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RESEARCH ARTICLE

Genetic analysis of sponge gourd for morphometric traits and physical sensory test

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Abstract

A total of 32 sponge-gourd (*Luffa cylindrica* L.) genotypes were screened for morphometric traits, yield performance, and sensory aroma. About 26 genotypes displayed medium-long fruits (15–25 cm), and 19 genotypes reached harvest within 55 days, demonstrating notable earliness. Yield showed a strong positive correlation with both fruit number and average fruit weight. Genotype × environment interaction was highly significant for yield, underscoring the importance of stability analysis. Eight genotypes (VRSG-10, VRSG-18, VRSG-171, VRSG-28, VRSG-68, VRSG-69, VRSG-69-1, and VRSG-77) exhibited regression coefficients (b = 0 or 1), indicating stable performance across environments. Moreover, Kashi Shreya, VRSG-195, VRSG-7-17, VRSG-10, and VRSG-171 achieved the highest yields per hectare, making them promising candidates for cultivation across major Indian agro-climatic zones. Cluster analysis grouped the 32 genotypes into eight distinct clusters; notably, VRSG-7-17 formed a singleton cluster and possessed a distinctive Basmati-rice-like aroma in leaves, vines, flowers, fruits, and peel, as confirmed by physical-sensory evaluation of both raw and cooked material. These findings highlight considerable genetic variability and identify stable, high-yielding, and aromatic lines for future breeding and aroma-targeted improvement programs.

Keywords: Sponge gourd; Correlation, AMMI Stability Analysis; Physical Sensory Test; Aroma.

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Introduction

Sponge gourd (*Luffa cylindrica* L.) is an important member of the cucurbit group. It is an annual climber and a cross-pollinated vegetable that expresses different forms of sex, i.e., hermaphrodite, staminate, and pistillate (Takahashi, 1980; Kumar et al., 2013; Phan et al., 2015). Being tropical and subtropical in nature, it is grown in both the rainy and summer seasons worldwide (Singh et al., 2018). Fruits of sponge gourd are edible at both the young and green stages, in raw as well as cooked form (Phan et al., 2015). Sponge gourd exhibits rich variability in leaf size and shape, fruit shape, size, and colour, which are governed by numerous genes (Beyer et al., 2002; Zalapa et al., 2006; Kumar et al., 2013). Genetic variability, heritability, character association, diversity, and stability analysis are desirable goals for germplasm collection and successful breeding programs aimed at developing high-yielding and stable varieties (Kumar et al., 2013).

Sponge gourd is easily cultivated in farmers' fields, where seeds of local varieties are often preserved for the next season. Farmers usually avoid selfing and crossing procedures and restrict themselves to growing newly introduced varieties. As a result, the quality of local varieties deteriorates, leading to reduced crop yield. To identify new sponge gourd varieties with specific and unique quality

traits, 32 genotypes of this vegetable crop were evaluated for genetic variability and trait characterization. We report the identification of improved, stable, high-yielding, disease-resistant, and aromatic varieties of *Luffa cylindrica* L.

Materials and Methods

Plant materials and experimental design

A total of 32 genotypes of sponge gourd, including two known cultivars (Kashi Divya and Kashi Shreya), were selected from the germplasm stock maintained at ICAR–Indian Institute of Vegetable Research (ICAR-IIVR), Varanasi, India (Table 1). Evaluation of the genotypes was conducted over two years, 2016–17 (E1 and E2) and 2017–18 (E3 and E4), during two consecutive seasons (rainy and summer) at the ICAR-IIVR Research Farm. The experiment was laid out in a randomized complete block design (RCBD) with three replications. Each replication comprised two rows, and each row had six plants in a plot size of 7.0 m^2. Spacing was maintained at 65 cm between plants and 150 cm between rows (Choudhary et al., 2014). All recommended agronomic and cultural practices, protection measures, and recommended doses of manures and fertilizers were applied to raise a healthy crop (Halder et al., 2017).

Observation

Data were recorded from eight randomly selected plants per replication. Observations were taken for morphological traits (based on visual observation), viz., leaf colour, fruit size, fruit colour at first harvest, and earliness (Table 2). Fruit size was determined based on fruit length, and earliness was assessed by the duration from seed sowing to first commercial harvest. Data were also recorded for eight quantitative traits, viz., days to first male and female flower appearance, days to first harvest, fruit length (cm), fruit width (cm), number of fruits per plant, average fruit weight (g), and fruit yield (q/ha), following the sponge gourd guidelines of the national technical regulations QCVN 2013 DUS of Angel Loofah (*Luffa acutangula*) (MARD, 2013).

For the physical sensory test, samples were collected from leaves, flowers, and fruits of all 32 genotypes. A team of five individuals verified each sample by smelling at the green stage of fruits, leaves, and flowers, as well as after cooking the fruits. The presence or absence of aroma at both raw and cooked stages was noted and scored.

Statistical analysis

Statistical analyses, including correlations among genotypic, phenotypic, and environmental factors; stability analysis; principal component analysis (PCA); covariances between genotypic and phenotypic data; heritability; co-heritability of yield traits; and cluster analysis were computed using the methods suggested by Al-Jibouri et al. (1958), Dewey and Lu (1959), and Eberhart & Russel (1966). The additive main effect and multiplicative interaction (AMMI) model, as suggested by Gauch (1988), was also utilized for stability analysis. GenStat 8.0 software was used to determine the stability of the genotypes across environments (Payne et al., 2009).

