

**MOLECULAR DIVERSITY ASSESSMENT AND
MANIFESTATION OF HETEROSIS FOR GROWTH
AND YIELD IN SPONGE GOURD
(*Luffa cylindrica* (L.) Roem.)**

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**MOLECULAR DIVERSITY ASSESSMENT AND
MANIFESTATION OF HETEROSIS FOR GROWTH
AND YIELD IN SPONGE GOURD
(*Luffa cylindrica* (L.) Roem.)**

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By

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CERTIFICATE

This is to certify that the thesis entitled '**MOLECULAR DIVERSITY ASSESSMENT AND MANIFESTATION OF HETEROSIS FOR GROWTH AND YIELD IN SPONGE GOURD (*Luffa cylindrica* (L.) Roem.)**' submitted by **Ms. CHITHRA K., UHS19PGD355** for the degree of **DOCTOR OF PHILOSOPHY in VEGETABLE SCIENCE** to the University of Horticultural Sciences, Bagalkot is a record of bonafide research work done by her during the period of her study at University of Horticultural Sciences, Bagalkot under my guidance and supervision and the thesis has not previously been formed the basis of the award of any other degree, diploma, associateship, fellowship or similar titles.

**BAGALKOT
FEBRUARY, 2023**

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CONTENTS

Sl. No.	Chapter particulars	Page No.
	CERTIFICATE	iii
	ACKNOWLEDGEMENT	iv
	LIST OF ABBREVIATIONS	viii
	LIST OF TABLES	x
	LIST OF PLATES	xiv
	LIST OF FIGURES	xvi
	LIST OF APPENDICES	xvii
1.	INTRODUCTION	1-4
2.	REVIEW OF LITERATURE	5-82
	2.1 Genetic variability, heritability and genetic advance	5
	2.2 Genetic diversity study	31
	2.3 Molecular characterization in sponge gourd	37
	2.4 Correlation co-efficient analysis	42
	2.5 Path co-efficient analysis	50
	2.6 Magnitude of heterosis	55
	2.7 General and specific combining ability studies	71
3.	MATERIAL AND METHODS	83-114
	3.1 Experimental site	83
	3.2 Location and Climate	83
	3.3 Experimental details	83
	3.4 Experiment-I: Morphological characterization of sponge gourd genotypes	85
	3.5 Experiment-II: Molecular characterization of sponge gourd genotypes	86
	3.6 Experiment-III: Development of F ₁ hybrids and their evaluation	89
	3.7 Observations recorded	92
	3.8 Statistical analysis	103

Sl. No.	Chapter particulars	Page No.
4.	EXPERIMENTAL RESULTS	115-222
	4.1 Analysis of variance	115
	4.2 Morphological characterization	117
	4.3 Genetic variability	120
	4.4 Genetic diversity studies	135
	4.5 Molecular characterization	143
	4.6 Correlation co-efficient analysis	145
	4.7 Path co-efficient analysis	152
	4.8 Magnitude of heterosis	160
	4.9 Combining ability effects and variances	201
5.	DISCUSSION	223-257
	5.1 Analysis of variance	224
	5.2 Genetic variability	224
	5.3 Genetic diversity studies	228
	5.4 Molecular characterization	234
	5.5 Correlation co-efficient analysis	235
	5.6 Path co-efficient analysis	237
	5.7 Magnitude of heterosis	239
	5.8 Combining ability effects and variances	246
6.	SUMMARY AND CONCLUSION	258-265
7.	REFERENCES	266-287
	APPENDICES	288-292

LIST OF ABBREVIATIONS

%	Per cent
$^{\circ}\text{C}$	Degree Celsius
$^{\circ}\text{brix}$	Degree brix
No.	Number
σ_s^2	Variance due to specific combining ability
cm	Centimetre
g	Gram
df	Degrees of freedom
Fig.	Figure
FYM	Farm Yard Manure
ANOVA	Analysis of variance
CD	Critical difference
CTAB	Cetyl Trimethyl Ammonium Bromide
DAS	Days after sowing
DNA	Deoxyribonucleic Acid
GA	Genetic Advance
GAM	Genetic Advance as per cent over Mean
GCA	General Combining Ability
GCV	Genotypic Coefficient of Variation
GV	Genotypic Variance
h^2	Heritability (in broad sense)
ha	Hectare
kg	Kilogram
m	Meter

mg	Milligram
ml	Millilitres
mm	Millimetres
RCBD	Randomized Complete Block Design
PCV	Phenotypic Coefficient of Variation
PV	Phenotypic variance
<i>QTL</i>	Quantitative Trait Loci
Rpm	Revolutions per minute
SCA	Specific Combining Ability (variance)
SSR	Simple Sequence Repeats
T	Tonnes
<i>i.e.</i>	That is
<i>viz.</i>	Namely/Videlicet
<i>via.</i>	Through
Vs	Versus
<i>et al.</i>	co-workers
S.Em. $\pm$	Standard Error mean
SC	Standard check
BP	Better Parent
BST	Best Parent

LIST OF TABLES

Table No.	Title	Page No.
1.	Review of literature on mean, range, components of variance, heritability and genetic advance as per cent over mean for different characters in sponge gourd and other related cucurbit	7
2.	Review of literature on heterosis for different characters in sponge gourd and other related cucurbits	58
3.	Review of literature on combining ability and gene action on various traits in sponge gourd and other related cucurbits	71
4.	List of sponge gourd genotypes used in the experiment and their source of collection	84
5.	Details of SSR primers used for molecular characterization of sponge gourd genotypes	88
6a.	PCR reactions for microsatellite primers	89
6b.	PCR protocol followed for microsatellite primers of 40 sponge gourd genotypes	89
7.	Details of lines, tester and standard checks used in this study	90
8.	Analysis of variance (ANOVA) for growth, yield and quality parameters in sponge gourd	116
9.	Morphological characterization of sponge gourd genotypes for leaf color, leaf shape, leaf lobe and flower color	118
10.	Morphological characterization of sponge gourd genotypes for fruit shape, fruit color and flesh color	119
11.	Estimates of genetic variability parameters for growth, yield and quality traits in sponge gourd genotypes	122
12.	<i>Per se</i> performance of sponge gourd genotypes for growth and earliness parameters	125
13.	<i>Per se</i> performance of sponge gourd genotypes for earliness and yield parameters	126
14.	<i>Per se</i> performance of sponge gourd genotypes for yield and yield parameters	129
15.	<i>Per se</i> performance of sponge gourd genotypes for sponge yield and quality parameters	131
16.	Nutritional composition and antioxidant properties of sponge gourd genotypes	134

Table No.	Title	Page No.
17.	Per cent contribution of seventeen characters towards total divergence in sponge gourd genotypes	137
18.	Classification of sponge gourd genotypes into different clusters based on D^2 statistics	138
19.	Average intra cluster (diagonal) and inter cluster D^2 values in sponge gourd genotypes	138
20.	Cluster mean values for yield and its components in sponge gourd genotypes	140
21.	Details of the genetic parameters of molecular markers used for characterizing sponge gourd genotypes	144
22.	Clustering pattern of forty genotypes of sponge gourd on the basis of molecular marker analysis	147
23.	Estimates of phenotypic correlation coefficients for yield and its attributing traits in sponge gourd genotypes	148
24.	Estimates of genotypic correlation coefficients for yield and its attributing traits in sponge gourd genotypes	150
25.	Phenotypic path coefficient analysis for yield and its attributing characters in sponge gourd genotypes	154
26.	Genotypic path coefficient analysis for yield and its attributing characters in sponge gourd genotypes	158
27.	Analysis of variance (mean sum of squares) of line $\times$ tester analysis for various characters in sponge gourd	162
28.	<i>Per se</i> performance of crosses and parents for growth and earliness parameters in sponge gourd	165
29.	Heterosis (%) over better parent, best parent and standard check for vine length in sponge gourd	167
30.	Heterosis (%) over better parent, best parent and standard check for number of branches in sponge gourd	169
31.	Heterosis (%) over better parent, best parent and standard check for days to first male and female flower in sponge gourd	170
32.	<i>Per se</i> performance of crosses and parents for earliness and yield parameters in sponge gourd	172
33.	Heterosis (%) over better parent, best parent and standard check for node at first male and female flower in sponge gourd	174

Table No.	Title	Page No.
34.	Heterosis (%) over better parent, best parent and standard check for days to first harvest and last harvest in sponge gourd	176
35.	Heterosis (%) over better parent, best parent and standard check for fruit length and fruit diameter in sponge gourd	177
36.	<i>Per se</i> performance of crosses and parents for yield and yield parameters in sponge gourd	180
37.	Heterosis (%) over better parent, best parent and standard check for average fruit weight and number of fruits per vine in sponge gourd	182
38.	Heterosis (%) over better parent, best parent and standard check for fruit yield per vine and fruit yield per plot in sponge gourd	183
39.	Heterosis (%) over better parent, best parent and standard check for fruit yield per hectare and number of seeds per fruit in sponge gourd	185
40.	<i>Per se</i> performance of crosses and parents for sponge yield and quality parameters in sponge gourd	186
41.	Heterosis (%) over better parent, best parent and standard check for sponge yield and total soluble solids in sponge gourd	188
42.	Heterosis (%) over better parent, best parent and standard check for fruit firmness and fruit color (L*) in sponge gourd	190
43.	Heterosis (%) over better parent, best parent and standard check for fruit color (a*) and fruit color (b*) in sponge gourd	191
44.	Heterosis (%) over better parent, best parent and standard check for protein and ascorbic acid content in sponge gourd	193
45.	<i>Per se</i> performance of crosses and parents for quality parameters in sponge gourd genotypes	195
46.	Heterosis (%) over better parent, best parent and standard check for potassium and phenol content in sponge gourd	197
47.	Heterosis (%) over better parent, best parent and standard check for total antioxidants and total flavonoids in sponge gourd	199
48.	Heterosis (%) over better parent, best parent and standard check for crude fiber and ash content in sponge gourd	200
49.	Variance due to general and specific combining ability for different characters in sponge gourd	202
50.	General combining ability effects for growth parameters in sponge gourd	204

Table No.	Title	Page No.
51.	Specific combining ability effects for growth parameter in sponge gourd	205
52.	General combining ability effects for earliness and yield parameters in sponge gourd	207
53.	Specific combining ability effects for earliness and yield parameters in sponge gourd	208
54.	General combining ability effects for yield and yield parameters in sponge gourd	211
55.	Specific combining ability effects for yield and yield parameters in sponge gourd	212
56.	General combining ability effects for sponge yield and quality parameters in sponge gourd	215
57.	Specific combining ability effects for sponge yield and quality parameters in sponge gourd	216
58.	General combining ability effects for quality parameters in sponge gourd	220
59.	Specific combining ability effects for quality parameters in sponge gourd	221
60.	Over all analysis of general combining ability status of parents in sponge gourd	255
61.	Overall analysis of heterosis status of hybrids/ crosses in sponge gourd	256

LIST OF PLATES

Plate No.	Title	Between Pages
1.	General view of the experimental plot of experiment-I	86-87
2a.	Fruits of parents (lines and testers) and commercial check used in the experiment	90-91
2b.	Fruits of parents (lines and testers) and commercial check used in the experiment	90-91
3.	General view of the crossing block	92-93
4.	General view of the hybrids and parents evaluation block during summer 2022	92-93
5.	Morphological characterization of sponge gourd genotypes for leaf shape	118-119
6.	Morphological characterization of sponge gourd genotypes for leaf lobe	118-119
7.	Morphological characterization of sponge gourd genotypes for leaf color	118-119
8.	Morphological characterization of sponge gourd genotypes for fruit flower color	118-119
9.	Morphological characterization of sponge gourd genotypes for flesh color	118-119
10.	Morphological characterization of sponge gourd genotypes for fruit shape	120-121
11.	Morphological characterization of sponge gourd genotypes for fruit color	120-121
12a.	Variation in fruit characters of sponge gourd genotypes	134-135
12b.	Variation in fruit characters of sponge gourd genotypes	134-135
12c.	Variation in fruit characters of sponge gourd genotypes	134-135
12d.	Variation in fruit characters of sponge gourd genotypes	134-135
12e.	Variation in fruit characters of sponge gourd genotypes	134-135
13a.	Banding profile of SSR marker (SG_La_1) obtained on agarose gel of sponge gourd genotypes	144-145

Plate No.	Title	Between Pages
13b.	Banding profile of SSR marker (SG_La_4) obtained on agarose gel of sponge gourd genotypes	144-145
13c.	Banding profile of SSR marker (SG_La_11) obtained on agarose gel of sponge gourd genotypes	144-145
13d.	Banding profile of SSR marker (SG_La_28) obtained on agarose gel of sponge gourd genotypes	144-145
14.	Top four high yielding genotypes of sponge gourd	240-241
15a.	Fruits of top hybrid (L2 × T1) identified for fruit yield	252-253
15b.	Fruits of top hybrid (L6 × T1) identified for fruit yield	252-253
15c.	Fruits of top hybrid (L2 × T2) identified for fruit yield	252-253

LIST OF FIGURES

Figure No.	Title	Between Pages
1.	Dendrogram of clustering pattern of forty genotypes of sponge gourd	136-137
2.	Unweighted neighbour joining cluster analysis showing relationship and diversity among 40 sponge gourd genotypes	146-147
3.	Genetic variation for growth and yield in sponge gourd genotypes	224-225
4.	Genetic variation for different quality traits in sponge gourd genotypes	224-225

LIST OF APPENDICES

Appendix No.	Title	Page No.
I	Meteorological data during the experimental period recorded at the meteorological observatory of MHREC, UHS, Bagalkot	288
II	Reaction of sponge gourd F ₁ hybrids and their parents to fruit fly, leaf miner, downy mildew and powdery mildew incidence	289
III	Fruit characteristics of crosses, parents and commercial check	291

1. INTRODUCTION

Sponge gourd (*Luffa cylindrica* (L.) Roem.) is one of the minor cucurbitaceous vegetable crop cultivated in tropical and sub-tropical areas of the world. It is a diploid species with $2n=26$ chromosome number belonging to the family cucurbitaceae. This crop is indigenous to Tropical Asia, probably India and South East Asia. It has several other names like, towel gourd, smooth gourd, smooth luffa, dishcloth gourd, bath sponge, vegetable sponge, Chinese luffa. It is also called ghiya tori, nenua and turai in Hindi and tuppada hirekayi in Kannada (Nath and Swamy, 2016). There are nine species in *Luffa* out of which *Luffa acutangula* (L.) Roxb. and *Luffa cylindrica* (L.) Roem. are grown in large scale.

The crop sponge gourd is usually cultivated in small area for local consumption in Karnataka and little more area in some of the North Indian states. Hence, exact area and production are not documented. It has been cultivating extensively in Tropical and sub-tropical climatic conditions for centuries in the Middle East, India, China, Japan and Malaysia (Porterfield, 1955). In India, the crop is widely cultivated in Uttar Pradesh, Bihar, West Bengal, Orissa, Assam, Andhra Pradesh and Kerala (Arya and Prakash, 2002). In Karnataka, it is grown mainly in kitchen gardens during the spring summer and rainy seasons.

Sponge gourd is an annual climber with branched tendrils. It is highly cross pollinated crop due to the presence of monoecious sex form, however, other sex forms like hermaphrodite, staminate and pistillate flowers were also found in nature. Flowers are large, deep yellow in colour with having five petals. The inflorescence of staminate flower is emerged in racemes while, the pistillate flowers are solitary with short and long pendunculate. The anthesis usually starts in the morning hours between 4.00 to 7.00 am. Pollen fertility is maximum on the day of anthesis and lasts till two to three days after anthesis in winter and one and half days in rainy season. Stigma receptivity is seen six hour before anthesis and retained up to 24 hours after anthesis (Singh, 1957).

It is highly cross pollinated vegetable, thus, its natural population has tremendous variability for fruit length, shape, colour and taste *etc.* There is a wide variability with reference to fruit size ranging from few centimetres to one meter, fruit

shapes like lengthened cylindrical to club shaped, spindle type, elliptical and elongated and fruit colour variations like light green, intermediate green, dark green with white strips (Kumar *et al.*, 2013).

