



Character association and path coefficient analysis of indigenous and exotic bitter gourd (*Momordica charantia*) germplasm

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ABSTRACT

Fifty indigenous and exotic genotypes of bitter gourd (*Momordica charantia* L.) were evaluated for 12 quantitative traits during spring-summer seasons of year 2008–09 and 2009–10, respectively and the pooled data was analysed. The mean, range, phenotypic and genotypic variance, genotypic and phenotypic coefficient of variation, heritability in broad sense and genetic advance were calculated. Path coefficient analysis was carried out using correlation coefficients to know the yield- contributing traits having true associations with yield/plant. Improvement in yield/plant can be achieved by selection using the correlation and path analysis data generated in this study. Ovary length, fruit L: D ratio, fruit weight and number of fruits/plant were positively correlated with yield/plant. Number of fruits/plant, fruit weight, ovary length and fruit L: D ratio also had high phenotypic and genotypic direct effects on yield/plant, revealing that indirect selection for these traits would be effective in improving yield/plant. Higher genotypic coefficient of variance along with high heritability and genetic advance for number of fruits/plant and fruit weight would also be of great use for indirect selection for improvement in yield/plant. The material used in the study is of diverse nature and can be used in the breeding programme for development of improved genotypes in bitter gourd.

Key words: Coefficient of variation, Genetic advance, Heritability, *Momordica charantia*

Bitter gourd (syn bitter melon, balsam pear, *Momordica charantia* L.) is a tropical and subtropical vine of the family Cucurbitaceae. It is widely grown in Asia, especially in China, India and Southeast Asia. It is an important vegetable crop grown for edible fruits, both in rainy and spring-summer seasons in India. Bitter gourd demonstrates wide diversity especially the fruit morphology varies greatly in color, size, and exocarp characteristics. The center of bitter gourd domestication likely lies in eastern Asia, possibly eastern India or southern China. The critical assessment of magnitude of diversity is pre-requisite for any breeding programme for developing superior genotypes with desirable yield and quality traits. Thus, determining genetic diversity through variation between genotypes, genotype groups or populations is most important breeding tool to select better genotypes for improvement in desired traits. An estimate of genetic advance along with heritability is helpful in assessing the reliability of character for selection. Knowledge of the mechanisms underlying the correlations between different traits is fundamental for understanding the degree of integration of the

phenotype and to resolve the constraints imposed on evolutionary processes. Correlation and path co-efficient analysis determines nature and magnitude of association among variables and is the measurement of direct influence of one variable upon the other. All these measures are important for the identification of genetically distant parental combinations, aiming to use distinct gene sets in crossings for getting superior hybrids and segregants, to evaluate the degree of genetic erosion, or even to determine the extent of the genetic base of cultivated forms to develop heterotic groups. Genetic diversity assessments and linkage map construction can increase the effectiveness of breeding programs.

Keeping in view the present study is, therefore, designed to evaluate and characterize exotic accessions and define their relationship with indigenous accessions and to the commercial cultivars of economic importance of bitter gourd.

MATERIALS AND METHODS

The experimental materials comprised fifty indigenous and exotic accessions of bitter gourd, exotic genotypes obtained from Asian Vegetable Research and Development (AVRDC)-World Vegetable Centre, Taiwan and maintained at Division of Vegetable Science, Indian Agricultural Research Institute, New Delhi. The indigenous accessions are two

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from Kerala (DBG 13, DBG 14), twenty one from West Bengal (DBG 18, DBG 33, DBG 34, DBG 35, DBG 36, DBG 37, DBG 38, DBG 39, DBG 40, DBG 41, DBG 42, DBG 43, DBG 44, DBG 45, DBG 46, DBG 47, DBG 48, DBG 49, DBG 50, DBG 51, DBG 52), eight from New Delhi (two gynocious lines, viz. DBGy201 and DBGy 202; six monoecious lines DBG 17, Pusa Do Mausami, Pusa Vishesh, Sel 1, Sel 2, Nakhra Local), nineteen exotic accessions from AVRDC, Taiwan (EC620325, EC620326, EC620329, EC620330, EC620331, EC620332, EC620333, EC620334, EC620335, EC620337, EC620338, EC620344, EC620346, EC620353, EC620354, EC620355, EC620356, EC620357, EC620358).

The experiment was laid out in a randomized complete block design with 3 replications for phenotypic evaluation during spring–summer (dry) seasons of year 2008–2009 and 2009–2010. The recommended dose of fertilizer and agronomic practices were done to raise a successful crop during the spring-summer seasons of both years. Five plants were selected for taking observation after discarding the border plants at both ends and were examined for 12 traits, viz. leaf L: D ratio, internode length, node bearing first female flower, ovary length, fruit L: D ratio, fruit weight, number of fruits/plant, yield/plant, vine length, seed L: D ratio, number of seeds/fruit and 100 seed weight.

Analysis of variance was performed following the standard procedures. The phenotypic and genotypic coefficient of variation were calculated according to Burton and De Vane (1953), heritability, genetic advance, genetic gain and correlation coefficients were calculated according to the formulae of Johnson *et al.* (1955). The path coefficient analysis was done as per Dewey and Lu (1959).

