitter gourd genotypes. High heritability coupled with high genetic advance as percent of mean was observed for fruit yield per vine, average fruit weight, total soluble solids, number of fruits per vine, vine length and fruit length suggesting early generation improvement for these traits. The multivariate analysis also reflected considerable genetic diversity in the genotypes studied and were grouped in five clusters with maximum number of genotypes in cluster I. Ascorbic acid content contributed maximum towards total genetic divergence followed by total soluble solids and fruit yield per vine. Hence, the traits namely ascorbic acid, total soluble solids, fruit yield per vine, vine length, number of fruits per vine and fruit length will enable better selection outcomes in the form of superior genotypes in bitter gourd.

Key words: *Momordica charantia*, genetic variability, genetic divergence.

Bitter gourd (*Momordica charantia* L.), a member of the Cucurbitaceae family, is known as bitter melon, balsam pear and karela. The crop is native to South Asia and is extensively grown in China, Japan, South East Asia, Africa and South America. In India the area under bitter gourd is 99,000 hectares with the production of 11,98,000 MT (Anonymous, 1). Bitter gourd is rich in ascorbic acid and iron content. The bitter principle in bitter gourd is cucurbitacin, a glucoside which prevents the spoilage of cooked vegetable and keeps it fit for consumption even for two to three days. It is also used for reduction of blood sugar levels in the treatment of diabetes (Singh *et al.*, 6). In bitter gourd, wide variability in respect of vegetative and fruit characters is seen in India than in Africa / South East Asia region. Many varieties/hybrids have been developed utilizing this variability. Eastern and north eastern India being an important center of diversity of bitter gourd provides great range of variation for its genetic improvement. It is possible to develop high-yielding open-pollinated varieties, or hybrids, by utilizing existing variability and this technique could be used in improvement of bitter gourd.

Keeping in view of the above context, this experiment was conducted at the Vegetable Science Research Farm, Bihar Agricultural University, Sabour (Bhagalpur), Bihar during summer-2018. The experiment comprised of 17 genotypes (Pusa Ausadhi, Konkan Tara, Pusa Rasdar and 14 improved lines developed through hybridization followed by selection of BAU, Sabour) of bitter gourd with one check (Palee from East West Seed Company Ltd.) sown in a randomized block design with two replications. All the genotypes along with one check planted with spacing 75 cm × 60 cm × 90 cm, in a double row planting fashion on raised bed (Zig-Zag). The Observations were recorded for fourteen quantitative and two biochemical traits namely germination percentage (%), node to first male flower, days to first male flower, node to first female flower, days to first female flower, days to first fruit harvest, fruit length (cm), fruit girth (cm), flesh thickness (cm), number of primary branches, vine length (cm), average fruit weight (g), number of fruits per vine, fruit yield per vine (Kg), total soluble solids (^{0} Brix) and ascorbic acid (mg/100g) . The analysis of variance for the design of experiment (RBD) was carried out according to the set statistical procedures. The genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and heritability in broad sense (h^2bs) were computed following the methodology given by Burton and deVane (2). Genetic advance (G.A.) as percent of mean was estimated by the method suggested by Johnson *et al.* (3). Genetic divergence was chalked out by Mahalanobis (4) D^2 statistics.

In the present study, the analysis of variance showed significant and good amount of variability present among the genotypes for all the characters studied except germination percentage. GCV in numerical terms was lesser than the PCV for all the traits studied (Table 1) reflecting the influence of environment; hence one has to be more cautious

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while selecting the elite lines for these traits on the basis of GCV alone (Talukder *et al*., 8). High magnitude of GCV and PCV were noticed for fruit yield per plant, average fruit weight, total soluble solids, number of fruits per plant, vine length and fruit length (Table 1) indicating promising nature of these traits for effective selection. Moderate GCV and PCV were noticed for fruit girth and node to first male flower. These moderate results suggested for the selection of these traits with special caution. The similar kinds of results were also reported by earlier researchers namely Yadagiri *et al*. (10) and Tyagi *et al*. (9). Low GCV and PCV were recorded for germination percentage and node to first female flower which indicates low variability for these traits. Earlier researchers also reported low GCV and PCV for different traits in their study (Singh *et al.,* 6).

