Variability, correlations, and path co-efficient analysis in snake gourd (*Trichosanthes cucumirana* L.) inbreds

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ABSTRACT

Background and Objective: The present study was undertaken to determine the genetic variation, the correlation coefficient, the interrelationship between the different characters, and the direct and indirect contribution of these characters to the yield of snake gourd inbreds.

Methodology: Fifteen snake gourd inbreds were evaluated to measure the genetic variability, heritability, and path coefficient analysis for association among the characters and their contribution to yield.

Main Results: A significant variation was observed for all the characters among the inbreds. High genotypic coefficient of variation (GCV) along with high phenotypic coefficient of variation (PCV) was found for the characters like fruit length (103.80% and 104.42%), individual fruit weight (31.27% and 33.47%), and yield per plant (25.11% and 33.81%). Whereas high heritability, coupled with the high genetic advance in percent means, was observed for fruit length (98.82% and 73.41%), individual fruit weight (87.30% and 60.19%), and number of fruits per plant (86.56% and 47.79%) which indicates that these characters are controlled by additive gene effect with minimum environment effect. Hence, direct selection can be the way out for further improvement of snake gourd inbreds. The highest positive direct effects were recorded for individual fruit weight (0.69), number of fruits per plant (0.31), and harvest duration (0.62). Correlation studies revealed that fruit yield had a significant positive correlation with individual fruit weight, number of fruits per plant, and harvest duration.

Conclusions: So, the direct selection of high-yielding inbreds of snake gourd should emphasize the individual fruit weight and number of fruits per plant.

Keywords: Snake gourd, genetic variability, heritability, path analysis, correlation

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INTRODUCTION

Snake gourd is a monoecious crop. It is diploid (2n=2x=22) and belongs to the family Cucurbitaceae. It is an annual creeper and a day-neutral type of vegetable. It is highly cross-pollinated, and due to its out-crossing characteristics, diverse genotypes are always generated in this crop (Islam *et al*., 2020). Snake gourd (*Trichosanthes cucumirana* L.) is an important summer vegetable in Bangladesh. A wide range of variability exists in the size, shape, and color of fruits in Bangladesh. Snake gourd is one of the leading summer vegetables. Though it is grown predominantly in the summer season, it can also be grown around the year except in extreme winter. It can meet the vegetable demand during the early Kharif season when there exists an acute shortage of vegetables in Bangladesh. It plays a vital role in mitigating vegetable demand during the lean period of vegetable supply in Bangladesh. It is important as a good source of minerals, fiber, nutrients, and antioxidants to make food wholesome and healthy (Ahmed *et al*., 2004). It is also one of the important vegetables that fetch more yields per unit area, but the average yield of the crop is low. In addition, it has tremendous export potential because of its excellent keeping quality and shelf life (Podder *et al*., 2010). Snake gourd is one of the leading summer vegetables. The total production of snake gourd during 2019–2020 was 42,938 MT on an area of 19,778 acres of land, and the average yield is 5.36 t/ha (BBS, 2021), which is very low. There are many reasons for this low yield. Lack of high-yielding variety i.e., non-availability of high-yielding variety to the farmers/producers, is one of the main reasons for this low yield. Although Bangladesh exports a limited scale of snake gourd.

The desirable fruit variations, particularly for fruit type and quality have been preserved by the farmers. Along with fruit morphotypes, variation for other plant characters is also available. Some seed companies also import hybrid types from China and other countries although the quality of these hybrids is not better considering the climatic conditions of Bangladesh. In many cases, the varieties are susceptible to many diseases and insects. Besides, the number of snake gourd types that are now available is insufficient to meet farmers' demands. To boost the production of this vegetable, there is no alternative way to develop high-yielding open-pollinated and good hybrid varieties. Therefore, there is a need to improve the productivity and fruit yield of this vegetable. Fruit yield is a complex association among several agronomic traits also to plan an efficient snake gourd breeding program or crop selection program. The knowledge of interrelations among yield and yield contributing characteristics is necessary, and correlation studies among yield and other crop traits could be of interest to breeders in planning hybridization programs and evaluating the individual plants in the segregating populations.

