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RESEARCH ARTICLE

Assessing *per se* performance, variability, association and principal component analysis in sponge gourd (*Luffa cylindrica* [L.]Roem.) genotypes for different horticultural attributes

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Abstract

Luffa cylindrica [L.] Roem., known as sponge gourd, belongs to the Cucurbitaceae family and the present investigation, conducted with 48 sponge gourd genotypes, aimed to evaluate various horticultural traits at the Department of Vegetable Science, Horticultural College and Research Institute, Tamil Nadu Agricultural University in Coimbatore. The experimental results exhibited significant differences among the genotypes evaluated, with a higher PCV compared to the GCV, suggesting that environmental factors strongly influence the expression of these characters. The high heritability, coupled with high genetic advance, was observed for most characters studied, indicating that they are primarily controlled by additive gene action. This suggests that selection based on these characters would be effective for identifying suitable genotypes. The correlation study among various traits showed the highest positive significant association for the weight of individual fruit (0.86), followed by the number of fruits vine^{-1} (0.67) and fruit diameter (0.45). With fruit yield vine^{-1} as the designating trait, these traits were identified as the most important yield determinant characters. Principal Component Analysis revealed that days to first male flower anthesis, days to first female flower anthesis, node bearing first male flower and node bearing first female flower components exhibited with an eigenvalue of unity and accounting for 67.91 % of total variance. Characters with positive values in each PC are the important yield-determining characters and hence, all these characters can be well relied upon for the selection of a suitable genotype.

Keywords: correlation; heatmap; PCA; sponge gourd; variability

Introduction

Vegetables play a crucial role in a balanced diet, providing not only energy but also essential nutrients such as vitamins, minerals, micronutrients, antioxidants and bioactive phytochemicals that promotes overall health (1). Among these, cucurbitaceous vegetables are particularly important, offering significant nutritional value. One such vegetable is the sponge gourd (*Luffa cylindrica* (L.) Roem.), an herbaceous vine with a diploid chromosome number of 2n = 26, which is native to the subtropical regions of Asia, especially India (2). Sponge gourd is widely recognized by various names, including dishcloth gourd, Egyptian cucumber, towel gourd, vegetable sponge and smooth gourd (3).This plant thrives in both tropical and subtropical climates and is widely cultivated throughout India, particularly in states such as Uttar Pradesh, Kerala, Odisha, Assam, West Bengal and Bihar (4). The young, tender fruits are commonly used in cooking, appearing in dishes such as chutneys and curries, known for being easy to digest, they are believed to stimulate the appetite when consumed (5). The variability in the shape, size and color of fruits is highly noticeable. India is home to a diverse array of crop varieties, but only a few are considered promising for commercial cultivation and breeding.

To improve these varieties and develop new, high-yielding ones, it is essential to focus on key genetic factors, including genetic variability, heritability, genetic advancement and principal component analysis (PCA). These factors play a crucial role in identifying superior genotypes that are more likely to express desirable traits, such as yield and other desirable traits (6). Genetic variability allows breeders to explore a wide range of traits, while heritability indicates the potential for these traits to be passed on to future generations. Genetic advancement measures the progress made in improving these traits over generations. PCA helps identify the most important traits influencing genetic variation, thereby streamlining the breeding process. The ultimate goal of breeding programs is to identify high-yielding genotypes, which can then be used to develop promising hybrids or new varieties. These improved genotypes are crucial for increasing productivity and ensuring the availability of high-quality crops for commercial cultivation, benefiting both farmers and consumers. This study was conducted with the aim of contributing to the development of high-yielding genotypes and further developing promising hybrids or varieties, making them available for commercial cultivation.

Materials and Methods

The experiment was conducted in two seasons (November 2023 and June 2024) at the Department of Vegetable Science, Horticultural College and Research Institute, Tamil Nadu Agricultural University in Coimbatore, using a Randomized Block Design with two replications. The experimental material consists of 48 various sponge gourd genotypes collected from different parts of our country (Table S1). Observations were recorded on various growth and yield attributes *viz*., days to first male flower anthesis (DFMFA), days to first female flower anthesis (DFFFA), node bearing first male flower (NBFMF), node bearing first female flower (NBFFF), vine length at the time of flowering (VL), number of primary branches vine^{-1} at the time of flowering (NPBV), days to first fruit harvest (DFFH), fruit length (FL), fruit girth (FG), weight of individual fruit (WIF), fruit diameter (FD), number of fruits vine^{-1} (NFV) and fruit yield vine^{-1} (FYV). The data collected from the two seasons were pooled for comprehensive statistical analysis, in which ANOVA was used to assess significant differences among genotypes and environments (7). Genotypic and phenotypic variability were estimated to evaluate trait variation as proposed (8). Heritability and genetic advance were calculated to determine the potential for selection (9, 10). Correlation coefficients helped identify relationships among key agronomic traits. PCA was applied to reduce dimensionality and highlight major contributing traits. PCA also facilitated the clustering of genotypes based on shared characteristics for breeding purposes. The statistical analysis was carried out for the *per se* performance, variability, heritability, correlation and PCA by using 'Grapes 1.1.0. software' (General R-based Analysis Platform Empowered by Statistics).

