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SHORT RESEARCH ARTICLE

Genetic variation, trait interrelationships and cluster analysis in indigenous sponge gourd (*Luffa cylindrica* L. Roem.) germplasm of Assam

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Abstract

Morpho-metric characterization of sponge gourd germplasm revealed polymorphism in 12 qualitative traits. Primary branches per plant, internode length, peduncle length, fruit length, fruits per plant, seeds per fruit and marketable fruit yield per plant registered high genotypic and phenotypic coefficients of variation. The heritability in broad sense and expected genetic advance as percent of mean were high for all the traits except vine length. The genetic correlation of marketable fruit yield per plant was highly significant and positive with primary branches, internode number, fruit length, female flowers per plant, fruits per plant and fruit weight. Marketable fruit yield had a significant negative genetic correlation with internode length, days to the appearance of first male flower, days to the appearance of the first female flower, node number at which first female flower appears, days to first fruit harvest, fruit diameter and male-female flower ratio. Genetic path analysis revealed high direct effects of fruits per plant and fruit weight on marketable fruit yield. An Unweighted Neighbour-Joining (UNJ) clustering based on usual Euclidean distances grouped the sponge gourd germplasm into three distinct clusters. The information accrued may be useful in sponge gourd improvement.

Keywords: Cluster analysis, Genetic correlation, Genetic parameters, Path coefficient analysis, Polymorphic traits.

Sponge gourd (*Luffa cylindrica* L. Roem.) is a nutritious and tasty vegetable belonging to the family Cucurbitaceae. Its fruits contain several vital nutrients and dietary fibres. It is a very useful crop for smallholder farmers of Asian countries for increasing their income (FAOSTAT 2021). The natural population of sponge gourd (*Luffa cylindrica* L. Roem.) has considerable variability for different traits. Large variation is evident for various qualitative and quantitative traits, including the fruit size which ranges from a few centimeters to one metre among the cultivars grown in India. Phenotypically diverse types are common in homestead gardens and local markets of Assam, reflecting a relatively broad spectrum of variability among the sponge-gourd genetic resources of the region. Profuse morphological variability was found among the test cultigens of *Luffa* in different growing areas of India (Prakash et al. 2013). The information on variability and diversity is an essential prerequisite for improving the crop for a region but that is lacking in the local sponge gourd germplasm of Assam. The coefficient of variation gives an idea of the extent of variability present while the heritability implies the extent of transmissibility of a trait into the progeny generation. Further, high heritability coupled with high genetic advance indicates a preponderant role of additive gene action for a trait. Correlation and path analysis gives an insight into the nature and magnitude of the association of fruit yield and other attributes along with direct and indirect effects of an independent trait on fruit yield. Certain morphological qualitative characters can distinguish the germplasm appropriately based on the polymorphism they exhibit.

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Table 1. Genotypic correlation coefficients among the 18 morpho-metric traits in sponge gourd germplasm.

