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Original Article

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

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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.,

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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).

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		

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):

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

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

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

where $\mathrm{Ms_e}$ is the mean square error, $\mathrm{Ms_t}$ 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):

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