Result and Discussion

The *per se* performance of sponge gourd genotypes for their different horticultural attributes is shown in Table 1, which indicates that they are significantly different for the recorded traits. The character days to first male flower anthesis recorded a mean value of 39.46 and three out of 48 genotypes, viz., VRSG -51 (35.95), VRSG -15 (36.12) and VRSG -3-17 (36.58), took significantly fewer days than the grand mean for this character. The mean observed value was 41.84 for the days to first female flower anthesis, which ranged from 39.58 (Naduvalasu Local) to 45.31 days (VRSG -50). Among the 48 genotypes evaluated, a total number of 14 genotypes showed significantly lower value than the grand mean (9.25) for the node bearing the first male flower and 13 genotypes for the node bearing first female flower with a mean value of 11.65. Vine length at the time of flowering was maximum in the genotype L.C. 7 (116.93 cm) followed by Nallampatti Local (115.13 cm). A total number of 25 genotypes recorded significantly higher values than the grand mean of 4.64 for a number of primary branches vine^{-1} at the time of flowering. A number of days taken for first harvest of fruit ranged between 44.25 (Naduvalasu Local) to 52.41 (VRSG -50), with a grand mean of 48.12. The length of the fruits observed among the genotypes varied from 20.53 cm (L.C. 1) to 41.16 cm (VRSG -26) and twenty genotypes recorded higher values than the grand mean of 32.23 cm. The maximum fruit girth of 19.98 cm was recorded in L.C. 9 and the minimum girth of 14.35 cm in VRSG -50 which produced slender fruits. The individual fruit weight in sponge gourd genotypes recorded a grand mean of 210.40 g and twenty genotypes produced significantly greater fruit weights than the grand mean. The genotype VRSG -84 recorded the maximum weight of 262.40 g, followed by Embalam Local with a weight of 256.80 g. Fruit diameter had a range of 4.34 cm (Kashi Jyoti) to 6.28 cm (VRSG -3-14). The higher number of fruits was observed (24.62) in Oddanchatram Local, followed by Kashi Shreya (21.75) and VRSG -26 (21.52). Fruit yield vine^{-1} had a grand mean of 3.92 kg and thirteen genotypes recorded a significantly higher yield, with a maximum of 5.41 kg in Oddanchatram Local, followed by 5.34 kg in VRSG -26, 5.21 kg in VRSG -3-5 and 5.19 kg in VRSG -68-1. Similar evaluation studies were performed and reported in sponge gourd (11-14).

The extent of variability was measured in terms of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV). The heritability in a broad sense and genetic advance (GA) were worked out and represented in Fig. 1. The assessment of variability offers valuable insights into the nature and magnitude of genetic diversity within the population. In the present study, PCV values were consistently higher than the corresponding GCV values for most of the traits examined (Fig. 1), indicating a considerable influence of environmental factors on the expression of these traits. This suggests that while genetic variability is present, environmental conditions also play a significant role in shaping phenotypic performance. Among the traits studied, the fruit yield of vine^{-1} exhibited both high PCV and GCV, signifying the presence of substantial genetic variation and relatively less environmental influence. This is indicative of a trait that is more amenable to improvement through direct selection. These findings are in agreement with earlier reports in sponge gourds and in bitter gourd (15, 16). Moderate PCV and GCV estimates were recorded for traits such as number of primary branches vine^{-1} at the time of flowering, fruit length, weight of individual fruit and number of fruits vine^{-1}. This level of variability suggests that these traits possess moderate heritable variation and could respond to selection with some degree of environmental modulation. These results are supported by the findings in sponge gourd and in ridge gourd (17, 18). The trait, node bearing the first male flower, demonstrated moderate PCV but low GCV values, suggesting that environmental factors have a more substantial influence on its expression. This pattern indicates that genetic improvement through selection may be more challenging for this trait unless environmental influences are minimized. A similar trend of the result was reported in ridge gourd (19). The study on variability analysis highlights the potentiality for genetic improvement, particularly for yield-contributing traits of sponge gourd.