Traits	IL	PL	DAFMF	DAFFF	IN	VL	NNFFFA	DFFH	PDL	FL	FD	FFPP	FPP	FW	MFFR	SPF	MFYPP
PB	-0.383*	-0.306	-0.179	-0.224	0.610**	0.234	-0.208	-0.214	0.135	0.432*	-0.329	0.617**	0.670**	0.270	-0.321	0.128	0.590**
IL		0.039	0.091	0.164	-0.797**	0.597**	-0.054	0.170	0.084	-0.101	0.031	-0.655**	-0.571**	-0.576**	0.459**	-0.045	-0.635**
PL			0.409*	0.442*	-0.233	-0.217	0.205	0.458**	-0.003	-0.049	-0.076	0.106	-0.151	-0.450**	-0.191	-0.178	-0.323
DAFMF				0.980**	-0.396*	-0.339	0.648**	0.975**	0.016	0.085	0.143	-0.046	-0.179	-0.562**	-0.040	0.138	-0.415*
DAFFF					-0.470**	-0.324	0.689**	1.002**	-0.006	0.016	0.193	-0.098	-0.252	-0.639**	-0.002	0.062	-0.497**
IN						-0.016	-0.214	-0.473**	-0.282	0.026	-0.020	0.707**	0.628**	0.585**	-0.570**	0.187	0.691**
VL							-0.401*	-0.305	-0.231	-0.079	-0.079	-0.073	-0.078	-0.215	-0.091	0.199	-0.137
NNFFFA								0.698**	-0.061	0.204	0.188	-0.100	-0.253	-0.367*	-0.087	-0.050	-0.358*
DFFH									-0.009	0.030	0.178	-0.107	-0.246	-0.630**	-0.015	0.044	-0.488**
PDL										0.158	-0.188	-0.014	0.076	0.271	0.310	0.314	0.193
FL											-0.485**	0.325	0.441*	0.332	-0.154	-0.111	0.467**
FD												-0.245	-0.451**	-0.186	-0.054	0.039	-0.344*
FFPP	-												0.913**	0.139	-0.772	0.208	0.668**
FPP														0.486**	-0.497**	0.146	0.894**
FW															-0.055	0.109	0.818**
MFFR																-0.022	-0.347*
SPF																	0.109

PB = Primary branches per plant, IL = Internode length, PL= Petiole length, DAFMF = Days to the appearance of first male flower, DAFFF= Days to appearance of first female flower, IN = Internode number, VL= Vine length, NNFFFA= Node number at which first female flower appears, DFFH= Days to first fruit harvest, PDL= Peduncle length, FL = Fruit length, FD = Fruit diameter, FFPP= Female flowers per plant, FPP= Fruits per plant, FW= Fruit weight, MFFR= Male-female flower ratio, SPF=Seeds per fruit, MFYPP = Marketable fruit yield per plant.

*, ** Significant at 5% and 1% levels, respective.

Table 2. Genotypic path coefficients of different traits on marketable fruit yield per plant.

Trait	PB	IN	FL	FFPP	FPP	FW	riy
Primary branches (PB)	0.0056	0.0282	0.0126	-0.0675	0.4925	0.1181	0.5895
Internode number (IN)	0.0034	0.0463	0.0008	-0.0774	0.4620	0.2562	0.6912
Fruit length (FL)	0.0024	0.0012	0.0291	-0.0357	0.3241	0.1453	0.4665
Female flowers per plant (FFPP)	0.0034	0.0327	0.0095	-0.1095	0.6711	0.0610	0.6682
Fruits per plant (FPP)	0.0037	0.0291	0.0129	-0.1000	0.7351	0.2128	0.8936
Fruit weight (FW)	0.0015	0.0271	0.0097	-0.0153	0.3573	0.4379	0.8182
Residual = 0.0092							

Table 3. Cluster composition of the 33 sponge gourd genotypes.

Cluster	Sub-cluster	No. of genotypes	Composition
I	A	13	ASG21, ASG2, ASG15, NSG1, ASG20, ASG6, ASG8, ASG24, NSG2, ASG3, ASG25, ASG9, ASG1
	B	9	ASG17, ASG12, ASG13, ASG18, ASG16, ASG11, ASG10, ASG5, ASG28
II	A	8	ASG27, ASG26, ASG7, ASG30, ASG23, Pusa Sneha, ASG19, ASG14
	B	2	ASG29, ASG22
III	-	1	ASG4

Cluster analysis classifies germplasm into some genetically diverse groups and subgroups, enabling the breeder to choose suitably diverse parents for the future hybrid breeding programme. Considering the above, the present investigation was undertaken to assess the genetic variation, correlation and clustering pattern in a collection of sponge gourd germplasm indigenous to Assam.