The tender or immature fruits of sponge gourd are eaten as cooked vegetable, used in the preparation of chutneys and curries. The tender fruits are easily digestible and increase appetite when consumed. It is nutritive vegetable rich in vitamin A, vitamin C and minerals (Mg, Ca, Na, K, Fe, Cu, Zn and Mn). It contains moisture of 93.2 g, protein 1.2 g, fat 0.2 g, carbohydrates 2.9 g and vitamins like, thiamine (0.02 mg), riboflavin (0.06 mg) and fibres (0.20 g) per 100 g of edible portion. The fruits of sponge gourd also have higher levels of protein and carotene than the ridge gourd (More and Shinde, 2001).

The sponge gourd fruits contains multiple bioactivators, such as alkaloids, flavonoids, sterols, glycosides, glycoproteins and thus possesses anti-inflammation, anti-fungal, anti-bacterial, anti-mycordical, sedative and analgesic activities. Fruits of this crop are best for the treatment of fever, jaundice, diabeties and hypertension. The presence of ribosome-inactivating protein in the seeds of sponge gourd said to be had anti-HIV activity. The oil extracted from the seeds of this crop is used for industrial purpose, treatment of leprosy and against many skin diseases (Partap *et al.*, 2012).

The mature dry fruits of this crop consists of dense network of cellulose fibers called as sponge or luffa which is used as filter and cleaning the motor car, glass wares, kitchen utensils and preparation of bathing accessories which increases the blood circulation and it is also credited as relief for rheumatic and arthritic suffers (Kumar *et al.*, 2013).

Inspite of being native to Tropical Asia and endowed with enormous variability and genetic divergence in the country but the scientific research to exploit this variability were limited. The research work on “crop improvement of this crop” in Karnataka is still megere. Hence, to exploit this variability, 40 genotypes of sponge gourd were collected from different parts of the state and country and are used for crop improvement. The study on variability of this crop is first step in crop improvement programme. However, an insight into the magnitude of variability, heritability and gene

effects present in available accessions provides information on the extent of possible improvement can be done in different characters.

The studies on components of variability and heritability do not throw light on the extent and nature of relationship existing between yield and various contributory characters. Hence, the correlation and path analysis are known to help the breeder in prioritizing the selection of yield and yield related characters. Correlation coefficient analysis measures the mutual relationship between various plant characters and determines the component characters on which selection can be based for improvement in yield (Fisher, 1918). Path analysis permits identification of direct and indirect causes of association and measures the relative importance of each character to a plant breeder for initiating a judicious breeding programme. Similarly, the information on genetic divergence among the available germplasm is also vital to a plant breeder for selecting more diverse parents to exploit high heterotic F_1 s and to create more variability in the segregating generations (Arunachalam, 1981). Among the different methods to study the available diversity, Mahalanobis generalized distance estimated by D^2 statistic (Rao, 1952) serves to be a good index for estimating genetic diversity.

Molecular markers provide reliable estimates of genetic diversity may improve screening efficiency of many traits through their linkage having alleles with small and large effects and will provide the first understanding of biology and architecture of quantitative traits at the DNA level. Use of such sophisticated molecular markers to characterize the germplasm is order of the day as morphology is influence by environment. These markers are powerful tools that can provide significant information which may enhance the scope of diversified use of germplasm in the crop improvement program. It also reveals the extent of relationship among the genotypes and to estimate genetic diversity or relatedness. Simple Sequence Repeats (SSR) are widely used for genetic diversity analysis because of their simplicity, effectiveness, abundance, co-dominant inheritance, extensive genomic coverage, high polymorphism and high reproducibility of results (Powell *et al.*, 1996). Hence, it is an important to consider a molecular diversity analysis in available germplasm.

Sponge gourd being monoecious in sex expression can be profitably utilized for the production of F_1 hybrid seeds at cheaper rate. High number of hybrid seeds per cross

makes it more economical. Thus, the development of F₁ hybrids manually is simple and less costly which enable the breeders to exploit hybrid vigour commercially in this crop. This crop has a broad spectrum of variation for early maturity, high fruit yield, different fruit size, shape, colour, cluster types and dwarf to long vine types. Therefore, sponge gourd offers greater scope for exploitation of hybrid vigour on commercial scale to increase the productivity and production. In this connection an attempt has been made to identify superior heterotic F₁ hybrids for yield, quality and earliness in this crop.

However, it never happens that each hybridization is accompanied by manifestation of hybrid vigour. Only certain pair of parents gives heterotic progeny. Therefore, for development of effective heterosis breeding programme in sponge gourd one need to elucidate the genetic nature and magnitude of quantitative inherited traits and estimated prepotency of parents in hybrid combinations. In this connection, the combining ability studies are essential to identify potential parents. Mating designs like line $\times$ tester (L $\times$ T) analysis which was first developed by Kempthorne (1957) provides information of combining ability and gene action. The general combining ability (gca) effects helps in selection of superior parents whereas, specific combining ability (sca) effects helps in selection of parental combination (hybrids).

Based on the crop importance and above mentioned facts, it was decided to take up an experiment on “Molecular diversity assessment and manifestation of heterosis for growth and yield in sponge gourd (*Luffa cylindrica* (L.) Roem.)” with the following objectives.

1. To study the genetic variability in sponge gourd genotypes for growth, yield and quality attributes.
2. Morphological and molecular characterization of sponge gourd genotypes.
3. To study the correlation and path coefficient analysis for yield and yield attributes.
4. To investigate the heterosis and combining ability for productivity traits in sponge gourd.

2. REVIEW OF LITERATURE

Sponge gourd is one of the important minor cucurbitaceous vegetable crop in which less breeding work has been done. Therefore, the plant breeder primary concern with the genetic improvement of both quantitative and qualitative traits is the information on various traits particularly of those that contribute to yield and quality would be the most useful in planning the appropriate breeding programs. Hence, in the present study an attempt was made to study the morphological and molecular diversity, variability, heritability, magnitude of heterosis and combining ability for various characters in sponge gourd genotypes. Further, the literature pertaining to this work in sponge gourd and similar aspect in other related crops has been summarized under the following sub-headings.

2.1 Genetic variability, heritability and genetic advance

2.2 Genetic diversity study

2.3 Molecular characterization in sponge gourd

2.4 Correlation co-efficient analysis

2.5 Path co-efficient analysis

2.6 Magnitude of heterosis

2.7 General and specific combining ability studies

2.1 Genetic variability, heritability and genetic advance

The magnitude of variability and its genetic components are the most important aspects of breeding material. Hence, the basic understanding of genetic variability is a prerequisite for the planning of breeding programme. Generally, genotypic coefficient of variability (GCV) and phenotypic coefficient of variability (PCV) are measured to study the variability.

The phenotypic expression of the plant characters is mainly controlled by the genetic makeup of the plant and its growing environment. Further, the genetic variance

of any quantitative trait is composed of additive variance (heritable) and non-additive variance which include dominance and epistasis (non-allelic interaction). Therefore, it becomes necessary to partition the observed phenotypic variability into its heritable and non-heritable components with suitable parameters such as phenotypic and genotypic coefficient of variation, heritability and genetic advance.

Heritability is the heritable portion of phenotypic variation and also a good index in providing information on the degree of inheritance of characters from parent to progeny. The estimates of heritability help in the selection of elite genotypes from diverse genetic population. Genetic advance measures the amount of progress that could be expected with selection in a character. However, the character showing high heritability need not exhibit high genetic advance (Johnson *et al.*, 1955). High heritability coupled with high genetic advance indicates that the improvement could be made for a character by simple selection.

Genetic advance under selection is the improvement in the mean genotypic value of the selected families over base population which depends upon the genetic variability existing in the population. Hence, the components of variances and heritable components with genetic parameters, such as genetic coefficient of variation, heritability estimate and genetic advance are important tools for the breeders to plan suitable breeding strategy.

A comprehensive review on mean, range, components of variance, broad sense heritability, genetic advance and genetic advance over percent mean (GAM) in sponge gourd and ridge gourd for different quantitative and qualitative traits are presented in the Table 1.

2.2 Genetic diversity study

Genetic diversity is an important factor for heritable improvement in any crop and the knowledge of genetic diversity, its nature and degree of variability would be useful for selecting desirable parents from available germplasm for a successful breeding programme. The genetically diversified genotypes could be used as parent in hybridization program for getting desirable segregants and in creating good scope for

Table 1. Review of literature on mean, range, components of variance, heritability and genetic advance as per cent over mean for different characters in sponge gourd and other related cucurbit

Sl. No.	Characters	Crop	Mean	Range	PV	GV	PCV (%)	GCV (%)	h^2 (%)	GA	GAM (%)	References
1.	Vine length at harvest time (m)	SG	5.36	4.25 - 7.75	-	-	16.49	10.22	42.40	0.72	-	Singh <i>et al.</i> (2009b)
		SG	3.17	2.71 - 3.54	-	-	10.39	9.72	87.51	0.59	18.73	Samadia (2010)
		SG	-	-	-	-	20.93	18.89	81.50	-	35.13	Pandey <i>et al.</i> (2012b)
		SG	1.72	1.43 - 2.36	1107.07	698.64	19.39	15.40	63.11	43.25	25.20	Dubey <i>et al.</i> (2013)
		SG	-	-	-	-	9.53	9.33	95.81	93.99	18.82	Kumar <i>et al.</i> (2013)
		SG	7.82	4.60 - 10.03	1.91	1.68	17.67	16.57	87.97	-	32.02	Patidar (2014)
		SG	3.36	2.27 - 3.82	-	-	11.91	10.76	81.62	67.21	20.03	Sharma <i>et al.</i> (2017)
		SG	4.20	2.20 - 6.20	-	-	28.84	27.39	90.00	-	53.61	Singh <i>et al.</i> (2017b)
		SG	6.45	3.40 - 9.51	-	-	22.48	21.93	95.20	-	44.09	Abhijeet <i>et al.</i> (2018b)
		SG	3.29	4.85 - 1.98	-	-	14.30	12.55	89.55	-	22.70	Kumar <i>et al.</i> (2019)
		SG	2.93	1.86 - 4.60	-	-	26.99	25.56	89.70	-	49.87	Singh <i>et al.</i> (2019c)
		SG	4.38	2.95 - 6.36	-	-	25.00	24.16	93.30	210.60	48.07	Annigeri (2020)
		SG	5.05	2.36 - 8.93	-	-	40.09	39.53	97.24	4.06	80.31	Kumar <i>et al.</i> (2020b)
		SG	2.34	1.75 - 3.47	-	-	18.86	16.05	72.40	-	28.12	Som <i>et al.</i> (2020a)
		SG	4.04	2.87 - 2.93	-	-	25.27	19.72	60.90	1.28	31.70	Ray (2021)
		SG	6.87	4.23 - 10.14	-	-	25.28	24.10	90.09	-	47.35	Purushottama (2022)
		RG	3.50	2.16 - 4.69	-	-	20.87	15.05	51.98	0.78	22.35	Choudhary and Kumar (2011)
		RG	2.91	2.51 - 3.69	-	-	13.00	12.37	90.42	0.70	24.23	Samadia (2011)
		RG	5.48	2.35 - 9.56	-	-	33.55	29.61	77.70	-	-	Rabbani <i>et al.</i> (2012)

Table 1. *Contd...*

Sl. No.	Characters	Crop	Mean	Range	PV	GV	PCV (%)	GCV (%)	h ² (%)	GA	GAM (%)	References
1.	Vine length at harvest time (m)	RG	2.44	2.00 - 2.91	880.35	775.59	12.17	11.42	88.00	53.85	22.09	Koppad <i>et al.</i> (2015)
		RG	3.90	2.20 - 6.50	1.40	0.80	30.90	23.60	58.20	1.40	37.00	Varalakshmi <i>et al.</i> (2015)
		RG	2.85	1.97 - 4.09	5640.66	5540.00	26.39	26.16	98.20	151.96	53.40	Saklesh (2016)
		RG	3.13	2.43 - 3.71	-	-	15.12	11.25	55.30	0.54	-	Bhargava <i>et al.</i> (2017)
		RG	2.87	2.07 - 3.63	-	-	17.85	12.52	49.23	-	18.10	Karthik <i>et al.</i> (2017)
		RG	3.03	2.45 - 3.73	0.09	0.08	10.16	9.45	86.52	-	18.12	Manoj <i>et al.</i> (2018)
		RG	3.98	1.52 - 4.61	5859.68	5708.12	19.25	19.00	97.00	153.61	38.63	Ramesh <i>et al.</i> (2018b)
		RG	-	-	2834.35	2796.92	13.32	13.23	98.70	108.22	27.08	Divyaraj <i>et al.</i> (2019)
		RG	4.39	2.20 - 8.19	28770.1	28379.47	38.67	38.40	98.64	344.67	78.57	Harshitha <i>et al.</i> (2019a)
		RG	8.09	-	-	-	5.27	4.76	81.40	-	8.81	Kannan <i>et al.</i> (2019)
		RG	7.76	-	-	-	4.39	3.63	84.73	-	7.42	Kannan and Rajamanickam (2019)
		RG	7.19	4.92 - 9.88	194.10	193.27	19.36	19.35	99.93	286.74	39.86	Methela <i>et al.</i> (2019)
		RG	2.64	1.92 - 3.26	-	-	13.97	13.57	94.90	72.22	27.24	Akhila and Singh (2020)
		RG	7.07	6.22 - 10.18	0.81	0.80	21.24	21.14	98.00	-	43.32	Krishnamoorthy (2020a)
		RG	10.21	-	-	-	6.57	4.22	41.27	-	5.59	Vijayakumar <i>et al.</i> (2020)
		RG	5.69	-	6239.98	5748.05	13.88	13.32	92.12	149.89	26.33	Vinitha <i>et al.</i> (2021)
		RG	2.91	1.82 - 4.56	3422.56	2096.13	15.72	20.09	61.24	73.80	25.34	Panda <i>et al.</i> (2022)
2.	Number of primary branches per plant	SG	4.52	3.05 - 5.70	-	-	18.17	13.16	55.20	0.92	-	Singh <i>et al.</i> (2009b)
		SG	3.96	3.08 - 5.00	0.46	0.32	17.06	14.33	70.60	0.98	24.80	Dubey <i>et al.</i> (2013)
		SG	-	-	-	-	13.22	12.71	92.47	3.22	25.17	Kumar <i>et al.</i> (2013)
		SG	4.70	3.26 - 7.40	1.17	0.91	23.06	20.32	77.67	-	36.89	Patidar (2014)

Table 1. *Contd...*

Sl. No.	Characters	Crop	Mean	Range	PV	GV	PCV (%)	GCV (%)	h ² (%)	GA	GAM (%)	References
2.	Number of primary branches per plant	SG	4.72	3.17 - 5.67	-	-	15.7	15.46	96.91	1.48	31.39	Sharma <i>et al.</i> (2017)
		SG	6.02	4.33 - 9.10	-	-	24.18	22.41	86.00	-	42.81	Singh <i>et al.</i> (2017b)
		SG	3.09	1.80 - 4.80	-	-	24.94	24.56	96.99	-	49.83	Kumar <i>et al.</i> (2019)
		SG	5.35	3.26 - 8.26	-	-	22.90	21.50	88.19	-	41.60	Singh <i>et al.</i> (2019c)
		SG	4.25	3.47 - 5.33	-	-	14.11	10.35	55.55	0.67	15.75	Annigeri (2020)
		SG	5.51	3.76 - 8.73	-	-	22.28	20.24	82.47	2.08	37.86	Kumar <i>et al.</i> (2020b)
		SG	3.89	3.29 - 4.05	-	-	6.07	4.29	49.98	-	6.25	Som <i>et al.</i> (2020a)
		SG	7.06	-	11.27	10.14	47.58	45.13	89.97	6.22	88.19	Yadav (2020)
		SG	2.65	2.23 - 2.93	-	-	12.84	6.90	28.90	0.20	7.64	Ray (2021)
		SG	5.42	3.09 - 8.12	-	-	23.67	22.94	91.42	-	45.79	Purushottama (2022)
		RG	4.53	3.47 - 6.33	-	-	21.86	12.88	34.71	0.71	15.63	Choudhary and Kumar (2011)
		RG	3.00	1.57 - 4.23	-	-	24.90	22.24	79.78	-	-	Rabbani <i>et al.</i> (2012)
		RG	4.68	2.33 - 6.17	0.98	0.88	21.42	20.34	90.00	18.40	39.80	Koppad <i>et al.</i> (2015)
		RG	6.90	2.90 - 13.3	9.00	7.30	43.40	39.00	80.80	5.00	72.30	Varalakshmi <i>et al.</i> (2015)
		RG	5.88	4.40 - 7.87	1.21	1.04	18.74	17.33	85.50	1.94	33.00	Saklesh (2016)
		RG	4.13	3.60 - 4.93	-	-	10.34	6.77	42.90	3.37	-	Bhargava <i>et al.</i> (2017)
		RG	5.08	4.00 - 6.40	0.35	0.03	11.79	10.56	80.26	-	19.49	Manoj <i>et al.</i> (2018)
		RG	4.09	3.00 - 7.40	1.09	0.96	25.50	23.96	88.23	1.89	46.89	Harshitha <i>et al.</i> (2019a)
		RG	7.78	6.00 - 9.70	-	-	18.86	6.75	12.82	-	4.98	Karthik <i>et al.</i> (2017)
		RG	2.53	1.61 - 3.71	0.29	0.18	21.25	17.08	64.56	0.71	28.27	Panda <i>et al.</i> (2022)

Table 1. Contd...