Table. 1. *Per se* performance of sponge gourd genotypes for different horticultural attributes

	DFMFA	DFFFA	NBFMF	NBFFF	VL	NPBV	DFFH	FL	FG	WIF	FD	NFV	FYV
SG1	41.09	43.27	10.10	12.00	89.55	3.94	49.55	34.51	15.50	204.19	5.46	17.49	3.58
SG2	40.64	40.35	8.83	11.90	103.34	4.16	48.42	37.57	16.40	239.54	6.18	21.42	5.03
SG3	41.24	41.57	9.36	12.29	100.73	4.35	47.91	35.47	17.44	241.66	6.01	20.23	4.94
SG4	38.00	40.60	9.16	11.74	107.15	4.63	48.66	24.28	17.17	246.79	5.69	20.86	5.21
SG5	41.45	42.52	9.47	10.91	100.57	5.24	48.45	38.03	18.54	200.77	5.71	19.10	3.91
SG6	38.06	44.20	8.25	11.01	111.81	5.01	44.82	26.62	16.42	223.87	6.28	18.69	4.15
SG7	36.58	41.43	8.05	9.98	94.05	4.92	47.45	24.39	16.25	128.15	5.63	16.52	2.17
SG8	39.05	41.98	9.57	11.94	101.91	4.66	48.77	37.36	18.79	213.02	5.01	15.21	3.31
SG9	40.86	42.31	7.42	10.27	91.89	4.18	48.71	31.73	17.63	165.30	5.39	15.22	2.53
SG10	38.41	41.79	9.86	11.58	99.63	4.86	47.22	32.84	15.40	200.82	6.18	18.07	3.62
SG11	36.12	41.48	8.95	10.92	98.01	4.84	44.70	33.86	17.80	150.83	4.91	18.30	2.75
SG12	38.57	42.79	9.69	11.59	90.42	4.99	47.60	33.89	15.76	200.03	4.65	18.27	3.55
SG13	40.43	42.55	10.79	13.05	94.19	4.56	49.02	36.14	19.19	204.03	5.18	17.22	3.55
SG14	40.87	41.40	9.03	11.87	104.69	4.76	47.99	41.16	18.95	242.70	5.82	21.52	5.34
SG15	39.00	41.75	9.49	11.37	102.44	3.92	47.64	32.61	18.80	227.33	5.80	22.76	4.98
SG16	39.81	45.31	10.39	12.23	101.19	4.71	52.41	29.01	14.35	153.64	4.60	19.21	2.97
SG17	35.95	41.73	7.73	10.20	96.79	4.47	45.23	27.68	17.89	179.16	5.61	16.24	2.92
SG18	39.33	40.93	9.57	12.01	88.37	4.10	48.00	34.35	18.61	201.12	5.73	17.27	3.50
SG19	37.96	41.37	8.74	11.24	104.68	3.97	46.77	28.47	17.14	211.25	5.50	18.63	3.90
SG20	39.28	41.00	9.59	13.23	105.32	4.54	47.71	39.98	18.35	249.24	6.11	20.30	5.19
SG21	37.82	40.29	9.41	11.55	92.59	5.44	48.01	31.20	16.19	225.22	4.84	17.74	3.98
SG22	38.12	40.61	9.41	12.33	102.68	3.90	47.43	36.56	18.90	262.40	6.19	19.82	5.11
SG23	38.15	40.64	7.55	10.18	103.08	4.59	47.30	32.39	16.44	221.25	5.39	16.50	3.68
SG24	38.92	39.98	10.43	12.65	90.90	5.32	44.86	36.78	15.60	203.28	4.97	18.87	3.81
