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

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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 are more reliable (Johnson et al., 1955). Heritability provides information on the magnitude of the inheritance of characters from parent to offspring, while genetic advance is helpful in finding the actual gain expected under selection (Larik et al., 2000; Nwangburuka and Denton, 2012; Ogunniyan and Olaoko, 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., 2012; Ogunniyan and Olakojo, 2015).
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 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.

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):

Environmental variance $(\sigma^2e) = M_{Se}$ (1)

Phenotypic variance $(\sigma^2p) = (\sigma^2g + \sigma^2e)$ (2)

Genotypic variance $(\sigma^2g) = (M_{Se} - M_{St})/r$ (3)

where $M_{Se}$ is the mean square error, $M_{Se}$ is the mean square treatment and $r$ is the number of replications.

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

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

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

Estimation of heritability in broad sense: Broad sense heritability ($h^2_b$) 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):

$h^2_b = \frac{GCV}{PCV}$ (6)
where $h^2 B$ is the heritability in a broad sense, $\sigma^2 p$ is the phenotypic variance and $\sigma^2 g$ 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):

$$GA = \frac{K \times \sqrt{(\sigma^2 p \times \sigma^2 g)}}{\sigma^2 p} \times 100$$  \hspace{1cm} (7)

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

$$GAM(\%) = \frac{GA}{X} \times 100$$  \hspace{1cm} (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):

$$r_g = \frac{P_{xy}}{\sqrt{\sigma^2 _{gx} \sigma^2 _{gy}}}$$  \hspace{1cm} (9)

and

$$r_p = \frac{G_{xy}}{\sqrt{\sigma^2 _{px} \sigma^2 _{py}}}$$  \hspace{1cm} (10)

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

$$r_{ij} = P_{ij} + \sum r_{ik} \times P_{kj}$$  \hspace{1cm} (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):

$$h = \sqrt{(1 - R^2)}$$  \hspace{1cm} (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, ($D^2$ 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

<table>
<thead>
<tr>
<th>Character</th>
<th>Range</th>
<th>Mean ± SE</th>
<th>CV (%)</th>
<th>$\sigma^2 g$ (%)</th>
<th>$\sigma^2 p$ (%)</th>
<th>GCV (%)</th>
<th>PCV (%)</th>
<th>$h^2 B$ (%)</th>
<th>GA (%)</th>
<th>GAM (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Vine length</td>
<td>0.83–3.82</td>
<td>2.208 ± 0.149</td>
<td>12.04</td>
<td>0.447</td>
<td>0.518</td>
<td>30.29</td>
<td>32.61</td>
<td>86.30</td>
<td>1.280</td>
<td>57.97</td>
</tr>
<tr>
<td>Nodes with male flower</td>
<td>14.00–31.00</td>
<td>19,857 ± 911</td>
<td>3.66</td>
<td>17,253</td>
<td>17,781</td>
<td>20.92</td>
<td>21.24</td>
<td>97.03</td>
<td>8.428</td>
<td>42.45</td>
</tr>
<tr>
<td>Days to male flower</td>
<td>60.00–89.00</td>
<td>72,048 ± 1,688</td>
<td>1.37</td>
<td>58,424</td>
<td>59,396</td>
<td>10.61</td>
<td>10.70</td>
<td>98.36</td>
<td>15,616</td>
<td>21.68</td>
</tr>
<tr>
<td>Fruit length (cm)</td>
<td>18.84–60.08</td>
<td>34.00 ± 2.072</td>
<td>2.02</td>
<td>90,079</td>
<td>90,550</td>
<td>27.91</td>
<td>27.99</td>
<td>99.48</td>
<td>19,501</td>
<td>57.36</td>
</tr>
<tr>
<td>Fruit width (cm)</td>
<td>3.33–9.07</td>
<td>6.790 ± 0.269</td>
<td>4.22</td>
<td>1.492</td>
<td>1.574</td>
<td>17.99</td>
<td>18.48</td>
<td>94.79</td>
<td>2,450</td>
<td>36.08</td>
</tr>
<tr>
<td>Single fruit weight (g)</td>
<td>87.50–325.00</td>
<td>198,897 ± 13,724</td>
<td>1.04</td>
<td>39,547</td>
<td>39,582</td>
<td>31.61</td>
<td>31.63</td>
<td>99.89</td>
<td>129,464</td>
<td>65.09</td>
</tr>
<tr>
<td>Number of fruit/vine</td>
<td>9.00–44.00</td>
<td>19,000 ± 1,884</td>
<td>4.30</td>
<td>74,378</td>
<td>75,044</td>
<td>45.39</td>
<td>45.69</td>
<td>99.11</td>
<td>17,687</td>
<td>93.09</td>
</tr>
<tr>
<td>Fruit yield/vine (kg)</td>
<td>1.10–8.36</td>
<td>3,684 ± 0.401</td>
<td>5.33</td>
<td>3,377</td>
<td>3,416</td>
<td>49.88</td>
<td>50.17</td>
<td>98.86</td>
<td>3.764</td>
<td>102.17</td>
</tr>
</tbody>
</table>