Sl. No.	Characters	Crop	Mean	Range	PV	GV	PCV (%)	GCV (%)	h ² (%)	GA	GAM (%)	References
3.	Days to first male flower	SG	50.78	31.95 - 64.77	-	-	16.35	16.18	98.02	16.76	33.01	Samadia (2010)
		SG	-	-	-	-	5.80	4.50	60.20	-	7.19	Pandey <i>et al.</i> (2012b)
		SG	35.20	31.75 - 37.50	6.25	4.12	7.10	5.76	65.87	3.39	9.64	Dubey <i>et al.</i> (2013)
		SG	-	-	-	-	7.97	7.22	82.08	4.89	13.47	Kumar <i>et al.</i> (2013)
		SG	39.02	30.55 - 48.00	26.94	25.30	13.30	12.89	93.92	-	25.73	Patidar (2014)
		SG	24.24	22.00 - 26.20	-	-	4.76	3.97	69.56	1.65	6.82	Sharma <i>et al.</i> (2017)
		SG	36.23	28.50 - 48.47	-	-	15.68	13.35	73.00	-	23.42	Singh <i>et al.</i> (2017b)
		SG	41.43	34.00 - 60.33	-	-	12.64	11.31	80.10	-	20.86	Abhijeet <i>et al.</i> (2018b)
		SG	42.26	30.88 - 49.85	-	-	12.45	10.71	73.91	-	18.96	Kumar <i>et al.</i> (2019)
		SG	38.67	25.10 - 47.93	-	-	16.58	14.52	76.69	-	26.20	Singh <i>et al.</i> (2019c)
		SG	51.36	47.67 - 56.80	-	-	3.27	6.83	23.01	1.66	3.23	Annigeri (2020)
		SG	40.58	31.67 - 48.63	-	-	13.69	12.57	84.36	9.66	23.80	Kumar <i>et al.</i> (2020b)
		SG	62.22	55.00 - 70.66	-	-	7.83	4.05	26.75	-	9.14	Som <i>et al.</i> (2020a)
		SG	34.55	-	5.24	3.77	6.62	5.62	71.93	3.39	9.81	Yadav (2020)
		SG	42.46	40.08 - 45.06	-	-	4.68	3.33	50.60	1.97	4.88	Ray (2021)
		SG	44.18	31.34 - 51.91	-	-	17.07	15.74	85.00	-	29.89	Purushottama (2022)
		RG	38.47	29.00 - 53.00	-	-	12.21	11.61	90.46	8.75	22.74	Singh <i>et al.</i> (2008)
		RG	37.83	34.26 - 45.03	-	-	7.62	6.37	69.96	4.15	10.98	Samadia (2011)
		RG	38.55	33.93 - 45.73	10.74	9.96	8.50	8.19	92.70	6.26	16.23	Saklesh (2016)
		RG	38.64	25.66 - 49.46	-	-	16.96	14.34	71.40	9.65	-	Bhargava <i>et al.</i> (2017)
		RG	42.37	38.30 - 53.06	-	-	13.64	7.55	30.63	-	8.60	Karthik <i>et al.</i> (2017)
		RG	34.40	31.10 - 39.95	5.34	5.01	6.71	6.50	93.83	-	12.98	Manoj <i>et al.</i> (2018)
		RG	38.40	33.00 - 44.00	11.93	11.35	8.99	8.77	95.00	6.77	17.62	Ramesh <i>et al.</i> (2018b)

Table 1. *Contd...*

Sl. No.	Characters	Crop	Mean	Range	PV	GV	PCV (%)	GCV (%)	h ² (%)	GA	GAM (%)	References
3.	Days to first male flower	RG	-	-	13.56	11.06	8.43	7.61	81.60	6.19	14.17	Divyaraj <i>et al.</i> (2019)
		RG	25.85	21.00 - 42.78	28.50	22.77	20.65	18.40	79.90	8.70	33.99	Harshitha <i>et al.</i> (2019a)
		RG	38.36	-	-	-	12.57	10.07	64.15	-	16.61	Kannan <i>et al.</i> (2019)
		RG	26.43	-	-	-	8.04	7.18	79.43	-	13.16	Kannan and Rajamanickam (2019)
		RG	61.55	59.33 - 64.33	3.82	1.07	3.18	1.68	28.01	1.13	1.83	Methela <i>et al.</i> (2019)
		RG	42.95	34.89 - 47.45	-	-	8.49	7.53	78.70	5.87	13.77	Akhila and Singh (2020)
		RG	35.77	32.20 - 41.80	6.79	3.02	7.29	4.86	44.00	-	6.67	Krishnamoorthy (2020a)
		RG	34.42	-	-	-	6.40	4.62	52.17	-	6.88	Vijayakumar <i>et al.</i> (2020)
		RG	30.12	-	-	-	8.31	7.62	84.05	4.33	14.39	Chinthalapudi <i>et al.</i> (2021)
		RG	26.25	-	-	-	8.97	7.45	68.09	3.34	12.74	Sravani <i>et al.</i> (2021)
4.	Days to first female flower	SG	42.50	32.44 - 52.40	-	-	9.29	9.11	87.30	6.57	-	Singh <i>et al.</i> (2009b)
		SG	60.24	43.23 - 74.18	-	-	13.17	12.95	96.74	15.81	26.24	Samadia (2010)
		SG	-	-			4.25	3.94	85.90	-	7.52	Pandey <i>et al.</i> (2012b)
		SG	41.45	37.50 - 43.75	8.79	5.84	7.15	5.83	66.44	4.06	9.79	Dubey <i>et al.</i> (2013)
		SG	-	-	-	-	8.95	8.12	82.35	5.24	15.18	Kumar <i>et al.</i> (2013)
		SG	47.89	38.00 - 58.55	32.54	27.08	11.91	10.87	83.23	-	20.42	Patidar (2014)
		SG	26.46	24.40 - 28.00	-	-	7.86	4.22	75.43	2.00	7.56	Sharma <i>et al.</i> (2017)

Table 1. Contd...

Sl. No.	Characters	Crop	Mean	Range	PV	GV	PCV (%)	GCV (%)	h ² (%)	GA	GAM (%)	References
4.	Days to first female flower	SG	39.99	34.37 - 50.33	-	-	13.38	10.99	67.00	-	18.60	Singh <i>et al.</i> (2017b)
		SG	47.72	39.66 - 63.00	-	-	10.09	8.56	72.00	-	14.96	Abhijeet <i>et al.</i> (2018b)
		SG	46.54	55.50 - 35.23	-	-	11.89	11.13	87.58	-	21.45	Kumar <i>et al.</i> (2019)
		SG	41.52	31.66 - 50.16	-	-	14.73	12.24	69.10	-	20.97	Singh <i>et al.</i> (2019c)
		SG	46.67	43.73 - 53.53	-	-	7.18	3.47	23.46	1.62	3.47	Annigeri (2020)
		SG	44.67	32.33 - 51.67	-	-	14.78	13.69	85.76	11.66	26.12	Kumar <i>et al.</i> (2020b)
		SG	65.11	56.00 - 69.33	-	-	5.91	4.96	70.41	-	28.52	Som <i>et al.</i> (2020a)
		SG	40.61	-	11.47	8.63	8.34	7.23	75.25	5.25	12.93	Yadav (2020)
		SG	40.25	38.04 - 42.64	-	-	4.26	3.36	62.20	2.31	5.46	Ray (2021)
		SG	48.57	35.34 - 57.91	-	-	15.47	13.85	80.16	-	25.55	Purushottama (2022)
		RG	40.99	29.00 - 55.00			12.96	13.42	93.18	10.56	25.76	Singh <i>et al.</i> (2008)
		RG	48.60	42.27 - 53.60			8.78	4.85	30.56	2.69	5.33	Choudhary and Kumar (2011)
		RG	47.05	40.66 - 57.23			9.45	8.91	88.84	8.14	17.30	Samadia (2011)
		RG	49.78	46.33 - 54.00	8.26	4.81	5.77	4.41	58.00	3.45	6.93	Koppad <i>et al.</i> (2015)
		RG	47.70	37.00 - 66.40	56.10	27.60	15.70	11.00	49.20	7.60	15.90	Varalakshmi <i>et al.</i> (2015)
		RG	44.24	38.13 - 51.20	17.51	16.95	9.46	9.31	96.80	8.34	18.86	Saklesh (2016)
		RG	-	-	-	-	14.21	13.88	95.00	-	27.92	Ananthan and Krishnamoorthy (2017)
		RG	42.64	30.40 - 53.46	-	-	13.69	10.81	62.30	7.49	-	Bhargava <i>et al.</i> (2017)
		RG	49.07	41.28 - 56.17	-	-	10.73	7.89	54.07	-	11.95	Karthik <i>et al.</i> (2017)
		RG	40.81	36.30 - 45.95	8.59	8.12	7.18	6.98	94.43	-	13.97	Manoj <i>et al.</i> (2018)
		RG	42.43	36.00 - 52.00	18.90	18.23	10.25	10.06	96.00	8.64	20.36	Ramesh <i>et al.</i> (2018b)
		RG	-	-	13.42	10.69	7.60	6.78	79.70	6.01	12.47	Divyaraj <i>et al.</i> (2019)
		RG	34.59	23.80 - 47.34	27.23	12.79	15.09	10.34	46.98	5.05	14.60	Harshitha <i>et al.</i> (2019a)
		RG	34.17	-	-	-	6.04	5.32	73.34	-	8.72	Kannan and Rajamanickam (2019)
		RG	44.13	-	-	-	7.37	5.35	52.73	-	8.01	Kannan <i>et al.</i> (2019)

Table 1. Contd...

Sl. No.	Characters	Crop	Mean	Range	PV	GV	PCV (%)	GCV (%)	h ² (%)	GA	GAM (%)	References
4.	Days to first female flower	RG	66.73	64.67 - 70.33	4.35	1.34	3.13	1.73	30.78	1.32	1.98	Methela <i>et al.</i> (2019)
		RG	-	-	-	-	7.37	6.99	90.01	6.87	-	Parveen <i>et al.</i> (2019)
		RG	46.96	39.8 - 52.15	-	-	7.19	6.26	75.80	5.26	11.22	Akhila and Singh (2020)
		RG	46.01	39.40 - 55.00	14.83	9.80	8.37	6.80	66.00	-	11.39	Krishnamoorthy (2020a)
		RG	43.50	-	-	-	9.57	7.54	62.22	-	12.26	Vijayakumar <i>et al.</i> (2020)
		RG	39.62	-	-	-	6.34	5.81	84.13	4.35	10.98	Chinthalapudi <i>et al.</i> (2021)
		RG	34.48	-	-	-	10.00	6.82	46.56	3.30	9.59	Sravani <i>et al.</i> (2021)
5.	Node at first male flower	SG	-	-	-	-	28.68	23.87	69.20	-	40.90	Pandey <i>et al.</i> (2012b)
		SG	7.07	5.26 - 9.60	1.66	1.43	18.33	17.01	86.16	-	32.53	Patidar (2014)
		SG	1.84	1.11 - 4.21	-	-	49.41	45.81	85.96	1.61	87.38	Sharma <i>et al.</i> (2017)
		SG	7.69	4.73 - 15.33	-	-	33.51	32.95	97.00	-	66.75	Singh <i>et al.</i> (2017b)
		SG	7.71	3.66 - 18.33	-	-	40.09	36.20	81.50	-	67.33	Abhijeet <i>et al.</i> (2018b)
		SG	5.41	3.03 - 9.23	-	-	32.00	30.88	93.16	-	61.41	Singh <i>et al.</i> (2019c)
		SG	5.76	4.00 - 9.40	-	-	25.00	18.06	51.92	1.54	26.78	Annigeri (2020)
		SG	6.72	3.67 - 12.26	-	-	34.13	33.12	94.21	4.45	66.23	Kumar <i>et al.</i> (2020b)
		SG	7.54	6.20 - 8.53	-	-	9.30	8.29	79.50	-	28.51	Som <i>et al.</i> (2020a)
		SG	9.82	-	6.25	4.83	25.46	22.38	77.29	3.98	40.53	Yadav (2020)
		RG	8.63	3.00 - 22.00	-	-	42.77	41.43	93.83	7.14	82.73	Singh <i>et al.</i> (2008)
		RG	3.87	2.93 - 5.13	0.19	0.45	18.12	17.31	91.20	1.32	34.04	Saklesh (2016)
		RG	9.18	3.70 - 19.06	-	-	45.78	44.64	95.10	8.24	-	Bhargava <i>et al.</i> (2017)
		RG	3.32	2.67 - 3.78	-	-	15.58	2.64	2.87	-	0.92	Karthik <i>et al.</i> (2017)
		RG	3.56	3.10 - 4.30	0.16	0.11	11.24	9.54	72.13	-	16.70	Manoj <i>et al.</i> (2018)
		RG	4.18	2.90 - 5.53	0.61	0.56	18.63	17.84	92.00	1.47	35.20	Ramesh <i>et al.</i> (2018b)

Table 1. *Contd...*

Sl. No.	Characters	Crop	Mean	Range	PV	GV	PCV (%)	GCV (%)	h ² (%)	GA	GAM (%)	References
5.	Node at first male flower	RG	6.65	-	-	-	16.38	14.51	78.48	1.76	26.48	Suresh and Balamohan(2018)
		RG	-	-	0.55	0.55	17.11	17.08	99.70	1.53	35.15	Divyaraj <i>et al.</i> (2019)
		RG	4.01	2.05 - 6.40	1.27	0.79	28.11	22.16	62.11	1.44	35.97	Harshitha <i>et al.</i> (2019a)
		RG	9.00	-	-	-	9.04	6.40	60.66	-	24.04	Kannan <i>et al.</i> (2019)
		RG	5.87	-	-	-	8.45	5.12	78.48	-	26.80	Kannan and Rajamanickam (2019)
		RG	4.38	3.04 - 5.74	-	-	15.85	15.78	99.10	1.44	32.36	Akhila and Singh (2020)
		RG	9.14	3.80 - 17.00	8.73	3.71	32.34	21.08	42.00	-	28.31	Krishnamoorthy (2020a)
		RG	7.83	-	-	-	7.83	5.19	43.88	-	7.08	Vijayakumar <i>et al.</i> (2020)
		RG	2.46	-	-	-	38.35	32.53	71.93	1.40	56.83	Chinthalapudi <i>et al.</i> (2021)
		RG	2.75	-	-	-	32.32	12.68	15.40	0.28	10.25	Sravani <i>et al.</i> (2021)
6.	Node at first female flower	SG	11.25	7.53 - 14.33	-	-	24.23	22.41	86.00	6.15	-	Singh <i>et al.</i> (2009b)
		SG	-	-	-	-	18.71	15.54	69.00	-	26.60	Pandey <i>et al.</i> (2012b)
		SG	-	-	-	-	10.42	9.44	82.12	1.88	17.63	Kumar <i>et al.</i> (2013)
		SG	11.84	8.73 - 14.66	4.36	2.34	12.92	17.64	53.66	-	19.50	Patidar (2014)
		SG	6.99	4.66 - 9.29	-	-	26.27	18.85	51.47	1.95	27.85	Sharma <i>et al.</i> (2017)
		SG	11.51	7.10 - 18.23	-	-	24.79	23.93	93.00	-	47.60	Singh <i>et al.</i> (2017b)
		SG	13.72	6.66 - 27.00	-	-	31.82	30.26	90.40	-	59.27	Abhijeet <i>et al.</i> (2018b)
		SG	13.03	6.56 - 19.05	-	-	19.59	18.73	91.44	-	36.89	Kumar <i>et al.</i> (2019)
		SG	9.97	6.06 - 14.36	-	-	23.05	21.74	88.98	-	42.25	Singh <i>et al.</i> (2019c)
		SG	12.97	10.87 - 15.87	-	-	27.14	26.06	91.93	1.74	13.39	Annigeri (2020)
		SG	11.18	7.13 - 15.43	-	-	20.14	19.19	90.72	4.20	37.65	Kumar <i>et al.</i> (2020b)
		SG	13.89	12.46 - 15.06	-	-	5.96	5.60	88.50	-	25.26	Som <i>et al.</i> (2020a)
		SG	18.23	-	8.38	6.60	15.88	14.10	78.77	4.70	25.77	Yadav (2020)
		SG	11.48	10.33 - 12.66	-	-	5.81	7.62	36.70	0.83	7.25	Ray (2021)
		SG	9.05	8.10 - 12.50	-	-	12.52	11.85	89.61	-	23.11	Purushottama (2022)