SG25	38.93	42.95	8.55	10.08	88.56	4.26	47.86	25.95	17.50	150.11	5.45	20.86	3.10
SG26	39.83	41.33	8.23	10.68	92.88	5.32	48.02	38.07	16.71	215.94	4.34	18.16	4.03
SG27	39.44	42.31	11.06	13.13	91.67	5.16	50.75	31.73	18.63	215.67	4.86	17.14	3.82
SG28	38.79	40.92	9.64	11.41	104.99	5.41	48.61	27.76	17.89	218.75	5.49	21.91	4.97
SG29	40.83	42.89	10.83	12.84	95.61	4.79	51.54	36.28	18.17	210.94	5.54	18.69	3.91
SG30	39.74	41.41	7.75	11.82	95.00	4.34	47.92	20.53	17.25	227.74	5.65	17.55	3.90
SG31	40.74	44.01	8.94	10.95	99.49	5.04	49.05	29.85	16.63	198.80	4.68	15.34	3.04
SG32	40.16	42.36	7.70	11.16	113.51	4.73	49.21	21.70	17.12	213.48	5.38	17.44	3.69
SG33	39.42	41.00	9.64	12.51	113.00	4.15	48.00	30.66	14.61	239.93	5.48	17.78	4.17
SG34	40.38	42.70	9.40	11.86	107.14	5.22	48.29	34.78	17.81	228.29	4.70	17.63	4.05
SG35	42.31	43.73	9.76	11.44	116.93	3.80	49.22	29.35	17.90	233.28	5.76	15.33	3.48
SG36	39.77	42.63	9.54	12.45	110.22	3.93	48.75	30.65	19.42	178.83	5.71	16.82	3.04
SG37	40.68	40.17	9.35	12.07	100.82	4.13	50.25	32.75	19.98	245.54	5.73	20.01	4.94
SG38	40.34	41.99	9.45	11.24	95.67	6.44	48.68	35.13	18.30	200.88	4.82	19.02	3.78
SG39	40.11	41.63	10.34	13.25	92.34	5.20	48.94	36.35	17.49	171.89	5.77	19.70	3.41
SG40	39.51	41.78	8.46	10.99	102.67	4.65	47.22	35.56	19.52	230.89	5.75	21.77	5.00
SG41	41.65	42.48	10.05	11.91	96.65	4.91	48.07	35.40	16.75	230.48	5.54	16.15	3.73
SG42	38.45	40.41	9.78	11.81	106.58	4.07	46.98	33.65	17.10	203.08	4.86	14.78	3.03
SG43	38.20	41.84	8.21	12.21	106.24	3.79	48.34	26.50	19.45	256.80	5.94	20.17	5.14
SG44	42.39	43.71	9.07	10.87	111.09	4.16	48.98	22.01	16.58	109.36	5.06	20.24	2.34
SG45	37.68	39.58	8.51	10.94	105.54	5.06	44.25	36.00	17.67	231.68	5.47	15.31	3.54
SG46	38.12	40.55	10.92	13.04	115.13	4.85	49.57	34.55	18.60	248.33	5.32	20.06	5.05
SG47	40.33	41.35	10.03	11.94	106.69	4.46	48.58	34.35	19.03	243.70	5.54	24.62	5.41
SG48	40.69	42.52	8.13	10.52	112.27	4.97	48.29	30.75	18.05	199.39	5.19	20.06	3.84
GM	39.46	41.84	9.25	11.65	101.18	4.64	48.12	32.23	17.54	210.40	5.43	18.58	3.92
SE	0.64	0.81	0.15	0.18	1.84	0.08	1.01	0.58	0.32	4.00	0.11	0.13	0.07
CD(5 %)	1.82	2.32	0.56	0.51	5.24	0.23	2.88	1.66	0.92	11.39	0.31	1.23	0.31

