Agriculture and Natural Resources 50 (2016) 483–489

Contents lists available at ScienceDirect

Agriculture and Natural Resources

journal homepage: http://www.journals.elsevier.com/agriculture-and-natural-resources/

Original Article

Variability, heritability, character association, path analysis and morphological diversity in snake gourd

A.S.M. Mahbubur Rahman Khan,[a] Rabeya Eyasmin,[b] M. Harunur Rashid,[a, c, *] Sheikh Ishtiaque,[a] Apurbo Kumar Chaki[a]

[a] *Bangladesh Agricultural Research Institute (BARI), Joydebpur, Gazipur 1701, Bangladesh*
[b] *Department of Biotechnology, Bangladesh Agricultural University, Mymensingh 2202, Bangladesh*
[c] *Department of Plant Science, University of Manitoba, Winnipeg MB R3T 2N2, Canada*

ARTICLE INFO

Article history:
Received 12 February 2016
Accepted 15 July 2016
Available online 3 January 2017

Keywords:
Correlation
Genetic diversity
Heritability
Path analysis
Thrichosamthes anguina

ABSTRACT

Genetic variability, heritability and path coefficient analysis were studied in 21 genotypes of snake gourd. The phenotypic coefficient of variations was found slightly higher than the genotypic coefficient of variations for all characters studied, indicating that the apparent variation is not only genetic but also influenced by the growing environment in the expression of the traits. The genotypic coefficient of variation was high for the fruit yield, number of fruits per vine, length of fruit and single fruit weight. High heritability coupled with high-to-moderate genetic advance was estimated for all characters studied. Correlation studies revealed that the fruit yield had a significant, positive correlation with the number of fruits per vine, length of fruit and single fruit weight. Importantly, more than 90% of the genotypic total variation was contributed by the characters included in the path analysis. The highest, direct, positive effect was recorded for the number of fruits per vine. The divergence value for cluster analysis indicated that the genotypes from clusters II and III had the highest inter-cluster distance and were expected to provide high heterosis in hybridization and to show wide variability in genetic architecture. The selection of high yielding genotypes should give emphasis to the number of fruits per vine, length of fruit and single fruit weight.

Introduction

Snake gourd (*Thrichosamthes anguina* L.) is a cultivated species of the genus *Trichosanthes* in the family Cucurbitaceae and while its center of origin is not precisely known, most authors agree that India or the Indo-Malayan region is its original home (Choudhury, 1967; Seshadri, 1986; Roy et al., 1991). Currently, it is grown throughout tropical or subtropical regions (Ahmed et al., 2000). In spite of its diverse germplasm, the average productivity of the crop is low (Khatun et al., 2010) due to the cultivation of local cultivars. The diverse morphological characters of *T. anguina* in Bangladesh provide relatively broad phenotypic species variation (Ahsan et al., 2014; Rabbani et al., 2012; Ahmed et al., 2000), indicating great scope for genetic improvement as well as for increasing the productivity of the crop through varietal improvement.

For developing a superior variety, it is essential to improve the yield components; however, yield is a complex character and is associated with many other contributing traits which are simply inherited (Rao et al., 1990). The assessment of existing genetic variability in any crop species is essential for formulating effective breeding strategies as the existing variability can be used to enhance the yield level of the cultivars (Patil et al., 2012; Belaj et al., 2002). The information on heritability alone may not help in identifying characters for enforcing selection; therefore, heritability estimates in conjunction with predicted genetic advance is more reliable (Johnson et al., 1955). Heritability provides information on the magnitude of the inheritance of characters from parent to off spring, while genetic advance is helpful in finding the actual gain expected under selection (Larik et al., 2000; Nwangburuka and Denton, 2012; Ogunniyan and Olakojo, 2015). Correlation and path coefficient analysis provide information about the association between two traits and the partitioning of the relationship into direct and indirect effects showing the relative importance of each of the causal factors (Bhatt, 1973; Diz et al., 1994; Mihretu et al.,

* Corresponding author. Bangladesh Agricultural Research Institute (BARI), Joydebpur, Gazipur 1701, Bangladesh.
E-mail address: rashidhrc@gmail.com (M.H. Rashid).

http://dx.doi.org/10.1016/j.anres.2016.07.005

2014). Characters having a high genotypic coefficient of variation indicate high potential for effective selection (Burton and DeVane, 1953). To the best of the authors' knowledge, no serious attempts have so far been made to upgrade the productivity of snake gourd varieties in Bangladesh. Therefore, the present study was undertaken to find out the genetic variability, genetic advancement, diversity and interrelationships among different characters and the direct and indirect contribution of these characters towards the yield of snake gourd varieties.

Materials and methods

Experimental site

The experiment was conducted at the research farm of the Plant Genetic Resources Centre (PGRC), Bangladesh Agricultural Research Institute (BARI), Gazipur, Bangladesh during February to December, 2011. The experimental site is situated in the subtropical zone and characterized by heavy rainfall during May to September and scant rainfall during the rest of the year (BBS, 2012). The soil in the experimental field was a clay loam in texture with a pH of around 6.0 and poor fertility status. It belongs to the “Shallow red-brown terrace” soil of the Madhupur tract (Haider et al., 1991).