Table 1. *Contd...*

Sl. No.	Characters	Crop	Mean	Range	PV	GV	PCV (%)	GCV (%)	h^2 (%)	GA	GAM (%)	References
6.	Node at first female flower	RG	13.57	5.00 - 31.00	-	-	41.42	40.71	96.58	11.18	82.38	Singh <i>et al.</i> (2008)
		RG	14.59	2.93 - 20.27	-	-	32.29	29.40	82.91	8.04	55.14	Choudhary and Kumar (2011)
		RG	9.80	5.30 - 19.90	11.50	8.60	34.70	29.90	74.30	5.20	53.10	Varalakshmi <i>et al.</i> (2015)
		RG	10.81	6.33 - 16.73	10.99	10.61	30.68	30.13	96.50	6.59	60.96	Saklesh (2016)
		RG	-	-	-	-	14.69	14.32	95.00	-	28.73	Ananthan and Krishnamoorthy (2017)
		RG	11.68	3.00 - 21.00	-	-	32.95	31.45	91.10	7.22	-	Bhargava <i>et al.</i> (2017)
		RG	8.02	6.33 - 10.87	-	-	20.23	15.65	59.84	-	24.94	Karthik <i>et al.</i> (2017)
		RG	11.31	9.00 - 13.10	0.92	0.77	8.51	7.79	83.97	-	14.72	Manoj <i>et al.</i> (2018)
		RG	16.43	8.00 - 22.00	17.96	17.13	25.79	25.18	95.00	8.33	50.66	Ramesh <i>et al.</i> (2018b)
		RG	17.14	-	-	-	17.86	16.39	84.23	5.31	30.98	Suresh and Balamohan (2018)
		RG	-	-	11.71	11.05	21.03	20.38	93.90	6.62	40.70	Divyaraj <i>et al.</i> (2019)
		RG	9.18	4.40 - 21.54	12.99	10.45	39.25	35.19	80.42	5.97	65.01	Harshitha <i>et al.</i> (2019a)
		RG	16.28	-	-	-	17.70	16.13	84.56	-	31.68	Kannan and Rajamanickam (2019)
		RG	19.55	-	-	-	17.78	16.79	84.98	-	30.46	Kannan <i>et al.</i> (2019)
		RG	15.04	7.87 - 20.44	-	-	21.01	20.13	91.80	6.11	39.73	Akhila and Singh (2020)
		RG	23.61	15.4 - 27.80	8.48	3.49	12.34	7.87	40.00	-	10.36	Krishnamoorthy (2020a)
		RG	20.21	-	-	-	8.28	3.62	19.15	-	3.26	Vijayakumar <i>et al.</i> (2020)

Table 1. *Contd...*

Sl. No.	Characters	Crop	Mean	Range	PV	GV	PCV (%)	GCV (%)	h ² (%)	GA	GAM (%)	References
6.	Node at first female flower	RG	11.14	-	-	-	24.40	23.74	97.84	2.80	25.13	Chinthalapudi <i>et al.</i> (2021)
		RG	9.36	-	-	-	28.89	14.69	25.88	1.44	15.40	Sravani <i>et al.</i> (2021)
		RG	7.59	-	1.27	1.07	14.85	13.63	84.21	1.95	25.76	Vinitha <i>et al.</i> (2021)
		RG	13.76	9.64 - 18.46	5.21	4.58	15.55	16.59	87.81	4.13	30.02	Panda <i>et al.</i> (2022)
7.	Days to first harvest	SG	49.33	40.12 - 49.33	-	-	8.62	8.22	92.00	7.98	-	Singh <i>et al.</i> (2009b)
		SG	69.88	53.84 - 83.61	-	-	11.05	10.90	97.42	15.49	22.16	Samadia (2010)
		SG	-	-	-	-	4.53	2.99	43.60	-	4.06	Pandey <i>et al.</i> (2012b)
		SG	50.83	47.75 - 53.00	6.61	4.17	5.06	4.02	63.08	3.34	6.57	Dubey <i>et al.</i> (2013)
		SG	-	-	-	-	12.10	10.74	78.72	1.93	19.63	Kumar <i>et al.</i> (2013)
		SG	58.62	48.49 - 67.66	35.61	30.04	10.18	9.35	84.36	-	17.69	Patidar (2014)
		SG	34.58	-	37.66	32.12	4.87	4.63	90.13	3.13	9.05	Sharma <i>et al.</i> (2017)
		SG	53.91	47.50 - 62.50	-	-	11.73	7.49	41.00	-	9.85	Singh <i>et al.</i> (2017b)
		SG	61.44	52.00 - 76.00	-	-	8.89	7.07	63.30	-	11.59	Abhijeet <i>et al.</i> (2018b)
		SG	54.04	43.60 - 63.33	-	-	11.39	9.34	67.29	-	15.79	Singh <i>et al.</i> (2019c)
		SG	72.97	62.93 - 78.60	-	-	4.12	8.24	25.40	3.15	4.31	Annigeri (2020)
		SG	57.68	44.87 - 68.50	-	-	13.28	11.79	78.91	12.45	21.58	Kumar <i>et al.</i> (2020b)
		SG	90.38	82.53 - 88.00	-	-	2.56	0.88	11.88	-	58.00	Som <i>et al.</i> (2020a)
		SG	51.84	-	9.58	7.66	5.97	5.34	79.95	5.10	9.83	Yadav (2020)
		RG	50.47	39.00 - 61.00			12.73	12.39	94.64	12.53	24.82	Singh <i>et al.</i> (2008)
		RG	58.02	50.70 - 67.00	-	-	9.30	9.00	93.74	10.42	17.96	Samadia (2011)
		RG	54.60	48.27 - 61.13	-	-	8.03	5.00	38.81	3.51	6.42	Choudhary and Kumar (2011)
		RG	53.55	45.07 - 57.67	-	-	6.38	4.77	55.90	3.94	7.36	Choudhary <i>et al.</i> (2014)
		RG	64.07	58.33 - 71.33	24.43	21.28	7.71	7.20	87.00	8.87	13.85	Koppad <i>et al.</i> (2015)

Table 1. *Contd...*

Sl. No.	Characters	Crop	Mean	Range	PV	GV	PCV (%)	GCV (%)	h ² (%)	GA	GAM (%)	References
7.	Days to first harvest	RG	52.74	48.93 - 56.33	5.73	4.90	4.54	4.20	85.60	4.22	8.00	Saklesh (2016)
		RG	54.61	43.00 - 65.26	-	-	10.91	7.47	46.80	5.74	-	Bhargava <i>et al.</i> (2017)
		RG	53.32	46.50 - 59.75	10.72	9.13	6.14	5.66	85.10	-	10.76	Manoj <i>et al.</i> (2018)
		RG	50.69	45.00 - 58.33	9.39	8.29	6.05	5.68	88.00	5.57	11.00	Ramesh <i>et al.</i> (2018b)
		RG	-	-	13.83	11.07	6.27	5.61	80.10	6.13	10.35	Divyaraj <i>et al.</i> (2019)
		RG	47.98	39.55 - 58.58	20.57	10.15	9.45	6.64	49.37	4.61	9.61	Harshitha <i>et al.</i> (2019a)
		RG	65.17	-	-	-	7.39	5.96	86.63	-	13.42	Kannan and Rajamanickam (2019)
		RG	61.17	-	-	-	7.85	6.12	81.86	-	11.03	Kannan <i>et al.</i> (2019)
		RG	-	-	-	-	10.02	9.75	94.70	11.55	-	Parveen <i>et al.</i> (2019)
		RG	58.30	49.88-63.48	-	-	6.20	5.45	77.30	5.73	9.87	Akhila and Singh (2020)
		RG	57.19	-	-	-	6.47	4.72	53.27	-	7.11	Vijayakumar <i>et al.</i> (2020)
		RG	46.21	-	71.46	52.39	18.29	15.66	73.31	12.77	27.63	Vinitha <i>et al.</i> (2021)
		RG	45.60	37.00 - 56.00	18.75	10.40	7.45	9.26	64.78	5.63	12.36	Panda <i>et al.</i> (2022)
8.	Days to last harvest	RG	72.34	62.00 - 80.00	-	-	6.36	5.72	80.76	7.66	10.58	Singh <i>et al.</i> (2008)
		RG	90.69	87.30 - 94.83	7.23	4.07	2.97	2.22	56.00	3.12	3.44	Koppad <i>et al.</i> (2015)
		RG	87.21	88.67- 106.67	35.75	22.30	6.15	4.86	62.40	7.68	7.90	Saklesh (2016)
		RG	88.76	77.00 -95.00	16.95	13.97	4.64	4.21	82.00	6.99	7.88	Ramesh <i>et al.</i> (2018b)
		RG	-	-	19.57	18.61	4.80	4.68	95.10	8.66	9.42	Divyaraj <i>et al.</i> (2019)
		RG	43.55	84.50- 114.98	105.66	43.55	10.47	6.72	41.22	8.73	8.89	Harshitha <i>et al.</i> (2019a)
		RG	89.81	79.78 - 96.26	-	-	4.72	4.46	89.40	7.80	8.68	Akhila and Singh (2020)
		RG	81.03	61.01- 98.18	94.56	89.53	12.00	11.67	94.00	-	23.40	Krishnamoorthy (2020a)
9.	Fruit length (cm)	SG	19.22	10.10 - 29.33	-	-	26.79	25.22	90.30	9.75	-	Singh <i>et al.</i> (2009b)
		SG	19.35	14.42 - 24.17	-	-	12.25	11.69	91.09	4.44	22.99	Samadia (2010)
		SG	-	-	-	-	22.86	22.44	96.30	-	45.37	Pandey <i>et al.</i> (2012b)

Table 1. Contd...

Sl. No.	Characters	Crop	Mean	Range	PV	GV	PCV (%)	GCV (%)	h ² (%)	GA	GAM (%)	References
9.	Fruit length (cm)	SG	10.03	6.16 - 13.38	7.91	5.89	28.03	24.18	74.45	4.31	42.98	Dubey <i>et al.</i> (2013)
		SG	-	-	-	-	16.44	15.96	94.21	7.66	31.90	Kumar <i>et al.</i> (2013)
		SG	24.26	18.93 - 28.40	10.85	4.85	13.57	9.07	44.67	-	12.49	Patidar (2014)
		SG	24.36	19.70 - 35.60	-	-	17.68	14.80	70.12	6.22	25.54	Sharma <i>et al.</i> (2017)
		SG	29.30	15.30 - 38.40	-	-	20.50	18.52	82.00	-	34.47	Singh <i>et al.</i> (2017b)
		SG	23.63	15.23 - 35.43	-	-	24.87	23.78	91.40	-	46.84	Abhijeet <i>et al.</i> (2018b)
		SG	19.49	11.37 - 25.54	-	-	20.91	18.92	81.86	-	35.26	Kumar <i>et al.</i> (2019)
		SG	22.58	14.56 - 30.10	-	-	19.37	18.17	87.96	-	35.11	Singh <i>et al.</i> (2019c)
		SG	16.04	13.75 - 18.76	-	-	11.85	9.54	63.91	2.52	15.63	Annigeri (2020)
		SG	24.83	17.36 - 38.93	-	-	21.09	19.57	86.05	9.28	37.40	Kumar <i>et al.</i> (2020b)
		SG	20.25	8.64 - 25.14	-	-	18.98	17.64	86.35	-	62.42	Som <i>et al.</i> (2020a)
		SG	20.49	-	33.64	24.41	28.30	24.11	72.56	8.67	42.30	Yadav (2020)
		SG	21.70	13.10 - 26.30	-	-	20.97	16.02	58.40	5.47	25.22	Ray (2021)
		SG	22.57	16.89 - 28.87	-	-	17.17	16.41	91.31	-	32.29	Purushottama (2022)
		RG	14.96	4.40 - 26.00			35.82	35.51	98.25	10.85	72.52	Singh <i>et al.</i> (2008)
		RG	20.85	3.67 - 26.93	-	-	24.88	22.74	83.60	8.93	42.84	Choudhary and Kumar (2011)
		RG	22.71	7.60 - 36.36			30.53	29.99	96.46	13.78	60.68	Samadia (2011)
		RG	19.16	8.00 - 34.67	-	-	31.81	26.54	69.63	-	-	Rabbani <i>et al.</i> (2012)
		RG	12.09	3.90 - 16.42			25.39	24.56	93.50	5.91	48.88	Choudhary <i>et al.</i> (2014)
		RG	25.34	19.70 - 33.03	23.09	15.56	18.95	15.56	67.00	6.67	26.33	Koppad <i>et al.</i> (2015)
		RG	22.50	10.50 - 41.30	77.50	60.90	39.10	34.70	78.60	14.20	63.40	Varalakshmi <i>et al.</i> (2015)
		RG	23.15	16.75 - 33.49	27.09	25.36	22.48	21.75	93.60	10.04	43.34	Saklesh (2016)

Table 1. *Contd...*

Sl. No.	Characters	Crop	Mean	Range	PV	GV	PCV (%)	GCV (%)	h^2 (%)	GA	GAM (%)	References
9.	Fruit length (cm)	RG	-	-	-	-	27.88	27.69	98.00	-	56.66	Ananthan and Krishnamoorthy (2017)
		RG	34.32	25.26 - 50.63	-	-	17.79	14.31	64.80	8.14	-	Bhargava <i>et al.</i> (2017)
		RG	19.52	12.13 - 32.28	-	-	34.26	33.81	97.40	-	68.74	Karthik <i>et al.</i> (2017)
		RG	23.06	16.24 - 31.03	16.84	15.21	17.79	16.91	90.30	-	33.10	Manoj <i>et al.</i> (2018)
		RG	26.04	14.73 - 34.67	28.22	27.15	20.40	20.01	96.00	10.53	40.44	Ramesh <i>et al.</i> (2018b)
		RG	25.21	-	-	-	23.73	22.76	91.95	11.33	44.95	Suresh and Balamohan (2018)
		RG	-	-	33.41	33.08	24.35	24.23	99.00	11.79	49.68	Divyaraj <i>et al.</i> (2019)
		RG	27.07	18.10 - 39.80	35.34	20.61	21.96	16.77	58.33	7.14	26.39	Harshitha <i>et al.</i> (2019a)
		RG	27.50	-	-	-	19.07	16.60	89.59	-	34.92	Kannan and Rajamanickam (2019)
		RG	34.51	-	-	-	21.02	18.87	80.59	-	34.89	Kannan <i>et al.</i> (2019)
		RG	23.96	8.73 - 42.07	52.01	49.02	30.09	29.22	94.25	14.00	58.43	Methela <i>et al.</i> (2019)
		RG	-	-	-	-	17.23	16.389	90.41	5.22	-	Parveen <i>et al.</i> (2019)
		RG	23.63	14.53 - 31.75	-	-	27.53	27.18	97.40	12.73	55.26	Akhila and Singh (2020)
		RG	29.13	19.70 - 45.00	48.04	44.86	24.94	24.11	93.00	-	47.99	Krishnamoorthy (2020a)
		RG	30.72	-	-	-	14.06	13.14	87.44	-	25.32	Vijayakumar <i>et al.</i> (2020)
		RG	22.70	-	-	-	18.45	18.08	96.01	8.29	36.50	Chinthalapudi <i>et al.</i> (2021)
		RG	17.67	-	-	-	27.65	11.87	18.42	1.85	10.49	Sravani <i>et al.</i> (2021)
		RG	20.69	-	67.19	62.78	39.61	38.29	93.44	15.78	76.25	Vinitha <i>et al.</i> (2021)
		RG	20.28	16.00-30.68	14.51	13.39	18.03	18.77	92.27	7.24	35.69	Panda <i>et al.</i> (2022)