*Note: DFMFA: Days to first male flower anthesis; DFFFA: Days to first female flower anthesis; NBFMF Node bearing first male flower; NBFFF: Node bearing first female flower; VL: Vine length at the time of flowering; NPBV: Number. of primary branches vine^{-1} at the time of flowering; DFFH, Days to first fruit harvest; FL: Fruit length (cm); FG: Fruit girth (cm); WIF: Weight of individual fruit (g); FD: Fruit diameter (cm); NFV: Number of fruits vine^{-1}; FYV: Fruit yield vine^{-1}(kg)

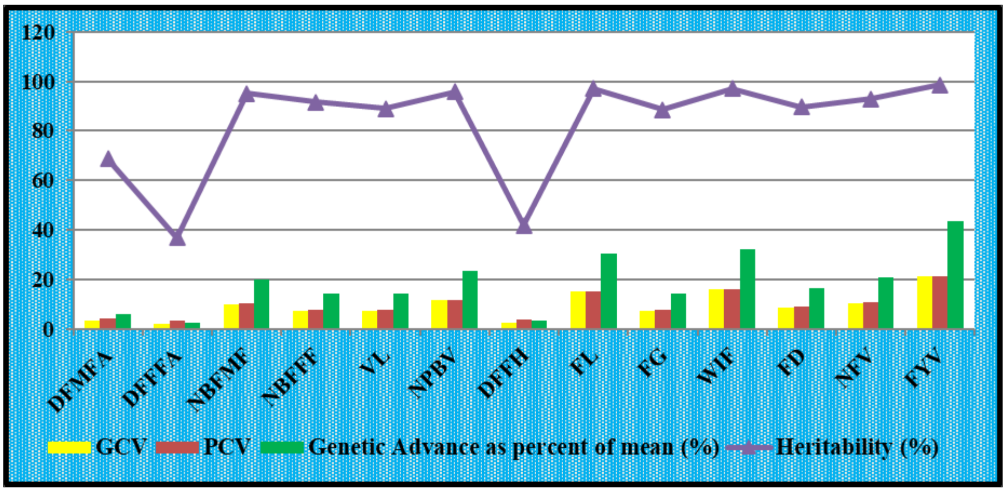

Fig. 1. Variability, heritability and genetic advance for various characters of sponge gourd genotypes *Note: DFMFA: Days to first male flower anthesis; DFFFA: Days to first female flower anthesis; NBFMF Node bearing first male flower; NBFFF: Node bearing first female flower; VL: Vine length at the time of flowering; NPBV: Number. of primary branches vine^{-1} at the time of flowering; DFFH, Days to first fruit harvest; FL: Fruit length (cm); FG: Fruit girth (cm); WIF: Weight of individual fruit (g); FD: Fruit diameter (cm); NFV: Number of fruits vine^{-1}; FYV: Fruit yield vine^{-1}(kg).

Estimating heritability in the broad sense is crucial in plant breeding, as it helps distinguish between genetic and environmental components of observed phenotypic variation. Since field-level variability alone cannot determine the extent to which a trait is genetically controlled, heritability estimates provide a more precise understanding of the inheritance potential. However, heritability on its own is not a definitive indicator of the effectiveness of selection. Therefore, combining heritability estimates with genetic advance (GA) offers a more reliable prediction of the selection response. From Fig. 1 and Table S2, it is observed that traits such as number of primary branches vine^{-1} at the time of flowering, fruit length, weight of individual fruit, number of fruits vine^{-1} and fruit yield vine^{-1} exhibited high heritability coupled with high genetic advance. This suggests that these traits are predominantly governed by additive gene action and are less influenced by environmental factors. Hence, they are ideal traits for improvement through direct selection. These results corroborate the findings in sponge gourd, further reinforcing their reliability (20).

On the other hand, traits such as node bearing the first male flower, node bearing the first female flower, vine length at the time of flowering, fruit girth and fruit diameter showed high heritability but moderate genetic advance. This suggests that both additive and non-additive gene actions may influence these traits and that the environment may still play a considerable role. Although selection for such traits can still be effective, it may require more precise breeding strategies. Similar trends have been reported in previous studies in sponge gourds and in ridge gourds (21-23). The combined interpretation of heritability and genetic advancement in this study highlights key traits with strong genetic control that can be efficiently improved through selection, thereby offering valuable direction for future breeding programs focused on yield enhancement and trait improvement in cucurbits.

Correlation analysis serves as a vital tool for understanding the relationships between yield and its contributing traits. Given the complexity of yield, a polygenic trait influenced by multiple physiological and morphological characteristics, identifying traits that are positively associated with yield is crucial for formulating effective selection strategies in breeding programs. The colour gradient from Fig. 2 illustrate the strength and direction of correlations between traits. Dark purple plots signify strong positive correlations, orange denotes negative correlations and white indicates negligible or no correlation. This intuitive visualization helps quickly identify key relationships relevant to yield improvement. Among the traits analyzed, weight of individual fruit (0.86), number of fruits vine^{-1} (0.67) and fruit diameter (0.45) exhibited a highly significant positive correlation with fruit yield vine^{-1}. This implies that selection for these traits could directly contribute to enhancing overall yield.

Additionally, traits like fruit girth (0.37) and vine length at the time of flowering (0.30) also showed significant positive associations with yield, although to a lesser extent. Research indicates similar findings in their studies, further validating the consistency of these associations across studies (24-26). Conversely, days to first female flower anthesis (-0.42) and number of primary branches vine^{-1} at the time of flowering (-0.07) were negatively correlated with fruit yield vine^{-1}. These negative associations suggest that delayed flowering or excessive vegetative branching may be detrimental to yield, likely due to altered resource allocation. A similar trend was observed in sponge gourd and in ridge gourd, indicating a consistent pattern across cucurbitaceous crops (26, 27). The correlation analysis highlights several traits with strong and positive associations with fruit yield, which can be prioritized in selection to achieve genetic improvement. At the same time, negatively associated traits should be carefully monitored during selection to avoid inadvertent yield penalties.

Principal Component Analysis (PCA) was performed to assess the relative contribution of different traits toward genetic variability and to identify the most influential characters that can be targeted in selection. PCA is particularly valuable in multivariate trait analysis, as it reduces dimensionality while retaining most of the variation present in the dataset, thereby highlighting the most critical traits contributing to overall divergence. The analysis revealed that four principal components (PCs) had eigenvalues greater than one, collectively accounting for 67.91 % of the total genetic variation among the genotypes (Table 2). PC1 explained the largest portion of variance (26.70 %, with an eigenvalue of 3.47), followed by PC2 (18.92 %),