Plant materials

Twenty-one genotypes of snake gourd were used in this study that had been collected by the PGRC during 2010 from different locations in Bangladesh (Table 1).

Experimental design and layout

The experiment was laid out in a randomized complete block design with three replications. Inter- and intra-row spacings were maintained at 2 m × 2 m. There were two pits per replication and two plants per pit on the raised bed; the pits were prepared and left open for 1 wk prior to transplanting.

Seedling raising and transplanting

Seeds of all genotypes were soaked in water for 48 h. The soaked seeds were then sown in polyvinyl pots containing a mixture of soil and well-decomposed cow dung (1:1) in February, 2011. At age 20 d, seedlings were transplanted into the pits of the experimental field in March 2011.

Land and pit preparation

The experimental plots were prepared by ploughing, harrowing and laddering to achieve a desirable tilth. Final land preparation was done 1 wk before the pit preparation. Recommended doses of manure and fertilizers—cow dung, urea, triple super phosphate (TSP), muriate of potash (MP), gypsum, sulfur, zinc oxide and boron at 10,000 kg/ha, 80 kg/ha, 65 kg/ha, 35 kg/ha, 75 kg/ha, 18 kg/ha, 4.50 kg/ha and 1.70 kg/ha, respectively—were applied in the experimental field (Salim and Masud, 2015). All cow dung and half the TSP and MP were applied in the field at the time of land preparation. The remaining TSP and MP and all the gypsum and zinc oxide and one-third of the urea were applied in the pit 1 wk prior to transplantation. The remaining urea was applied as top dressing in two installments at 20 d and 40 d after transplanting.

Table 1
Snake gourd genotypes used in the study.

Accession number	Location	Accession number	Location
TA0001	Comilla	TA0012	Jamalpur
TA0002	Comilla	TA0013	Jamalpur
TA0003	Comilla	TA0014	Faridpur
TA0004	Chandpur	TA0015	Faridpur
TA0005	Chandpur	TA0016	Tangail
TA0006	Chandpur	TA0017	Tangail
TA0007	B. Baria	TA0018	Tangail
TA0008	Comilla	TA0019	Laxmipur
TA0009	Mymensingh	TA0020	Feni
TA0010	Mymensingh	TA0021	Chittagong
TA0011	Mymensingh		

Intercultural operation and plant protection

The soil around the base of each seedling was pulverized after the establishment of seedlings. Necessary intercultural operations were done to ensure normal growth and development of the plants. Bamboo sticks were used to support the growing plants and allowed them to grow along string netting. Irrigation was applied to the plants in pits as and when required. Adult red pumpkin beetle was controlled by hand removal twice daily whereas fruit fly was controlled at the fruiting stage using poison bait. The bait was prepared with 15–20 drops of Nogos 100 EC per 100 g of crushed sweet gourd placed in earthen pots in the field at a distance of 8.0 m between pots and at about 1.0 m height from the ground using split bamboo sticks.

Data analysis

ANOVA analysis of the yield and yield-contributing characters was applied to each quantitative trait using the SAS version 9.2 software (SAS, 2008) and treatment means were tested as significant at the 5% probability level and as highly significant at the 1% probability level (SAS, 2008). The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were estimated according to the method suggested by Burton and DeVane (1953) using Equations (1)–(5):

$$\text{Environmental variance}\left(\sigma^2 e\right) = Ms_e \tag{1}$$

$$\text{Phenotypic variance}\left(\sigma^2 p\right) = \left(\sigma^2 g + \sigma^2 e\right) \tag{2}$$

$$\text{Genotypic variance}\left(\sigma^2 g\right) = (Ms_e - Ms_t)/r \tag{3}$$

where Ms_e is the mean square error, Ms_t is the mean square treatment and r is the number of replications.

$$PCV = \frac{\sqrt{\sigma^2 p}}{\bar{x}} \times 100 \tag{4}$$

$$GCV = \frac{\sqrt{\sigma^2 g}}{\bar{x}} \times 100 \tag{5}$$

where $\sigma^2 p$ is the phenotypic variance, $\sigma^2 g$ is the genotypic variance and $\bar{x}$ is the grand mean of a character.

Estimation of heritability in broad sense: Broad sense heritability (h^2) expressed as the percentage of the ratio of the genotypic variance (g) to the phenotypic variance (p) and was estimated on genotype mean basis as described by Allard (1960) as Equation (6):

$$h^2B = \frac{\sqrt{\sigma^2 g}}{\sigma^2 p} \times 100 \quad (6)$$

where h^2B is the heritability in a broad sense, σ^2p is the phenotypic variance and σ^2g is the genotypic variance.

Genetic Advance (GA) and the percentage of the mean (GAM) assuming selection of the superior 5% of the genotypes was estimated in accordance with the methods illustrated by Johnson et al. (1955) and Equations (7) and (8):

$$GA = \frac{K \times \sqrt{(\sigma^2 p \times \sigma^2 g)}}{\sigma^2 p} \quad (7)$$

where GA is the expected genetic advance, K is the standardized selection differential at 5% selection intensity (K = 2.063), σ^2p is the phenotypic variance and σ^2g is the genotypic variance.

$$GAM(\%) = \frac{GA}{\bar{x}} \times 100 \quad (8)$$

where GAM is the genetic advance as a percentage of the mean, GA is the expected genetic advance and x is the grand mean of a character.