The present investigation was carried out at the Krishi Vigyan Kendra, Jorhat Farm of Assam Agricultural University in *kharif* 2017. The materials consisted of 30 germplasm lines (ASG1 to ASG30) collected from different places of Assam, NSG1 and NSG 2 from Nagaland and an improved variety, Pusa Sneha, from IARI, New Delhi. The experiment was conducted in a randomized block design (RBD) with two replications keeping a spacing of 2.0 m x 1.2 m. All the plants climbed onto bamboo poles provided for support. Twenty-four qualitative traits were recorded as per descriptors (Joshi *et al.* 2004). However, 18 quantitative traits were considered for assessment of variability, estimation of correlations and cluster analysis among the germplasm studied (Table 1).

Genetic parameters, namely, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in the broad sense (h^2_{bs}), and genetic advance as per cent of mean (GAM) were estimated by using standard statistical procedures. The estimates of h^2_{bs} and GAM were categorized as suggested by Johnson et al. (1955) while the estimates of GCV and PCV were classified following the procedure of Sivasubramanian and Madhavamenon (1973). Standard statistical procedures were followed to generate the genetic correlation matrix. This matrix was, in turn, used for path analysis following the procedure of Dewey and Lu (1959). Cluster analysis was done using DARwin version 6.0.021 (http://darwin.cirad.fr) developed by Perrier and Jacquemoud-Collet (2006). The usual Euclidean distances for 18 morpho-metric traits constituted the Unweighted Neighbour-Joining (UNJ) clustering dissimilarity measures.

Among the qualitative traits, twelve traits were found monomorphic and all the germplasm under study had angular stem, branched tendril, dentate leaf margin, low dorsal as well as low ventral leaf pubescence without any leaf spot, thin stem pubescence, prostrate growth habit, yellow flower, white flesh, black seed and monoecious sex-type. The remaining twelve traits were polymorphic and there was variation from tetramorph to dimorph with fruit shape being tetramorphic, seven traits being trimorphic (leaf shape, leaf size, leaf lobes, fruit ribs, fruit colour, flesh flavor and flesh taste) and four being dimorphic traits (blossom end fruit shape, stem end fruit shape, fruit skin texture and hardness) (Supplementary Tables 1 and 2).

The quantitative traits, namely, marketable fruit yield per plant, primary branches, internode length, peduncle length, fruit length, fruits per plant and seeds per fruit, had high estimates (>20%) of GCV and PCV (trait-wise estimates not shown). A high GCV for these traits revealed more significant genetic variability among the germplasm under study, suggesting the prospect of improvement through selection. Earlier, Tyagi et al. (2020) have reported moderate magnitude of variability in *Luffa*. The range of h^2_{bs} observed for the traits was 46.50 - 99.60%, while GAM varied from 15.45-82.42% for different traits. All the traits except vine length had high h^2_{bs} values (>60%) concurrent with high GAM values (>20%). Primarily, the genes with additive effects govern the traits with high heritability and high expected genetic advance. Simple selection methods such as mass selection without progeny testing would improve a genetically variable population of plants selected for traits largely governed by genes with additive effects.

Trait inter-relationship

Marketable fruit yield per plant showed a highly significant and positive genotypic correlation with primary branches, internode number, and female flowers per plant, fruit length, fruits per plant and fruit weight (Table 1). Literature on work regarding trait relationships is scanty. Significant positive yield correlations with average fruit weight and fruits per plant and the significant positive correlation between fruit yield and fruit length in sponge gourd have been reported earlier. Significant and positive associations of marketable fruit yield per plant with fruits per plant and fruit weight were observed in ridge gourd (Choudhary et al. 2014) and bottle gourd (Chouhan *et al.* 2020). In the present study, primary branches per plant and internode number had a positive and highly significant genetic correlation, and both had significant to highly significant genetic correlation with fruit length, female flowers per plant, fruits per plant, fruit weight and marketable fruit yield per plant in sponge gourd. Female flowers per plant had a positive and highly significant genetic correlation with fruits per plant and marketable fruit yield per plant, while fruits per plant had a positive and highly significant genetic correlation with fruit weight and marketable fruit yield per plant. The results reported above exhibited that fruit yield had a positive genetic correlation with a few simply inherited traits with high heritability. Primary branches, internode number, female flowers per plant, fruits per plant, and fruit weight are some of the corollary traits the cucurbit breeders might consider to improve marketable fruit yield. Such secondary traits could be the basis of indirect selection of plants reflecting a possibility of correlated response in fruit yield.