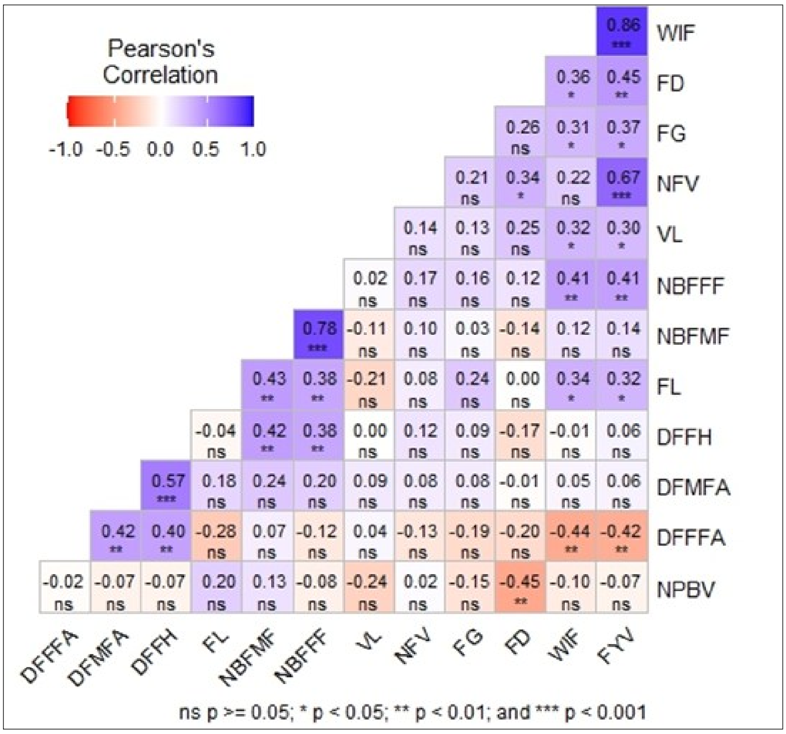

Fig. 2. Correlation plot representing the various characters association with yield of sponge gourd genotypes..*Note: DFMFA: Days to first male flower anthesis; DFFFA: Days to first female flower anthesis; NBFMF Node bearing first male flower; NBFFF: Node bearing first female flower; VL: Vine length at the time of flowering; NPBV: Number. of primary branches vine^{-1} at the time of flowering; DFFH, Days to first fruit harvest; FL: Fruit length (cm); FG: Fruit girth (cm); WIF: Weight of individual fruit (g); FD: Fruit diameter (cm); NFV: Number of fruits vine^{-1}; FYV: Fruit yield vine^{-1}(kg).

PC3 (14.11 %) and PC4 (8.19 %), as depicted in Fig. 3. The remaining components (PC5 to PC13) contributed minimally to the total variation and were thus not considered critical for trait-based selection.

In PC1, traits such as days to first female flower anthesis and number of primary branches vine^{-1} at the time of flowering showed positive contributions, indicating their significant influence on the primary axis of genetic divergence. PC2 included positive contributions from a wider array of traits, including days to first male and female flower anthesis, node bearing first male and female flowers, number of primary branches vine^{-1} at the time of flowering, days to first fruit harvest and fruit length. The consistent positive loadings of these traits suggest that they collectively play a pivotal role in defining genetic diversity and should be emphasized in breeding programs aimed at developing high-yielding genotypes. These findings align with similar PCA-based studies in sponge gourd, confirming that traits associated with flowering time, fruit morphology and early growth attributes are critical determinants of genetic divergence (28). Identifying traits with high positive loadings in principal components allows breeders to focus on a reduced set of informative characters, enhancing the efficiency of genotype selection. Therefore, traits that contribute positively to the major principal components should be prioritized in selection indices, particularly for improving complex traits such as yield, where indirect selection based on correlated components can significantly accelerate breeding gains.

Table 2. Eigenvalues and percentage of variation for different traits of sponge gourd genotypes

Component axis	Principle component characters	Eigen value	Variance %	Cumulative %	Component loading			
					1 vector	2 vector	3 vector	4 vector
1	DFMFA	3.47	26.70	26.70	-0.09	0.39	-0.32	0.13
2	DFFFA	2.46	18.92	45.62	0.23	0.33	-0.39	0.13
3	NBFMF	1.83	14.11	59.72	-0.21	0.46	0.19	-0.19
4	NBFFF	1.06	8.19	67.91	-0.35	0.33	0.09	-0.31
5	VL	0.93	7.12	75.03	-0.15	-0.15	-0.39	0.06
6	NPBV	0.87	6.72	81.75	0.09	0.13	0.45	0.59
7	DFFH	0.69	5.36	87.11	-0.09	0.48	-0.29	0.09
8	FL	0.58	4.43	91.54	-0.26	0.17	0.41	-0.09
9	FG	0.41	3.15	94.69	-0.27	-0.06	-0.01	-0.04
10	WIF	0.33	2.54	97.23	-0.44	-0.13	0.05	-0.03
11	FD	0.22	1.69	98.92	-0.27	-0.28	-0.28	-0.19
12	NFV	0.14	1.04	99.96	-0.290	-0.05	-0.11	0.59
13	FYV	0.00	0.04	100	-0.49	-0.13	-0.01	0.26