To create efficient breeding techniques, it is crucial to examine the genetic diversity that already exists in every crop species. This is because the present variability can be leveraged to raise cultivar production levels (Patil *et al*., 2012). Heritability provides details on the extent of character inheritance from parents to offspring, whereas genetic progress is useful in determining the actual gain anticipated under selection (Narayanankutty *et al*., 2006; Nwangburuka and Denton, 2012; Ogunniyan and Olakojo, 2014). The partitioning of the relationship into direct and indirect effects, which illustrates the relative relevance of each of the causal components, can be done using route coefficient analysis and correlation to learn more about the association between two features (Rana and Pandit, 2011; Khan *et al*., 2016). A statistical approach called path-coefficient analysis aids plant breeders in understanding the kinds of relationships that exist between two factors (Wright, 1921; Islam *et al*., 2014; Yonas *et al*., 2014). The relationship between two variables can be such that one variable directly causes and then affects the other variable. Path analysis would help partition the correlation into direct and indirect effects of various traits on fruit yield. The concept of path analysis was originally developed by Wright (1921). However, the technique was first used for plant selection by Dewey and Lu (1959). Path coefficient analysis is simply a standardized partial regression coefficient that splits the correlation coefficient into the measures of direct and indirect effects (Wright, 1934).

Nevertheless, the correlation, along with path analysis, would give a better appreciation of the cause-and-effect relationship between pairs of characters. Knowledge of correlations, if accompanied by the understanding of the magnitude of contribution (direct and indirect) of each component character to the final makeup of the fruit yield, the criteria formulated would be effective in selecting the genotypes and using themselves in the crop improvement program. Therefore, the present study was undertaken to determine the genetic variation, the correlation coefficient, and the path coefficient in snake gourd (*Trichosanthes cucumirana* L.) inbreds.

MATERIALS AND METHODS

Location of the Observation

The experiment was conducted at the Olericulture Division of Horticulture Research Centre of Bangladesh Agricultural Research Institute (BARI), Gazipur, Dhaka.

Plant Materials and Culture

The seeds of 15 inbred lines (viz., TA01-1, TA01-2, TA02-1, TA03-3, TA04-4, TA05-4, TA06-1, TA07-5, TA08-2, TA001-6, TA002-2, TA003-5, TA004-3, TA005-8, and TA01-2-A) were sown on poly bag on April 2, 2022. The inbred lines were selected based on their horticultural traits, and insect-pest reactions from the previous year were recorded. The samples were collected from different locations in Bangladesh through a crop improvement program.

Seeds of all genotypes were soaked in water for 48 hours. The soaked seeds were then sown in polyvinyl pots containing a mixture of soil and well-decomposed cow dung (1:1) in March 2022. At age 19 days, seedlings were transplanted into the pits of the experimental field in April 2022. The experiment was laid out using a randomized complete block design with three replications. The unit plot size was 7.5 m × 1.0 m, and five plants were accommodated in a plot with a plant spacing of 1.5 m apart single plant maintaining a row-to-row distance of 1.0 m. Fertilizers were applied at 10,000-81-35-75-18-4.3-2 kg/ha of cowdung-N-P-K-S-Zn-B [cowdung at 10 t/ha, urea at 176 kg/ha, TSP (Triple Super Phosphate) at 175 kg/ha, MoP (Muriate of Potash) at 150 kg/ha, gypsum at 99 kg/ha, zinc sulphate at 12 kg/ha, and boric acid at 10 kg/ha]. The sources of N, P, K, S, Zn, and B were urea, TSP, MoP, gypsum, zinc sulphate, and boric acid (medicated), respectively. Moreover, the entire amount of cow dung, P, S, Zn, B, and 1/3rd of K, was applied during pit preparation as basal to each plot. The rest of K was applied in two equal installments at 20 and 35 days after transplanting (DAT). N was applied in four equal installments at 7, 20, 35, and 50 DAT. Furthermore, necessary intercultural operations were done during the crop period for the proper growth and development of the plants. The fruits were harvested in the maturity stage.

Data and Their Analysis Process

Data were collected from all the individual plants of inbred lines. Data were recorded for days to 1st male flower, days to 1st female flower, node order 1st male flower, node order 1st female flower, fruit length (cm), fruit breadth (cm), individual fruit weight (g), number of fruits per plant, harvest duration (day), and yield per plant (kg). However, the data were analyzed to estimate genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) using the formula of Burton and DeVane (1953), heritability in a broad sense using the formula of Hanson *et al.* (1956), the genetic advance was estimated by the using formula suggested by Johnson *et al.* (1955). Correlation coefficient and path coefficient analysis were worked out as suggested by Singh and Chaudhary (1985) and Dewey and Lu (1959), respectively.