Table 1. *Contd...*

Sl. No.	Characters	Crop	Mean	Range	PV	GV	PCV (%)	GCV (%)	h^2 (%)	GA	GAM (%)	References
10.	Fruit diameter (cm)	SG	3.62	3.18 - 4.25	-	-	10.68	10.58	98.55	0.78	21.65	Samadia (2010)
		SG	-	-	-	-	20.38	19.67	93.20	-	39.10	Pandey <i>et al.</i> (2012b)
		SG	3.51	2.65 - 4.45	1.01	0.70	19.38	16.12	69.22	1.43	27.64	Dubey <i>et al.</i> (2013)
		SG	-	-	-	-	10.72	9.88	84.82	1.83	18.74	Kumar <i>et al.</i> (2013)
		SG	4.52	3.56 - 5.43	0.25	4.52	11.00	8.82	64.25	-	14.57	Patidar (2014)
		SG	2.67	2.25 - 3.11	-	-	10.18	10.08	98.08	0.55	20.57	Sharma <i>et al.</i> (2017)
		SG	2.84	2.17 - 4.10	-	-	17.07	14.56	73.00	-	25.59	Singh <i>et al.</i> (2017b)
		SG	3.19	2.18 - 4.18	-	-	17.22	15.88	85.00	-	30.17	Abhijeet <i>et al.</i> (2018b)
		SG	5.21	4.20 - 6.40	-	-	12.45	11.35	83.06	-	21.31	Kumar <i>et al.</i> (2019)
		SG	3.67	2.40 - 4.93	-	-	20.28	18.44	82.65	-	34.54	Singh <i>et al.</i> (2019c)
		SG	2.64	2.24 - 3.13	-	-	11.66	9.92	72.51	4.59	17.39	Annigeri (2020)
		SG	3.57	2.43 - 4.86	-	-	17.71	16.00	81.64	1.06	29.79	Kumar <i>et al.</i> (2020b)
		SG	10.30	6.40 - 11.69	-	-	13.53	10.66	62.12	-	56.12	Som <i>et al.</i> (2020a)
		SG	2.58	-	1.43	1.33	46.47	44.82	93.02	2.29	89.05	Yadav (2020)
		SG	14.23	12.70 - 15.60	-	-	8.87	5.37	36.60	0.95	6.69	Ray (2021)
		SG	6.38	5.60 - 7.06	-	-	9.17	8.54	86.59	-	16.38	Purushottama (2022)
		RG	3.41	2.40 - 4.70	-	-	15.19	14.05	85.58	0.91	26.68	Singh <i>et al.</i> (2008)
		RG	4.70	3.47 - 7.10	-	-	26.13	21.67	68.78	1.74	37.02	Choudhary and Kumar (2011)
		RG	3.14	2.31 - 4.14	-	-	14.07	13.95	98.38	0.89	28.51	Samadia (2011)
		RG	11.66	8.95 - 20.67	-	-	25.43	20.23	63.27	-	-	Rabbani <i>et al.</i> (2012)

Table 1. *Contd...*

Sl. No.	Characters	Crop	Mean	Range	PV	GV	PCV (%)	GCV (%)	h^2 (%)	GA	GAM (%)	References
10.	Fruit diameter (cm)	RG	2.73	2.23 - 3.20	26.46	4.38	18.85	7.66	16.00	1.75	6.42	Koppad <i>et al.</i> (2015)
		RG	11.80	8.10 - 16.90	8.80	2.80	25.20	14.10	31.50	1.90	16.40	Varalakshmi <i>et al.</i> (2015)
		RG	4.34	3.53 - 5.25	59.51	12.14	17.79	8.04	20.40	3.24	7.48	Saklesh (2016)
		RG	3.01	2.33 - 4.20	-	-	21.42	14.11	43.40	0.57	-	Bhargava <i>et al.</i> (2017)
		RG	13.38	12.05 - 15.50	-	-	9.79	5.98	37.36	-	7.53	Karthik <i>et al.</i> (2017)
		RG	4.03	3.29 - 4.81	0.15	0.13	9.61	9.08	89.37	-	17.69	Manoj <i>et al.</i> (2018)
		RG	5.31	3.20 - 7.45	253.27	248.94	30.00	29.74	98.00	32.22	60.75	Ramesh <i>et al.</i> (2018b)
		RG	13.20	-	-	-	18.41	14.20	59.45	2.98	22.55	Suresh and Balamohan (2018)
		RG	-	-	47.56	47.17	17.52	17.44	99.20	14.08	35.79	Divyaraj <i>et al.</i> (2019)
		RG	4.63	3.78 - 5.61	28.29	11.67	11.50	7.38	41.23	4.52	9.76	Harshitha <i>et al.</i> (2019a)
		RG	4.38	-	-	-	9.21	5.48	54.45	-	19.21	Kannan and Rajamanickam (2019)
		RG	4.41	-	-	-	11.50	4.38	14.48	-	3.43	Kannan <i>et al.</i> (2019)
		RG	4.56	3.43 - 5.20	0.22	0.12	10.29	7.60	54.55	0.53	11.57	Methela <i>et al.</i> (2019)
		RG	-	-	-	-	11.86	10.18	73.59	3.31	-	Parveen <i>et al.</i> (2019)
		RG	4.48	3.70 - 6.00	-	-	14.58	14.33	96.50	13.27	29.00	Akhila and Singh (2020)
		RG	4.38	3.20 - 05.50	0.32	0.28	13.45	12.25	83.00	-	23.01	Krishnamoorthy (2020a)
		RG	5.38	-	-	-	8.47	7.03	69.06	-	12.05	Vijayakumar <i>et al.</i> (2020)
		RG	12.82	-	-	-	15.10	14.83	96.33	3.84	29.98	Chinthalapudi <i>et al.</i> (2021)
		RG	17.17	-	-	-	23.66	22.04	86.76	7.26	42.30	Sravani <i>et al.</i> (2021)
		RG	15.32	-	3.87	3.54	12.85	12.28	91.35	3.70	24.18	Vinitha <i>et al.</i> (2021)
		RG	12.34	10.02-14.02	1.07	0.68	6.71	8.39	63.96	1.36	11.06	Panda <i>et al.</i> (2022)

Table 1. Contd...

Sl. No.	Characters	Crop	Mean	Range	PV	GV	PCV (%)	GCV (%)	h ² (%)	GA	GAM (%)	References
11.	Average fruit weight (g)	SG	92.84	53.15 -172.35	-	-	40.65	40.38	97.80	65.47	-	Singh <i>et al.</i> (2009b)
		SG	110.00	76.00 -125.00	-	-	14.28	13.87	94.36	0.03	27.76	Samadia (2010)
		SG	-	-	-	-	26.48	25.58	93.30	-	50.88	Pandey <i>et al.</i> (2012b)
		SG	201.54	167.71- 262.3	1271.49	703.03	17.69	13.16	55.29	40.62	20.15	Dubey <i>et al.</i> (2013)
		SG	-	-	-	-	22.77	22.49	97.60	67.94	45.78	Kumar <i>et al.</i> (2013)
		SG	150.81	118.66 -179.7	367.12	197.80	12.70	9.33	53.87	-	14.10	Patidar (2014)
		SG	96.58	63.33 - 122.2	-	-	17.32	14.81	73.18	25.21	26.10	Sharma <i>et al.</i> (2017)
		SG	167.88	96.23 - 220.3	-	-	20.48	18.99	86.00	-	36.27	Singh <i>et al.</i> (2017b)
		SG	144.12	85.53 -210.40	-	-	27.07	25.59	89.40	-	49.85	Abhijeet <i>et al.</i> (2018b)
		SG	137.25	74.96-184.30	-	-	16.49	14.20	74.15	-	25.19	Kumar <i>et al.</i> (2019)
		SG	148.97	114.23-192.4	-	-	15.40	14.00	82.62	-	26.21	Singh <i>et al.</i> (2019c)
		SG	170.87	137.67-197.3	-	-	10.42	8.49	66.31	24.31	14.23	Annigeri (2020)
		SG	154.20	106.40 -211.5	-	-	17.94	16.61	85.70	48.86	31.68	Kumar <i>et al.</i> (2020b)
		SG	494.11	276.66- 560.0	-	-	17.27	11.66	45.61	-	68.84	Som <i>et al.</i> (2020a)
		SG	87.62	-	110.01	88.56	11.97	10.74	80.50	17.39	19.85	Yadav (2020)
		SG	144.72	120.85-165.2	-	-	10.77	9.77	82.30	26.41	18.25	Ray (2021)
		SG	153.46	102.92-188.9	-	-	14.28	13.70	92.05	-	27.08	Purushottama (2022)
		RG	79.95	20.00-313.33	-	-	43.86	43.70	99.30	71.74	89.73	Singh <i>et al.</i> (2008)
		RG	84.16	18.25-112.16	-	-	24.67	23.28	89.09	38.12	45.27	Choudhary and Kumar (2011)
		RG	104.04	43.10-162.90	-	-	32.70	32.50	98.79	69.24	66.55	Samadia (2011)
		RG	93.31	39.73 -173.69	-	-	33.25	31.56	90.07	-	-	Rabbani <i>et al.</i> (2012)

Table 1. Contd...

Sl. No.	Characters	Crop	Mean	Range	PV	GV	PCV (%)	GCV (%)	h ² (%)	GA	GAM (%)	References
11.	Average fruit weight (g)	RG	27.09	18.42 - 38.64	-	-	19.57	14.97	58.5	6.39	23.59	Choudhary <i>et al.</i> (2014)
		RG	147.31	125.03-182.3	489.60	284.84	15.02	11.45	58.00	0.26	18.00	Koppad <i>et al.</i> (2015)
		RG	169.80	79.80-300.80	4004.10	2915.40	37.30	31.80	72.80	94.90	55.90	Varalakshmi <i>et al.</i> (2015)
		RG	137.99	74.31-217.3	1889.59	1820.67	31.50	30.92	96.40	86.28	62.53	Saklesh (2016)
		RG	-	-	-	-	29.41	28.86	96.00	-	58.37	Ananthan and Krishnamoorthy (2017)
		RG	114.78	100.33 -124.0	-	-	6.38	4.70	54.20	8.18	-	Bhargava <i>et al.</i> (2017)
		RG	130.00	90.00 -183.00	-	-	22.32	19.00	72.49	-	33.33	Karthik <i>et al.</i> (2017)
		RG	154.58	96.54-216.01	783.66	729.51	18.10	17.47	93.09	-	34.72	Manoj <i>et al.</i> (2018)
		RG	194.21	81.67-277.67	267.36	2570.21	26.62	26.10	96.00	102.40	52.72	Ramesh <i>et al.</i> (2018b)
		RG	168.81	-	-	-	20.76	20.19	94.55	68.27	40.44	Suresh and Balamohan (2018)
		RG	-	-	1150.29	1149.41	27.04	27.03	99.90	69.81	55.67	Divyaraj <i>et al.</i> (2019)
		RG	208.75	141.40-267.9	1589.63	1132.67	19.10	16.12	71.25	58.52	28.03	Harshitha <i>et al.</i> (2019a)
		RG	270.00	-	-	-	13.78	12.25	78.65	-	25.03	Kannan and Rajamanickam (2019)
		RG	320.00	-	-	-	16.95	13.00	60.84	-	20.55	Kannan <i>et al.</i> (2019)
		RG	157.71	43.77-258.90	2499.79	2480.09	31.58	31.7	99.21	102.18	64.79	Methela <i>et al.</i> (2019)
		RG	-	-	-	-	21.39	20.79	94.49	23.08	-	Parveen <i>et al.</i> (2019)
		RG	132.56	98.54-182.82	-	-	30.80	29.50	91.70	9.20	58.20	Akhila and Singh (2020)
		RG	223.94	111.0-295.00	5189.41	5146.51	30.30	30.17	99.00	-	61.91	Krishnamoorthy (2020a)
		RG	391.34	-	-	-	9.38	7.77	68.64	-	13.27	Vijayakumar <i>et al.</i> (2020)
		RG	230.54	-	-	-	35.00	34.98	99.88	166.05	72.03	Chinthalapudi <i>et al.</i> (2021)
		RG	270.63	-	-	-	43.66	42.01	92.57	225.34	83.26	Sravani <i>et al.</i> (2021)

Table 1. Contd...

Sl. No.	Characters	Crop	Mean	Range	PV	GV	PCV (%)	GCV (%)	h ² (%)	GA	GAM (%)	References
11.	Average fruit weight (g)	RG	179.42	-	10904.6	10040.99	58.19	55.85	92.08	198.08	110.39	Vinitha <i>et al.</i> (2021)
		RG	121.71	86.33-168.29	347.16	295.64	14.12	15.30	85.16	32.68	26.85	Panda <i>et al.</i> (2022)
12.	Number of fruits per vine	SG	23.42	17.22 - 36.23	-	-	24.00	21.32	85.70	8.66	-	Singh <i>et al.</i> (2009b)
		SG	8.06	4.55 - 12.34	-	-	28.00	28.37	97.42	4.59	56.93	Samadia (2010)
		SG	-	-	-	-	26.03	25.01	93.40	-	49.54	Pandey <i>et al.</i> (2012b)
		SG	17.66	14.55-22.00	10.84	8.05	18.65	16.07	74.32	5.04	28.54	Dubey <i>et al.</i> (2013)
		SG	-	-	-	-	14.01	13.40	91.54	6.72	26.42	Kumar <i>et al.</i> (2013)
		SG	11.18	7.26 - 15.33	4.21	2.98	18.35	15.44	70.80	-	26.76	Patidar (2014)
		SG	29.34	19.53 - 35.06	-	-	16.01	13.82	74.52	7.21	24.58	Sharma <i>et al.</i> (2017)
		SG	23.54	12.33 - 33.60	-	-	25.59	23.86	87.00	-	45.84	Singh <i>et al.</i> (2017b)
		SG	21.81	12.56 - 34.23	-	-	26.05	25.10	92.80	-	49.83	Abhijeet <i>et al.</i> (2018b)
		SG	10.93	7.41 - 18.89	-	-	23.61	22.97	94.58	-	46.01	Kumar <i>et al.</i> (2019)
		SG	16.68	8.73 - 26.60	-	-	30.45	29.19	91.86	-	57.63	Singh <i>et al.</i> (2019c)
		SG	24.21	16.60 - 32.80	-	-	20.07	18.42	48.19	8.43	34.84	Annigeri (2020)
		SG	20.27	10.70 - 32.26	-	-	23.96	23.04	92.49	9.25	45.65	Kumar <i>et al.</i> (2020b)
		SG	21.65	18.80 - 30.13	-	-	20.18	12.95	41.15	-	83.18	Som <i>et al.</i> (2020a)
		SG	27.55	-	86.59	70.09	33.78	30.39	80.94	15.52	56.32	Yadav (2020)
		SG	14.84	13.11 - 15.86	-	-	9.13	5.35	34.30	0.96	6.45	Ray (2021)
		SG	10.52	7.05 - 15.68	-	-	23.50	22.65	92.84	-	44.95	Purushottama (2022)
		RG	21.4	16.67 - 42.80	-	-	28.12	25.48	82.05	10.17	47.54	Choudhary and Kumar (2011)
		RG	9.08	6.70 - 12.60	-	-	22.53	21.61	91.95	3.87	42.69	Samadia (2011)
		RG	9.96	4.67 - 19.00	-	-	40.36	39.28	94.69	-	-	Rabbani <i>et al.</i> (2012)

Table 1. *Contd...*

Sl. No.	Characters	Crop	Mean	Range	PV	GV	PCV (%)	GCV (%)	h ² (%)	GA	GAM (%)	References
12.	Number of fruits per vine	RG	138.67	122.93-147.5	-	-	8.07	2.66	10.90	2.51	1.81	Choudhary <i>et al.</i> (2014)
		RG	6.71	5.50 - 9.66	1.28	0.94	16.86	14.49	73.00	1.72	25.66	Koppad <i>et al.</i> (2015)
		RG	13.60	4.70- 33.80	43.80	29.20	48.80	39.80	66.70	9.10	67.00	Varalakshmi <i>et al.</i> (2015)
		RG	5.94	4.10-8.63	1.83	1.43	22.77	20.12	78.10	2.18	36.63	Saklesh (2016)
		RG	-	-	-	-	15.33	14.96	95.00	-	30.06	Ananthan and Krishnamoorthy (2017)
		RG	15.11	12.23-19.06	-	-	15.76	10.10	41.10	2.01	-	Bhargava <i>et al.</i> (2017)
		RG	7.79	4.09 - 13.15	-	-	36.72	35.09	91.35	-	69.09	Karthik <i>et al.</i> (2017)
		RG	5.64	4.40-6.90	0.39	0.31	11.11	9.95	80.22	-	18.36	Manoj <i>et al.</i> (2018)
		RG	13.24	8.67-20.67	14.04	13.17	28.31	27.42	94.00	7.24	54.70	Ramesh <i>et al.</i> (2018b)
		RG	14.02	-	-	-	15.60	14.52	86.67	3.91	27.85	Suresh and Balamohan (2018)
		RG	-	-	4.25	4.07	21.77	21.32	95.90	4.07	43.02	Divyaraj <i>et al.</i> (2019)
		RG	4.47	1.60 - 8.00	2.96	2.45	38.50	35.02	82.78	2.93	65.64	Harshitha <i>et al.</i> (2019a)
		RG	12.19	-	-	-	15.24	14.47	93.47	-	32.28	Kannan and Rajamanickam (2019)
		RG	16.52	-	-	-	18.03	17.41	94.46	-	35.06	Kannan <i>et al.</i> (2019)
		RG	14.02	6.00 - 28.67	23.95	21.43	34.90	33.01	89.48	9.02	64.32	Methela <i>et al.</i> (2019)
		RG	-	-	-	-	27.85	21.05	57.14	4.27	-	Parveen <i>et al.</i> (2019)
		RG	12.24	6.98 - 14.95	-	-	15.91	14.87	87.40	3.59	28.63	Akhila and Singh (2020)
		RG	13.84	9.00 - 17.60	8.68	5.56	21.11	16.90	64.00	-	27.88	Krishnamoorthy (2020a)
		RG	15.21	-	-	-	6.51	5.16	63.00	-	8.45	Vijayakumar <i>et al.</i> (2020)
		RG	17.74	-	-	-	25.05	24.73	97.47	8.92	50.29	Chinthalapudi <i>et al.</i> (2021)
		RG	12.52	-	-	-	23.43	19.74	71.00	4.29	34.27	Sravani <i>et al.</i> (2021)

Table 1. Contd...

