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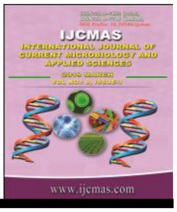

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Genetic Variability, Diversity and Character Association in Sponge Gourd [*Luffacylindrica* (Roem.) L.]

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ABSTRACT

The present study was conducted to determine phenotypic performance, genetic variability, heritability, genetic advance, diversity, correlation and path analysis for yield and seventeen yield attributing characters of forty five sponge gourd germplasm. PCV was higher than GCV for all the traits studied. High PCV and GCV were recorded for number of primary branches, number of fruiting nodes on main stem, sex ratio, fruits per plant and yield per plant. Thirteen characters showed high heritability coupled with high genetic advance. Correlation coefficient study indicated that yield per plant had highly significant positive relationship with number of primary branches, fruiting nodes on main stem, fruit length, fruit weight, fruits per plant, seeds per fruit and 100 seed weight. Path co-efficient analysis showed that fruits per plant (0.7013) and number of seeds per fruit (0.6833) exhibited the highest positive direct effect on yield per plant. Based on Mahalanobis' D^2 statistics, the forty five genotypes were grouped into seven different clusters. Maximum intra cluster distance was in cluster- III (541.13) where maximum inter-cluster distance was between cluster- IV and cluster- V (5177.9). Characters namely yield per plant, fruit weight and number of fruiting nodes on main stem showed maximum contribution towards divergence, hence considering these characters in selection of diverse parents during hybridization program manifests high heterosis.

Keywords

Genetic variability, Diversity, Yield, Correlation coefficient, Path analysis

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Introduction

Sponge gourd or smooth gourd or dishcloth gourd or smooth loofah or vegetable sponge [*Luffa cylindrica* (Roem.) L.] (2n=2x=26) is one of the minor cucurbitaceous vegetable crop with old world origin in subtropical Asian region including particularly India (Kalloo, 1993; Swarup, 2006). This crop has been cultivating for centuries in the Middle East, India, China, Japan and Malaysia. In India, it is cultivated on both commercial scale and in kitchen gardens during the spring summer and rainy season. *Luffa* has nine species out of which *Luffa acutangula* (L.) Roxb., *L. cylindrica* M. Roem., *L. echinta* Roxb., *L. graveolens*, *L. tuberose* Roxb., *L. umbellata* are found in India. *Luffa acutangula* (ridge gourd) and *Luffa cylindrica* (sponge gourd) are grown throughout India in tropical and subtropical climate. *Luffa acutangula* has three varieties: var. *acutangula* is grown in South East Asia and other tropical areas; var. *amara*, a wild form is confined to peninsular India, while var. *forskallii* (Harms.) Heiser and Schilling, another wild form is confined to Yemen. *Luffa echinata* grows in natural habitat in western Himalayas, central India and Gangetic plains. *Luffa graveolens* is a wild species distributed in parts of North Central India

The tender or immature fruits are cooked as vegetable, used in the preparation of chutneys and curries and tender fruits are easily digestible and increase appetite when consumed. Sponge gourd is a highly nutritive vegetable and contains moisture of 93.2 g, protein 1.2 g, fat 0.2 g, carbohydrates 2.9 g, vitamins (thiamine 0.02 mg, riboflavin 0.06mg, niacin 0.4 mg and β carotene 120 mg), minerals (calcium 36 mg, phosphorous 19 mg and iron 1.1 mg) and fibers 0.20 g per 100 g of edible portion (Gopalan *et al.,* 1999). Sponge gourd fruits contain more protein and carotene than ridge gourd (More and Shinde, 2001). Sponge gourd is a minor crop and its cultivation is not yet flourished at commercial scale and exact area of cultivation is not known.