Phenotypic and genotypic correlation coefficients were estimated using the standard procedure suggested by Miller et al. (1958) using the corresponding variance and covariance components as shown in Equations (9) and (10):

$$r_g = \frac{P_{cov} x.y}{\sqrt{\sigma^2 gx.\sigma^2 gy}} \quad (9)$$

and

$$r_p = \frac{G_{cov} x.y}{\sqrt{\sigma^2 px.\sigma^2 py}} \quad (10)$$

where r_p is the phenotypic correlation coefficient, r_g is the genotypic correlation coefficient between the characters x and y, $P_{cov}x.y$ is the phenotypic covariance and $G_{cov}x.y$ is the genotypic covariance between the characters x and y.

Path coefficient analysis was conducted as suggested by Dewey and Lu (1959) using the phenotypic and genotypic correlation coefficients to determine the direct and indirect effects of the yield component on the fruit yield based on Equation (11):

$$r_{ij} = P_{ij} + \sum r_{ik} \times P_{kj} \quad (11)$$

where r_{ij} is the mutual association between the independent trait (i) and the dependent trait (j) as measured by the correlation coefficient, p_{ij} is the component of direct effects of the independent trait (i) on the dependent variable (j) and $r_{ik}p_{kj}$ is the assumption of components of the indirect effect of a given independent trait via all other independent traits.

The residual effect (h) was calculated using the formula from Dewey and Lu (1959) as shown in Equation (12):

$$h = \sqrt{(1 - R^2)} \quad (12)$$

where R^2 is calculated as $\sum r_{ij}p_{ij}$.

Path coefficient analysis was calculated using the GENES software package (Cosme, 2013).

Divergence was estimated using the Mahalanobis generalized distance, (the D^2 statistic) according to Mahalanobis (1936) and as extended by Rao (1952) to clustering using Tocher's method.

However, there are three ways to estimate variability in a given population: 1) using simple measures such as the range, arithmetic mean, standard deviation, standard error and coefficient of variation; 2) estimating the various components of variation such as the GCV and PCV; and 3) studying genetic diversity (Singh, 2000). All three approaches were tried in the present study with the 21 *T. anguina* genotypes.

Results and discussion

Variance components and coefficients of variation

Estimates of variances and their components are given in Table 2. The phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all characters studied, indicating that the apparent variation was not only genetic but also was influenced by the growing environment in the expression of the traits. In general, the quantitative characters were highly influenced by the environment. The GCV values were a bit lower ranging from 7.73% to 49.95% while the PCV values ranged from 7.94% to 50.17% (Table 2). According to Deshmukh et al. (1986), PCV and GCV values greater than 20% are regarded as high, whereas values less

Table 2
Genetic variability and heritability parameters for yield and yield contributing characters of snake gourd.

Character	Range	Mean ± SE	CV[a] (%)	σ^2g[b]	σ^2p[c]	GCV[d] (%)	PCV[e] (%)	h^2 B[f] (%)	GA[g]	GAM[h]
Vine length	0.83–3.82	2.208 ± 0.149	12.04	0.447	0.518	30.29	32.61	86.30	1.280	57.97
Nodes with male flower	14.00–31.00	19.857 ± 0.911	3.66	17.253	17.781	20.92	21.24	97.03	8.428	42.45
Nodes with female flower	17.00–42.00	27.00 ± 1.283	3.74	34.259	35.281	21.68	22.00	97.10	11.882	44.01
Days to male flower	60.00–89.00	72.048 ± 1.688	1.37	58.424	59.396	10.61	10.70	98.36	15.616	21.68
Days to female flower	69.00–91.00	77.619 ± 1.320	1.81	35.990	37.963	7.73	7.94	94.80	12.033	15.50
Fruit length (cm)	18.84–60.08	34.00 ± 2.072	2.02	90.079	90.550	27.91	27.99	99.48	19.501	57.36
Fruit width (cm)	3.33–9.07	6.790 ± 0.269	4.22	1.492	1.574	17.99	18.48	94.79	2.450	36.08
Single fruit weight (g)	87.50–325.00	198.897 ± 13.724	1.04	39.547	39.582	31.61	31.63	99.89	129.464	65.09
Number of fruit/vine	9.00–44.00	19.000 ± 1.884	4.30	74.378	75.044	45.39	45.60	99.11	17.687	93.09
Fruit yield/vine (kg)	1.10–8.36	3.684 ± 0.401	5.33	3.377	3.416	49.88	50.17	98.86	3.764	102.17

[a] Coefficient of variation.
[b] Genotypic variance.
[c] Phenotypic variance.
[d] Genotypic coefficient of variation.
[e] Phenotypic coefficient of variation.
[f] Heritability.
[g] Genetic advance.
[h] Genetic advance as percentage of mean.

than 10% are considered to be low and values between 10 and 20% to be medium. Based on this classification, high GCV and PCV values were observed for the number of fruits per vine (45.39% and 45.60%, respectively), fruit yield per plant (49.88% and 50.17%, respectively), yield per hectare (49.95% and 50.03%, respectively), vine length (30.29% and 32.61%, respectively), length of fruit (27.91% and 27.99%, respectively), single fruit weight (31.61% and 31.63%, respectively), node number with first male flower (20.92% and 21.24%, respectively) and female flower (21.68% and 22.00%, respectively), whereas moderate GCV and PCV values were observed from days to first male flower opening (10.61% and 10.70%, respectively) and width of fruit (17.99% and 18.48, respectively). Therefore, the study of GCV and PCV in snake gourd genotypes exhibited variability for almost all characters (Table 2) indicating the existence of wider genetic variation in Bangladeshi genotypes and these results were strongly supported by previous studies in snake gourd (Varghese and Rajan, 1993; Rahman et al., 2002; Rana and Pandit, 2011; Deepa and Mariappan, 2013; Ahsan et al., 2014). The GCV and PCV for days to first female flower opening (7.73% and 7.94%) were low, which was in agreement with the findings of Miah et al. (2000) and Rahman et al. (2002).