Sl. No.	Characters	Crop	Mean	Range	PV	GV	PCV (%)	GCV (%)	h ² (%)	GA	GAM (%)	References
12.	Number of fruits per vine	RG	52.08		244.58	68.01	30.02	15.83	27.80	8.96	17.20	Vinitha <i>et al.</i> (2021)
		RG	13.20	6.90-20.33	11.10	8.59	22.21	25.24	77.44	5.31	40.26	Panda <i>et al.</i> (2022)
13.	Fruit yield per vine (kg)	SG	1.88	0.97 - 3.12	-	-	36.35	34.26	89.90	1.01	-	Singh <i>et al.</i> (2009b)
		SG	0.87	0.38 - 1.42	-	-	35.48	34.88	96.65	0.61	70.64	Samadia (2010)
		SG	-	-	-	-	13.78	12.88	87.40	-	24.17	Pandey <i>et al.</i> (2012b)
		SG	3.51	2.65 - 4.45	0.47	0.25	19.56	14.35	53.80	0.76	21.68	Dubey <i>et al.</i> (2013)
		SG	-	-	-	-	29.92	29.48	97.13	2.63	59.86	Kumar <i>et al.</i> (2013)
		SG	1.60	1.18 - 2.75	0.17	0.13	24.61	21.60	77.03	-	39.06	Patidar (2014)
		SG	2.43	1.81 - 3.14	-	-	20.82	17.12	67.65	0.70	28.98	Sharma <i>et al.</i> (2017)
		SG	3.40	1.64 - 3.76	-	-	23.10	21.83	89.00	-	42.35	Singh <i>et al.</i> (2017b)
		SG	2.61	1.94 - 3.40	-	-	16.54	15.19	84.30	-	28.74	Abhijeet <i>et al.</i> (2018b)
		SG	1.46	0.65 - 2.26	-	-	46.66	44.16	89.55	-	86.08	Kumar <i>et al.</i> (2019)
		SG	2.03	1.28 - 3.08	-	-	27.13	25.35	87.34	-	48.81	Singh <i>et al.</i> (2019c)
		SG	0.72	0.52 - 1.03	-	-	20.09	18.43	48.18	265.71	34.84	Annigeri (2020)
		SG	2.69	1.55 - 3.75	-	-	22.33	20.41	83.52	1.03	38.42	Kumar <i>et al.</i> (2020b)
		SG	2.51	-	0.99	0.89	39.68	37.62	89.90	1.84	73.48	Yadav (2020)
		SG	2.26	1.65 - 2.83	-	-	20.12	13.63	45.90	0.43	19.04	Ray (2021)
		SG	1.61	1.06 - 2.63	-	-	26.19	25.70	96.26	-	51.94	Purushottama (2022)
		RG	0.98	0.25-2.89			42.59	40.9	92.24	0.79	80.61	Singh <i>et al.</i> (2008)
		RG	1.72	0.77-2.21			24.76	19.94	64.86	0.57	33.09	Choudhary and Kumar (2011)
		RG	0.94	0.36-2.00			45.7	45.41	98.72	0.76	92.94	Samadia (2011)

Table 1. *Contd...*

Sl. No.	Characters	Crop	Mean	Range	PV	GV	PCV (%)	GCV (%)	h ² (%)	GA	GAM (%)	References
13.	Fruit yield per vine (kg)	RG	9.53	3.06 - 24.68	-	-	59.77	58.00	94.16	-	-	Rabbani <i>et al.</i> (2012)
		RG	3.74	1.60 - 4.69	-	-	20.36	14.99	54.20	0.85	22.73	Choudhary <i>et al.</i> (2014)
		RG	1.01	0.70 - 1.76	91377.3	75630.00	30.09	27.37	62.00	515.39	51.30	Koppad <i>et al.</i> (2015)
		RG	1.80	0.60 - 2.80	0.40	0.20	35.00	26.60	57.70	0.70	41.70	Varalakshmi <i>et al.</i> (2015)
		RG	0.87	0.39 - 1.83	248508	244368.0	57.04	56.56	98.30	1009.8	115.55	Saklesh (2016)
		RG	-	-	-	-	32.86	31.55	92.00	-	62.39	Ananthan and Krishnamoorthy (2017)
		RG	2.11	1.21 - 3.31	-	-	26.29	24.21	84.80	0.97	-	Bhargava <i>et al.</i> (2017)
		RG	0.96	0.52 - 1.64	-	-	38.59	35.41	84.23	-	66.95	Karthik <i>et al.</i> (2017)
		RG	0.90	0.49 - 1.56	0.05	0.04	24.87	24.06	93.56	-	47.94	Manoj <i>et al.</i> (2018)
		RG	2.65	0.71 - 4.91	148.70	143.35	45.92	45.09	96.00	2.42	91.20	Ramesh <i>et al.</i> (2018b)
		RG	2.37	-	-	-	27.88	25.37	82.76	1.13	47.54	Suresh and Balamohan (2018)
		RG	-	-	0.23	0.231	40.82	40.57	98.80	0.98	83.07	Divyaraj <i>et al.</i> (2019)
		RG	0.95	0.30 - 1.82	176442	144803.2	44.29	40.12	82.07	710.14	74.87	Harshitha <i>et al.</i> (2019a)
		RG	4.42	-	-	-	15.24	12.42	84.84	-	22.58	Kannan and Rajamanickam (2019)
		RG	5.22	-	-	-	16.50	12.14	54.15	-	18.41	Kannan <i>et al.</i> (2019)
		RG	2.13	0.77 - 4.41	0.76	0.71	40.96	39.59	93.42	1.68	78.82	Methela <i>et al.</i> (2019)
		RG	-	-	-	-	20.98	20.19	92.62	6.93	-	Parveen <i>et al.</i> (2019)
		RG	1.64	0.76 - 2.72	-	-	19.55	18.80	92.40	51.50	37.24	Akhila and Singh (2020)
		RG	3.10	1.58 - 04.75	1.01	0.95	31.84	30.92	94.00	-	61.85	Krishnamoorthy (2020a)
		RG	5.92	-	-	-	10.65	9.09	72.87	-	15.99	Vijayakumar <i>et al.</i> (2020)
		RG	3.63	-	-	-	36.11	36.03	99.56	2.69	74.06	Chinthalapudi <i>et al.</i> (2021)

Table 1. *Contd...*

Sl. No.	Characters	Crop	Mean	Range	PV	GV	PCV (%)	GCV (%)	h ² (%)	GA	GAM (%)	References
13.	Fruit yield per vine (kg)	RG	3.38	-	-	-	48.94	46.75	91.23	3.11	91.99	Sravani <i>et al.</i> (2021)
		RG	11.79	-	10.42	8.69	27.37	24.99	83.39	5.55	47.03	Vinitha <i>et al.</i> (2021)
		RG	1.57	1.06 - 2.83	0.14	0.11	21.29	24.41	76.08	0.60	38.26	Panda <i>et al.</i> (2022)
14.	Fruit yield per plot (kg)	SG	25.39	18.60 - 33.06	-	-	15.98	15.44	93.32	7.80	30.73	Sharma <i>et al.</i> (2017)
		SG	15.13	10.28 - 23.70	-	-	30.90	16.37	28.05	-	83.93	Som <i>et al.</i> (2020a)
		RG	7.76	3.67 - 14.91	12.94	12.46	46.33	45.47	96.30	7.14	91.92	Saklesh (2016)
		RG	11.80	8.01-13.58	4.63	2.75	14.06	18.23	59.46	2.63	22.34	Panda <i>et al.</i> (2022)
15.	Fruit yield per hectare (t/ha)	SG	226.5	165.94-294.9	-	-	15.98	15.44	93.31	69.59	30.72	Sharma <i>et al.</i> (2017)
		SG	126.9	87.15-172.23	-	-	20.82	18.16	20.82	41.43	32.63	Annigeri (2020)
		SG	110.0	71.41-164.83	-	-	31.87	23.87	56.09	-	83.93	Som <i>et al.</i> (2020a)
		RG	23.30	8.50- 37.90	65.80	37.30	34.80	26.20	56.80	9.50	40.70	Varalakshmi <i>et al.</i> (2015)
		RG	86.04	40.81 - 163.5	1575.97	1518.15	46.14	45.29	96.30	78.78	91.56	Saklesh (2016)
		RG	25.50	6.80-47.22	13695.5	13216.57	45.91	45.10	97.00	232.65	91.26	Ramesh <i>et al.</i> (2018b)
		RG	-	-	1776.49	16.48.37	43.37	41.78	92.80	80.56	82.90	Divyaraj <i>et al.</i> (2019)
		RG	19.76	-	-	-	16.21	13.98	89.14	-	35.18	Kannan and Rajamanickam (2019)
		RG	12.81	6.90 - 21.91	-	-	38.65	35.45	84.17	-	67.01	Karthik <i>et al.</i> (2017)
		RG	14.80	6.84-24.48	-	-	30.80	29.50	91.70	1.00	58.20	Akhila and Singh (2020)
16.	Number of seeds per fruit	SG	246.94	123.49-405.3	-	-	32.66	32.59	99.61	165.51	67.02	Samadia (2010)
		SG	-	-	-	-	27.15	26.90	98.17	78.68	54.91	Kumar (2011)
		SG	294.2	192.00-358.0	2493.99	2121.52	16.97	15.66	85.06	-	29.75	Patidar (2014)

Table 1. *Contd...*

Sl. No.	Characters	Crop	Mean	Range	PV	GV	PCV (%)	GCV (%)	h ² (%)	GA	GAM (%)	References
16.	Number of seeds per fruit	SG	90.99	47.22-125.32	-	-	20.64	16.31	62.41	-	26.54	Kumar <i>et al.</i> (2019)
		SG	108.17	85.54-118.23	-	-	10.55	8.31	62.10	14.60	13.49	Ray (2021)
		SG	210.54	162.45-285.3	-	-	21.60	20.89	94.41	-	42.00	Purushottama (2022)
		RG	105.05	55.83-194.93			26.23	25.89	97.41	55.30	52.64	Samadia (2011)
		RG	68.36	32.13 - 118.5	652.64	593.39	37.37	35.63	90.90	47.85	69.99	Saklesh (2016)
		RG	145.36	-	-	-	25.58	25.05	95.93	73.48	50.55	Suresh and Balamohan (2018)
		RG	121.37	55.09 -198.32	1972.22	1296.27	36.59	29.66	65.73	60.13	49.54	Harshitha <i>et al.</i> (2019a)
		RG	125.36	-	-	-	29.90	29.87	99.79	77.05	61.46	Chinthalapudi <i>et al.</i> (2021)
		RG	118.13	-	-	-	37.04	30.14	66.20	59.68	50.53	Sravani <i>et al.</i> (2021)
		RG	56.32	44.73 - 69.68	34.83	25.57	8.97	10.48	73.41	8.92	15.84	Panda <i>et al.</i> (2022)
		SG	-	-	-	-	22.21	21.32	92.17	1.50	42.17	Kumar <i>et al.</i> (2013)
		SG	5.28	-	0.98	0.73	18.78	16.21	74.58	1.52	28.85	Yadav (2020)
		SG	4.88	4.47 - 5.35	-	-	6.15	3.48	27.46	0.17	3.55	Annigeri (2020)
		RG	4.45	3.50 - 5.67	0.37	0.31	13.61	12.57	85.30	1.06	23.92	Methela <i>et al.</i> (2019)
		RG	3.89	-	-	-	4.31	3.95	94.65	-	24.63	Kannan and Rajamanickam (2019)
		RG	3.07	-	-	-	12.31	11.96	94.26	-	23.91	Kannan <i>et al.</i> (2019)
		RG	4.00	3.69 - 4.33	-	-	9.17	3.54	14.90	0.11	2.81	Akhila and Singh (2020)
		RG	3.20	2.10 - 5.00	0.39	0.33	18.87	17.39	86.00	-	33.03	Krishnamoorthy (2020a)
		RG	1.34	-	-	-	33.34	32.82	96.88	-	66.54	Vijayakumar <i>et al.</i> (2020)
		RG	2.50	-	-	-	45.02	36.61	66.12	1.53	61.32	Sravani <i>et al.</i> (2021)

Table 1. *Contd...*

Sl. No.	Characters	Crop	Mean	Range	PV	GV	PCV (%)	GCV (%)	h ² (%)	GA	GAM (%)	References
18.	Fruit tenderness (kg/cm ²)	SG	4.02	2.93 - 6.11	-	-	19.45	18.80	93.40	-	37.29	Purushottama (2022)
19.	Crude fiber (%)	RG	0.48	-	-	-	9.34	8.28	78.62	-	15.40	Kannan and Rajamanickam (2019)
		RG	0.47	-	-	-	9.12	8.23	78.45	-	15.45	Kannan <i>et al.</i> (2019)
		RG	0.48	0.39 - 0.58	-	0.00	9.73	9.37	92.00	-	18.61	Krishnamoorthy (2020a)
		RG	0.47	-	-	-	4.74	3.89	67.33	-	6.58	Vijayakumar <i>et al.</i> (2020)
		RG	0.97	-	-	-	89.31	28.99	10.53	0.18	19.38	Sravani <i>et al.</i> (2021)

GV-Genotypic Variance
PV-Phenotypic variance

GCV-Genotypic co-efficient of variance
PCV-Phenotypic co-efficient of variance

h²-heritability (broad sense)
GA-Genetic advance

GAM-Genetic advance as per cent of mean
SG-Sponge gourd RG-Ridge gourd

improvement of the crop through rational selection for developing open pollinated varieties as well as parents for hybrid development.

Germplasm evaluation and characterization for economically important traits are pre-requisites for genetic improvement of crop. Mahalanobis D^2 statistic technique is a powerful tool for measuring genetic divergence which is based on multivariate analysis of quantitative traits. Later, the degree of genetic diversity is worked out between any two populations over all the characters taken under study. Genetically divergent population falls into different groups on clustering of genotypes thus enabling selection of parents. The geographic distributions of genotypes are compared with genetic diversity, which very often exhibit parallelism.

This generalized distance method has been extensively used in various crop plants for elucidating information on the available genetic diversity. The outcome of various studies, for genetic diversity is briefly reviewed here with respect to sponge gourd and closely related cucurbit crop like ridge gourd.

