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Shailesh Singh
Department of Vegetable Science, Narendra Deva University of Agriculture and Technology, Kumarganj, Faizabad, Uttar Pradesh, India

VB Singh
Department of Vegetable Science, Narendra Deva University of Agriculture and Technology, Kumarganj, Faizabad, Uttar Pradesh, India

Nidhi Tyagi
Department of Vegetable Science, Dr. Y.S. Parmar University of Horticulture and Forestry, Nauni, Solan, Himachal Pradesh, India

Studies on genetic variability of sponge gourd genotypes

Shailesh Singh, VB Singh and Nidhi Tyagi

Abstract

Sponge gourd is cultivated and marketed by smallholder farmers, and are important crop in home gardens throughout southern and southeastern Asia. Twenty eight genotypes of sponge gourd were evaluated for their genetic variability, heritability and potential for screening suitable genotypes for future improvement programmes. The genotypes exhibited highly significant differences for all the traits under study. A wide range of variability along with high estimates of PCV and GCV was observed for node number to anthesis first staminate flower, node number to anthesis first pistillate flower, vine length, number of fruits per plant and average fruit yield per plant indicating high variability available in the germplasm for these characters for further improvement. High heritability coupled with high genetic advance as per cent of mean was observed for node number to anthesis of first staminate flower, node number to anthesis of first pistillate flower, days to anthesis of first staminate flower, vine length, number of nodes per vine, number of primary branches per plant, fruit length, fruit diameter, number of fruits per plant, average fruit weight and average fruit yield per plant indicated these characters had additive gene effect and therefore, these are more reliable for effective selection.

Keywords: Sponge gourd, variability, phenotypic coefficient of variation, genotypic coefficient of variation

Introduction

Among the cucurbits sponge gourd [*Luffa cylindrica* (L.) syn. *Luffa aegyptiaca* Mill] is one of important summer vegetable crop. Its immature fruit and seed oil have many medicinal and nutritional properties (Yawalkar, 2004 and Demir *et al.*, 2008) [29, 7] therefore, it play significant role in human diet especially in the tropical and subtropical countries. In sponge gourd, wide range of variability is found in vegetative and fruit characteristics in India because it highly cross pollinated crop (Singh *et al*., 2009) [23] and south-east Asia was reported native of this crop (Kalloo, 1993) [13]. Inbreeding depression is very low in sponge gourd so it is behave as self-pollinated crop therefore crossing pollinating cause degraded and adulterated, thus leading to decreased quality of local variety (Phan *et al*., 2015) [20]. Now, there is a need for improved varieties in respect of heat, drought and disease tolerance and germplasm is the important natural resource that should be used by the breeders to develop new cultivars. Genetic variability is a prerequisite for a successful breeding programme of any crop species and a critical survey of genetic variability is essential before initiating an improvement programme aiming to develop high yielding varieties (Falconer, 1989) [9]. The variability analysis and partitioning of the total variation into heritable and nonheritable components with suitable genetic parameters like genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), percent heritability, percent genetic advance etc. is therefore, a necessity (Barma *et al*., 1990) [2]. The magnitude of these components is a measure of the type of gene action involved in the expression of various traits. The information about gene action helps in deciding a breeding procedure for the genetic improvement of traits (Singh and Narayanan, 2007) [22]. However, it is possible to develop high-yielding open pollinated varieties, or hybrids, by utilizing existing variability (Islam *et al.*, 2009) [11] and this technique could be used in improvement of sponge gourd. Therefore, an attempt was made in the present investigation to estimate the magnitude of genetic variability, heritability, genetic advance in twenty eight sponge gourd genotypes, which can be utilized as donors in hybridization programme.

Materials and Methods

The present investigation was carried out at Main Experimental Station of Vegetable Science, N.D.U.A. & T., Faizabad (Uttar Pradesh) during summer season, 2015. Geographically, Narendra Nagar, falls under humid sub-tropical climate and is located in between 24.47^0 and 26.56^0 N latitude and 82.12^0 and 83.98^0 E longitude at an altitude of 113 m above the mean sea

Correspondence
Nidhi Tyagi
Department of Vegetable Science, Dr. Y.S. Parmar University of Horticulture and Forestry, Nauni, Solan, Himachal Pradesh, India

level in the Gangetic Alluvial Plains of Eastern Uttar Pradesh. The experiment was conducted in Randomized Complete Block Design with three replications to assess the performance of 28 genotypes of sponge gourd including check variety Pusa Chikini. The plot size was of 3 m × 2.5 m with row to row spacing of 2.5 m and plant to plant spacing of 0.50 m. All the recommended package of practices was followed to raise a healthy crop. The observations were recorded on five randomly selected plants from each genotype in each replication for the characters *viz.*, node number to anthesis of first staminate flower, node number to anthesis of first pistillate flower, days to anthesis of first staminate flower, days to anthesis of first pistillate flower, days to first fruit harvest, vine length (m), number of nodes per vine, number of primary branches per plant, fruit length (cm), fruit diameter (cm), number of fruits per plant, average fruit weight (g) and average fruit yield per plant (kg). The analysis of variance for the design of experiment (RBD) was carried out according to the procedure outlined by Panse and Sukhatme (1967) [18]. The data were analyzed for phenotypic and genotypic variances (Johnson *et al.*, 1955) [12]. The Genotypic and phenotypic coefficients of variations were estimated according to the formula suggested by Burton (1952) [6]. Heritability in broad sense (h^2bs), genetic advance (GA), and genetic advance in percent of mean (GA%) were estimated for different characters by the formula suggested by Johnson *et al.* (1955) [12].