Heritability and genetic advance

Heritability values are helpful in predicting the expected progress to be achieved through the process of selection; high heritability coupled with high genetic advance is an indicator of a greater proportion of the additive genetic variance and consequently a high genetic gain is expected from selection (Singh and Rai, 1981). In the current study, the heritability ranged from 86.30% to 99.89%, while genetic advance as a percentage of the mean showed a wider gain ranging from 15.50% to 102.76% (Table 2). According to Singh (2000), heritability values greater than 80% are very high, values 60–79% are moderately high, values from 40 to 59% are medium and values less than 40% are low. Therefore, the traits under study (Table 2) fall into the high category since heritability >80%. Johnson et al. (1955) classified genetic advance as a percentage of the mean; values 0–10% are low, 10–20% are moderate and 20% and above are high. Based on this measure, the traits under study have high heritability value coupled with high-to-moderate genetic advance as a percentage of the mean (ranging from 15.50% to 102.76%) as shown in Table 2. Johnson et al. (1955) and Panse (1957) suggested that the estimation of heritability and the expected genetic advance should be considered jointly. However, the results from the combination of heritability and genetic advance indicated that the variation is attributable to a high degree of additive effect; therefore, the characters can be improved by selection (Chauhan and Nanda, 1983). The presence of heritability and additive gene action in the present study were supported by the findings reported for various cucurbits (Prasad and Singh, 1989; Sharma and Dhankar, 1990; Saha et al., 1991; Islam et al., 1993; Mathew and Khader, 1999; Miah et al., 2000; Singh et al., 2002; Kutty and Dharmatti, 2004; Rana and Pandit, 2011; Rabbani et al., 2012; Kumar et al., 2013; Deepa and Mariappan, 2013; Ahsan et al., 2014).

Association among characters

The phenotypic and genotypic correlations of yield with yield component characters are indicated in Table 3. Yield is the result of many characters which are interdependent. Breeders always look for genetic variation among traits to select desirable types as some of these characters are highly correlated among themselves and with yield, so that the analysis of the relationship among these characters and their correlation with yield is essential to establish selection criteria (Singh, 2000). Most of the genotypic correlation coefficients were higher than their corresponding phenotypic correlation coefficient indicating the masking of the efficiency of the environment which modified the expression of a character thereby reducing the phenotypic expression (Saha et al., 1992; Islam et al., 1993). All characters observed for quantitative data showed positive genotypic and phenotypic correlations with the fruit yield (Table 3). The fruit yield had a highly significant, positive, genotypic and phenotypic correlation with the total number of fruits and single fruit weight, while the vine length and nodes with male flowers appearing showed significant, positive, genotypic and phenotypic correlation and none of the characters showed a negative correlation with the fruit yield (Table 3). Negative genotypic and phenotypic correlations were observed for the number of fruits per plant with fruit length and width, single fruit weight, node with female flowers appearing and days to female flower opening. The single fruit weight had a highly significant, positive, genotypic and phenotypic correlation with fruit length, while fruit

Table 3
Genotypic (G) and phenotypic (P) correlation coefficients among important quantitative traits in snake gourd genotypes.

Character		Vine length	Nodes with male flower	Nodes with female flower	Days to male flower	Days to female flower	Fruit length (cm)	Fruit width (cm)	Single fruit weight (g)	Number of fruits/vine	Fruits yield/vine (kg)
Vine length	G	1	0.613**[a]	0.361*	0.830**	0.650**	0.015	0.072	0.154	0.291	0.376*
	P		0.601**	0.352*	0.829**	0.629**	0.011	0.070	0.155	0.280	0.362*
Nodes with male flower	G		1	0.542**	0.590**	0.555**	0.118	0.017	0.113	0.268	0.362*
	P			0.532**	0.578**	0.548**	0.117	0.016	0.103	0.256	0.341*
Nodes with female flower	G			1	0.309*	0.388*	0.351*	0.102	0.267	−0.076	0.085
	P				0.307*	0.381*	0.350*	0.103	0.257	−0.077	0.085
Days to male flower	G				1	0.769**	0.150	−0.036	0.178	0.138	0.209
	P					0.762**	0.149	−0.036	0.177	0.132	0.198
Days to female flower	G					1	0.221	0.003	0.233	−0.032	0.056
	P						0.220	0.003	0.231	−0.030	0.057
Fruit length (cm)	G						1	−0.083	0.689**	−0.276	0.143
	P							−0.082	0.683**	−0.273	0.141
Fruit width (cm)	G							1	0.312*	−0.299	0.037
	P								0.311*	−0.301	0.037
Single fruit weight (g)	G								1	−0.184	0.435**
	P									−0.183	0.432**
Number of fruit/vine	G									1	0.774**
	P										0.762**
Fruit yield/vine (kg)	G										1
	P										

[a] * = significant at 5% of probability,** = significant at 1% level.

width had a significant, positive, genotypic and phenotypic correlation. Similar correlation has been observed in different cucurbits (Islam et al., 1993; Rahman et al., 2002; Rana and Pandit, 2011). Days to female and male flower opening had highly significant, positive, genotypic and phenotypic correlation to node number at the appearance of first female and male flowering.