*Note: DFMFA: Days to first male flower anthesis; DFFFA: Days to first female flower anthesis; NBFMF Node bearing first male flower; NBFFF: Node bearing first female flower; VL: Vine length at the time of flowering; NPBV: Number. of primary branches vine^{-1} at the time of flowering; DFFH, Days to first fruit harvest; FL: Fruit length (cm); FG: Fruit girth (cm); WIF: Weight of individual fruit (g); FD: Fruit diameter (cm); NFV: Number of fruits vine^{-1}; FYV: Fruit yield vine^{-1}(kg)

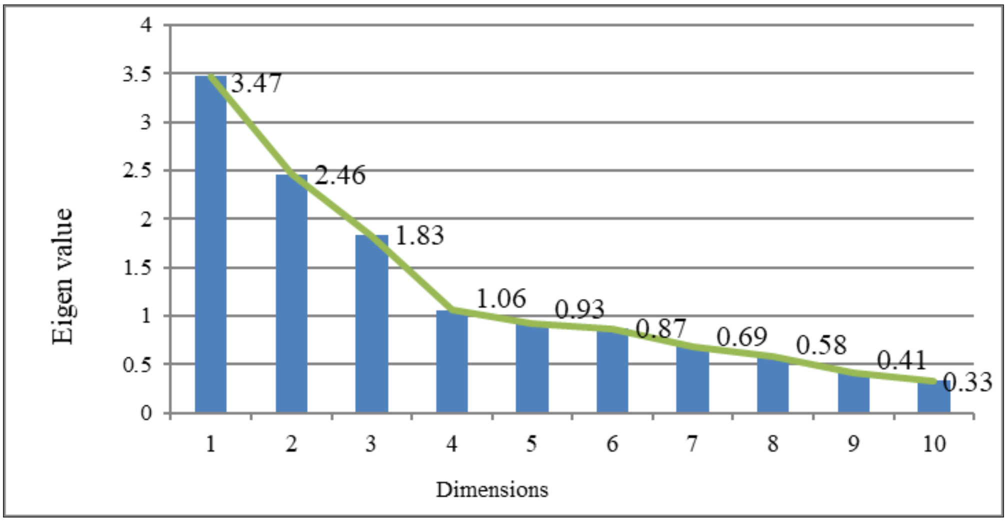

Fig. 3. Scree plot of sponge gourd genotypes.

The heat map analysis (Fig. 4) provided a comprehensive visual summary of the performance of various genotypes across multiple traits. It serves as a powerful analytical and visual tool, enabling the identification of superior genotypes and simplifying the complexity associated with multivariate trait evaluation. This aids breeders in prioritizing genotypes for advanced testing and selection. In this graphical representation, each cell corresponds to the intersection of a trait (column) and a genotype (row), with the colour intensity of the cell indicating the magnitude of the trait value for that genotype. The use of colour gradients not only enhances interpretability but also supports data-driven decision-making by clearly illustrating the genotypes excel in key traits. Dark green shades represented higher performance values, suggesting that the corresponding genotypes exhibited superior expression for the respective traits.

In contrast, lighter colours indicated lower performance levels, allowing for quick visual identification of genotypes with weaker trait expression. This gradient-based visualization effectively distinguishes high-performing genotypes from less desirable ones. By simultaneously displaying all traits and genotypes, the heat map facilitated pattern recognition and cluster formation, highlighting groups of genotypes that consistently performed well across multiple traits, which was similar to the previous research (29). Such grouping is valuable for identifying promising lines for selection and further evaluation in breeding programs.