Sponge gourd is an annual climber and monoecious vegetable but different sex forms like hermaphrodite, staminate and pistillate etc. are commonly found in nature (Takahashi, 1980) flowers are large yellow in colour, Group of male and single female flowers are formed in leaf axil. The existence of different size of fruits ranging from a few centimetres to one meter, different fruit shapes and colours (light green, green and dark green with light white stripes, etc.) indicates the presence of wide genetic variability. To develop a new variety there is need of high magnitude of genetic variability in the base material and the vast of variability for desired characters, variation may exist or created, is the first step to any crop improvement programme (Singh, 2000). To know the extent of variability present in a population, evaluation of large number of germplasm lines is the first line of work. This improvement in any crop is based on the extent of genetic variation and magnitude of available beneficial genetic variability. Some of the biometric parameters include genotypic (GCV) and phenotypic (PCV) coefficients of variation. High value of these coefficients indicates wider diversity. Similarly, narrow difference between GCV and PCV reveals low sensitivity to the environmental effects. Another indicator of variability is heritability, which is the ratio of genetic variance to total variance. This is broad sense heritability and gives an idea about that portion of observed variability which is attributable to genetic differences. Heritability estimates supplemented by genetic variance are more meaningful. Heritability is a component in the computation of expected progress which is most meaningful when accompanied by genetic advance. Genetic advance would be more in cases where the additive genetic variance is more than non-additive genetic variance (Lush, 1949).

Crop improvement through successful selection programme is only achieved using valid information about the correlation and genetic variability of traits of interest. Correlation studies among yield and other traits of the crop will be of interest to breeders in planning hybridization programmes and evaluating the individual plants in the segregating populations. Knowledge of genetic diversity among existing cultivars of any crop is essential for long term success in breeding programme and to maximize the exploitation of the germplasm resources (Rabbani *et al.,* 2012). The genetically diverse parents are always able to produce high heterotic effects and great frequency of desirable segregants in further generations. D^2

statistic is a useful tool to measure genetic divergence among genotypes in any crop as developed by Mahalanobis (1936). However, in the present study, an attempt has been made together information on genetic variability, heritability, genetic gain, correlation and path analysis for different characteristics of sponge gourd, so as to select the potential parents for breeding programme to attain the anticipated improvement in fruit yield per plant.

Materials and Methods

Location and experiment

The study was conducted in Alluvial zone of West Bengal at Horticultural Research Station, Mandouri, Bidhan Chandra KrishiViswavidyala, West Bengal, India during March 2014 and July 2015.

Plant material and source

Total forty five genotypes were collected from ICAR-NBPGR, New Delhi; ICAR-IIVR, Varanasi; parts of West Bengal, Andhra Pradesh and Bihar states of India. It was evaluated for two years during March 2014 and March 2015. The seeds were sown in pits taken at a row spacing of 1.0m and intra row spacing of 0.75m in randomized block design (RBD). Well decomposed FYM (Farm Yard Manure) was incorporated into the soil @ 10 tonnes per hectare.

The experimental plots were fertilized @ 40 kg N, 20 kg P_2O_5 and 20 kg K_2O per hectare. Half of the nitrogen, full dose of phosphorus and potash were applied as basal. The remaining half of the nitrogen was applied in two equal splits at an interval of one month starting from sowing. The crop was grown under irrigated conditions duly adopting recommended cultural practices (Singh and Singh, 2009). Need based plant protection measures were also taken up to control the pests and diseases.

Observations

The observations were recorded in five randomly selected plants from each replication for vine length, number of primary branches, number of fruiting nodes on main stem, days to first staminate flower appearance, days to first pistillate flower appearance, days to 50% flowering, span of flowering, sex ratio, node at which 1st female flower appearance, days to harvestable maturity from anthesis, fruit length, diameter of the fruit, fruit weight, number of fruits per plant, number of seeds per fruit, seed index (100 seed weight) and fruit yield per plant.

Statistical analysis

The data recorded were subjected to genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad sense heritability(H^2), genetic advance as per cent of mean (GAM), correlation (genotypic and phenotypic) and path coefficients were computed by the methods suggested by Panse and Sukhatme (1985). Analysis of genetic divergence was done according to Mahalanobis' D^2 (1936) statistics. The analysis was computed by using computer software program Windostat version 9.3 from Indostat services, Hyderabad, India.