Path coefficient analysis

The association of characters as determined by the simple correlation coefficient may not provide an exact representation of the relationship between yield and yield attributes. In contrast, path coefficient analysis permits a critical examination of specific direct and indirect effects of characters and measures the relative importance of each of them in determining the ultimate goal yield. The genotypic path coefficient analysis (Table 4) showed that the number of fruits per plant had the maximum direct effect (0.836) followed by the single fruit weight (0.671). The fruit width, fruit length, days to first female flower opening, node with male flower bearing and vine length had moderate direct effects on the yield, while node with female flower and days to first male flower opening had negative direct effects. On the other hand, phenotypic path coefficient analysis showed that the single fruit weight had the maximum direct effect (0.988) followed by the number of fruits per plant (0.788), whereas nodes bearing female flower, days to male and female flowers opening and fruit yield per plant had negative direct effects. The remaining characters had moderate direct effects on the yield (Table 4). Importantly, the residual effect was 9.25% for the genotypic coefficient and 2.4% for the phenotypic coefficient indicating that about 91% of the genotypic total variation and 98% of the phenotypic total variation were contributed by the characters included in the path analysis. The residual effects determine how the best the causal factors account for the variability of the dependent factor, that is, yields per plant. Therefore, the present studies indicated that the number of fruits per plant, single fruit weight and fruit width had positive direct effects on the fruit yield per plant. Similarly, a positive direct effect of the yield component characters on yield was reported in bottle gourd (Rahman et al., 1986), cucumber (Islam et al., 1993) and snake gourd (Rana and Pandit, 2011). The vine length and days to female flowering had determinative indirect effects toward the yield and need to be considered for simultaneous selection. Thus, emphasis should be given to selection of these characters for the yield improvement in snake gourd.

Diversity analysis

Genotypes were mostly distributed in five different clusters with cluster II having almost half of the genotypes (47.62%) followed by Cluster I which contained four genotypes (Table 5). On the other hand, clusters III and V each contained only two genotypes. The clustering pattern was consistent with Khatun et al. (2010) and Rabbani et al. (2012) who reported four and five clusters, respectively. Though many of the genotypes from the same or nearby areas fell in the same clusters, some genotypes collected from the same region did not fall in a single cluster, indicating that geographical proximity does not always result in genetic similarity. Thus, there are factors other than geographical diversity that are responsible for genetic diversity, and genotypes that have been collected from the same place may have different genetic make-up. These findings were also in agreement with Rahman et al. (2002), Khatun et al. (2010) and Rabbani et al. (2012). The magnitudes of the intra-cluster distances were not always proportional to the number of genotypes in the cluster (Table 6). It was observed that the cluster II contained 10 genotypes (Table 5) but its intra-cluster distance (2139.47) was not necessarily the highest, whereas cluster V had only two genotypes but its intra-cluster distance (5325.11) was the highest (Table 4). The intra-cluster distances in some of the clusters were less than the inter-cluster distances which indicated that the genotypes within the same cluster were closely related. On the other hand, the maximum inter-cluster D^2 value (12,602.50) was observed between clusters II and III and the minimum was between clusters I and III (3551.24). The lower intra-cluster and higher inter-cluster values also suggested that the genotypes were homogeneous within and heterogeneous between clusters. Therefore, the genotypes grouped in clusters II and III are expected to provide high heterosis in hybridization and to show wide variability in genetic architecture. Larger inter cluster distances compared to intra-cluster distances were observed in previous studies (Khatun et al., 2010; Rabbani et al., 2012).

The characters which contributed most toward the D^2 matrix are presented in Table 7. It was observed that cluster I contained the

Table 4
Path analysis showing direct (bold-diagonal) and indirect (off-diagonal) effect at genotypic (G) and phenotypic (P) level of yield component traits on yield in snake gourd genotypes (genotypic and phenotypic residual effect was 9.25% and 2.4%, respectively).