Environmental variance (σ^2e) = Ms_e ------- (1)
Phenotypic variance (σ^2p) = ($\sigma^2g + \sigma^2e$) ------- (2)
Genotypic variance (σ^2g) = ($Ms_e - Ms_t$)/r ------- (3)

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

$$\text{PCV} = \frac{\sqrt{\sigma^2 p}}{\bar{X}} \times 100 \quad \text{-------(4)}$$

$$\text{GCV} = \frac{\sqrt{\sigma^2 g}}{\bar{X}} \times 100 \quad \text{-------(5)}$$

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

Estimation of heritability in a broad sense (h^2) was expressed as the percentage of the ratio of the genotypic variance (σ^2g) to the phenotypic variance (σ^2p)

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

Genetic advance (GA) and the percentage of the mean (GAM) assuming selection of the superior 5% of the genotypes was estimated as per methods described by Johnson *et al*. (1955):

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

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.

$$GAM\ (\%) = \frac{GA}{\overline{X}} \times 100 \quad \text{------- (8)}$$

where GAM is the genetic advance as a percentage of the mean, GA is the expected genetic advance, and $\overline{X}$ 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 component.

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

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

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 the equation:

$$r_{ij} = p_{ij} + \sum r_{ik}\, p_{kj} \quad \text{-------(11)}$$

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.

RESULTS AND DISCUSSION

Genetic Parameters

To create well-organized breeding techniques, it is vital to observe the genetic diversity that already exists in the desirable crop species (Patil *et al*., 2012). In the current study, the snake gourd inbreds exhibited significant differences for all the ten characters under study. Heritability, genetic advance, genetic advance in percent of the mean, genotypic coefficient of variation, and phenotypic coefficient of variation are presented in Table 1. The PCV was the highest in yield per plant (33.81%), followed by individual fruit weight (33.47%), harvest duration (27.63%), and number of fruits per plant (26.89%). Bartaula *et al.* (2019) reported that high PCV indicates the existence of a wide scope of selection for the improvement of the traits. Comparatively low PCV was observed for days to 1st male flower (9.96%), Fruit breadth (10.48%), and days to 1st female flower (10.60%), node order of 1st female flower (13.24%), fruit length (14.42%) and node order of 1st male flower (17.94%) indicating less scope for selection.

The highest GCV was found for individual fruit weight (31.27%), followed by harvest duration (26.07%) and yield per plant (25.11%). Lamara *et al*. (2022) reported that high GCV indicates exploitable genetic variability for these traits, which may facilitate the selection. Comparatively low PCV was observed for days to 1st male flower (7.98%) followed by fruit breadth (8.64%), days to 1st female flower (9.16%), node order of 1st female flower (11.96%), node order of 1st male flower (12.77%), etc. indicating less scope for selection.

Table 1 Estimation of genetic parameters for different traits in 15 snake gourd inbreds

Characters	Genotypic coefficient of variation (%)	Phenotypic coefficient of variation (%)	Heritability (%)	Genetic advance	Genetic advance in percent means
Days to 1st male flower	7.98	9.96	64.19	5.44	13.17
Days to 1st female flower	9.16	10.60	74.61	7.49	16.29
Node order of 1st male flower	12.77	17.94	50.65	2.41	18.72
Node order of 1st female flower	11.96	13.24	81.54	5.12	22.24
Fruit length (cm)	13.80	14.42	98.82	89.70	73.41
Fruit breadth (cm)	8.64	10.48	68.05	0.62	14.69
Individual fruit weight (g)	31.27	33.47	87.30	111.13	60.19
Number of fruits per plant	18.35	26.89	86.56	14.23	47.79
Harvest duration	26.07	27.63	89.01	16.77	50.66
Yield per plant (kg)	25.11	33.81	55.12	2.11	38.40

Moreover, narrow range of difference between PCV and GCV was observed for fruit length (14.42% and 13.80%) followed by node order of 1st female flower (13.24% and 11.26%), days to 1st female flower (10.60% and 9.16%), harvest duration (27.63% and 26.07%), fruit breadth (10.48% and 8.64%), days to 1st male flower (9.96% and 7.98%) and individual fruit weight (33.47% and 31.27%) etc. indicating that the traits are mostly governed by genetic factors with minimal environmental influence on the phenotype.