Results and Discussion

The analysis of variance showed highly significant differences among 45 genotypes for all the characters indicating differences among the genotypes under study. The extent of variability in sponge gourd genotypes were measured in terms of mean, range, PCV, GCV, heritability and genetic advance (Table 1). Range of all traits revealed that there was a wide variation among the collected genotypes. The range of variation was widest for fruit weight (74.96 to 184.29 g) followed by fruit length (11.37 to 25.54 cm). The narrowest range was observed in seed index (10.73 to 13.01). PCV were higher than their corresponding GCV, which is obvious due to environmental influence. Relatively higher magnitude (>20.01%) of PCV and GCV were recorded in number of primary branches (24.56%, 24.94%), number of fruiting nodes on main stem (34.46%, 34.67%), sex ratio (22.29%, 24.35%), fruits per plant (22.97%, 23.61%) and yield per plant (44.16%, 46.66%). This implies that maximum variability is existed in the genotypes for aforesaid traits and there is good scope for improvement of these characters. Similar results were also reported byGowda *et al.,* (2011), Rabbani *et al.,* (2012), Dubey *et al.,* (2013), Choudhary *et al.,* (2014), Koppad *et al.,* (2015), Ananthan and Krishnamoorthy (2017), Karthik *et al.,* (2017) in ridge gourd, Khule *et al.,* (2011), Kumar *et al.,* (2013), Sharma *et al.,* (2017) in sponge gourd. The differences between values of PCV and GCV were less for all traits except number of seeds per fruit (16.31%, 20.64%). This suggests that the traits were less influenced by environment and hence they could be improved by following simple phenotypic selection. Similar results were also reported by Gowda *et al.,* (2011), Rabbani *et al.,* (2012), Choudhary *et al.,* (2014) and Koppad *et al.,* (2015) in ridge gourd.

GCV can further be investigated with the help of heritability estimates. While co-efficient of variation measure the magnitude of variability present in a population, heritability indicates the reliability with which the genotype is recognized by its phenotypic expression. High heritability estimates provides a clue that the characters would exhibit high response to selection. High heritability(>60%, Robinson 1966) and genetic advance as per cent of mean (>20%, Johnson *et al.,* 1955) estimates were recorded for vine length (89.55, 22.70), number of primary branches (96.99, 49.83), number of fruiting nodes on main stem (98.79, 70.55), sex ratio (83.81, 42.04), fruits per plant (94.58, 46.01), yield per plant (89.55, 86.08), days to pistillate flower appearance (87.58, 21.45), days to 50% flowering (85.29, 22.85), node at first female flower appearance (91.44, 36.89), fruit length (81.86, 35.26), fruit diameter (83.06, 21.31), fruit weight (74.15, 25.19) and number of seeds per fruit (62.41, 26.54) respectively. This indicated that all the above said traits were under the influence of additive gene action and simple selection based on phenotypic performance of these traits would be effective. Similar findings were reported by Choudhary *et al.,* (2014), Ananthan and Krishnamoorthy (2017) in ridge gourd, Khule *et al.,* (2011), Kumar *et al.,* (2013), Sharama *et al.,* (2017) in sponge gourd.

Correlation studies showed that for most character pairs, genotypic and phenotypic associations were in the same direction and genotypic estimates were higher than the phenotypic ones, indicating an inherent association between the characters (Table 2). The correlation studies revealed that yield per plant had positive and highly significant correlation with number of primary branches (0.4689, 0.4747), fruiting nodes on main stem (0.6141, 0.6168), fruit length (0.3309, 0.3396), fruit weight (0.4677, 0.4475), fruits per plant (0.6607, 0.6648), seeds per fruit (0.5401, 0.4772) and 100 seed weight (0.2462, 0.1978). These characters were most important selection criteria as they showed significant positive correlation and positive direct effect with yield. Days taken for first staminate flower appearance, days taken for first pistillate flower appearance, days to 50 % flowering, sex ratio, node at which first female flower appearance and days to harvestable maturity from anthesis were found to be negatively associated with total yield per vine but in desirable direction because negative values of these traits are beneficial and contribute positively to the yield per vine. This suggested that direct selection based on these traits would be rewarding for yield improvement. Such results were earlier reported by Pandey *et al.,* (2012), Kumar *et al.,* (2013), Dubey *et al.,* (2013), Yadav *et al.,* (2017) in sponge gourd. Rabbani *et al.,* (2012), Gowda *et al.,* (2012), Dubey *et al.,* (2013), Narasannavar *et al.,* (2014), Choudhary *et al.,* (2014) and Koppad *et al.,* (2015), Varalaxmi *et al.,* (2015), Ananthan and Krishnamoorthy (2017) in ridge gourd.