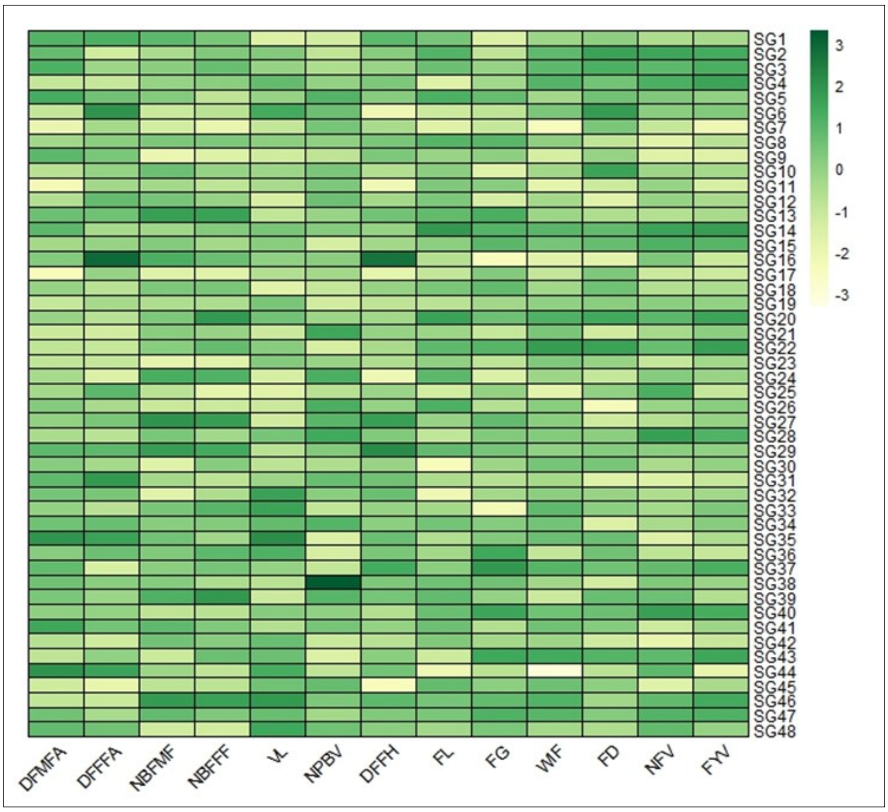

Fig. 4. Heat map showing the relationships among the yield and its contributing characters of sponge gourd genotypes. *Note: DFMFA: Days to first male flower anthesis; DFFFA: Days to first female flower anthesis; NBFMF Node bearing first male flower; NBFFF: Node bearing first female flower; VL: Vine length at the time of flowering; NPBV: Number. of primary branches vine^{-1} at the time of flowering; DFFH, Days to first fruit harvest; FL: Fruit length (cm); FG: Fruit girth (cm); WIF: Weight of individual fruit (g); FD: Fruit diameter (cm); NFV: Number of fruits vine^{-1}; FYV: Fruit yield vine^{-1}(kg).

Conclusion

The *per se* performance on 48 sponge gourd genotypes results revealed that the genotypes Naduvalasu Local, VRSG -186, L.C. 9， Nallampatti Local, for early to female flower anthesis and days to first harvest; the genotype VRSG -26, Naduvalasu Local, VRSG -68-1 for length of the fruit, the genotypes Oddanchatram Local, Kashi Shreya, Pusa sponge gourd 29, VRSG -26, Embalam Local, Nallampatti Local for several fruits vine^{-1} and the genotypes Oddanchatram Local, VRSG -26, Embalam Local, Nallampatti Local for fruit yield vine^{-1} were performed best. There was a significant variability among the genotypes for various horticultural traits. The variability study showed a high PCV compared to GCV for many traits, highlighting that traits with high genetic variability, such as fruit yield vine^{-1}, are suitable for genetic improvement through selection. In contrast, traits influenced more by environmental factors may require controlled conditions for effective improvement. This emphasizes the potential for enhancing yield-contributing traits in breeding programs. Traits with high heritability, combined with high genetic advance, were observed in characters such as the number of primary branches at the time of flowering, fruit length, weight of individual fruit, number of fruits vine^{-1} and fruit yield vine^{-1}, which are primarily controlled by additive genetic factors, making selection effective for these traits. Correlation analysis revealed a significant positive correlation between traits such as the weight of individual fruit, the number of fruits vine^{-1} and fruit diameter and fruit yield vine^{-1}, which can be prioritized in selection to achieve genetic improvement. Principal Component Analysis (PCA) identified key traits contributing to genetic variation, with four principal components accounting for 67.91 % of the total variability. These findings emphasize the importance of specific traits in improving yield and the potential of genotypes to be utilized in breeding programs to develop high-yielding sponge gourd varieties or hybrids. The study results showed that the genotypes oddanchatram local, Embalam local, Nallampatti local, VRSG -3-5, VRSG -26 were identified as best performer due to the favourable values recorded on desirable traits indicating their potentiality based on the assessment of genetic parameters and regarded as superior performers.

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Authors' contributions

GPP and SP have prepared the original manuscript with the support of all authors. The visualization and data analysis process was carried out by SH, NMB, DK and KC. All authors read and approved the final version of the manuscript.

Compliance with ethical standards

Conflict of interest: The author declares no conflicts of interest relevant to this.

Ethical issues: None

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