The magnitude of heritability in broad sense is an important tool for revealing the potential of a trait on the basis of phenotypic expression. High heritability estimates were recorded for all almost all the traits suggested the lesser role of environment and influential role of genetic component of variation. But the heritability estimates alone are not enough to provide effective improvement in the genetic material because high genetic advance does not bring high expected genetic advance always. That is why; both the parameters are useful in predicting the improvement. High heritability coupled with high genetic advance as per cent of mean was recorded for fruit yield per plant followed by average fruit weight, total soluble solids, number of fruits per plant, vine length, fruit length, ascorbic acid, fruit girth, node to first male flower and number of primary branches (Table 1). These results indicate that these characters were controlled by additive gene effects and phenotypic selection for these characters is likely to be effective. The previous researchers also found high heritability coupled with high genetic advance as per cent of mean for most of the traits under study (Yadagiri *et al*., 10 and Tyagi *et al*., 9). High heritability coupled with moderate genetic advance as per cent of mean was noticed for days to first female flower, days to first male flower, days to first harvest, node to first female flower and flesh thickness (Table 1). The breeder should adopt efficient 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 gourd.

In D^2 analysis all the eighteen genotypes were grouped into five clusters. Out of the five clusters, cluster I showed maximum number of genotypes (8) followed by cluster II (3) and V (3) (Table 2). The remaining clusters namely III and IV were bi-genotypic.

Table 1. Range, grand mean and parameters of genetic variability for yield and horticultural traits in bitter gourd genotypes.

Traits	Range	Population mean	PCV (%)	GCV (%)	GA (% of mean)	H^2_{bs}(%)
Germination percentage (%)	62.22 - 86.16	75.99	9.91	5.51	6.32	30.94
Node to first male flower	6.13 - 10.13	7.91	14.00	12.17	21.77	75.46
Days to first male flower	37.5 - 52.63	42.39	11.56	9.64	16.56	69.55
Node to first female flower	11.5 - 15.25	13.48	9.57	8.16	14.34	72.73
Days to first female flower	39.75 - 56.13	45.49	10.99	9.61	17.33	76.58
Days to first fruit harvest	47.67 – 68.00	55.8	12.02	9.71	16.15	65.21
Fruit length (cm)	8.48 - 19.96	14.29	22.14	20.69	39.81	87.27
Fruit girth (cm)	8.43 - 13.50	10.69	16.60	13.55	22.79	66.64
Flesh thickness (cm)	0.47 - 0.65	0.53	11.97	8.56	12.60	51.13
Number of primary branches	14.96 - 28.50	21.77	20.27	14.77	22.18	53.12
Vine length (cm)	198.4 - 409.4	290.67	22.25	21.35	42.21	92.07
Average fruit weight (g)	34.32 - 117.43	84.86	31.05	28.58	54.18	84.70
Number of fruits per vine	14.59 - 34.53	26.44	22.66	22.09	44.37	95.05
Total soluble solids (^{0} Brix)	4.00 - 8.85	5.91	23.51	23.06	46.58	96.18
Ascorbic acid (mg / 100g)	74.75 - 115.18	98.03	12.30	11.91	23.73	93.65
Fruit yield per vine (Kg)	1.14 - 3.55	2.20	36.00	33.43	63.95	86.24

Where, PCV and GCV (%) = Phenotypic and genotypic coefficient of variation in percentage, GA (% of mean) = Genetic advance as percent of mean; and H 2bs(%) = Heritability in broad sense (%)

The maximum intra-cluster distance was found in cluster V followed by cluster II and I. Since the intra-cluster distance was less, the chances of attaining best recombinants by hybridization among parents within cluster would be less. Therefore, there is a need to attempt hybridization between genotypes falling under different clusters based on inter-cluster distance. The highest inter-cluster genetic divergence was recorded between clusters IV and V followed by clusters I and clusters IV, clusters III and V and clusters III and V (Table 3). Earlier workers (Singh *et al.,* 5) also reported higher inter cluster genetic divergence in their studies. The wide range of dissimilarity values revealed that the germplasm collection represents a genetically diverse population and presence of adequate amount of genetic diversity among the bitter gourd genotypes used in the study. Hybridisation between the parents from these diverse clusters results in greater heterosis than those between closely related strains.

Cluster means for all the sixteen characters showed considerable variability among the clusters for each of them (Table 4). The present study revealed that the cluster I showed highest mean values for fruit yield per plant, average fruit weight and flesh thickness. Therefore, greater emphasis should be given to cluster I for selecting genotypes as parents to produce new recombination with desired yield characters. Cluster II observed to be superior for germination percentage, fruit length and number of primary branches. Cluster III came out to be superior for node to first male flower, days to first harvest, fruit girth and total soluble solids. Cluster IV observed to be superior for days to first male flower, node to first female flower, days to first female flower

Table 2. Cluster composition of bitter gourd genotypes based on Mahalanobis D^2 values.