Path analysis helps in understanding the magnitude of direct and indirect contribution of each character on the dependent character, *viz.,* yield. The results presented in Table 3, revealed that's different component traits *viz.,* fruits per plant (0.7013), Number of seeds per fruit (0.6833) and seed index (0.2293) exhibited positive direct effects towards yield per vine along with significant positive correlation with yield, indicating the importance of these characters in direct selection for yield. Similar results were reported by Pandey *et al.,* (2012), Kumar *et al.,* (2013), Yadav *et al.,* (2017), Sharma *et al.,* (2017) in sponge gourd, Rabbani *et al.,* (2012), Singh *et al.,* (2012), Dubey *et al.,* (2013), Narsannavar *et al.,* (2014), Choudhary *et al.,* (2014), Koppad *et al.,* (2015), Varalaxmi *et al.,* (2015), Ananthan and Krishnamoorthy (2017) in ridge gourd.

All the forty five genotypes were grouped into 7 different non-overlapping clusters following Mahalanobis's methods (Table 4). Out of the seven clusters, cluster- I was largest comprising 18 genotypes, followed by cluster- II comprising 12 genotypes, cluster -III with 9 genotypes, cluster -IV with 3 genotypes. Three clusters were single genotype clusters, these clusters were V, VI and VII. The inter cluster distances were higher than intra cluster distances (Table 5). Maximum intra cluster D^2distance was found to be in cluster- IV(541.13) followed by cluster-III (519.62) and cluster- II (351.53). Maximum inter cluster distance was found to be between cluster- IV and cluster- V (5177.9) followed by cluster- IV and cluster- VI (4034.09) and cluster- IV and cluster- VII (3552.24). genotypes belonging to distant clusters may be used as parents in hybridization programme for exploiting high heterosis in F_1generation as reported by Choudhary *et al.,* (2011), Rabbani *et al.,* (2012), Yadav *et al.,*(2016), Quamruzzaman *et al.,* (2011), Khule *et al.,* (2012), Singh *et al.,* (2008).

The comparison of clusters means revealed considerable differences among the clusters of different quantitative characters (Table 6). The cluster mean for vine length was highest in cluster- I (3.45 m) followed by cluster –II and IV (3.25 m) and lowest vine length for the cluster-VII (2.74 m). For number of primary branches cluster- II (3.89) had highest value followed by clusters- VI, VII (3.60) and lowest value for cluster-I (2.66). Number of fruiting nodes on main stem highest value was recorded by cluster- II (5.92) and lowest by cluster- V (3.20). For days to first staminate flowers appearance cluster-VII (47.96) has taken more number of days while cluster- IV (37.95 days) recorded minimum number of days. Maximum number of days to first pistillate flower appearance was observed in cluster-VII (52.63 days), while minimum number of days was observed in cluster- IV (41.71 days). Cluster- IV (45.08) recorded minimum days to 50 % flowering and maximum for the cluster- VII (57.50). Cluster mean value for span of flowering ranged from 36.49 to 38.43, highest being for the cluster-III and lowest in the cluster VII. Sex ratio on whole plant ranged from 16.09 to 24.67; the highest is being for the cluster- I and the lowest for the cluster VI. Cluster –IV had recorded lowest (10.72) for the node at which the first female flower appeared, while cluster- I (14.37) recorded highest node for this trait.

Table.1 Estimation of variability, heritability and genetic advance as per cent of mean for seventeen characters in 45 genotypes of sponge gourd

Sl.No	Character	Range		Mean	GCV %	PCV %	h^2 (Broad sense)	Genetic Adv. As % of Mean
		Maximum	Minimum					
1	Vine length (m) (90 DAS)	4.85	01.98	03.29	12.55	14.30	89.55	22.70
2	No. of primary branches	4.80	01.80	03.09	24.56	24.94	96.99	49.83
3	No. of fruiting nodes on main stem	7.20	02.20	04.20	34.46	34.67	98.79	70.55
4	Days to first staminate flower appearance	49.85	30.88	42.26	10.71	12.45	73.91	18.96
5	Days to first pistillate flower appearance	55.50	35.23	46.54	11.13	11.89	87.58	21.45
6	Days to 50% flowering	60.00	37.00	50.26	12.01	13.01	85.29	22.85
7	Span of flowering	42.23	35.27	37.63	03.71	04.85	58.69	05.86
8	Sex ratio (M/F)	37.15	14.93	22.76	22.29	24.35	83.81	42.04
9	Node of 1st female flower appearance	19.05	06.56	13.03	18.73	19.59	91.44	36.89
10	Days to harvestable maturity from anthesis	07.45	05.30	06.45	06.95	07.54	85.07	13.21
11	Fruit length (cm)	25.54	11.37	19.49	18.92	20.91	81.86	35.26
12	Fruit diameter (cm)	06.40	04.20	05.21	11.35	12.45	83.06	21.31
13	fruit weight (g)	184.29	74.96	137.25	14.20	16.49	74.15	25.19
14	Fruits per plant	18.89	07.41	10.93	22.97	23.61	94.58	46.01
15	No. of seeds per fruit	125.32	47.22	90.99	16.31	20.64	62.41	26.54
16	Seed index (100 seed weight)	13.01	10.73	11.91	04.69	05.20	81.40	08.72
17	Yield per plant (kg)	02.26	00.65	01.46	44.16	46.66	89.55	86.08