Character		Vine length (m)	Nodes with male flower	Nodes with female flower	Days to male flowering	Days to female flowering	Fruit length (cm)	Fruit width (cm)	Single fruit weight (g)	Number of fruits/vine	Fruits yield/vine (kg)
Vine length	G	**0.304**	0.258	−0.112	−0.474	0.105	0.0035	0.032	0.257	0.825	−0.825
	P	**0.156**	0.168	−0.0452	−0.0742	−0.157	0.0015	0.0197	0.169	0.501	−0.387
Nodes with male flower	G	0.186	**0.422**	−0.168	−0.336	0.0895	0.0273	0.076	0.189	0.760	−0.795
	P	0.0938	**0.280**	0.0683	−0.0517	−0.136	0.0169	0.00450	0.112	0.458	−0.364
Nodes with female flower	G	0.110	0.229	**−0.309**	−0.176	0.0626	0.0813	0.0454	0.446	−0.216	−0.187
	P	0.0549	0.1489	**−0.128**	−0.0275	−0.0949	0.0507	0.0289	0.280	−0.138	−0.091
Days to male flowering	G	0.253	0.249	−0.0958	**−0.569**	0.124	0.0347	−0.016	0.297	0.391	−0.459
	P	0.129	0.162	−0.0394	**−0.0895**	−0.189	0.0216	−0.0101	0.193	0.236	−0.211
Days to female flowering	G	0.198	0.234	−0.120	−0.438	**0.161**	0.0511	0.0013	0.389	−0.091	−0.330
	P	0.0982	0.153	−0.0489	−0.0682	**−0.249**	0.0318	0.00084	0.252	−0.054	−0.061
Fruit length (cm))	G	0.0046	0.050	−0.109	−0.0854	0.0356	**0.232**	−0.0369	0.989	−0.783	−0.314
	P	0.00172	0.0327	−0.0449	−0.0133	−0.548	**0.145**	−0.0231	0.744	−0.488	−0.151
Fruit width (cm)	G	0.0219	0.0072	−0.0316	0.0205	0.00048	−0.0192	**0.445**	0.521	−0.848	−0.082
	P	0.0109	0.00448	−0.0132	0.00322	−0.00075	−0.0119	**0.281**	0.339	−0.538	−0.039
Single fruit weight (g)	G	0.0469	0.0477	−0.0828	−0.101	0.0376	0.160	0.139	**0.671**	−0.522	−0.956
	P	0.0242	0.0288	−0.0330	−0.0158	−0.0575	0.0989	0.0875	**0.988**	−0.327	−0.462
Number of fruit/vine	G	0.0885	0.113	0.0206	−0.0786	−0.0516	−0.0639	−0.133	−0.307	**0.836**	−0.970
	P	0.0437	0.0717	0.00988	−0.118	0.00747	−0.0395	−0.0847	−0.199	**0.788**	−0.814
Fruit yield/vine (kg)	G	0.144	0.1528	−0.0263	−0.119	0.0242	0.0331	0.0165	0.727	0.951	**−0.967**
	P	0.0565	0.095	−0.0109	−0.177	−0.0141	0.0204	0.0104	0.470	0.962	**−0.986**

Table 5
Distribution of snake gourd genotypes in different clusters.

Cluster	Number of genotypes	Percentage	Accession numbers
I	4	19.05	TA0001, TA0003, TA0009, TA0021
II	10	47.62	TA0002, TA0004, TA0005, TA0006, TA0008, TA00010, TA0011, TA0013, TA0014, TA0020
III	2	9.52	TA0007, TA0019
IV	3	14.29	TA0012, TA0016, TA0017
V	2	9.52	TA0015, TA0018

Table 6
Mean intra-(bold) and inter-cluster distance (D^2) based on morphological characters.

Cluster	I	II	III	IV	V
I	**2119.14**	5687.98	3551.24	4874.98	7599.51
II		**2139.47**	12,602.50	3956.79	11,941.35
III			**2305.41**	9995.95	12,118.91
IV				**3077.25**	5650.98
V					**5325.11**

genotypes producing a shorter main vine and required the minimum number of days to first male (65.00) and female (73.00) flower opening. The genotypes requiring the maximum number of days to first male flower opening belonged to cluster III whereas the genotypes requiring maximum days for the first female flower opening were in cluster IV. The genotypes of cluster III produced the first male flower at a lower node (17.50), while the genotypes from cluster IV produced this at a higher node (26.33). The genotypes comprising cluster IV produced the first female flower at node 36.33 while in cluster V this was at 23.5. The genotypes in cluster III produced the longest type of fruits whereas the shortest types of fruit were produced by the genotypes in cluster II. The heaviest fruits were produced by the genotypes from cluster III while the lightest fruits were produced by the genotypes of cluster II. The genotypes of cluster V produced the highest number of fruits per vine (36.5) and this resulted also in the highest yield per vine (8.29).

Genetic improvement in snake gourd is possible through selection exercised for the vine length, length of fruit, single fruit weight, number of fruits per vine and yield of fruits per vine, which all showed high values of GCV and PCV coupled with high heritability and genetic advance. These characters also exerted moderate-to-high positive or negative direct effects on the fruit yield. Therefore, emphasis should be given to these characters for the improvement of the fruit yield of snake gourd in a breeding program. The divergence study provides an opportunity to select better recombinants for various characters and thereby create greater variability in these characters in future generations. However, characters predominantly controlled by additive gene action would be amenable to conventional breeding methods. Therefore, these characters could be used for the development of high yielding varieties through selection.

Table 7
Cluster means of snake gourd genotypes for yield and yield-contributing characters.