RESULTS AND DISCUSSION

Analysis of variance revealed significant differences for

individual as well as pooled data amongst genotypes for all the twelve traits studied. Variance due to genotype was highly significant for all the twelve traits indicating the presence of sufficient variability in the genotypes selected for this study. High magnitude of variability has been reported in bitter gourd germplasm and varieties for various characters by many workers for vine length, branch number per vine, flowering duration, harvesting span, fruit length, average fruit weight, seed number per fruit, fruit number per vine, dry matter per vine, biological yield per vine and total fruit yield per vine (Bhave *et al.* 2003). The high coefficients of variation was observed for fruit traits like number of fruits per plant, number of seeds per fruit, fruit weight, fruit L: D ratio and ovary length due to heterogeneity existing among the accessions. The high magnitude of variability in the present study may be due the fact that the genotypes were collected from different agroclimatic conditions throughout world and were developed in different breeding programmes. Phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the observed traits indicating that genotypic expression was superimposed by the environmental influence (Table 1).

High PCV and GCV were observed for number of fruits/plant, number of seeds/fruit, fruit weight, fruit L: D ratio and ovary length. Kumar *et al.* (2008) reported high estimates of PCV and GCV for number of fruits/plant and fruit weight in cucumber; Rakhi and Rajamony (2005) for fruit weight and fruits/plant in culinary melons. The estimates of GCV and PCV for all the characters correspond closely which indicated that the variability existing in them was mainly due to their genetic makeup. Thus, selection can be effective on the basis of phenotypic appearance alone. Similar findings were reported by Bhave *et al.* (2003). The results revealed presence of high amount of genetic variability in the evaluated genotypes for the major yield contributing characters which

Table 1 Estimates of different genetic parameters of variation over two seasons (pooled data)

Characters	Mean	Range	PCV	GCV	h ² (%)	Genetic advance	GA as percentage of mean
Leaf L:D ratio	0.80	0.65-0.92	8.64	5.40	39.10	0.06	7.50
Internode length (cm)	4.69	3.05-6.63	18.70	15.03	64.60	1.17	24.94
Node bearing first female flower	15.64	9.20-27.93	28.45	25.91	82.90	7.60	48.59
Ovary length (cm)	1.61	0.60-2.93	31.87	29.19	83.90	0.89	55.28
Fruit L:D ratio	2.43	1.26-5.50	37.57	35.08	87.20	1.64	66.25
Fruit weight (g)	60.79	17.55-129.85	38.67	38.08	97.00	46.96	77.25
Number of fruits/plant	15.85	5.67-48.24	70.55	68.85	95.20	21.94	138.42
Yield/plant (g)	760.43	408.32-1222.51	28.21	21.43	57.70	254.95	33.52
Vine length (cm)	160.60	112.47-262.79	16.21	14.61	81.20	43.55	27.11
Seed L:D ratio	1.50	1.19-1.83	12.76	9.87	59.90	0.24	16.00
Number of seeds/fruit	17.74	4.75-35.37	42.89	41.06	91.60	14.36	80.94
100 seed weight (g)	14.03	7.67-23.00	25.45	21.60	72.10	5.30	37.77

indicated that further improvement for these traits is possible.

Heritability estimate is an informative parameter to the breeder for selecting the varieties for further use. The estimate of heritability was high for fruit weight, number of fruits per plant, number of seeds per fruit, fruit L: D ratio, ovary length, node bearing first female flower and vine length indicating the major role of genotypes in expression of these characters (Table 1). Heritable variation can be found out with greater degree of accuracy when heritability is studied in conjunction with genetic advance. Traits like fruit weight, number of fruits/plant, number of seeds per fruit, node bearing first female flower and vine length recorded high heritability and genetic advance in the present study. Devmore *et al.* (2010) reported similar results for fruit weight, number of seeds/fruit, vine length and fruit number/vine in bitter gourd; Kanwar *et al.* (2003) for node of first female flower in cucumber.

High genetic advance as percentage mean were observed in number of seeds per fruit, fruit weight, fruit L: D ratio, ovary length, node bearing first female flower, 100 seed weight and yield/plant indicating that selection would be effective for the improvement of these traits. Similar findings

related to high genetic advance as per cent of mean have been reported by earlier workers for various traits (Devmore *et al.* 2010, Bhave *et al.* 2003) which support the results of the present investigation.

The correlation coefficient analysis revealed that all the traits were positively correlated with yield per plant at both genotypic and phenotypic levels except internode length and seed L: D ratio (Table 2). Yield/plant was positively correlated with fruit weight, ovary length, number of fruits/plant and fruit L: D ratio indicating that selection for these characters might be useful in increasing the yield/plant in this crop. Similar results were reported by Dey *et al.*, (2005); Sundaram (2010), Sharma and Bhutani (2001), in bitter gourd.

