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Exploring the Dynamics of Genetic Parameters: Genetic Variability, Heritability and Genetic Advance in Sponge Gourd

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ABSTRACT

Sponge gourd is a popular low cost vegetable in the tropical and subtropical regions. It is an important component of crop rotation during pre-*kharif* and *kharif* seasons in North Indian conditions and is cultivated both on a commercial scale and in kitchen gardens. The present study was conducted to find out the variation among the genotypes for different traits, like as the number of nodes at first male flower appearance, fruit yield per plant, number of nodes at first female flower appear, fruit diameter, number of fruits per plant, average fruit weight, fruit length, days to first fruit harvest, days to first female flower and days to first male flower. The mean sum of squares due to genotypes revealed that a wider range of variation among the traits for almost all of the traits. High PCV and GCV estimates for number of number of nodes at first male flower appear, fruit yield per plant and the number of nodes at first female flower appear suggest substantial variability for the traits, thereby ensuring ample scope for improvement of these traits through selection. High heritability coupled with high genetic advance as % mean were observed for number of node at first female flower appear, number of node at first male flower appear, fruit diameter, average fruit weight, number of fruits per plant and fruit yield per plant which revealed that these traits are governed by additive gene action and phenotypic selection would be effective for the improvement of these traits.

Keywords Sponge gourd, Variability, Heritability, Genetic advance.

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INTRODUCTION

Luffa (*Luffa cylindrica* Roem.) commonly known as sponge gourd. The loofah vegetable sponge, the species had diploid chromosome number 2n = 2x = 26. It is an annual climbing plant with cross pollinated nature. It is difficult to assign with accuracy the indigenous area of *Luffa* species. They have a long history of cultivation in tropical countries of Asia and Africa. Indo-Burma is reported to be the primary center of diversity for sponge gourd and is originated in subtropical Asian region particularly India". Luffa com-

monly called loofah, vegetable sponge, bath sponge or dish cloth gourd, is a member of Cucurbitaceous family. The vernacular names of sponge gourd are kali tori, ghia tori, torianemia, nenuwa, chiori, dundul, ghosaligilka, bhol or tarada and ghiraula in different parts of the world. The sponge cultivated worldwide with the area 1.6 million hectare and production 23.68 million tonnes including pumpkins and gourds (Anonymous 2023).

The leaves and fruits are good remedies for Jaundice. Roots have laxative effects and the oil from the seeds is used for cutaneous complaints (Chauhan 1972). Being a minor crop and its cultivation is not yet flourished at commercial scale and area of cultivation is not known. The sponge gourd large amount of variation has been observed for many economically important traits. In India, wide range of variability is available in the land races or cultivars, in terms of qualitative as well as quantitative characters of sponge gourd. The fruit number and weight, uniform thickness, cylindrical fruit free from bitterness, high female: Male sex ratio, earliness, non-fibrous fruit at edible stage and resistance to powdery and downy mildew. Variability in cucurbitaceous crop occurs in the form of land races, traditional cultivars, wild relatives form and related non edible wild weedy species. In India little attention has been given for the genetic improvement of sponge gourd by collecting diverse germplasm, their morphological characterization and assessing the variability parameters like coefficient of variation. The appropriate breeding methodologies may be adopted for genetic improvement of this crop for simultaneously improvement of different characters, information regarding mutual relationship among the characters and direction of correlation analysis provides an effective means of finding out direct and indirect causes of association among causal variables. Though the literature in respect of germplasm evaluation variability and correlation studies in sponge gourd is not meager but these are based on testing of limited number of germplasm. Moreover, the results of the earlier studies on such aspects are relevant only for the materials and environments involved in the particular study and cannot be generalized. Therefore, studies on above aspects on the available germplasm under the environment where, it is to be exploited, is essential for successful utilization of germplasm resources in the development of superior varieties.

MATERIALS AND METHODS

Statistical analysis

The average values for each genotype in each replication for the characters studied were used for further statistical analysis. A brief outline of the procedure adopted for the estimation of statistical parameters. The model described by Panse and Sukhatme (1984) was used for computation of analysis of variance in which, calculated 'F' values were compared with the tabulated 'F' values at 5.00% to know the level of significance. All the studied characters which, showed significant variation among genotypes were further subjected to the analysis for the different quantitative genetic parameters. The PCV (Phenotypic Coefficient of Variation), GCV (Genotypic Coefficient of Variation), ECV heritability in broad sense (h^2_{bs}) and the expected genetic advance for different characters were calculated as per the model given by Burton and De Vane (1953) and Johnson *et al.* (1955).

For categorizing the magnitude of different parameters, the following limits were used:

PCV and GCV and ECV	<10%	-	Low
	10-20%	-	Moderate
	>20%	-	High
Genetic advance (GA)	<15%	-	Low
	15-30%	-	Moderate
	>30%	-	High
Heritability	<60%	-	Low
	60%-80%	-	Moderate
	> 80%	-	High

RESULTS AND DISCUSSION

The estimates of PCV (Phenotypic Coefficient of Variation) (Table 1) were higher than corresponding GCV (Genotypic Coefficient of Variation) for most of the characters studied which indicated that the apparent variation is not only due to genotypes but, also due to the influence of environment. Low environmental coefficient of variation for all the characters studied which, indicated the existence of inherent genetic variability for most of the characters.

Table 1. Estimates of variability parameters for horticultural and yield traits in sponge during summer season, 2024.