Table 1: List of sponge gourd genotypes used in the present investigation

S. No.	*Genotypes*	*Genotype code*	*Remarks*
1	Kashi Divya	G1	Popular Check
2	Kashi Shreya	G2	Popular Check
3	VRSG-10	G3	Germplasm
4	VRSG-11	G4	Germplasm
5	VRSG-1-12	G5	Germplasm
6	VRSG-12	G6	Germplasm
7	VRSG-13	G7	Germplasm
8	VRSG-136	G8	Germplasm
9	VRSG-14-1	G9	Germplasm
10	VRSG-142-1	G10	Germplasm
11	VRSG-154	G11	Germplasm
12	VRSG-171	G12	Germplasm
13	VRSG-18	G13	Germplasm
14	VRSG-195	G14	Germplasm
15	VRSG-2-12	G15	Germplasm
16	VRSG-214	G16	Germplasm
17	VRSG-28	G17	Germplasm
18	VRSG-40	G18	Germplasm
19	VRSG-49-1	G19	Germplasm
20	VRSG-50	G20	Germplasm
21	VRSG-57	G21	Germplasm
22	VRSG-61	G22	Germplasm
23	VRSG-64	G23	Germplasm
24	VRSG-68	G24	Germplasm
25	VRSG-69	G25	Germplasm
26	VRSG-69-1	G26	Germplasm
27	VRSG-70	G27	Germplasm
28	VRSG-7-17	G28	Germplasm
29	VRSG-77	G29	Germplasm
30	VRSG-9	G30	Germplasm
31	VRSG-91	G31	Germplasm
32	VRSG-97	G32	Germplasm

Results

Characterization of morphological traits

All the 32 genotypes were evaluated and characterized during four seasons in two successive years. A total of 24 genotypes had green leaves, while 08 were having dark

green leaves. The fruit size was measured in the range of <15 cm to >25 cm, where 'VRSG-12' exhibited the smallest and Kashi Shreya the largest fruit size. While 26 and 5 cultivars were measured as medium long (15 – 25 cm) and long (>25 cm) in fruit size (Table 2). On fruit colour parameter at the first harvesting stage, 18 genotypes were of green colour, while 06 and 08 genotypes were dark green and light green colour, respectively. Among all the genotypes, no one genotype was observed for late, while 13 genotypes were classified as medium and 19 genotypes were represented by the early group based on first fruit harvesting.

In the physical sensory test, the team clarified that only 'VRSG-7-17' had a special aroma like Basmati rice during physical smelling and cooking (Fig. 1).

Correlation and heritability

For a better characterization of the association between yield and horticultural traits, a correlation-based approach was adopted using the Pearson coefficient as a correlation index. A total of 8 positive and 4 negative but significant genotypic correlations were observed between the traits (Table 3). The maximum genotypic correlation was found between days to first harvest and days to first female flower appearance (0.7991), followed by the association between number of fruit per plant and yield quintal per hectare (0.7982). Days to first harvest further established a positive and significant genotypic correlation with days to first male flower appearance. Similarly, fruit width, fruit number per plant and average fruit weight were positively correlated with fruit length (0.3521), fruit width (0.0983) and fruit length (0.5337), respectively. The fruit yield was positively and significantly correlated with the number of fruits (0.7982) and average fruit weight (0.5056). However, it had negative but significant genotypic correlations with days to first male flower appearance (-0.3079) and days to first female flower appearance (-0.1795). The maximum phenotypic correlation was recorded between yield and number of fruits per plant (0.7863), while maximum environmental correlation was observed between days to first male and female flower appearance (0.7087); both of these associations were statistically non-significant.

The phenotypic covariance was generally higher than the genotypic covariance value for each character (Table 4). Fruit yield had positive and high covariance between FW, NFPP, FL and AFW. However, negative covariance was observed between fruit yield and DMF, DFF and DFH.

The highest and lowest heritabilities were observed for NFP (0.9661) and FW (0.2120), respectively (Table 5). The highest co-heritability was observed between AFW and FW (6.994) and the lowest between FW and DFF (0.085). However, fruit yield showed maximum co-heritability with DFF (1.00) and NFPP (0.994) and minimum co-heritability with FW (0.736).

Stability, principal component and cluster analysis

The stability analysis of variance indicated highly significant effects ($p < 0.01$) for the treatment, genotype (G), environment (E), and interaction (GxE) for the fruit yield (Q/ha) of 32

Table 2: Observation on four pheno-morphological characters in 32 genotypes of sponge gourd

Trait	*Trait segment*	*No. of genotype*	*Genotype*
Leaf colour	Green Leaf	24	VRSG-11, VRSG-1-12, VRSG-12, VRSG-136, VRSG-14-1, VRSG-142-1, VRSG-154, VRSG-195, VRSG-2-12, VRSG-28, VRSG-40, VRSG-49-1, VRSG-50, VRSG-57, VRSG-61, VRSG-64, VRSG-68, VRSG-69, VRSG-70, VRSG-7-17, VRSG-77, VRSG-9, VRSG-91, VRSG-97
	Dark Green Leaf	08	Kashi Divya, Kashi Shreya, VRSG-10, VRSG-13, VRSG-171, VRSG-18, VRSG-214, VRSG-69-1
Fruit size at commercial harvesting	<15cm (small)	01	VRSG-12
	15-25cm (medium long)	26	Kashi Divya, VRSG-10, VRSG-13, VRSG-171, VRSG-18, VRSG-69-1, VRSG-11, VRSG-1-12, VRSG-2-12, VRSG-136, VRSG-14-1, VRSG-142-1, VRSG-195, VRSG-28, VRSG-40, VRSG-49-1, VRSG-50, VRSG-57, VRSG-61, VRSG-64, VRSG-68, VRSG-69, VRSG-70, VRSG-7-17, VRSG-9, VRSG-91,
	>25cm (long)	5	Kashi Shreya, VRSG-154, VRSG-214, VRSG-77, VRSG-97
Fruit colour at commercial harvesting	Light Green Fruit	08	VRSG-11, VRSG-1-12, VRSG-12, VRSG-2-12, VRSG-40, VRSG-57, VRSG-7-17, VRSG-97
	Green Fruit	18	VRSG-10, VRSG-13, VRSG-171, VRSG-18, VRSG-214, VRSG-69-1, VRSG-136, VRSG-14-1, VRSG-142-1, VRSG-154, VRSG-28, VRSG-49-1, VRSG-61, VRSG-64, VRSG-68, VRSG-70, VRSG-77, VRSG-91
	Dark Green Fruit	06	Kashi Divya, Kashi Shreya, VRSG-195, VRSG-50, VRSG-69, VRSG-9
Earliness* (from days of seed sowing to first commercial harvesting)	<55days (early)	19	VRSG-10, VRSG-171, VRSG-69-1, VRSG-12, VRSG-18, VRSG-136, VRSG-142-1, VRSG-195, VRSG-28, VRSG-40, VRSG-49-1, VRSG-57, VRSG-61, VRSG-64, VRSG-68, VRSG-70, VRSG-9, VRSG-91, VRSG-2-12
	55-65days (medium)	13	Kashi Divya, Kashi Shreya, VRSG-11, VRSG-1-12, VRSG-13, VRSG-14-1, VRSG-154, VRSG-214, VRSG-50, VRSG-69, VRSG-7-17, VRSG-77, VRSG-97
	>65days (late)	0	-