Table.2 Genotypic (G) and Phenotypic (P) correlation coefficients among important biometrical traits in sponge gourd

Charac ters		(PB)	(FN)	(DSF)	(DFF)	(DPF)	(SF)	(SR)	(NFA)	(DHM)	(FL)	(FD)	(FW)	(FPP)	(NSF)	(SI)	(Y)
VL	G	0.2705**	-0.0354	0.0107	0.0425	0.1267	0.4624**	0.4869**	0.1294	-0.0082	-0.0088	0.0309	0.0100	-0.1299	0.1251	0.5255**	-0.0152
	P	0.2696**	0.0117	0.2494**	0.1963*	0.2595**	0.5590**	0.5476**	0.2379**	0.1481	0.1609	0.1934*	0.2200*	-0.0184	0.3522**	0.1652	0.0353
PB	G		0.8599**	-0.6522**	-0.6120**	-0.6030**	0.0667	-0.4180**	-0.6577**	-0.2779**	0.1484	-0.2539**	-0.0427	0.5040**	-0.0049	0.0353	0.4689**
	P		0.8589**	-0.5024**	-0.5201**	-0.5241**	0.1310	-0.3537**	-0.5992**	-0.2089*	0.1811*	-0.1896*	0.0107	0.5149**	0.0494	0.0101	0.4747**
FN	G			-0.6712**	-0.6665**	-0.6492**	-0.1565	-0.4872**	-0.6833**	-0.4126**	0.2340**	-0.2589**	0.1500	0.5008**	0.1877*	0.0408	0.6141**
	P			-0.5404**	-0.5872**	-0.5824**	-0.0689	-0.4272**	-0.6350**	-0.3529**	0.2442**	-0.2078*	0.1603	0.5051**	0.1837	0.0235	0.6168**
DSF	G				0.9458**	0.9543**	0.0770	0.6166**	0.6890**	0.4038**	-0.5178**	0.4299**	-0.2273**	-0.3273**	-0.2245**	0.0617	-0.4906**
	P				0.9385**	0.9434**	0.2980**	0.6340**	0.6848**	0.4706**	-0.2473**	0.5245**	0.0018	-0.1952*	0.0330	-0.0773	-0.3729**
DFF	G					0.9530**	0.2843**	0.5934**	0.6781**	0.5352**	-0.5309**	0.4759**	-0.2119**	-0.2974**	-0.1928*	0.0141	-0.4766**
	P					0.9512**	0.3967**	0.6067**	0.6818**	0.5691**	-0.3246**	0.5340**	-0.0467	-0.2089*	-0.0015	-0.0752	-0.4024**
DPF	G						0.2480**	0.6529**	0.6818**	0.4750**	-0.5302**	0.4799**	-0.1703*	-0.3696**	-0.1485	0.0476	-0.5084**
	P						0.3429**	0.6678**	0.6908**	0.5132**	-0.3493**	0.5399**	-0.0225	-0.2857**	0.0212	-0.0464	-0.4423**
SF	G							0.4424**	0.1591	0.4064**	-0.2267**	0.1405	0.0174	-0.1811*	0.0738	0.2101*	-0.0729
	P							0.4604**	0.2290**	0.4806**	0.0407	0.2815**	0.2146*	-0.0267	0.3030**	-0.0038	0.0046
SR	G								0.7187**	0.3363**	-0.1623	0.2493**	0.1853*	-0.4152**	0.2205*	0.2949**	-0.2238**
	P								0.7295**	0.3745**	-0.0488	0.3153**	0.2759**	-0.3306**	0.3485**	0.1002	-0.1795*
NFA	G									0.4510**	-0.2172*	0.3334**	-0.0582	-0.4297**	-0.0302	0.0585	-0.4577**
	P									0.4639	-0.1222	0.3719**	0.0510	-0.3678**	0.0958	-0.0459	-0.4146**
DHM	G										-0.5552**	0.3949**	-0.2843**	-0.2328**	-0.2520**	0.0346	-0.4148**
	P										-0.3703**	0.4511**	-0.1199	-0.1445	-0.0434	-0.0540	-0.3463**
FL	G											-0.8009**	0.3530**	-0.0773	0.4026**	0.3937**	0.3309**
	P											-0.5656**	0.4261**	0.0052	0.4642**	0.2280**	0.3396**
FD	G												-0.4016**	0.1207	-0.3681**	-0.2037*	-0.2147*
	P												-0.2070*	0.1711*	-0.1344	-0.2569**	-0.1582
FW	G													-0.3733**	0.9570**	0.5530**	0.4677**
	P													-0.2393**	0.9251**	0.2974**	0.4475**
FPP	G														-0.2855**	-0.1478	0.6607**
	P														-0.1371	-0.1649	0.6648**
NSF	G															0.6836**	0.5401**
	P															0.2816**	0.4772**
SI	G																0.2462**
	P																0.1978*