Cluster Number	No. of Genotypes	Genotypes
I	8	BRBT 2, BRBT3, BRBT 4, BRBT 6, BRBT 10, BRBT 13, BRBT 14, Pusa Aushadhi
II	3	BRBT1, BRBT 12, Palee
III	2	BRBT 8, BRBT 9
IV	2	Konkan Tara, Pusa Rasdar
V	3	BRBT 5, BRBT 7, BRBT 11

Table 3. Inter and intra-cluster distance among five clusters of bitter gourd genotypes.

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	434.45	759.60	974.25	3394.89	1553.62
Cluster II		469.21	942.66	1587.76	3120.50
Cluster III			179.47	2782.97	3265.26
Cluster IV				307.39	7754.48
Cluster V					954.96

Table 4. Cluster means of five clusters for 16 traits in D^2 analysis.

Traits	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Mean	Max.	Min.
Germination percentage (%)	75.48	79.43	74.19	69.63	79.37	75.62	79.43	69.63
Node to first male flower	7.95	8.42	7.23	7.73	7.85	7.84	8.42	7.23
Days to first male flower	43.28	42.77	39.90	38.13	44.20	41.66	44.20	38.13
Node to first female flower	13.47	12.63	14.48	12.46	14.33	13.47	14.48	12.46
Days to first female flower	46.06	46.42	42.96	41.38	47.49	44.86	47.49	41.38
Days to first fruit harvest	56.42	61.00	50.69	52.71	54.39	55.04	61.00	50.69
Fruit length (cm)	15.04	16.76	14.70	12.49	10.75	13.95	16.76	10.75
Fruit girth (cm)	10.71	11.20	12.88	9.55	9.45	10.76	12.88	9.45
Fruit thickness (cm)	5.56	5.04	5.11	5.52	5.04	5.25	5.56	5.04
Number of primary branches	21.23	24.55	24.50	17.33	21.57	21.84	24.55	17.33
Vine length (cm)	287.92	288.21	281.40	201.21	366.25	284.99	366.25	201.21
Average fruit weight (g)	94.25	86.10	89.67	56.36	74.38	80.15	94.25	56.36
Number of fruits per vine	28.46	27.86	16.31	31.66	22.93	25.44	31.66	16.31
Fruit yield per vine (Kg)	2.66	2.40	1.49	1.78	1.50	1.97	2.66	1.49
Total soluble solids (^{0} Brix)	5.78	5.22	7.65	6.58	5.33	6.11	7.65	5.22
Ascorbic acid (mg/100g)	101.44	101.10	84.04	81.22	106.45	94.85	106.45	81.22

Where, Max.= maximum mean and Min. = minimum mean and number of fruits per plant. Cluster V observed to be superior for vine length and ascorbic acid (Table 4).

Among the sixteen characters studied, ascorbic acid contributed maximum towards genetic divergence followed by total soluble solids, fruit yield per vine, vine length, average fruit weight and fruit length (Table 5). Sundaram (7) also found similar results for different characters in their study. Ranking of genotypes based on intra-cluster mean performance for these traits which are major contributors of genetic diversity revealed its usefulness in selecting genotypes for heterosis breeding.

With the above studies and findings it can be concluded that the traits namely ascorbic acid, total soluble solids, fruit yield per vine, vine length, average fruit weight and fruit length were the major contributors towards the total genetic divergence and the same traits will also enable better selection outcomes in the form of superior genotypes for future breeding/hybridization programme.

Table 5. Percent contribution of various traits to genetic divergence.

Characters	Times ranked 1st	% Contribution
Germination percentage (%)	0	0
Node to first male flower	0	0
Days to first male flower	0	0
Node to first female flower	0	0
Days to first female flower	0	0
Days to first fruit harvest	0	0
Fruit length (cm)	2	1.30
Fruit girth (cm)	0	0
Flesh thickness (cm)	0	0
Number of primary branches	0	0
Vine length (cm)	3	1.96
Average fruit weight (g)	2	1.31
Number of fruits per vine	0	0
Fruit yield per vine (Kg)	7	4.58*
Total soluble solids (^{0}Brix)	28	18.30*
Ascorbic acid (mg/100 g)	111	72.55*

DECLARATION

The authors declare no conflict of interest.

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(Received : July, 2019; Revised : October, 2020; Accepted : November, 2020)