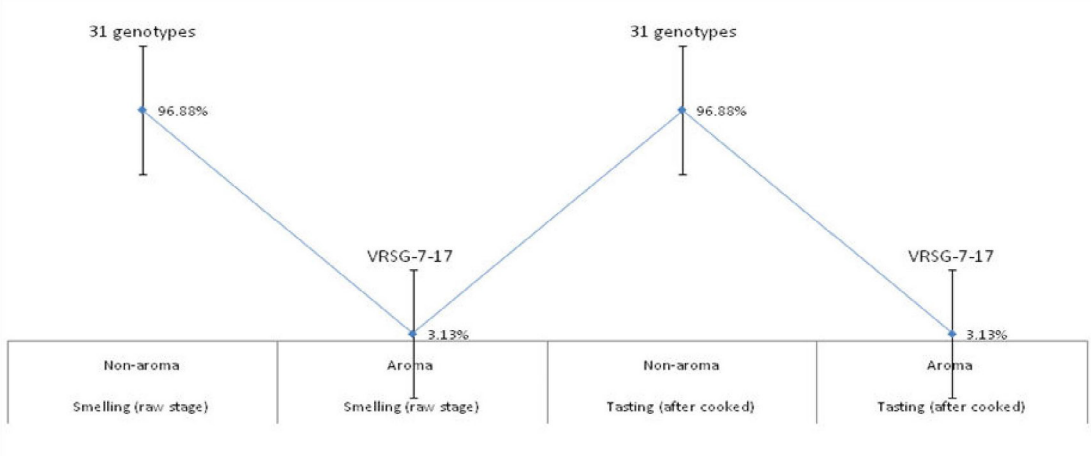

Fig. 1: Percentage of aromatic and non-aromatic genotypes during organoleptic test by smelling (raw stage) and tasting (after cooking)

Table 3: Genotypic, phenotypic and environmental correlation for 8 characters

Traits	*Components*	*DMF*	*DFF*	*DFH*	*FL*	*FW*	*NFPP*	*AFW*
DMF	G	1.0000						
	P	1.0000						
	E	1.0000						
DFF	G	0.6667**	1.0000					
	P	0.6715	1.0000					
	E	0.7087	1.0000					
DFH	G	0.6671**	0.7991**	1.0000				
	P	0.6382	0.7034	1.0000				
	E	0.6714	0.5439	1.0000				
FL	G	-0.1646	0.2835	0.3172	1.0000			
	P	-0.0560	0.2174	0.2736	1.0000			
	E	0.1092	0.0699	0.1546	1.0000			
FW	G	-0.0556	-0.0200	-0.0615	0.3521**	1.0000		
	P	-0.1660	-0.0835	-0.0410	0.2755	1.0000		
	E	-0.2139	-0.1351	-0.0350	0.3492	1.0000		
NFPP	G	-0.0869	-0.1802*	-0.3297	-0.1037	0.0983*	1.0000	
	P	-0.0721	-0.1512	-0.2677	-0.1017	0.0422	1.0000	
	E	-0.1365	-0.1260	-0.0164	-0.1167	-0.0141	1.0000	
AFW	G	-0.4570*	-0.0934	0.0084	0.5337**	-0.0385	-0.1090	1.0000
	P	-0.2610	-0.0506	-0.0184	0.4820	0.0024	-0.1233	1.0000
	E	0.0201	0.0920	-0.1433	0.1506	0.0713	-0.3788	1.0000
FY	G	-0.3079*	-0.1795*	-0.2442	0.2373	0.0693	0.7982**	0.5056**
	P	-0.2008	-0.1353	-0.2094	0.2128	0.0425	0.7863	0.5072
	E	-0.1029	0.0005	-0.1126	0.0143	0.0614	0.4893	0.5751

**Correlation is significant at the 0.01 level, *Correlation is significant at the 0.05 level. DMF=Days to Ist male flower appearance; DFF=Days to Ist female flower appearance; DFH= Days to first harvesting; FL=Fruit Length (cm); FW=Fruit width (cm); NFPP=Number of fruit per plant; AFW=Average fruit wt.(g) and FY=Fruit yield (q/ha).