*****: Significant at p = 0.05, **: Significant at p = 0.01

(VL)- Vine length (cm); (PB)-No. of primary branches; (FN)-No. of fruiting nodes on main stem; (DSF)-Days to first staminate flower appearance; (DFF)-Days to 50% flowering; (DPF)-Days to first pistillate flower appearance; (SF)-Span of flowering; (SR)-Sex ratio (M/F); (NFA)-Node at which 1st female flower appearance; (DHM)-Days to harvestable maturity from anthesis; (FL)-Fruit length (cm); (FD)-Fruit diameter (cm); (FW)-Fruit weight (g); (FPP)-Fruits per plant; (NSF)-No. of seeds per fruit; (SI)-Seed index (100 seed weight); (Y)- Yield per plant (kg)

Table.3 Path Coefficients (Genotypic) showing direct (Bold) and indirect effects of component traits in sponge gourd genotypes

Characters	(VL)	(PB)	(FN)	(DSF)	(DFF)	(DPF)	(SF)	(SR)	(NFA)	(DHM)	(FL)	(FD)	(FW)	(FPP)	(NSF)	(SI)	r
VL	**-0.3629**	0.0461	0.0058	-0.0079	0.0163	-0.0009	-0.0423	0.2268	-0.0087	0.0023	0.0029	-0.0054	-0.0023	-0.0911	0.0855	0.1205	-0.0152
PB	-0.0982	**0.1705**	-0.1398	0.4825	-0.2349	0.0041	-0.0061	-0.1947	0.0441	0.078	-0.0488	0.0443	0.0097	0.3535	-0.0033	0.0081	0.4689**
FN	0.0129	0.1466	**-0.1626**	0.4966	-0.2558	0.0044	0.0143	-0.2269	0.0458	0.1159	-0.077	0.0452	-0.0339	0.3512	0.1282	0.0094	0.6141**
DSF	-0.0039	-0.1112	0.1091	**-0.7398**	0.363	-0.0065	-0.007	0.2872	-0.0462	-0.1134	0.1705	-0.0751	0.0515	-0.2295	-0.1534	0.0141	-0.4906**
DFF	-0.0154	-0.1043	0.1084	-0.6997	**0.3838**	-0.0065	-0.026	0.2764	-0.0455	-0.1503	0.1748	-0.0831	0.048	-0.2086	-0.1318	0.0032	-0.4766**
DPF	-0.046	-0.1028	0.1056	-0.706	0.3657	**-0.0068**	-0.0227	0.3041	-0.0457	-0.1334	0.1745	-0.0838	0.0386	-0.2592	-0.1015	0.0109	-0.5084**
SF	-0.1678	0.0114	0.0255	-0.057	0.1091	-0.0017	**-0.0914**	0.2061	-0.0107	-0.1141	0.0746	-0.0245	-0.0039	-0.127	0.0504	0.0482	-0.0729
SR	-0.1767	-0.0713	0.0792	-0.4562	0.2277	-0.0044	-0.0404	**0.4657**	-0.0482	-0.0944	0.0534	-0.0435	-0.0419	-0.2912	0.1507	0.0676	-0.2238**
NFA	-0.047	-0.1121	0.1111	-0.5097	0.2603	-0.0046	-0.0145	0.3347	**-0.0671**	-0.1266	0.0715	-0.0582	0.0132	-0.3013	-0.0207	0.0134	-0.4577**
DHM	0.003	-0.0474	0.0671	-0.2987	0.2054	-0.0032	-0.0371	0.1566	-0.0303	**-0.2808**	0.1828	-0.069	0.0643	-0.1633	-0.1722	0.0079	-0.4148**
FL	0.0032	0.0253	-0.0381	0.3831	-0.2038	0.0036	0.0207	-0.0756	0.0146	0.1559	**-0.3292**	0.1399	-0.0799	-0.0542	0.2751	0.0903	0.3309**
FD	-0.0112	-0.0433	0.0421	-0.318	0.1827	-0.0032	-0.0128	0.1161	-0.0224	-0.1109	0.2637	**-0.1747**	0.0909	0.0847	-0.2515	-0.0467	-0.2147*
FW	-0.0036	-0.0073	-0.0244	0.1682	-0.0813	0.0012	-0.0016	0.0863	0.0039	0.0798	-0.1162	0.0701	**-0.2264**	-0.2618	0.6539	0.1268	0.4677**
FPP	0.0471	0.0859	-0.0814	0.2421	-0.1141	0.0025	0.0166	-0.1934	0.0288	0.0654	0.0254	-0.0211	0.0845	**0.7013**	-0.1951	-0.0339	0.6607**
NSF	-0.0454	-0.0008	-0.0305	0.1661	-0.074	0.001	-0.0067	0.1027	0.002	0.0708	-0.1326	0.0643	-0.2166	-0.2002	**0.6833**	0.1567	0.5401**
SI	-0.1907	0.006	-0.0066	-0.0456	0.0054	-0.0003	-0.0192	0.1373	-0.0039	-0.0097	-0.1296	0.0356	-0.1252	-0.1036	0.4671	**0.2293**	0.2462**