Path analysis helps in partitioning the genotypic correlation coefficients into direct and indirect effects of component characters in yield. Results of path analysis indicated that number of fruits/plant, fruit weight, ovary length and fruit L: D ratio exhibited positive genotypic effects on yield/plant (Table 3). Thus, the correlation coefficient between yield per plant and these four traits is real one, revealing that indirect selection for these traits would be effective in improving yield per plant. Islam *et al.* (2009),

Table 2 Genotypic (G) and phenotypic (P) correlation coefficient among different pairs of traits of bitter gourd genotypes (pooled data)

		X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12
X1	G	0.000											
	P	0.000											
X2	G	-0.042	0.000										
	P	-0.002	0.000										
X3	G	-0.042	-0.252	0.000									
	P	0.029	-0.197	0.000									
X4	G	0.098	0.224	-0.186	0.000								
	P	0.031	0.172	-0.166	0.000								
X5	G	-0.108	0.077	-0.034	0.734**	0.000							
	P	-0.077	0.063	-0.027	0.630**	0.000							
X6	G	0.156	0.200	-0.276	0.749**	0.638**	0.000						
	P	0.103	0.158	-0.248	0.666**	0.577**	0.000						
X7	G	-0.007	-0.347*	0.276	-0.605**	-0.431**	-0.806**	0.000					
	P	0.003	-0.302*	0.235	-0.548**	-0.394**	-0.776**	0.000					
X8	G	0.132	-0.302*	0.087	0.397**	0.325*	0.415**	0.388**	0.000				
	P	0.113	-0.253	0.047	0.334*	0.230	0.322*	0.373**	0.000				
X9	G	0.441**	0.306*	-0.214	0.316*	0.191	0.086	0.014	0.235	0.000			
	P	0.128	0.162	-0.180	0.252	0.174	0.067	0.012	0.156	0.000			
X10	G	0.418**	0.159	-0.143	-0.041	0.022	0.078	-0.094	-0.089	0.076	0.000		
	P	0.222	0.099	-0.112	-0.035	0.005	0.058	-0.061	-0.038	0.054	0.000		
X11	G	0.172	0.135	-0.070	0.361*	0.450**	0.496**	-0.388**	0.183	0.108	0.152	0.000	
	P	0.105	0.110	-0.058	0.314*	0.400**	0.464**	-0.372**	0.096	0.089	0.100	0.000	
X12	G	0.258	0.048	0.057	0.418**	0.280	-0.102	0.107	0.062	0.235	0.124	0.097	0.000
	P	-0.037	0.020	0.055	0.380**	0.176	-0.078	0.083	0.013	0.145	0.114	0.086	0.000

*, ** Significant at 0.05 and 0.01 levels, respectively

X1. Leaf L: D ratio, X2. Internode length (cm), X3. Node bearing first female flower, X4. Ovary length (cm), X5. Fruit L: D ratio, X6. Fruit weight (g), X7. Number of fruits/plant, X8. Yield/plant (g), X9. Vine length (cm), X10. Seed L: D ratio, X11. Number of seeds/fruit, X12. 100 seed weight (g)

Table 3 Genotypic path coefficient among different traits of bitter gourd genotypes (pooled data)

Characters	Leaf L: D ratio	Internode length	Node bearing first female flower	Ovary length	Fruit L: D ratio	Fruit weight	Number of fruits/plant	Vine length	Seed L: D ratio	Number of seeds/fruit	100 seed weight	Correlation with yield/plant
Leaf L: D ratio.	0.048	0.004	0.003	0.027	-0.027	0.065	0.003	0.109	-0.025	0.032	0.004	0.132
Internode length	-0.002	-0.088	0.016	0.063	0.019	0.100	-0.364	0.097	-0.009	0.025	-0.003	-0.092
Node bearing first female flower	-0.002	0.022	-0.062	-0.052	-0.008	-0.157	0.245	0.052	0.008	-0.013	-0.004	0.087
Ovary length	0.005	-0.020	0.012	0.279	0.182	0.421	-0.570	0.024	0.002	0.067	-0.008	0.197
Fruit L: D ratio	-0.005	-0.007	0.002	0.205	0.248	0.364	-0.430	0.015	-0.001	0.084	-0.005	0.325
Fruit weight	0.007	-0.018	0.017	0.209	0.158	0.632	-0.807	0.007	-0.005	0.093	0.007	0.015
Number of fruits/plant	0.000	0.017	-0.017	-0.169	-0.107	-0.490	1.040	0.001	0.006	-0.072	-0.007	0.373
Vine length	0.012	-0.018	-0.013	0.083	0.047	0.042	0.015	0.180	-0.005	0.020	-0.015	0.235
Seed L: D ratio	0.020	-0.014	0.009	-0.010	0.005	0.037	-0.093	0.006	-0.059	0.028	-0.008	-0.089
Number of seeds/fruit	0.008	-0.012	0.004	0.101	0.112	0.293	-0.387	0.009	-0.009	0.187	0.000	0.183
100 seed weight	-0.003	-0.004	-0.004	0.033	0.020	-0.049	0.087	0.019	-0.007	0.001	-0.064	0.062

Sundaram (2010), Sharma and Bhutani (2001) also revealed maximum direct contribution of number of fruits per plant in bitter gourd. Thus, the diverse genetic material of the present study can be used in the future breeding programme for improvement of bitter gourd yield.

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