Parameters / Characters	General mean	Exp mean next Generation	Coefficient of Variation (%) Phenotypic	Genotypic	Environmental	h^2 (Broad sense)	Genetic advancement 5%	Gen adv as % of mean 5%
Number of node at first female flower appear	9.55	13.77	21.43	21.42	0.42	100.00	4.21	44.13
Number of node at first male flower appear	3.74	5.55	23.43	23.41	0.70	99.00	1.80	48.222
Days to first male flower	37.89	40.27	3.05	3.05	0.16	99.00	2.38	6.284
Days to first female flower	36.93	40.98	5.32	5.32	0.16	99.00	4.04	10.958
Days to first fruit harvest	46.86	52.00	5.39	5.38	0.26	99.00	5.19	11.083
Fruit length (cm)	23.33	27.98	9.65	9.65	0.09	100.00	4.64	19.896
Fruit diameter (cm)	4.22	5.83	18.54	18.52	1.01	99.00	1.61	38.095
Average fruit weight (g)	110.27	140.03	13.13	13.11	0.62	99.00	29.76	26.988
Number of fruits per plant	12.45	16.08	14.19	14.16	0.92	99.00	3.62	29.120
Fruit yield per plant (kg)	1.38	2.00	22.00	21.90	2.07	99.00	0.62	44.918

During summer season, 2023-24, high phenotypic and genotypic coefficient of variation was obtained for number of node at first male flower appear (23.43% & 23.41%), fruit yield per plant (22.00% & 21.90%) and number of node at first female flower appear (21.43% & 21.42%). However, moderate PCV (Phenotypic Coefficient of Variation) and GCV (Genotypic Coefficient of Variation) were observed for fruit diameter (18.54% & 18.52%), number of fruits per plant (14.19% & 14.16 %) and average fruit weight (13.13 & 13.11%). Low PCV & GCV values were observed for fruit length (9.65% & 9.65%), days to first fruit harvest (5.39% & 5.38%), days to first female flower (5.32% & 5.32 %) and days to first male flower (3.05% & 3.05%). Environmental coefficient of variation was observed low for all the characters subjected to analysis of genetic parameters. High PCV and GCV (Fig. 1) estimates for number of number of node at first male flower appear, fruit yield per plant and number of node at first female flower appear content suggest substantial variation among the studied plant material thereby, ensuring ample scope for improvement of these characters through phenotypic selection. Kumar *et al.* (2012), Kumar *et al.* (2019), Kumar *et al.* (2020) high GCV & PCV for staminate flower. Kumar and Pandit (2022), Myla *et al.* (2022), Kousthubha *et al*. (2023), Yadav *et al.* (2024) and Devi *et al.* (2025) have also high GCV and PCV values for fruit per plant and fruit yield due to differences in experimental material and growing environment.

High estimates for heritability in broad sense (Table 1) were observed for number of node at first female & male flower appear, days to first male & female flower, days to fruit harvest, fruit length, fruit diameter, average fruit weight, number fruits per plant, fruit yield per plant. High heritability coupled with high genetic advance as percentage mean were observed for number of node at first female flower appear, number of node at first male flower appear, fruit diameter, average fruit weight, number of fruits per plant and fruit yield per plant which revealed that these traits are governed by additive gene action and phenotypic selection would be effective for the improvement of these traits. High heritability along

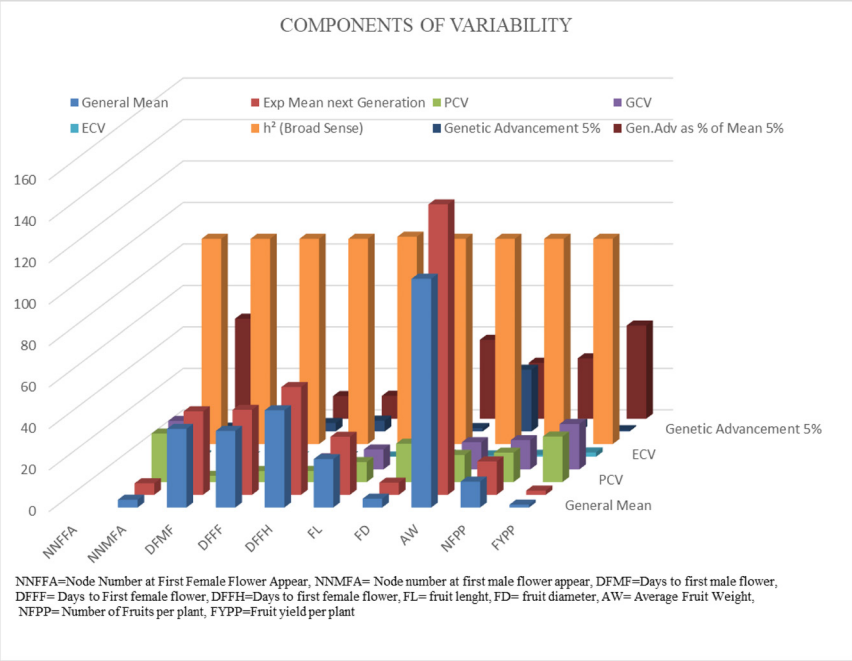

Fig. 1. Estimates of variability parameters for horticultural and yield traits in sponge during summer season, 2024.

with moderate genetic advance was observed for fruit length, days to first fruit harvest and days to first female flower. High heritability and low genetic advance were observed for days to first male flower which reveals that heterosis breeding would be effective for improvement of this trait. Presence of high heritability for above mentioned traits indicated that large proportion of phenotypic variance was attributable to the genotypic variance and the differences for the trait among the genotypes were real. Therefore, selection for these traits on the basis of phenotypic expression could be relied upon.

Kousthubha *et al.* (2023), has also reported high heritability and genetic advance for average fruit weight, number of fruits per plant which corroborate the present findings. number of node at first female flower appear, number of node at first male flower appear, fruit diameter, and fruit yield per plant Likewise Singh *et al.* (2019) observed 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 and present results for these traits are in agreement with their findings.

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