*: Significant at p = 0.05, **: Significant at p = 0.01 Residual effect: 0.1264

(VL)- Vine length (m); (PB)-No. of primary branches; (FN)-No. of fruiting nodes on main stem; (DSF)-Days to first staminate flower appearance; (DFF)-Days to 50% flowering; (DPF)-Days to first pistillate flower appearance; (SF)-Span of flowering; (SR)-Sex ratio (M/F); (NFA)-Node at which 1st female flower appearance; (DHM)-Days to harvestable maturity from anthesis; (FL)-Fruit length (cm); (FD)-Fruit diameter (cm); (FW)-Fruit weight (g); (FPP)-Fruits per plant; (NSF)-No. of seeds per fruit; (SI)-Seed index (100 seed weight)

Table.4 Grouping of 45 sponge gourd genotypes based on D2 analysis

S.No	Cluster number	No of genotypes	Name of genotypes
1	Cluster-I	18	Basantpur Local, Habra Local, IC-398694, IC-398572, IC-336981, IC-361081, IC-343029, IC-326772, VRSG-57, IC-276519, Rajahmundry Local, IC-544806, IC-355633, Kalyani Local-2, IC-538115, IC-538688, IC-397534 and Kalyani Local-1
2	Cluster-II	12	IC-336760, IC-284795, IC-092761, IC-336759, IC-549807, IC-276381, VRSG-167, VRSG-70, IC-550776, IC-274593, VRSG-08 and IC-284882
3	Cluster-III	9	IC-284877, VRSG-09, IC-284869, VRSG-199, IC-276284, IC-339218, Ghoragacha Local, IC-355635 and Kalyani Local-3
4	Cluster-IV	3	IC-343160, VRSG-12 and Patna Local
5	Cluster-V	1	IC-284948
6	Cluster-VI	1	IC-284941
7	Cluster-VII	1	IC-284840

Table.5 Inter and intra cluster D2 values

	Cluster-I	**Cluster-II**	**Cluster-III**	**Cluster-IV**	**Cluster-V**	**Cluster-VI**	**Cluster-VII**
Cluster-I	227.436	1643.740	555.056	2356.755	936.269	1081.514	1568.103
Cluster-II		351.528	1131.590	745.572	3399.356	2853.304	1959.682
Cluster-III			519.616	1775.888	1552.321	1463.971	1445.357
Cluster-IV				541.126	5177.897	4034.087	3552.242
Cluster-V					0.000	966.879	1276.876
Cluster-VI						0.000	732.866
Cluster-VII							0.000