Character	I	II	III	IV	V
Vine length (m)	1.59	2.02	2.78	3.03	2.62
Nodes with male flower	18.25	18.80	17.50	26.33	21.00
Nodes with male flower	29.00	24.40	25.50	36.33	23.50
Days to male flowering	65.00	70.30	81.50	79.67	73.50
Days to female flowering	73.00	76.00	85.00	85.67	75.50
Length of fruit (cm)	42.95	27.85	48.21	33.50	33.44
Width of fruit (cm)	6.59	6.79	6.58	7.11	6.91
Single fruit weight (g)	237.33	154.00	304.17	201.94	236.67
Number of fruit/vine	15.50	16.90	12.00	23.67	36.50
Fruit yield/vine (kg)	3.62	2.52	3.65	4.61	8.29

Conflicting interests

The authors declare that they have no conflict of interests.

Acknowledgements

The authors are grateful to colleagues at BARI for beneficial discussion on this manuscript. This work was supported by grants from the Bangladesh Agricultural Research Council (BARC), Bangladesh. The authors also acknowledge the Plant Genetic Resource Centre of BARI for providing the accessions of snake gourd. Dr. Zhongwei Zou is thanked for his technical criticism of the manuscript.

References

Ahmed, M.S., Rasul, M.G., Bashar, M.K., Mian, A.S.M., 2000. Variability and heterosis in snake gourd (*Trichosanthes anguina* L.). Bangladesh J. Plant Breed. Genet. 13, 27–32.
Ahsan, F.N., Islam, A.K.M.A., Rasul, M.G., Mian, M.A.K., Hossain, M.M., 2014. Genetic variability in snake gourd (*Tricosanthes cucurminata*). J. Agri. Tech. 10, 355–366.
Allard, R.W., 1960. Principles of Plant Breeding. John Wiley and Sons Inc, New York, NY, USA.
BBS, 2012. Statistical yearbook of Bangladesh. In: Statistics and Informatics Division (SID), 32nd ed. Ministry of Planning, Government of the People's Republic of Bangladesh, Dhaka, Bangladesh, p. 21.
Belaj, A., Satovic, Z., Rallo, L., Trujillo, I., 2002. Genetic diversity and relationship in olive (*Olea europea* L.) germplasm collection as determined by RAPD. Theor. Appl. Genet. 105, 638–644.
Bhatt, G.M., 1973. Significance of path coefficient analysis in determining nature of character association. Euphytica 22, 338–343.
Burton, G.W., DeVane, E.H., 1953. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. Agron. J. 45, 478–481.
Chauhan, J.S., Nanda, J.S., 1983. Genetic variability for physico-chemical characters of rice grain in segregating *Oryza sativa* L. Oryza 20, 209–215.
Choudhury, B., 1967. Vegetables. India, the Land and the People. National Book Trust, New Delhi, India.
Cosme, D.C., 2013. GENES – a software package for analysis in experimental statistics and quantitative genetics. Acta Sci. Agron. 35, 271.
Diz, D.A., Wofford, D.S., Schank, S.C., 1994. Correlation and path coefficient analyses of seed-yield components in pearl millet X elephant grass hybrids. Theor. Appl. Genet. 89, 112–115.
Deepa, N.D., Mariappan, S., 2013. Genetic variability, heritability and genetic advance for yield and its components snake gourd (*Trichosanthes anguina* L.). Afr. J. Agric. Res. 8, 3857–3859.
Deshmukh, S.N., Basu, M.S., Reddy, P.S., 1986. Genetic variability, character association and path coefficient analysis of quantitative traits in Virginia bunch varieties of groundnut. Indian J. Agric. Sci. 56, 816–821.
Dewey, D.R., Lu, K.H., 1959. A correlation and path-coefficient analysis of components of crested wheatgrass seed production. Argon. J. 51, 515–518.
Haider, J., Marumoto, T., Azad, A.K., 1991. Estimation of microbial biomass, carbon and nitrogen in Bangladesh soils. Sci. Plant Nutr. 37, 591–599.
Islam, M.S., Khan, S., Khanam, D., Malek, M.A., Hoque, A.M.M., 1993. Genetic variability and path analysis in cucumber (*Cucumis sativus* L.). Bangladesh J. Plant Breed. Genet. 6, 45–51.
Johnson, H.W., Robinson, H.F., Comstock, R.E., 1955. Estimates of genetic and environmental variability in soybeans. Agron. J. 47, 314–318.
Khatun, M., Rabbani, M.G., Rahaman, E.H.S., 2010. Estimate of genetic diversity in snake gourd (*Trichosanthes cucumerina*). Bangladesh J. Agric. Res. 35, 95–100.
Kumar, R., Ameta, K.D., Dubey, R.B., Pareek, S., 2013. Genetic variability, correlation and path analysis in sponge gourd (*Luffa cylindrica* Roem.). Afr. J. Biotechnol. 12, 539–543.
Kutty, M.S., Dharmatti, P.R., 2004. Genetic variability studies in bitter gourd (*Momordica charantia* L.). Karnataka J. Agric. Sci. 1, 11–15.
Larik, A.S., Malik, S.I., Kakar, A.A., Naz, M.A., 2000. Assessment of heritability and genetic advance for yield and yield components in *Gossypium hirsutum* L. Sci. Khyber 13, 39–44.
Mahalanobis, P.C., 1936. On the generalized distance in statistics. Proc. Nat. Acad. Sci. India 2, 49–55.
Mathew, S.S., Khader, A.K.M., 1999. Genetic studies in snake gourd (*Trichosanthes anguina* L.). J. Trop. Agri 37, 71–72.
Miah, M.A., Rahman, M.M., Uddin, M.S., Rahman, A.K.M.M., Ullah, M.H., 2000. Genetic association in bitter gourd (*Momordica charantia* L.). Bangladesh J. Sci. Tech. 2, 21–25.