Results and Discussion
Mean sum of square due to treatment was found highly significant for all the characters, indicated the presence of high magnitude of variability are present among the genotypes (Table 1). Estimates of high variability of 28 genotypes in respects of thirteen characters have been presented in Table 2. The node number to anthesis of first staminate flower ranged from 3.03 to 9.23, while, its mean was 5.41 node. In case of node number to anthesis of first pistillate flower ranged from 6.06 to 14.36 node however, its mean was 9.97 node. Significant early days to anthesis of first male and female flower was ranged from 25.10 to 47.93 days and 31.66 to 50.16 days over the mean was 38.67 days and 41.52 days, respectively. On the other hand, days to first fruit harvest ranged from 43.60 to 63.33 days, whereas, its general mean was 54.04. The vine length and number of nodes per vine ranged from 1.86 to 4.60 m and 32.26 to 62.46, respectively, while its general mean was 2.93 m and 45.14 nodes, respectively. The number of primary branches per plant ranged from 3.26 to 8.26, while its general mean was 5.35. The fruit length and fruit diameter ranged from 14.56 to 30.10 cm and 2.40 to 4.93 cm, respectively whereas, its general mean was 22.58 cm and 3.67 cm, respectively. The number of fruits per plant was ranged from 8.73 to 26.60, with mean 16.68. The mean value over the genotypes regarding average fruit weight was 148.97 g with a range of 114.23 to 192.40 g. The average fruits yield per plant (kg) ranged from 1.275 to 3.083 kg, while its general mean was 2.025 kg. These observations corroborate the findings of the previous worker (Tyagi *et al.*, 2017) [27] in bitter gourd. This measurement of variation indicated comparatively lesser influence of environment for the expression of characters under study and it was not entirely unexpected for the crop. It otherwise established the genotypic worth of the genotypes to express heritable differences for the concern characters.
The coefficient of genotypic and phenotypic variability is helpful to measure the extent of variability present in

particular trait. They also provide a helpful measure to compare the variability present among various quantitative traits. The estimates of coefficient of variances revealed that magnitude of phenotypic coefficient of variation for all the traits were higher than the magnitude of genotypic coefficient of variation that indicated the role of environment in expression of traits (Table 2). The estimates of phenotypic as well as genotypic coefficient of variations were observed higher for node number to anthesis of first staminate flower (PCV 32.00; GCV 30.88) followed by number of fruits per plant (PCV 30.45; GCV 29.19), average fruit yield per plant (PCV 27.13; GCV 25.35), vine length (PCV 26.99; GCV 25.56), node number to anthesis of first pistillate flower (PCV 23.05; GCV 21.74) and number of primary branches per plant (PCV 22.90; GCV 18.55) whereas, number of nodes per vine (PCV 19.66; GCV 18.55) and fruit length (PCV 19.37; GCV 18.17) were moderate coefficient of variability. These findings corroborate by the previous workers (Arora *et al.*, 1983; Krishna Prasad and Singh, 1990 in sponge gourd; Devi and Mariappan, 2013 in snake gourd; Singh *et al.*, 2015 in bottle gourd; Yadagiri *et al.*, 2017; Tyagi *et al.*, 2018 in bitter gourd) [1, 15, 8, 25, 28, 26].
Heritability is of interest to the plant breeders primarily as a measure of the value of selection for the particular character in various types of progeny and as an index of transmissibility of characters from parent to offspring (Hayes *et al.*, 1955) [10]. So, concept of heritability is important to evaluate the relative magnitude of the effect of genes and environments on total phenotypic variability. For this reason, Burton (1952) [6] suggested that genetic variability along with heritability should be considered for assessing the maximum and accurate effect of selection. The heritability estimates in broad sense were high for all the characters (Table 2), it indicating that though the character is least influenced by the environment effects, the selection for improvement of such character may be useful, because broad sense heritability is based on total genetic variance which includes both fixable (additive) and non-fixable (dominance and epistatic variance). The estimates of heritability in broad sense ranged from 67.29 (days to first fruit harvest) to 93.16 % (node number to anthesis of first staminate flower). Highest values of heritability in broad sense were shown in node number to anthesis of first staminate flower (93.16 %) followed by number of fruits per plant (91.86 %), vine length (89.70 %), number of nodes per vine (89.07 %), node number to anthesis of first pistillate flower (88.98 %), number of primary branches per plant (88.19 %), fruit length (87.96 %), average fruit yield per plant (87.34 %), fruit diameter (82.65 %), average fruit weight (82.62 %), days to anthesis of first staminate flower (76.69 %), while days to anthesis of first pistillate flower (69.10 %) and days to first fruit harvest (67.29 %) which indicated moderate heritability. Similar findings support from the previous studies (Singh and Kumar, 2002 in bottle gourd; Bharathi *et al.*, 2006 in spine gourd; Khule *et al.*, 2011 in sponge gourd; Behera, 2013 and Tyagi *et al.*, 2018 in bitter gourd) [21, 4, 14, 3, 26].
High heritability accompanied with high genetic advance as per cent of mean indicates that most likely the heritability is due to additive gene effects and selection may be effective (Table 2). However, it is not necessary that a character showing high heritability will also exhibit high genetic advance (Johnson *et al.*, 1955) [12]. High heritability coupled with high genetic advance as per cent of mean was observed for the characters node number to anthesis of first staminate flower, number of fruits per plant, vine length, average fruit