Heritability details the extent of character inheritance from parents to offspring, whereas genetic progress is useful in determining the actual gain anticipated under selection (Narayanankutty *et al*., 2006; Nwangburuka and Denton, 2012). A character can be improved only if it is highly heritable (Ogunniyan and Olakojo, 2014). Among the various characters of the current observation, high heritability coupled with high genetic advance over percent mean was noticed for fruit length (98.82% and 73.41%) followed by harvest duration (89.01% and 50.66%), individual fruit weight (87.30% and 60.19%), number of fruits per plant (86.56% and 47.79%) and yield per plant (55.12% and 38.40%), etc. High estimates of heritability with fairly high estimates of genetic advance over percent mean indicate the presence of additive gene effect, and selection for genetic improvement for these traits would be effective (Narayanankutty *et al*., 2006; Nwangburuka and Denton, 2012).

The Genotypic and Phenotypic Correlation Coefficient among Different Traits in 15 Snake Gourd Inbreds

The genotypic correlation coefficient and phenotypic correlation coefficient among different characters are presented in Table 2. The strong positive genotypic and phenotypic correlation of individual fruit weight (0.69 and 0.60) and harvest duration (0.61 and 0.54) with yield per plant indicates that if individual fruit weight and harvest duration increase, yield per plant increases.

Although correlation coefficients are useful for quantifying the magnitude and direction of correlations between traits (Rana and Pandit, 2011; Khan *et al*., 2016), they may result in misconceptions about selection strategies as a high magnitude of a correlation between two traits can occur due to the indirect effect of a third or a group of traits (Baye *et al*., 2020). Consequently, path analysis is a method that helps breeding programs perform indirect selection by confirming the obtained results from correlation analysis between traits and avoiding misconceptions throughout the selection (Wright, 1921; 1934).

Table 2 Genotypic and phenotypic correlation coefficient among different characters in 15 snake gourd inbreds

Characters		**DFM**	**DFF**	**NMF**	**NFF**	**FL**	**FB**	**IFW**	**F/pl.**	**HD**
DFF	r_g	0.93^{**}								
	r_p	0.87^{**}								
NMF	r_g	0.28^{NS}	0.07^{NS}							
	r_p	0.21^{NS}	0.11^{NS}							
NFF	r_g	-0.09^{NS}	-0.12^{NS}	0.82^{**}						
	r_p	-0.07^{NS}	-0.06^{NS}	0.76^{**}						
FL	r_g	-0.62^{**}	-0.62^{**}	0.65^{**}	0.72^{**}					
	r_p	-0.51^{**}	-0.56^{**}	0.45^{*}	0.62^{**}					
FB	r_g	0.38^{*}	0.35^{NS}	-1.07^{**}	-0.90^{**}	-0.95^{**}				
	r_p	0.20^{NS}	0.24^{NS}	-0.50^{**}	-0.59^{**}	-0.78^{**}				
IFW	r_g	-0.60^{**}	-0.58^{**}	0.68^{**}	0.54^{**}	0.96^{**}	-0.87^{**}			
	r_p	-0.39^{*}	-0.43^{*}	0.31^{NS}	0.40^{*}	0.89^{**}	-0.68^{**}			
F/pl.	r_g	0.62^{**}	0.42^{*}	-0.02^{NS}	-0.49^{**}	-0.61^{**}	0.27^{NS}	-0.47^{**}		
	r_p	0.18^{NS}	0.21^{NS}	0.01^{NS}	-0.14^{NS}	-0.46^{*}	0.32^{NS}	-0.32^{NS}		
HD	r_g	-0.50^{**}	-0.58^{**}	0.68^{**}	0.60^{**}	0.65^{**}	-0.77^{**}	0.54^{**}	0.20^{NS}	
	r_p	-0.40^{*}	-0.48^{**}	0.42^{*}	0.48^{**}	0.61^{**}	-0.52^{**}	0.53^{**}	0.18^{NS}	
Y/pl.	r_g	-0.17^{NS}	-0.26^{NS}	0.64^{**}	0.12^{NS}	0.51^{**}	-0.68^{**}	0.69^{**}	0.31^{NS}	0.61^{**}
	r_p	-0.17^{NS}	-0.17^{NS}	0.22^{NS}	0.14^{NS}	0.33^{NS}	-0.25^{NS}	0.60^{**}	0.54^{**}	0.54^{**}

Note: * Significant at 5% level, **Significant at 1% level, NS = non-significant. r_g = genotypic correlation coefficient, r_p = phenotypic correlation coefficient, DFM = days to 1st male flower, DFF = days to 1st female flower, NMF = node order of 1st male flower, NFF = node order of 1st female flower, FL = fruit length, FB = fruit breadth, IFW = individual fruit weight, F/pl. = number of fruits per plant, HD = harvest duration, Y/pl. = yield per plant.