Table 4: Genotypic and phenotypic covariance for 8 yield traits

Covariances between		*DMF*	*DFF*	*DFH*	*FL*	*FW*	*NFPP*	*AFW*	*FY*
DMF	G	1.6719							
	P	4.4804							
DFF	G	1.8593	4.6520						
	P	3.9788	7.8364						
DFH	G	2.4479	4.8910	8.0529					
	P	4.6710	6.8086	11.9566					
FL	G	-0.5923	1.7019	2.5053	7.7470				
	P	-0.3621	1.8589	2.8898	9.3308				
FW	G	-0.0054	-0.0032	-0.0130	0.0729	0.0055			
	P	-0.0567	-0.0378	-0.0229	0.1359	0.0261			
NFPP	G	-0.1504	-0.5199	-1.2518	-0.3861	0.0098	1.7898		
	P	-0.2077	-0.5763	-1.2599	-0.4229	0.0093	1.8525		
AFW	G	-8.1012	-2.7612	0.3263	20.3650	-0.0393	-1.9987	187.9648	
	P	-7.9530	-2.0403	-0.9176	21.1975	0.0056	-2.4156	207.2598	
FY	G	-7.6112	-7.4024	-13.2508	12.6283	0.0986	20.4171	132.5184	365.5486
	P	-8.3048	-7.3989	-14.1453	12.7005	0.1340	20.9101	142.6746	381.7146

DMF= Days to Ist male flower appearance; DFF=Days to Ist female flower appearance; DFH=Days to first harvesting; FL=Fruit Length (cm); FW=Fruit width (cm); NFPP=Number of fruits per plant; AFW=Average fruit wt.(g); and FY=Fruit yield (q/ha).

Table 5: Response of co-heritability between the 8 yield traits and heritability coefficient

Co-heritability between	*DMF*	*DFF*	*DFH*	*FL*	*FW*	*NFPP*	*AFW*	*FY*	*Heritability Coefficients*
DMF	0.000	0.467	0.524	1.636	0.094	0.720	1.02	0.916	0.373
DFF			0.718	0.916	0.085	0.902	1.35	1.00	0.594
DFH				0.867	0.567	0.994	0.356	0.936	0.674
FL					0.537	0.912	0.960	0.994	0.830
FW						1.055	6.994	0.736	0.212
NFPP							0.827	0.976	0.9661
AFW								0.929	0.9069
FY								0.000	0.9576

DMF= Days to Ist male flower appearance; DFF=Days to Ist female flower appearance; DFH=Days to first harvesting; FL=Fruit Length (cm); FW=Fruit width (cm); NFPP=Number of fruits per plant; AFW=Average fruit wt.(g); and FY=Fruit yield (q/ha).

genotypes when tested against pooled deviation (Table 6). Hence, a detailed stability analysis has been performed for yield in sponge gourd, including AMMI analysis. Following the E & R model, two genotypes, VRSG-10 and VRSG-18, were given significant responses for both conditions (b=0 and b=1), while VRSG-171 was significant for b=0. However, the genotypes VRSG-28, VRSG-68, VRSG-69, VRSG-69-1 and VRSG-77 were significant for b=1. The highest and lowest mean values were observed for VRSG-142-1 (68.44) and Kashi Divya (17.96) and both were non-significant deviations from the regression line for b=1 and b=0 (Table 7).

Analysis of variance of AMMI model for yield value, PC1, PC2, PC3 and PC4 score of 32 genotypes and four environments is presented in Table 8. The genotypes G2, G14, G28, G3, G12 and G27 yielded maximum, while maximum PCA scores were found for the genotypes G10 for PC4 (9.81), G26 for PC1 (3.51) and G16 for PC2 (3.72) and G1 for PC1 (1.84), respectively. AMMI analysis for yield revealed highly significant differences among genotypes and environments, and the genotypes G2 and G14 expressed better G × E interaction (Fig. 2). G2 and G14 were high yielder as well as stable genotypes as suggested by AMMI1 analysis. E1 was

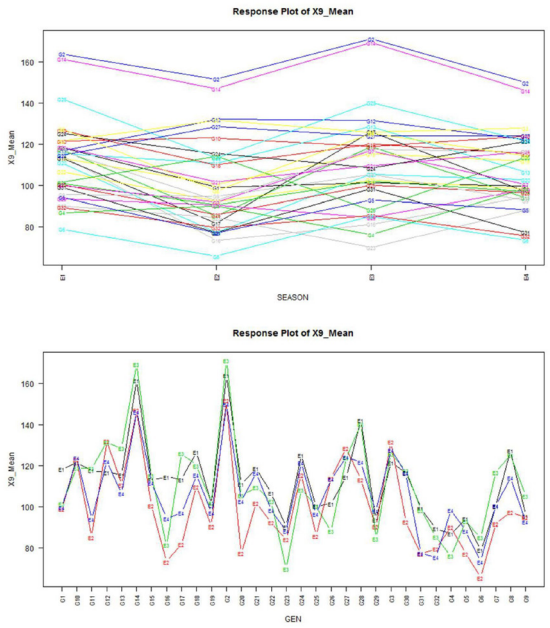

Fig. 2: Response plot of environment and genotypes for yield traits

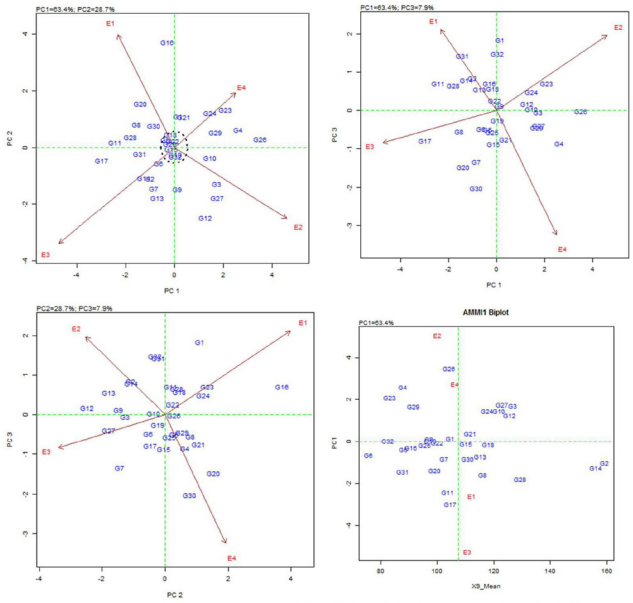

Fig. 3: AMMI Biplot for PCA 1 and PCA 2 displayed G1-G32 in E1-E4 for fruit yield

the highest-yielding environment, while E2 was the lowest-yielding environment. The G × E component was further explained by three principal component axes, namely PC1, PC2 & PC3 for the yield trait (Fig. 3). The IPCA (PC) score plots with 32 genotypes and four environments allowed us to cluster and separate into two different negative and positive fields. The PC1 score (PC1=63.4%) suggested that the location of 12 genotypes and environment E2 and E4 was positive in the field and the remaining 20 genotypes, along with the environment E1 and E3, were in a negative field. However, in PC2 score (PC2=28.7%), having 14 genotypes and environments E2 and E3 were in the negative field and the remaining 18 genotypes, along with environments E1 and E4, were presented in the positive field. While the PC3 score (7.9%) suggested that the location of 15 genotypes and environment E1 and E2 was positive in the field and the remaining 17 genotypes, along with the environment E3 and E4, were in a negative field, but G28 was stable with an E1 positive field in PC1 and PC2 plots (Fig. 3).