* 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 ranging from 50 to 79% are high, values 40–59% 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 shown 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>
<thead>
<tr>
<th>Character</th>
<th>Vine length</th>
<th>Nodes with male flower</th>
<th>Nodes with female flower</th>
<th>Days to male flower</th>
<th>Days to female flower</th>
<th>Fruit length (cm)</th>
<th>Fruit width (cm)</th>
<th>Single fruit weight (g)</th>
<th>Number of fruits/vine</th>
<th>Fruits yield/vine (kg)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Vine length</td>
<td>G</td>
<td>0.613***</td>
<td>0.361*</td>
<td>0.830**</td>
<td>0.650**</td>
<td>0.015</td>
<td>0.072</td>
<td>0.154</td>
<td>0.291</td>
<td>0.376*</td>
</tr>
<tr>
<td></td>
<td>P</td>
<td>0.601**</td>
<td>0.352*</td>
<td>0.829**</td>
<td>0.629**</td>
<td>0.011</td>
<td>0.070</td>
<td>0.155</td>
<td>0.280</td>
<td>0.362*</td>
</tr>
<tr>
<td>Nodes with male</td>
<td>G</td>
<td>0.542**</td>
<td>0.590</td>
<td>0.555</td>
<td>0.548**</td>
<td>0.117</td>
<td>0.016</td>
<td>0.103</td>
<td>0.256</td>
<td>0.341*</td>
</tr>
<tr>
<td></td>
<td>P</td>
<td>0.532**</td>
<td>0.578**</td>
<td>0.548**</td>
<td>0.548**</td>
<td>0.117</td>
<td>0.016</td>
<td>0.103</td>
<td>0.256</td>
<td>0.341*</td>
</tr>
<tr>
<td>Nodes with female</td>
<td>G</td>
<td>0.307*</td>
<td>0.388*</td>
<td>0.351*</td>
<td>0.102</td>
<td>0.267</td>
<td>0.086</td>
<td>0.077</td>
<td>0.085</td>
<td></td>
</tr>
<tr>
<td></td>
<td>P</td>
<td>1</td>
<td>0.769**</td>
<td>0.150</td>
<td>0.036</td>
<td>0.178</td>
<td>0.138</td>
<td>0.209</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Days to male flower</td>
<td>G</td>
<td>0.762**</td>
<td>0.149</td>
<td>0.036</td>
<td>0.177</td>
<td>0.132</td>
<td>0.198</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>P</td>
<td>1</td>
<td>0.221</td>
<td>0.001</td>
<td>0.231</td>
<td>0.032</td>
<td>0.056</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Days to female flower</td>
<td>G</td>
<td>0.220</td>
<td>0.003</td>
<td>0.231</td>
<td>0.030</td>
<td>0.057</td>
<td>0.057</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>P</td>
<td>1</td>
<td>0.083</td>
<td>0.689**</td>
<td>0.276</td>
<td>0.143</td>
<td>0.143</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Fruit length (cm)</td>
<td>G</td>
<td>0.036</td>
<td>0.683**</td>
<td>0.273</td>
<td>0.141</td>
<td>0.141</td>
<td>0.141</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>P</td>
<td>1</td>
<td>0.312*</td>
<td>0.299</td>
<td>0.037</td>
<td>0.037</td>
<td>0.037</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Single fruit weight (g)</td>
<td>G</td>
<td>0.311*</td>
<td>0.301</td>
<td>0.184</td>
<td>0.435**</td>
<td>0.183</td>
<td>0.432**</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>P</td>
<td>1</td>
<td>0.774**</td>
<td>0.762**</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

* — significant at 5% of probability, ** — significant at 1% level.
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 weight, 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 weight 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 D² 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 D² matrix are presented in Table 7. It was observed that cluster I contained the

### Table 4

<table>
<thead>
<tr>
<th>Character</th>
<th>Vine length (m)</th>
<th>Nodes with male flower</th>
<th>Nodes with female flower</th>
<th>Days to male flowering</th>
<th>Days to female flowering</th>
<th>Fruit length (cm)</th>
<th>Fruit width (cm)</th>
<th>Single fruit weight (g)</th>
<th>Number of fruits/vine</th>
<th>Fruits yield/vine (kg)</th>
</tr>
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<td>0.032</td>
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<td>0.168</td>
<td>–0.0452</td>
<td>–0.0742</td>
<td>–0.157</td>
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<td>–0.336</td>
<td>0.0895</td>
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<td>–0.136</td>
<td>0.0169</td>
<td>0.0450</td>
<td>0.112</td>
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<td>–0.176</td>
<td>0.0626</td>
<td>0.0813</td>
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<td>0.1489</td>
<td>0.128</td>
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<td>–0.0949</td>
<td>0.0507</td>
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<tr>
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<td>0.124</td>
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<td>–0.199</td>
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<td>0.0104</td>
<td>0.470</td>
<td>0.962</td>
<td>–0.986</td>
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</table>
genotypes producing a shorter main vine and required the minimum number of days to first male flower (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.

**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**