Table.6 Mean values of seven clusters for yield and its contributing characters

Cluster Number	Vine length (m) (90 DAS)	No. of primary branches	No. of fruiting nodes on main stem	Days to first staminate flower appearance	Days to first pistillate flower appearance	Days to 50% flowering	Span of flowering	Sex ratio (M/F)	Node at which 1st female flower appearance	Days to harvestable maturity from anthesis	Fruit length (cm)	Fruit diameter (cm)	Fruit weight (g)	Fruits per plant	No. of seeds per fruit	Seed index (100 seed weight)	Yield per plant (kg)
Cluster-I	3.45	2.66	3.09	43.99	48.44	52.20	37.52	24.67	14.37	6.52	19.99	5.21	136.84	09.19	89.74	11.97	1.25
Cluster-II	3.25	3.89	5.92	39.15	42.60	45.58	37.44	20.78	11.18	6.23	20.87	4.99	145.95	12.46	96.89	11.82	1.80
Cluster-III	3.13	2.78	3.93	43.47	48.60	53.03	38.43	23.29	13.72	6.63	18.17	5.33	137.89	10.32	91.99	12.04	1.42
Cluster-IV	3.25	3.13	4.87	37.95	41.71	45.08	37.30	21.06	10.72	6.02	21.43	4.95	159.75	13.41	112.22	12.62	2.14
Cluster-V	3.22	2.80	3.20	41.00	46.83	48.50	37.40	21.10	12.83	6.84	16.29	5.12	87.28	07.49	54.99	10.73	0.65
Cluster-VI	3.14	3.60	3.40	46.30	49.23	56.63	37.25	16.09	13.23	6.88	11.37	6.35	74.96	18.89	47.22	10.73	1.42
Cluster-VII	2.74	3.60	5.60	47.96	52.63	57.50	36.49	20.93	12.02	6.47	11.41	6.40	79.13	17.27	49.85	10.98	1.37
% Contribution towards divergence	4.20	5.31	7.27	7.84	3.76	3.48	5.18	7.31	3.15	5.14	6.89	3.54	9.48	5.78	3.43	2.91	15.33

Cluster- IV (6.02) recorded least number of days to harvestable maturity from anthesis, while cluster- VI (6.88) recorded maximum mean value. Maximum mean for fruit length was in the cluster-IV (21.43 cm) and minimum for the cluster-VI (11.37 cm). Diameter of fruit was maximum in the cluster-VII (6.40 cm) and minimum in the cluster- IV (4.95 cm). Fruit weight ranged from 74.96 to 159.75 g, with maximum fruit weight in the cluster- IV and minimum in the cluster- VI. Cluster- V (7.49) had recorded minimum number of fruits per plant, while cluster- VI (18.89) maximum number of fruits per plant. Number of seeds per fruit ranged from 47.22 to 112.22 with maximum number of seed per fruit in cluster- IV and minimum in cluster- VI. Seed index was highest in cluster- IV (12.62 g) and least in cluster- V and VI (10.73 g). Yield per plant was highest in the cluster- IV (2.14 Kg) while lowest yield in the cluster V (0.65 kg). For crop improvement in sponge gourd inter crossing among genotypes with outstanding mean performance was suggested by Singh *et al.*, (2008) in ridge gourd, Quamruzzaman *et al.*, (2011), Singh *et al.*, (2017) in sponge gourd.

Highest per cent contribution towards total genetic divergence (Table 6) was exhibited by yield per plant (15.33), followed by fruit weight (9.48), Days to first staminate flower appearance(7.84), sex ratio (7.31), number of fruiting nodes on main stem (7.27), fruit length (6.89), fruits per plant (5.78) and Number of primary branches (5.31) together contributing 57.37 percent towards divergence. Hence, these characters should be given high emphasis during hybridization programme. Rest of the characters exhibited 42.63 % contributed towards divergence.

On the basis of this study, it can be concluded that selection would be rewarding for number of primary branches, number of fruiting nodes on main stem, sex ratio, fruits per plant and yield per plant in bringing out the improvement in the sponge gourd as they appeared with high value of GCV, PCV, heritability and genetic gain. Further, correlation study also suggested that for improvement in yield, selection for such plants having more primary branches, fruiting nodes on main stem, fruit length, fruit weight, fruits per plant, seed per fruit and 100 seed weight would be beneficial. Yield per plant and fruit weight were found to be the important characters for increasing the yield potential in sponge gourd.

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