All the 32 genotypes were grouped into eight clusters (Table 9). Maximum genotypes were considered with cluster 1, 2 and 3, while the maximum value of intra-cluster was found for Cluster 6 and 8 (Table 8). Only genotype 'VRSG-7-17' (28) was alone in cluster 7 with '0' intra-cluster value. However, a dendogram exhibited 4 major clusters, including 2, 11, 2 and 17 genotypes in clusters 1, 2, 3 and 4, respectively (Fig. 4).

Discussion

Sponge gourd is a cross-pollinated crop and exhibits a wide range of variation in the colour, size, and shape of leaves, flowers, and fruits (Phan et al., 2015). Our observations validated the variation in leaf colour from green to dark green and fruit colour from light green to dark green. Earlier,

Table 6: Analysis of variance for stability analysis of 32 genotypes of sponge gourd for fruit yield (q/ha) by Eberhart and Russel (1966)

Source	*DF*	*SS*	*MSS*	*F (Div. Dev.)*	*F (Div. ME)*
Genotypes	31	31942.2813	1030.396	15.2217**	1.0907
Environment (Linear)	1	914.3438	914.3438	13.5073**	0.9679
G x E (Linear)	31	6596.0396	212.7755	3.1433**	0.2252
Env+ G x E	96	11842.6563	123.361	1.8224**	0.1306
Pooled Dev	64	4332.3188	67.6925	0.0717	
Pooled Error	248	702864	944.7097		
Total	127	43784.9375			

**Significant against pooled deviation M.S at 0.01 levels, respectively

Table 7: Analysis of variance for stability analysis of 32 genotypes of sponge gourd for fruit yield (q/ha).

S. No.	*Genotypes*	*Mean*	*PI*	*b*	*SE (b)*	*R Square*	*t (b=0)*	*t (b=1)*
1.	Kashi Divya	17.9658	-28.8895	3.1575	1.6417	0.6491	1.92ns	1.31ns
2.	Kashi Shreya	49.7883	2.9330	8.7768	4.7069	0.6348	1.86ns	1.65ns
3.	VRSG-10	34.7208	-12.1345	7.8705	1.5814	0.9253	4.98*	4.34*
4.	VRSG-11	41.0692	-5.7862	8.0024	2.9152	0.7903	2.75ns	2.40ns
5.	VRSG-1-12	25.8167	-21.0387	-0.0518	0.5696	0.0041	-0.09ns	-1.85ns
6.	VRSG-12	62.3742	15.5188	-1.1315	1.3116	0.2712	-0.86ns	-1.63ns
7.	VRSG-13	48.4083	1.5530	0.0317	1.0966	0.0004	0.03ns	-0.88ns
8.	VRSG-136	60.6942	13.8388	2.5653	1.1362	0.7182	2.26ns	1.38ns
9.	VRSG-14-1	24.1192	-22.7362	0.1876	0.5150	0.0622	0.36ns	-1.58ns
10.	VRSG-142-1	68.4375	21.5822	2.5885	2.8566	0.2911	0.91ns	0.56ns
11.	VRSG-154	51.3250	4.4697	1.3674	2.1023	0.1746	0.65ns	0.17ns
12.	VRSG-171	56.9275	10.0722	1.8466	0.4289	0.9026	4.31*	1.97ns
13.	VRSG-18	23.2192	-23.6362	-0.7614	0.0712	0.9828	-10.69**	-24.74**
14.	VRSG-195	64.0875	17.2322	-0.1084	1.5000	0.0026	-0.07ns	-0.74ns
15.	VRSG-2-12	45.5100	-1.3453	-3.2017	1.5537	0.6798	-2.06ns	-2.70ns
16.	VRSG-214	56.0342	9.1788	1.3474	0.4520	0.8163	2.98ns	0.77ns
17.	VRSG-28	22.9542	-23.9012	-0.2000	0.0820	0.7484	-2.44ns	-14.63**
18.	VRSG-40	64.7750	17.9197	-1.2582	0.9592	0.4624	-1.31ns	-2.35ns
19.	VRSG-49-1	51.2767	4.4213	0.8948	0.3598	0.7557	2.49ns	-0.29ns
20.	VRSG-50	60.9358	14.0805	-0.4852	1.5910	0.0444	-0.30ns	-0.93ns
21.	VRSG-57	21.1775	-25.6778	-0.0364	0.3288	0.0061	-0.11ns	-3.15ns
22.	VRSG-61	61.8517	14.9963	-1.2658	1.3567	0.3032	-0.93ns	-1.67ns
23.	VRSG-64	44.9442	-1.9112	0.3161	2.2201	0.0100	0.14ns	-0.31ns
24.	VRSG-68	51.2192	4.3638	-1.3079	0.4358	0.8183	-3.00ns	-5.30*
25.	VRSG-69	22.8642	-23.9912	-0.8883	0.2384	0.8741	-3.73ns	-7.92*
26.	VRSG-69-1	62.9142	16.0588	-1.1740	0.4733	0.7546	-2.48ns	-4.59*
27.	VRSG-70	48.2650	1.4097	0.9433	1.2253	0.2286	0.77ns	-0.05ns
28.	VRSG-7-17	57.5442	10.6888	-0.4834	0.7848	0.1595	-0.62ns	-1.89ns
29.	VRSG-77	22.5283	-24.3270	0.0186	0.2270	0.0034	0.08ns	-4.32*
30.	VRSG-9	64.4925	17.6372	0.5227	0.9976	0.1207	0.52ns	-0.48ns
31.	VRSG-91	52.6508	5.7955	2.0625	1.3324	0.5451	1.55ns	0.80ns
32.	VRSG-97	58.4800	11.6247	1.8529	1.2832	0.5104	1.44ns	0.66ns
	SE	4.83	1.56					