Nevertheless, marketable fruit yield per plant showed significant to highly significant negative genetic correlation with internode length, days to the appearance of first male flower, days to the appearance of the first female flower, node number at which first female flower appears, days to first fruit harvest, fruit diameter and male-female flower ratio. Both days to appearance of the first male flowers and days to appearance of first female flowers had significant to highly significant negative genetic correlations with internode number, fruit weight and marketable fruit yield per plant (Table 1). The present investigation also revealed that fruit diameter had a significant to highly significant negative genetic correlation with fruit length, fruits per plant and marketable fruit yield per plant. A significant negative genetic correlation was observed between days to the appearance of the first female flower and marketable fruit yield per plant in sponge gourd.

The genotypic path coefficient analysis revealed that fruits per plant and fruit weight were the two essential component traits of marketable fruit yield per plant because they had high and positive direct effects on fruit yield (Table 2).

Fruits per plant and fruit weight had positive and direct effects on yield per plant in sponge gourd. Narayanankutty *et al.* (2006) and Nisha *et al.* (2018) obtained similar results in snake gourd and watermelon, respectively. The indirect influence of fruits per plant via fruit weight indicated the importance of fruit weight towards the enhancement of marketable fruit yield per plant. So far as the indirect effect of fruit weight was concerned, fruit weight exerted a substantial indirect influence on marketable fruit yield through fruits per plant. The results of a genotypic path analysis revealed a high positive indirect effect of female flowers per plant via fruits per plant. As fruit length showed a high positive indirect effect via fruits per plant, the role of fruits per plant on marketable fruit yield per plant was found considerable. The indirect influences of internode number via fruits per plant and fruit weight were high and moderate, respectively, suggesting an appreciable relationship of fruits per plant and fruit weight to marketable fruit yield per plant. The residual of 0.0092 revealed that the six independent traits under consideration accounted for 99.08% of the total genetic variation in marketable fruit yield per plant.

Cluster analysis

UNJ clustering of the thirty-three-sponge gourd germplasm in the present study revealed three distinct clusters (Table 3). There were twenty-two genotypes in cluster I, ten in cluster II and one genotype in cluster III. The genotypes of cluster I registered the highest mean values for internode length, fruit length and fruit diameter. Cluster II recorded the highest mean values for primary branches, internode number, vine length, female flowers per plant, fruits per plant, fruit weight and marketable fruit yield per plant. In contrast, cluster III with a single genotype had the highest mean value for primary branches. Similar pattern of clustering using different sets of sponge gourd materials has been obtained earlier by several researches (Quamruzzaman et al. 2011). Therefore, selecting superior genotypes from clusters I and II as parents for hybridization would produce high yielding hybrids with desirable component traits. Few researchers grouped a number of sponge gourd genotypes in to various clusters in previous studies. The traits *viz*., fruit yield per vine, number of fruits per vine, and node at which first staminate flower appeared contributed the maximum towards the genetic divergence in earlier studies and played an essential role in the improvement programme. It could be concluded that the information generated from the study would be useful to plant breeders in selecting potential gene pools in sponge gourd breeding.

Author(s) contribution

Conceptualization of research (IS, DBP); Designing of the experiments (IS, DBP); Contribution of experimental materials (IS, DBP); Execution of field/lab experiments and data collection (IS, DBP); Analysis of data and interpretation (IS, DBP, AS, NSB, DS, DB); Preparation of manuscript (IS, DBP, AS, DS, NSB).

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