yield per plant, node number to anthesis of first pistillate flower, number of primary branches per plant indicating that these characters were also controlled by the additive action of polygene (Panse, 1957) [17] and would be considered for selection criteria. Results obtained here in agreement with the findings of Pandey et al. (2012) [16] in sponge gourd; Pathak et al. (2014) [19], Tyagi et al. (2018) [26] in bitter gourd. However, days to anthesis of first pistillate flower exhibited moderate heritability coupled with high genetic advance as per cent of mean, whereas character days to first fruit harvest showed moderate heritability coupled with moderate genetic advance as per cent of mean. These results corroborated with the findings of Bindu et al. (2000) [5] in pumpkin; Pandey et al. (2012) [16] in sponge gourd; Pathak et al. (2014) [19] and Tyagi et al. (2018) [26] in bitter gourd. From the result of genetic variability, node number to anthesis of first staminate flower, number of fruits per plant, vine length, average fruit yield per plant, node number to anthesis of first pistillate flower and number of primary branches per plant emerged as most reliable characters for selection because of their probable conditioning by the additive gene action.

Table 1: Analysis of variance for thirteen different characters in 28 genotypes of sponge gourd

Characters	Source of variation		
	Replications	Treatments	Error
d.f.	2	27	54
Node number to anthesis of first staminate flower	0.196	8.600**	0.205
Node number to anthesis of first pistillate flower	0.312	14.700**	0.583
Days to anthesis of first staminate flower	6.498	104.266**	9.590
Days to anthesis of first pistillate flower	19.905	89.175**	11.569
Days of first fruit harvest	17.226	88.915**	12.397
Vine length (m)	0.020	1.758**	0.064
Number of nodes per vine	1.087	219.179**	8.610
Number of primary branches per plant	0.015	4.162**	0.177
Fruit length (cm)	7.200	52.850**	2.305
Fruit diameter (cm)	0.011	1.470**	0.096
Number of fruits per plant	4.735	73.230**	2.102
Average fruit weight (g)	0.329	1397.084**	2.102
Average fruit yield per plant (kg)	0.008	0.829**	0.038

** Significant at 0.01 % level of probability

Table 2: Estimates of range, grand mean and genetic parameters for 13 characters of sponge gourd genotypes.

Characters	Range	Grand mean	PCV*	GCV**	Heritability in broad sense (h^2_{bs})	Genetic advance as per cent of mean
Node number to anthesis of first staminate flower	3.03-9.23	5.41	32.00	30.88	93.16	61.41
Node number to anthesis of first pistillate flower	6.06-14.36	9.97	23.05	21.74	88.98	42.25
Days to anthesis of first staminate flower	25.10-47.93	38.67	16.58	14.52	76.69	26.20
Days to anthesis of first pistillate flower	31.66-50.16	41.52	14.73	12.24	69.10	20.97
Days to first fruit harvest	43.60-63.33	54.04	11.39	9.34	67.29	15.79
Vine length (m)	1.86-4.60	2.93	26.99	25.56	89.70	49.87
Number of nodes per vine	32.26-62.46	45.14	19.66	18.55	89.07	36.07
Number of primary branches per plant	3.26-8.26	5.35	22.90	21.50	88.19	41.60
Fruit length (cm)	14.56-30.10	22.58	19.37	18.17	87.96	35.11
Fruit diameter (cm)	2.40-4.93	3.67	20.28	18.44	82.65	34.54
Number of fruit per plant	8.73-26.60	16.68	30.45	29.19	91.86	57.63
Average fruit weight (g)	114.23-192.40	148.97	15.40	14.00	82.62	26.21
Average fruit yield per plant (kg)	1.275-3.08	2.025	27.13	25.35	87.34	48.81

*GCV = Genotypic coefficient of variation; **PCV = Phenotypic coefficient of variation

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