Phan et al. (2015) reported light green, green, and dark green colours of leaves and fruits in sponge gourd. The majority of cultivars (>96%) were observed with medium fruit size. Fruit size, determined by fruit length and diameter, influences market demand; however, medium to average-sized fruits are generally preferred for domestic use (Davis and De Courley, 1993). More than 65.63% of genotypes belonged to the early group for first fruit harvesting. Genotypes producing early flowering and fruiting are valuable for enhancing yield capacity. Similar observations were reported in ridge gourd (*Luffa acutangula*) by Choudhary et al. (2008) and Hanumegowda et al. (2012).

Among the genotypes, VRSG-7-17 was identified with a distinct Basmati rice-like aroma during sensory evaluation

Table 8: Analysis of variance of AMMI model and AMMI score of 32 genotypes and four environments for fruit yield (q/ha) scheduled under four principal component analysis (PC1-PC4).

S. No.	*Components*	*PC1*	*PC2*	*PC3*	*PC4*
1	Percent	63.4	28.7	7.9	0.0
2	Df	33	31	29	27
3	Sum.Sq	13955.28	6327.62	1742.49	0.00
4	Mean.Sq	422.89**	204.12**	60.09**	0.00
5	F.value	5.98	2.89	0.85	0.00
AMMI score of genotypes and environments					
#Levels	Mean of YQPH	PC1	PC2	PC3	PC4
G1	104.50	0.14	1.09	1.84	-6.26
G10	121.79	1.46	-0.35	0.03	9.81
G11	103.77	-2.44	0.17	0.70	-5.82
G12	125.63	1.26	-2.49	0.17	-8.37
G13	115.28	-0.71	-1.79	0.56	1.92
G14	156.07	-1.27	-1.07	0.80	1.36
G15	110.14	-0.13	-0.05	-0.88	-1.29
G16	90.78	-0.30	3.72	0.70	1.12
G17	104.51	-2.99	-0.46	-0.79	-2.55
G18	118.02	-0.15	0.46	0.57	-1.27
G19	97.45	0.03	-0.24	-0.25	-5.78
G2	159.18	-1.01	-1.09	0.84	5.39
G20	99.08	-1.39	1.54	-1.47	-1.48
G21	111.54	0.39	1.06	-0.75	1.80
G22	99.88	-0.07	0.23	0.27	-1.38
G23	83.06	2.09	1.33	0.71	-9.66
G24	117.63	1.45	1.20	0.48	2.03
G25	95.63	-0.19	0.13	-0.57	-9.23
G26	104.22	3.51	0.29	-0.02	-1.60
G27	122.83	1.76	-1.78	-0.39	-2.41
G28	129.32	-1.80	0.37	0.66	4.84
G29	91.57	1.68	0.54	-0.44	2.58
G3	126.71	1.71	-1.28	-0.05	5.97
G30	110.77	-0.85	0.78	-2.03	-5.68
G31	87.87	-1.44	-0.21	1.43	3.23
G32	82.43	0.03	-0.33	1.48	-6.95
G4	87.84	2.59	0.62	-0.86	1.90
G5	88.07	-0.38	0.28	-0.49	-1.10
G6	75.62	-0.67	-0.55	-0.47	3.15
G7	102.29	-0.85	-1.45	-1.34	-5.35
G8	116.11	-1.58	0.81	-0.54	2.68
G9	97.01	0.12	-1.48	0.12	5.38
E1	112.39	-2.60	4.41	2.34	-5.16
E2	100.11	5.10	-2.79	2.19	-5.16
E3	110.77	-5.27	-3.76	-0.93	-5.16
E4	106.29	2.77	2.14	-3.60	-5.16

**Significant at the 0.01 level; #G1-G32 indicates to genotypes *e.g.,* G1=Kashi Divya; G2=Kashi Shreya; G3=VRSG-10; G 4=VRSG-11; G5=VRSG-1-12; G6=VRSG-12; G7=VRSG-13; G8=VRSG-136; G9=VRSG-14-1; G10=VRSG-142-1; G11=VRSG-154; G12=VRSG-171; G13=VRSG-18; G14=VRSG-195; G15=VRSG-2-12; G16=VRSG-214; G17=VRSG-28; G18=VRSG-40; G19=VRSG-49-1; G20=VRSG-50; G21=VRSG-57; G22=VRSG-61; G23=VRSG-64; G24=VRSG-68; G25=VRSG-69; G26=VRSG-69-1; G27=VRSG-70; G28=VRSG-7-17; G29=VRSG-77; G30=VRSG-9; G31=VRSG-91; G32=VRSG-97' and #E1-E4 indicates to 'Environments 1-4'.