Mihretu, Y., Weyessa, G., Adugna, D., 2014. Variability and association of quantitative characters among okra (*Abelmoschus esculentus* (L.) Moench) collection in South Western Ethiopia. J. Biol. Sci. 14, 336–342.

Miller, P.A., Williams, J.C., Robinson, H.F., Comstock, R.E., 1958. Estimates of genotypic and environmental variances and covariances in upland cotton and their implications in selection. Agron. J. 50, 126–131.

Nwangburuka, C.C., Denton, O.A., 2012. Heritability, character association and genetic advance in six agronomic and yield related characters in leaf *Corchorus olitorius*. Int. J. Agric. Res. 7, 367–375.

Ogunniyan, D.J., Olakojo, S.A., 2015. Genetic variation, heritability, genetic advance and agronomic character association of yellow elite inbred lines of maize (*Zea mays* L.). Niger. J. Genet. 28, 24–28.

Panse, V.G., 1957. Genetics of quantitative characters in relation to plant breeding. Indian J. Genet. Plant Breed. 17, 318–329.

Patil, P.R., Surve, V.H., Mehta, H.D., 2012. Line x Tester analysis in rice (*Oryza sativa* L.). Madras Agric. J. 99, 210–213.

Prasad, V.S.R.K., Singh, D.P., 1989. Studies on heritability, genetic advance and correlations in ridge gourd (*Luffa acutangula*, Roxb). Indian J. Hort. 46, 390–394.

Rabbani, M.G., Naher, M.J., Hoque, S., 2012. Variability, character association and diversity analysis of ridge gourd (*Luffa acutangula* Roxb.) genotypes of Bangladesh. SAARC J. Agric. 10, 1–10.

Rahman, M.A., Hossain, M.D., Islam, M.S., Biswas, D.K., Ahiduzzaman, M., 2002. Genetic variability, heritability and path analysis in snake gourd (*Trichosanthes anguina* L.). Pak. J. Biol. Sci. 5, 284–286.

Rahman, A.K.M.M., Das, M.K., Haque, M.M., 1986. Variability, correlation and path coefficient analysis in bottle gourd (*Lagenaria vulgaris* L.). Bangladesh J. Agric. 11, 13–19.

Rana, N.P., Pandit, M.K., 2011. Studies on genetic variability, character association and path analysis in snake gourd (*Trichosanthes anguina* L.) genotypes. J. Crop Weed 7, 91–96.

Rao, D.S.R.M., Singh, H., Singh, B., Khola, O.P.S., Faroda, A.S., 1990. Correlation and path coefficient analysis of seed yield and its components in sesame (*Sesamum indicum* L.). Haryana Agric. Univ. J. Res. 20, 273–276.

Rao, C.R., 1952. Advanced Statistical Methods in Biometric Research. John Wiley and Sons, New York, NY, USA.

Roy, R.P., Saran, S., Dutt, B., 1991. Cytogenetics of the cucurbitaceae. In: Tsuchiya, T., Gupta, P.K. (Eds.), Chromosome Engineering in Plants: Genetics, Breeding, Evolution. Elsevier, Amsterdam, The Netherlands, pp. 181–199.

Saha, S.R., Mitra, B.N., Hossain, A.E., Jalaluddin, M., Hoque, A.M.M., 1992. Genetic variability, character association and path coefficient analysis in pumpkin (*Cucurbita moschata* L.). Bangladesh Hortic. 20, 59–62.

Saha, M.C., Begum, R.A., Hamid, M.M., Hossain, S.M.M., 1991. Genetic variability and character association in teasel gourd. Bangladesh Hortic. 19, 25–30.

Salim, M.M.R., Masud, M.A.T., 2015. Advance yield Trial of Sponge Gourd Lines. Research Report on Horticultural Crops. Bangladesh Agricultural Research Institute, Gazipur, Bangladesh.

SAS, 2008. Statistical Analysis System. Version 9.2. SAS Institute Inc, Cary, NC., USA.

Seshadri, V.S., 1986. Cucurbits. In: Bose, T.K., Som, M.G. (Eds.), Vegetables Crops in India. Naya prokash, Calcutta-six, India, pp. 91–164.

Sharma, N.K., Dhankar, B.S., 1990. Variability studies in bottle gourd (*Lagenaria siceraria* Standl.). Haryana J. Hort. Sci. 19, 305–312.

Singh, R.P., Mohan, J., Singh, D., 2002. Studies on genetic variability and heritability in ridge gourd (*Luffa acutangula*). Agric. Sci. Dig. 22, 279–280.

Singh, B.D., 2000. Plant Breeding-principles and Methods, sixth ed. Kalyani Publishers, New Dehli, India.

Singh, R.P., Rai, J.N., 1981. Note on the heritability and genetic advance in chilli. (*Capsicum annuum* L. Prog. Hortic. 13, 89–92.

Varghese, P., Rajan, S., 1993. Genetic variability and heritability studies in snake gourd (*Trichosanthes anguina* L.). J. Trop. Agric. 31, 13–17.