Path Coefficient Analysis

The partitioning of genotypic correlation with yield per plant into direct and indirect components are presented in Table 3. According to the path coefficient analysis, a direct positive effect on yield per plant was observed for individual fruit weight, harvest duration, and node order of 1st male flower, etc. These traits showed the highest influence on yield per plant. Besides, individual fruit weight showed a positive indirect effect on yield per plant via node order of 1st male flower, node order of 1st female flower, fruit length, and harvest duration. Therefore, individual fruit weight can be considered a valuable option for snake gourd breeding in the case of an indirect selection for higher yield per plant.

The path coefficient analysis (Table 3) related that the highest positive direct effect was recorded in individual fruit weight (0.91) to fruit yield, and a high direct effect was found in total fruits per plant (0.42) followed by node order to 1st male flower (0.32). Considering the high direct contribution of individual fruit weight and total number of fruits per plant to the fruit yield, it would appear that these two characteristics are the most reliable selection criteria. The highest negative direct effect on yield was exhibited by days to 1st male flower (-0.33) and fruit length (-0.91). The results of our current study were also confirmed by several earlier studies conducted by Wright (1921), Islam *et al*. (2014), and Yonas *et al*. (2014), who stated that path coefficient analysis aids plant breeders in understanding the kinds of relationships that exist between two factors.

Table 3 Path analysis showing direct (bold-diagonal) and indirect (off-diagonal) effect at genotypic (G) level of yield component traits on yield in snake gourd genotypes (genotypic residual effect was 2.9%)

Characters	DFM	DFF	NMF	NFF	FL	FB	IFW	F/pl.	HD	Y/pl.
DFM	**-0.33**	0.09	0.09	0.00	0.99	0.05	-0.99	0.26	-0.11	-0.17
DFF	-0.31	**0.09**	0.02	-0.01	0.99	0.04	-0.96	0.17	-0.13	-0.24
NMF	-0.09	0.00	**0.32**	0.07	-0.93	-0.15	0.97	0.00	0.15	0.64
NFF	0.03	-0.01	0.27	**0.09**	-0.95	-0.12	0.99	-0.21	0.13	0.11
FL	0.21	-0.06	0.21	0.06	**-0.91**	-0.13	0.95	-0.26	0.14	0.51
FB	-0.13	0.03	-0.35	-0.08	0.98	**0.14**	-0.94	0.11	-0.17	-0.68
IFW	0.20	-0.06	0.22	0.05	-0.93	-0.12	**0.91**	-0.20	0.12	0.69
F/pl.	-0.21	0.04	-0.00	-0.04	0.96	0.03	-0.95	**0.42**	0.04	0.31
HD	0.11	-0.06	0.22	0.05	-0.94	-0.11	0.98	0.09	**0.21**	0.62

Note: Residual effect = 0.029. DFM = days to 1st male flower, DFF = days to 1st female flower, NMF = node order of 1st male flower, NFF = node order of 1st female flower, FL = fruit length, FB = fruit breadth, IFW = individual fruit weight, F/pl. = number of fruits per plant, HD = harvest duration, Y/pl. = yield per plant.

CONCLUSIONS

From the results of the present findings, it was indicated that the number of fruits per plant, fruit length, individual fruit weight, and harvest duration had moderate to high heritability and genetic advance. On the other hand, a strong positive genotypic and phenotypic correlation was found in individual fruit weight (0.69 and 0.60) and harvest duration (0.61 and 0.54) with fruit yield per plant. The individual fruit weight (0.91) and fruits per plant (0.42) also showed moderate to high positive direct effects on fruit yield. Therefore, emphasis should be given to these characters for the improvement of fruit yield of snake gourd aimed at in a hybridization program.

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