Table 9: Response of cluster and intra-cluster analysis of 32 genotypes

Clusters	*Number of genotypes*	*Details of genotypes*	*Intra-cluster*
1	10	8, 12, 13, 17, 19, 20, 22, 26, 27, 30	33.747
2	6	3, 10, 15, 18, 21, 24	26.665
3	6	1, 4, 7, 9, 16, 25	30.788
4	2	11, 29	29.033
5	3	5, 31, 32	37.407
6	2	6, 23	48.106
7	1	28	0
8	2	2, 14	43.495

Genotypes: 1=Kashi Divya; 2=Kashi Shreya; 3=VRSG-10; 4=VRSG-11; 5=VRSG-1-12; 6=VRSG-12; 7=VRSG-13; 8=VRSG-136; 9=VRSG-14-1; 10=VRSG-142-1; 11=VRSG-154; 12=VRSG-171; 13=VRSG-18; 14=VRSG-195; 15=VRSG-2-12; 16=VRSG-214; 17=VRSG-28; 18=VRSG-40; 19=VRSG-49-1; 20=VRSG-50; 21=VRSG-57; 22=VRSG-61; 23=VRSG-64; 24=VRSG-68; 25=VRSG-69; 26=VRSG-69-1; 27=VRSG-70; 28=VRSG-7-17; 29=VRSG-77; 30=VRSG-9; 31=VRSG-91; 32=VRSG-97.

and cooking. Supporting this finding, Phan et al. (2015) reported one sponge gourd accession ('B29') with aroma, although it degenerated after cooking.

Phenotypic correlation comprises both genotypic and environmental correlations. We observed eight positive and significant correlations and four negative but significant correlations. Similar positive and negative correlations at p <0.01 and p <0.05 were reported by Shah and Kale (2002) in ridge gourd. The strongest genotypic correlation was between days to first harvest and days to first female flower appearance, and between number of fruits per plant and yield (q/ha). The first harvesting of fruits depends on the early appearance of male and female flowers. Early flowering and fruiting, along with reduced fruit width, are considered desirable traits due to their market demand. In our study, fruit width, fruit number per plant, and average fruit weight were positively and significantly correlated with fruit length, fruit width, and fruit yield. Conversely, days to first male and female flower appearance showed negative but significant genotypic correlations. These findings align with Kumar et al. (2013), who reported that total yield per vine was significantly and positively correlated with the number of fruits per vine, average fruit weight, number of seeds per fruit, and total soluble solids at both genotypic and phenotypic levels. Badade et al. (2001) also found yield to be significantly but negatively correlated with days to first male and female flower appearance and weight of deformed fruits per vine in bottle gourd (*Lagenaria vulgaris*).

Correlation coefficients reflect variance and covariance matrices between variables and provide a basis for indirect selection of traits (Farshadfar et al., 2013). In the present study, genotypic covariances were lower than phenotypic covariances for all characters. Fruit yield showed high and positive covariance with NFP, AFW, FL, FW, and yield itself at

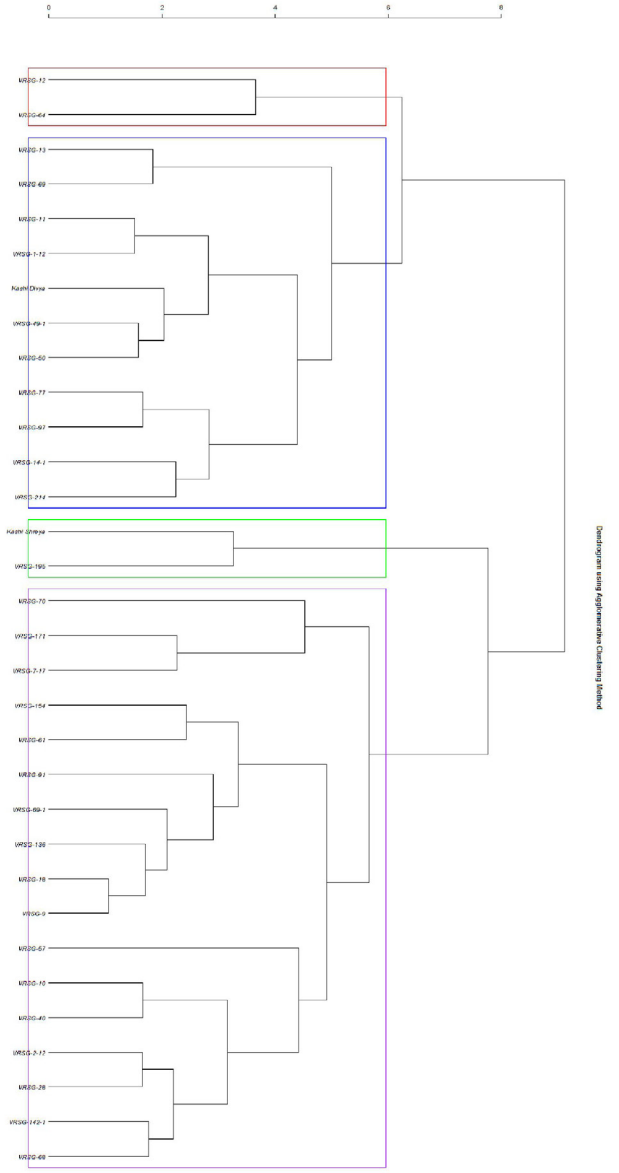

Fig. 4: Dendogram for cluster analysis using 32 genotypes

both genotypic and phenotypic levels. Enhanced covariance values between traits may represent high levels of genetic variation, which are useful in breeding programs (Farshadfar et al., 2013; Farshadfar and Estehghari, 2014).

Inter-character relationship studies are important in breeding for indirect selection of traits that are difficult to measure or exhibit low heritability. The lowest heritability in our study was observed for FW. Low to moderate heritability indicates the involvement of additive gene effects and average yield performance. Co-heritability was highest between DMF and FL and lowest between DMF and DFF, although FY showed maximum co-heritability with FL and FW. These observations suggest that the selection of certain traits would simultaneously affect yield and other traits (Farshadfar et al., 2013; Farshadfar and Estehghari, 2014).