2.2.1 Sponge gourd

Quamruzzaman *et al.* (2011) studied the genetic diversity with twenty local sponge gourd genotypes collected from Bangladesh by performing cluster analysis in which the genotypes were constellated into five distinct groups. Further, they also observed maximum inter-cluster distance between genotypes of cluster II and IV. Whereas, the highest intra cluster value was noticed in cluster II due to the presence of variations among the genotypes.

Khule *et al.* (2012) evaluated thirty genotypes of sponge gourd for genetic divergence using Mahalanobis's D^2 statistics. In this study, genotypes were grouped into four clusters by Tocher's method. The maximum numbers of genotypes were grouped in cluster IV followed by cluster II and the highest intra-cluster distance was observed in cluster II (2.637), then the highest inter-cluster distances were observed in cluster I and IV (5.080) followed by cluster I and II (4.726). They also reported that the traits like marketable fruit yield per plant (35.40 %), days to appearance of first male flower (20.22 %) and fruit length (18.62 %) were contributed maximum towards total genetic divergence.

A genetic divergence study in fifteen genotypes of sponge gourd (*Luffa cylindrica* L.) were assessed using D^2 statistics and principal component analysis by Gaffar *et al.* (2015). Where, genotypes were grouped into five different clusters. They noticed highest intra-cluster distance in cluster III that represent maximum variability within the cluster and the maximum inter-cluster distance was observed between the clusters IV and V. Later, they concluded that cluster with more distances was considered as more diverged than those with small distances.

Singh *et al.* (2017c) investigated 54 genotypes (10 lines, 4 testers and 40 F_1 's) of sponge gourd for cluster analysis and were grouped into eight distinct non over lapping clusters which indicated presence of considerable diversity among the genotypes. The maximum intra-cluster D^2 values were observed in VIII (420.45) and the maximum inter-cluster distance were observed between cluster II (63.09) and cluster VIII (504.73). They also reported that quantitative parameter like vine length was contributed maximum towards the total divergence while minimum contribution was reflected by days to first fruit harvest.

Abhijeet *et al.* (2018a) analyzed the thirty sponge gourd genotypes including Pusa Chikni for genetic diversity using Mahalanobis D^2 statistics. The tested genotypes were grouped into six non over lapping clusters. Among all the clusters formed, the maximum intra-cluster distance was observed in cluster V and the maximum inter cluster distance was observed between cluster I and cluster VI. The maximum contribution towards genetic divergence was shown by vine length (30.80 %) followed by fruit length (18.16 %). Similarly, Kumar *et al.* (2019) also conducted diversity assessment studies in sponge gourd genotypes. Based on the Mahalanobis' D^2 statistics, the forty five genotypes were constellated into seven different clusters. The maximum intra cluster distance was noticed in cluster III (541.13) whereas, maximum inter-cluster distance was observed between cluster IV and cluster V (5177.9). The per cent contribution towards genetic divergence revealed that the yield per plant, fruit weight and number of fruiting nodes on main stem were the major contributing characters towards total genetic divergence and they concluded that by considering these characters in selection for diverse parents during hybridization program manifests the high heterosis.

A genetic divergence study conducted by Singh *et al.* (2019b) in 28 sponge gourd genotypes through Mahalanobis D^2 statistics and grouped them into six distinct clusters. The intra-cluster value was highest in cluster VI and lowest in cluster II. The maximum inter cluster distance D^2 value was observed between cluster I and cluster IV indicating wide range of genetic diversity between these two clusters. Thus, these genetically diverged genotypes could be used as parents in hybridization program for getting desirable segregants. The maximum contribution towards genetic diversity was exhibited by average fruit yield per plant (41.27 %) followed by number of fruits per plant and node number to anthesis of first staminate flower (11.38 %).

Kumar *et al.* (2020c) studied the nature and magnitude of genetic divergence among the thirty genotypes of sponge gourd using Mahalanobis D^2 statistics. The thirty genotypes were grouped into seven different non overlapping clusters. Among all the clusters formed, highest number of genotypes were presented in cluster III which contained nine entries. The maximum intra-cluster distance was observed in case of cluster II (330.49), while the maximum inter-cluster distance was found between II and V (1084.58). The per cent contribution towards genetic divergence revealed that vine length (26.67 %), fruits per plant (25.75 %), days to anthesis of first pistillate flower (13.79 %), average fruit weight (9.43 %) and number of primary branches per plant (8.51 %) contributed maximum towards the total genetic divergence.

Sixteen genotypes of sponge gourd were grouped into four different clusters by using D^2 analysis (Yadav, 2020). The maximum intra cluster distance was observed in Cluster III (2304.49) followed by cluster I (2125.65) while, the maximum inter cluster distance was observed between cluster III and IV (9970.65) followed by cluster II and IV (9755.91). Further, the number of fruits per plant, fruit length, number of leaves per plant, node number of first female flower and fruit weight were principal contributing traits to total genetic divergence in sponge gourd.

A diversity assessment study was conducted by Ray (2021) with 14 genotypes of sponge gourd and grouped them into five clusters based on D^2 analysis. Among all the genotypes studied cluster I was found to be the largest with five genotypes followed by cluster V with four genotypes. It is also observed that the intra cluster distance was highest with cluster II (414.07) followed by cluster V (303.77). Similarly the highest

inter cluster distances was observed between cluster II and V (303.77) followed by cluster I and III (233.20). This indicated that the experimented genotypes grouped under I, II, V and III clusters were distinct and distantly related to each other.

Purushottama (2022) conducted a study with twenty two genotypes of sponge gourd and were grouped into six clusters using Tocher's method. Among the six clusters, cluster I was the largest, comprising of fourteen genotypes and it also showed maximum intra cluster diversity ($D^2=138.89$). The inter cluster diversity ($D^2= 907.36$) was maximum between cluster VI and IV.

2.2.2 Ridge gourd

Choudhary *et al.* (2011) carried out an investigation with 35 genotypes of ridge gourd for genetic diversity assessment based on Mahalanobis D^2 statistics and Tocchar's method. Considering eight quantitative characters, the 35 genotypes were grouped into four clusters. The maximum inter-cluster distance was exhibited between cluster II and IV ($D^2=7.867$) while the minimum was observed between clusters I and II ($D^2= 1.458$). Similarly, Rabbani *et al.* (2012) also assessed sixty genotypes of ridge gourd for magnitude of genetic diversity using Mahalanobis D^2 statistics and grouped them into four different clusters. The average inter-cluster distances were always higher than the average intra-cluster distances suggesting wider genetic diversity among the genotypes within the cluster. While the maximum intra cluster distance was observed in cluster III and the maximum inter cluster distance was observed between cluster III and cluster IV.

Singh *et al.* (2015) conducted an experiment with 110 genotypes of ridge gourd for genetic diversity analysis and grouped them into seven different clusters based on their D^2 values. They found that cluster VI was found to be the largest containing 22 genotypes followed by cluster I and II (20 genotypes each). The maximum intra-cluster distance was noticed in cluster VII (2.515) while the maximum inter-cluster distance was noticed between cluster IV and V (5.658). It suggested that selection of divergent parents may be useful for heterosis breeding in ridge gourd.

A genetic diversity study was conducted by Saklesh (2016) with 16 genotypes of ridge gourd and grouped them into five clusters based on intra and inter cluster

distances. The cluster I was the largest which comprised of nine genotypes. The highest intra-cluster distance was observed in cluster III ($D^2=1164.86$) followed by cluster I ($D^2=651.78$) and the maximum inter cluster distance was observed between cluster IV and I ($D^2=34428.80$). Among the characters studied, per cent of fruit set (19.18 %) contributed maximum towards the expression of genetic divergence followed by node to first female flower (8.34 %), fruit yield per plant (8.34 %), days to first harvest (6.68 %) and fruit length (5.82 %).

Yadav *et al.* (2016) examined 42 genotypes of ridge gourd using principal component analysis based on correlation matrix. Grouping of genotypes having heterogeneous origin in the same cluster indicated non-parallelism between genetic and geographical diversity. Out of the ten clusters formed, maximum intra-cluster distances were recorded in cluster VII followed by cluster VI while the maximum inter-cluster distance was calculated between cluster V and VI. Further, they found that cluster III was largest with eight genotypes while, cluster X was smallest with two genotypes.

Gautam *et al.* (2017) screened 42 ridge gourd genotypes which were grouped into three different clusters for genetic divergence using principal component analysis and non-hierarchical cluster analysis. They observed that intra-cluster distance was ranged between 2.724 (cluster I) to 3.550 (cluster II) while the inter-cluster distances were found maximum (5.984) between cluster I and II but minimum (3.419) between cluster III and II which suggested there is a scope for exploiting heterosis upon hybridization between genotypes.

Khatoon *et al.* (2017) evaluated for phenotypic diversity using 40 ridge gourd genotypes for 15 quantitative characters. Cluster analysis was used for grouping of genotypes and grouped them into six clusters. Where, cluster I had maximum (10) and cluster V had the minimum number (1) of genotypes. The highest (54.518) inter cluster distance was observed between cluster IV and VI and lowest (12.310) was between cluster I and II. Cluster VI ($D^2=24.606$) has exhibited highest intra cluster distance and lowest was observed in cluster I ($D^2=7.885$). Later, they concluded that days to first staminate flower, number of fruit per plant and days to first fruit harvest contributed maximum towards divergence.

An experiment was conducted by Rani *et al.* (2017) with an objective to study the thirty five genotypes of ridge gourd for magnitude of genetic diversity. The studied genotypes were grouped into five clusters based on D^2 values, which exhibited no association between geographical and genetic divergence. The maximum intra-cluster distance for cluster III (167.41) and minimum for cluster V (0) while the maximum inter-cluster distance was observed between cluster II and cluster V (535.54) followed by clusters III and II (195.34) which may serve as potential genotypes for hybridization programme in ridge gourd.

Umesh *et al.* (2017) evaluated 44 genotypes of ridge gourd for growth, earliness, yield parameters and genetic diversity was measured among the genotypes through D^2 statistics and seven different clusters were formed. Where, the cluster V was the largest with 18 genotypes and showed maximum intra-cluster diversity ($D^2 = 992.649$) and indicated that genotypes included in this cluster were very diverse. While the maximum inter-cluster distance was observed between clusters I and VI ($D^2 = 9848.6$). Hence the crosses between genotypes of these clusters can be tried for yield improvement. Also found that the fruit yield per plant was highest contributor to the total diversity (40.69 %).

Similar to above studies, Manoj *et al.* (2018) also conducted a research on genetic diversity in thirty five ridge gourd and grouped them into eight distinct clusters. Maximum intra-cluster diversity was recorded in cluster VI and maximum inter-cluster distance was recorded between cluster IV and VII. Flesh thickness contributed maximum to the total genetic diversity followed by rind thickness and fruit weight.

Methela *et al.* (2018) experimented with 29 genotypes of ridge gourd for genetic divergence using cluster analysis and principal component analysis and they grouped the genotypes into six classes. The highest inter cluster distance was observed between cluster III and V and the cluster VI (1.18) exhibited the highest intra cluster distance. Further, noticed larger inter cluster distances than the intra cluster distances which suggested the wider genetic diversity among the genotypes of different groups. The contribution of various characters towards the total divergence was recorded highest for days to first male flower, days to first female flower, node at first female flower, fruit

length, fruit weight and Total Soluble Solids (TSS). Similarly, Ramesh *et al.* (2018a) also studied the genetic divergence among 14 genotypes of ridge gourd using Mahalanobis D^2 statistics and grouped them into four distinct clusters and they observed highest intra-cluster distance in cluster IV and the highest inter cluster distance was observed between cluster II and IV (8506.65). Whereas, fruit yield per plant exhibited maximum towards divergence.

Genetic divergence study was conducted by Divyaraj *et al.* (2019) using fifteen ridge gourd genotypes which were grouped into four different clusters following Mahalanobis D^2 analysis. The clustering pattern indicated that cluster I was largest cluster comprising ten out of fifteen genotypes and the highest inter cluster distance was noticed between cluster II and III (81170.76). However, the highest contribution in manifestation of genetic divergence was exhibited by fruit yield per plant (45.71 %), average fruit weight (38.1 %), first male flowering node (5.71 %), flesh thickness (4.76 %) and (3.81 %) fruit yield per hectare (ha).

Shilpashree *et al.* (2022) analyzed genetic divergence with 55 diverse genotypes of ridge gourd through Mahalanobis D^2 statistics. The genotypes under this study were divided into nine clusters which showed sufficient variability. Among the different characters studied, fruit yield per vine (26.20 %) contributed maximum to the total genetic diversity followed by fruit length (19.06 %) and average fruit weight (13.60 %). The highest inter cluster distance (1173.86) was observed between cluster VII and IX. The genotypes belonging to the clusters with maximum inter cluster distance were genetically more divergent and these genotypes could be used in hybridization programme to obtain the promising segregants.

2.3 Molecular characterization in sponge gourd

Molecular marker is a distinguishing feature that can be used to identify a particular part or region of a genome, chromosome or genetic linkage group. Simple Sequence Repeat (SSR) or Microsatellite markers are widely used for genetic diversity analysis, genome mapping, cultivar identification, marker-assisted selection, phylogenetic relationships and population studies in plants because of their higher level

of polymorphism, random distribution across the genome with high reproducibility, simplicity, stability, co-dominance and due to its accuracy. Literature related to the molecular aspects of sponge gourd is scanty. Therefore, literature on other related cucurbitaceous crops are reviewed under:

Guo *et al.* (2012) evaluated 40 bitter gourd genotypes for genetic diversity. Twenty-five microsatellite loci were isolated from the genome using the Fast Isolation by AFLP of Sequences Containing Repeats (FIASCO) method. Ten loci were polymorphic and the number of alleles per locus ranged from 3 to 7, with the observed heterozygosity ranging from 0.46 to 0.65. These markers will have potential utility for applications in genetic diversity evaluation, molecular fingerprinting, identification, comparative genomics analysis, and genetic mapping in *Momordica* species. Out of 36 SSR markers tested, three primers did not amplify, only 13 produced polymorphic bands (100 %) and rest all other produced monomorphic bands. Out of 4 RAPD primers tested all of them were amplified.

Ji *et al.* (2012) developed 11 polymorphic *Momordica charantia* microsatellite loci and examined the genetic diversity of 55 Chinese *M. charantia* germplasm cultivars at these loci. The average number of alleles per locus ranged from 3 to 8, the expected heterozygosity of each locus varied from 0.132 to 0.786 with an average of 0.621 and the maximum polymorphism information content value was 0.744 with an average value of 0.572. These values suggested that the tested *M. charantia* germplasm had relatively high genetic diversity at the 11 microsatellite loci.

Guang-guang *et al.* (2013) examined 50 bitter gourd genotypes using 16 SSR molecular markers. A total of 90 alleles were amplified with 16 SSR primers and the average values of polymorphism loci percentage (P), genetic heterozygosity (He), effective number of alleles (Ne), Shannon-Wiener index (H), polymorphism information content (PIC) and genetic similarity coefficient were 97.78 %, 0.853, 7.728, 2.087, 0.834 and 0.706, respectively. The UP-GMA cluster analysis was performed and the results showed that the 50 bitter guard samples could be clustered into 6 groups. Since the genome was complex and the genetic information was ample amongst the 50 tested bitter gourd materials, directional continuity breeding played important roles in the accumulation of bitter gourd traits.

Unique primer-pairs were designed for 160 microsatellite loci and amplicons of expected length were obtained for 151 loci (94.4 %). Then evaluation of diversity in 54 bitter gourd accessions at 51 loci indicated that 20 per cent of the loci which were polymorphic with the PIC values ranging from 0.13 to 0.77. Thereafter, fifteen Indian varieties were clearly distinguished and indicated the usefulness of the markers developed. The microsatellite markers reported shall be further useful in various genetic and molecular studies in bitter gourd (Saxena *et al.*, 2014).

Hai-bin *et al.* (2015) conducted investigation using 17 Sequence Related Amplified Polymorphism (SRAP) markers and one EST-SSR marker derived from cucumber were used to evaluate the genetic diversity among 42 sponge gourd accessions. Total 197 bands were amplified using 18 primer pairs, 156 bands (79.18 %) of which were polymorphic ones. The number of loci detected by per primer pairs was ranged from 6 to 16, in which the average was 10.94 (with an average of 0.733). A dendrogram was constructed based on SRAP data using UP-GMA cluster method and divided 42 sponge gourd accessions into two major clusters, one comprising of 27 accessions of *Luffa acutangula* (L.) Roxb. and the remaining 15 accessions belonging to *Luffa cylindrica* (L.) Roem. The two clusters (inter-species) were very far in genetic relationship, whereas the intra-species accessions had extremely close genetic distance.