In this study, genotype × environment interaction was significant for yield traits. Genotypes VRSG-10, VRSG-18, VRSG-171, VRSG-28, VRSG-68, VRSG-69, VRSG-69-1, and VRSG-77 were significant for b=0 and/or b=1. The highest and lowest mean yields were observed for VRSG-142-1 and VRSG-17, respectively, but both showed non-significant deviations from the regression line under b=0 and b=1. An ideal cultivar is defined as one with the highest yield across a broad range of environments (Eberhart and Russell, 1966). A stable cultivar is characterized by regression coefficients (b) equal to one or zero. According to Oliveira and Godoy (2006), a genotype may be considered stable when environmental variance is small or parallel to the mean response of all genotypes.

Two-dimensional principal component analysis (PCA1 and PCA2) divided into positive and negative fields, revealed clustering of all 32 genotypes. This suggests that although genotypes may originate from the same region, geographic diversity does not necessarily correspond to genetic diversity (Jeger et al., 1983). Further, Hagos and Abay (2013), Prasad et al. (2016), and Moharana et al. (2025) demonstrated that AMMI analysis can be used to determine genotype stability across locations using PCA scores and AMMI stability values (ASV). In genotype × environment interaction, genetic variance changes across environments (Przystalski et al., 2008). Among the IPCA groups, PCs explained >90% of the variation, indicating that G×E interactions were well explained by the AMMI model. Such interactions may lead to inconsistent performance due to differences in genotype and environment responses.

Genotypes G2, G14, G28, G3, G12, and G27 yielded maximum values, while maximum PCA scores were observed for G10 (PC4), G26 (PC1), G16 (PC2), and G1 (PC1). These genotypes were stable across three environments for yield traits. Stable genotypes may survive in recommended climatic regions with specific traits, although stability does not always correspond to superior yield (Oliveira and Godoy, 2006). Genotypes G2 and G14 expressed better G×E interactions and showed maximum stability across all four environments for fruit yield, suggesting their potential for cultivation in diverse climatic zones. Similar results were reported for ridge gourd by Varalakshmi and Krishnamurthy (2017). The effectiveness of stable genotypes depends on consistent performance across environments (Agasimani et al., 2008; Shaikh et al., 2012).

IPCA score plots with 32 genotypes and four environments separated into positive and negative fields. Genotype G28 was stable in the E1-positive field in both PC groups, possibly due to a diverse genetic background (Zalapa et al., 2006). Genotypes with high and positive interactions can be utilized for specific environments (Yan and Tinker, 2006; Hagos and Abay, 2013). Biplots showed that environmental points were more scattered than genotype points, indicating greater variability due to environments.

The genotypes under study were grouped into eight clusters with varying intra-cluster values, suggesting ample variability for breeding programs. Genotype G28 was alone in a cluster and expressed high variability. This observation was consistent with findings by Zalapa et al. (2006) and Kumar et al. (2013).

Conclusion

In the present study, all 32 genotypes of sponge gourd were found to be highly significant based on correlation studies between yield and yield-related traits. Genotype × environment interaction illustrated its stability for yield traits across three or four environments. Twelve genotypes—Kashi Shreya, VRSG-10, VRSG-18, VRSG-171, VRSG-195, VRSG-28, VRSG-68, VRSG-69, VRSG-69-1, VRSG-77, VRSG-70, and VRSG-7-17—exhibited ample variability, stability, and significance, and can be cultivated in different agro-climatic zones and heterosis breeding programs. Genotype VRSG-7-17 was identified as genetically diverse and possessing a unique Basmati rice-like aroma, confirmed through sensory evaluation and cooking. This aromatic genotype can be utilized in aroma breeding programs.

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सारांश

नेनुआ (लुफ्फा सिलिंड्रिका एल.) की कुल 32 प्रभेदों/जीनोटाइप की आकारिकी विशेषताओं, उपज प्रदर्शन और सुगंध संबंधी विशेषताओं के लिए जांच की गई। छब्बीस जीनोटाइप में मध्यम लंबाई के फल (15-25 सेमी) पाए गए, और 19 जीनोटाइप 55 दिनों के भीतर औद्यानिक परिपक्वता के लिए तैयार हो गए, जो उल्लेखनीय अगेतीपन दर्शाते हैं।उपज का फलों की संख्या और औसत फल भार दोनों के साथ मजबूत सकारात्मक सहसंबंध पाया गया। जीनोटाइप × पर्यावरण की परस्पर क्रिया उपज के लिए अत्यधिक महत्वपूर्ण थी, जो स्थिरता विश्लेषण के महत्व को रेखांकित करती है। आठ जीनोटाइप (वीआरएसजी 10, वीआरएसजी 18, वीआरएसजी 171, वीआरएसजी 28, वीआरएसजी 68, वीआरएसजी 69, वीआरएसजी 691 और वीआरएसजी 77) ने प्रतिगमन गुणांक (b = 0 या 1) प्रदर्शित किए, जो विभिन्न वातावरणों में स्थिर प्रदर्शन को दर्शाता है। इसके अलावा, काशी श्रेया, वीआरएसजी 195, वीआरएसजी 7-17, वीआरएसजी 10 और वीआरएसजी 171 ने प्रति हेक्टेयर उच्चतम उपज प्राप्त की, जिससे वे प्रमुख भारतीय कृषि-जलवायु क्षेत्रों में खेती के लिए उत्कृष्ट प्रजाति बन सकते हैं। क्लस्टर विश्लेषण ने 32 जीनोटाइपों को आठ अलग-अलग समूहों में वर्गीकृत किया; विशेष रूप से, वीआरएसजी 7-17 ने एक एकल समूह बनाया और पत्तियों, लताओं, फूलों, फलों और छिलके में बासमती चावल जैसी विशिष्ट सुगंध पाई गई, जिसकी पुष्टि कच्चे और पके दोनों पदार्थों के भौतिक संवेदी मूल्यांकन से हुई। ये निष्कर्ष पर्याप्त आनुवंशिक विविधता को उजागर करते हैं और भविष्य के प्रजनन और सुगंध-लक्षित सुधार कार्यक्रमों के लिए स्थिर, उच्च उपज देने वाली और सुगंधित किस्मों की पहचान करते हैं।