Mashilo *et al.* (2016a) assessed the molecular diversity present amongst bottle gourd landraces for morphological characters and 11 selected polymorphic simple sequence repeat (SSR) markers. Further, the number of alleles varied from 3 to 9 with mean of 6 per SSR locus. Shannon's information index ranged from 0.95 to 2.01 with mean of 1.41. Expected heterozygosity values varied from 0.50 to 0.87 with a mean of 0.71 with PIC values of 0.5 to 0.85 and a mean of 0.7. Later, morphological characters and SSR marker analyses showed a significant correlation in clustering the landraces.

Mashilo *et al.* (2016b) used 14 SSR markers to investigate the genetic diversity in sixty-seven diverse bottle gourd landraces. The number of alleles detected per marker ranged from 4 to 11, with a total of 86 putative alleles. The mean PIC value was 0.57 and the expected heterozygosity (H_e) values ranged from 0.37 to 0.84 with a mean of 0.65. Jaccard's coefficient of similarity ranged from 0.00 to 1.00, with a mean of 0.63. Analysis of molecular variance (AMOVA) revealed that 79 %, 17 % and 4 % of the

variation in bottle gourd landraces was attributable to among landraces, within landraces and between populations, respectively. The study established the existence of considerable genetic diversity among South African bottle gourd landraces.

Bhutia *et al.* (2017) used 17 EST-SSR primers to analyze the molecular diversity study in forty seven *Luffa* genotypes which generated 34 alleles, ranged between 1-2 loci per primer. Forty seven genotypes were broadly organized into two different clusters. Cluster I included 11 genotypes, while Cluster II included 36 genotypes. EST-SSR primer C90830_G3 was noted to be highly informative with PIC value of 0.3750. Later, a high degree of molecular polymorphism was seen in all the studied markers. The PIC value ranged from 0.1124 to 0.3750. The present data had given adequate evidence of the applicability of EST-SSR markers for diversity analyses, cultivar identification and characterization of the *Luffa* germplasm.

A study conducted with 31 accessions of *luffa* spp including, 27 accessions of hermaphrodite *Luffa* (*L. hermaphrodita*), two lines of *L. acutangula* (Ridge gourd) and two lines of *L. aegyptiaca*. A total of 103 microsatellite markers were used for screening the genetic diversity among local landraces of *Luffa* species, 56 were found to be polymorphic, including 38 gSSR and 18 eSSR, respectively. A total of 197 amplification products were obtained. The mean number of alleles per locus was 3.52 with PIC ranged from 0.037 to 0.986. The Jaccard's coefficient ranged from 0.66 to 0.97 with an average of 0.81. This study provided information for future exploration, collection and utilization of *Luffa* genotypes, as well as the polymorphic markers identified could be available for the study of landmarks in linkages, genomic structures, evolutionary ecology and marker-assisted selection (MAS) in *Luffa* species (Pandey *et al.*, 2017).

Tyagi *et al.* (2018) conducted a study using 28 SSR primers generated by in-silico mining technology were employed for characterization of genetic diversity between 45 accessions of *L. cylindrica*. Amplification allowed the visualization of 35 bands with sizes between 90-400 bp, of which 7 bands were polymorphic with 0.25 polymorphic bands per primer suggesting very low polymorphism. The PIC and Rp values obtained were mostly zero or negative ones and signifying monomorphism. Hence, they concluded that newly developed SSR primers were ineffective in

differentiating these 45 accessions. The expected heterozygosity (H_e) varied between 0.022 - 0.506 with an average of 0.241. While mean observed heterozygosity (H_o) was observed which ranged from 0.022 to 0.955 with an average of 0.326 which indicated that selected accessions had a narrow genetic base.

Kumar *et al.* (2020a) carried out a study using twenty genotype of bitter gourd for molecular diversity analysis, out of 30 SSR markers screened, six were found to be polymorphic and remaining others showed monomorphic. PIC values varied from 0.22 to 0.94. From molecular characterization, two major clusters were formed. The genotypes namely, CO-1, BRBT-1, Katahi and Jhalari were found to be in the same cluster in both multivariate analysis and molecular characterization.

Sidhu and Pathak (2020) evaluated genetic relatedness of 36 genotypes of bitter gourd (*Momordica charantia* L.) collected from different parts of India were analyzed by combination of 4 RAPD and 36 SSR primers. Among the 40 primers screened only 11 primers showed polymorphism. The average number of polymorphic bands per primer was 2.1. The size of the amplified products varied from approximately 164 bp (MCMS 10) to 300 bp (MCMS 9). The dendrogram showed that all the accessions formed three main clusters with various degree of sub-clustering within the clusters. These results have implications for bitter gourd breeding and conservation in the future.

Alhariri *et al.* (2021) carried out an experiment using 51 diverse bitter gourd accessions as material for studying genetic diversity and relatedness using 61 SSR markers. Out of 61 SSR primers screened, 30 were polymorphic with a total of 99 alleles. The PIC value ranged from 0.038 to 0.721 with an average of 0.429. The numbers of alleles ranged from 2 to 5, with an average of 3.3 alleles per locus. Gene diversity ranged from 0.04 for BG_SSR-8 to 0.76 for S-24, showing a wide variation among the accessions. The UP-GMA cluster analysis grouped these accessions into three major clusters. The polymorphic SSR markers of the study will be highly useful in genetic fingerprinting, mapping and for association analysis in *Momordica* regarding several economic traits.

Mahapatra *et al.* (2022) employed 40 SSR primers to explore genetic diversity across 91 genotypes of bottle gourd, resulting in the detection of 39 alleles with average of 3.5 alleles per locus. The major allele frequency ranged from 0.6 (LSR-99) to 0.98

(LSR-002) with PIC value ranged from 0.05 to 0.52. The expected heterozygosity for the marker loci varied from 0.00 to 0.11. The UP-GMA dendrogram obtained by 11 SSRs distributed the 91 genotypes of bottle gourd into two major clusters. The cluster I predominantly consisted of only one genotype IC 0398552 which was completely diverse from other genotypes studied and can be utilized in heterosis breeding.

Bhutia *et al.* (2022) assessed genetic diversity with 36 genotypes of Satputia (*Luffa hermaphrodita*) collected from three phyto-geographical regions of India. Molecular characterization with EST-SSR primers and ISSR markers could delineate the genotypes into two distinct clusters belonging to *L. acutangula* and *L. hermaphrodita* with moderate diversity. Five ISSR primers with high resolving power and one EST-SSR primer pair were valuable for diversity analysis and DNA fingerprinting in *Luffa* spp. This investigation had revealed untapped variability in Satputia and identified promising genotypes that would play a significant role in ridge gourd improvement.

2.4 Correlation co-efficient analysis

Yield is a complex character and is governed by polygenes. Moreover, it is highly influenced by the environmental fluctuations. Correlation study measures the natural relationship between various characters with yield. It determines the component characters on which selection can be based for yield improvement. Correlation coefficient measures the degree of association either in positive or negative direction.

Phenotypic correlation is the observable correlation between two variables, which includes both genotypic and environmental effects. Genotypic correlation on the other hand, is the inherent association between two variables and it may be either due to pleotropic action of genes or linkage or both. Environmental correlation arises entirely due to environmental effects. The previous works done by different scientists on correlation studies at both phenotypic and genotypic level are reviewed and presented below.

2.4.1 Sponge gourd

Samadia (2010) studied correlation between different characters with yield in fifteen landraces of sponge gourd and the results revealed that the fruit yield per plant

showed significant positive correlation with number of fruits per plant and fruit weight. However, days to anthesis of first male flower, days to anthesis of first female flower and days to first fruit harvest showed negative and non-significant association with fruit yield per plant. Positive and significant association had been observed between days to anthesis of male and female flower with days to first harvesting indicating mutual association of these characters. Similarly, Khule *et al.* (2011) also studied correlation between different characters in thirty genotypes of sponge gourd. They noticed that number of fruits per plant and fruit length showed positive significant correlation with marketable fruit yield per plant at both genotypic and phenotypic levels whereas, node number at which first female flower appeared was correlated at genotypic level only. However, a negative and significant correlation was observed between days to first female flower appearance with marketable fruit yield per plant.

The correlation between different characters with yield was studied in 103 sponge gourd genotypes (Singh *et al.*, 2011). They observed genotypic correlations were higher than the corresponding phenotypic ones for most of traits implying inherent relationship among them. Fruit yield per plant was found significant and positively correlated with fruit length, fruit width, fruit weight and number of fruits per plant. While, it was negatively correlated with days to first male flower, days to first female flower and days to first fruit harvest which indicates earliness.

The scientist Pandey *et al.* (2012a) studied association between different characters in thirty sponge gourd genotypes and stated that days taken for anthesis of first female flower was positively and significantly associated with days to first marketable fruit harvest and fruit diameter. Further, days taken for anthesis of first male flower was found significant and positively associated with days taken for anthesis of first female flower and days to first marketable fruit harvest. Node number for appearance of first male flower was exhibited significantly positive association with node number for appearance of first female flower and the number of fruits per plant showed significantly negative association with average fruit weight. Similarly, Dubey *et al.* (2013) noticed positive and significant correlation between vine length, number of branches per plant, fruit diameter and number of fruit per plant at the genotypic and phenotypic levels with fruit yield per plant. These association characters were in desirable direction and selection of these traits may improve yield per plant.

Whereas, days to 50 per cent emergence showed significant and negative association with fruit yield per plant at the genotypic level.

The total yield per vine was positive and significantly correlated with number of fruits per vine, average fruit weight, number of seeds per fruit and total soluble solids both at genotypic and phenotypic levels in 20 sponge gourd genotypes tested (Kumar *et al.*, 2013). Similarly, average weight of fruit was significantly and positively correlated with number of seeds per fruit, total yield per vine, average length of fruit and number of fruits per vine.

An experiment was conducted by Patidar (2014) with twenty two genotypes of sponge gourd for correlation analysis and results revealed that yield per plant was found to be significant and positively correlated with number of primary branches per plant, fruit length, fruit diameter, per fruit weight, vine length and number of fruits per plant both at phenotypic and genotypic levels. This indicated that, these characters could be considered as criteria for selecting high yielding genotypes.

Sharma *et al.* (2017) reported that fruit yield per vine had significantly and positively correlation with number of leaves per vine at 45 days after sowing (DAS), number of branches and number of fruits per vine, fruit length and average fruit weight in fifteen sponge gourd genotypes. However, number of nodes at which appearance of first staminate and pistillate flower and days to first harvesting depicted negative and significant correlations. In an similar study by Yadav *et al.* (2017) with thirty genotypes of sponge gourd, observed that significant and positive correlation for yield per plant with average fruit weight, number of fruits per plant and days to anthesis of first pistillate flower at phenotypic level indicating that these traits were most important associates of fruit yield.

Singh and Tiwari (2018) conducted investigation on twenty one germplasm of sponge gourd for correlation between different characters and identified that the fruit yield per plant exhibited a positive and significant correlation with average fruit weight and number of fruits per plant. Kumar *et al.* (2019) also studied correlation between different characters in forty five genotypes of sponge gourd. They noticed that yield per plant had highly significant and positive correlation with number of primary branches, fruiting nodes on main stem, fruit length, fruit weight, fruits per plant, seeds per fruit

and 100 seed weight. However, days taken for first staminate flower appearance, days taken for first pistillate flower appearance, days to 50 per cent 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 they were in desirable direction.

The positive and significant association between fruit yield per plant and number of fruits per plant, fruit weight and length of fruit was observed by Parveen *et al.* (2019). However, days to first fruit picking exhibited negative and highly significant association with fruit yield per plant and negative relationship of this attribute with fruit yield was desirable.

A total of twenty eight genotypes of sponge gourd including check variety Pusa Chikini were evaluated for character association and revealed that fruit yield per plant and average fruit weight was positive and significantly correlated with number of fruits per plant at genotypic and phenotypic level (Singh *et al.*, 2019a).

Annigeri (2020) observed the characters like number of fruits per vine, average fruit yield per ha had exhibited high positive and significant association with fruit yield per plant in sponge gourd.

A correlation study conducted by Som *et al.* (2020b) on fifteen genotypes of sponge gourd noticed that the characters like fruit yield per plot was found to be positively and significantly correlated with number of fruit per plant, duration of crop, vine length, fruit length and node number of male flower and indicating that any increase in these five characters would bring about an enhancement in the yield of sponge gourd. Yadav (2020) also reported similar results like fruit yield per plant was positive and significantly correlated with fruit weight, fruit length, number of fruits per plant and number of branches at both genotypic and phenotypic levels in sponge gourd.

Ray (2021) conducted correlation analysis with 14 genotypes of sponge gourd and found that the characters *via* average fruit weight, inter node length, fruit girth, number of fruits per plant and number of seeds per fruit were positive and significantly correlated with fruit yield per plant at phenotypic level. Similarly, the characters like

number of fruits plant, average fruit weight and number of seeds per fruit were also positively and significantly correlated with fruit yield per plant at genotypic level.

The characters like number of primary branches per vine, number of nodes on the main vine, fruit length and number of fruits per vine had high significant positive association with yield per plant in sponge gourd as reported by Purushottama (2022). While, it exhibited negative significant association with days to appearance of first male and female flower and sex ratio at both genotypic and phenotypic level.

2.4.2 Ridge gourd

Choudhary and Kumar (2011) reported that, days to first female flower appearance, node at first female flower emergence, fruit length, days to first fruit harvest and average fruit weight showed positive and significant correlation with fruit yield per vine in twenty genotypes of ridge gourd while, the vine length showed negative and significant correlation with fruit yield per vine.

The scientist Hanumegowda *et al.* (2012) examined thirty ridge gourd genotypes for correlation analysis and noticed that yield per vine showed positive and significant association with number of fruits per vine, fruit weight, fruit length, fruit diameter, number of seeds per fruit and rind thickness at both genotypic and phenotypic level.

An experiment was conducted with sixty landraces of ridge gourd for correlation coefficient analysis and indicated that yield per plant had highly significant and positive relationship with the number of fruits per plant, average fruit weight, vine length at harvest and length of fruit. On the other hand, the sex ratio and fruit diameter exhibited negative association with fruit yield per plant (Rabbani *et al.*, 2012).

The correlation between different characters with yield was conducted by Choudhary *et al.* (2014) with six genotypes of ridge gourd. They reported that, marketable yield per plant had positive and highly significant correlation with fruit weight and number of marketable fruits per plant at only phenotypic level. Days to first female flower had negative and significant correlation with marketable fruit yield per vine which is desirable. Thus, selection of genotypes producing early female flowers would increase yield of ridge gourd.

Koppad *et al.* (2015) evaluated eighteen genotypes of ridge gourd and noticed that, the vine length at 45 DAS, number of branches at 90 DAS, number of fruits per vine, average fruit weight, fruit length and fruit diameter had positive and significant correlation with the yield. Whereas, the sex ratio and days to first female flowering had the negative significant association with the fruit yield per vine. Similarly, Varalakshmi *et al.* (2015) also reported that ridge gourd fruit yield/ha was significantly and positively associated with peduncle length, fruit length, number of fruits/vine, fruit weight and fruit yield/vine. Whereas, number of fruits/vine had significant positive association with fruit yield/vine and fruit weight/plant. This implies that indirect selection for these traits can also help to improve fruit yield in ridge gourd.

A correlation study conducted with eighteen genotypes of ridge gourd and found that fruit yield per vine showed significant positive correlation with number of leaves, number of fruits, average fruit weight, flesh thickness and rind thickness. Days to first female flowering exhibited negative significant correlation with fruit yield which is in desirable direction and implying that selection for this trait leads to early yield (Koppad *et al.*, 2016).

Ananthan and Krishnamoorthy (2017) assessed twenty ridge gourd genotypes for correlation study. The fruit yield per vine was found to be significantly and positively correlated with fruit weight, fruit diameter, number of fruits per plant and first female flowering node at both genotypic and phenotypic levels indicated that any increase in these four characters shall bring an enhancement in the yield. Gautam *et al.* (2017) also noticed similar results like fruit yield per plant had positive and significant correlation with the characters like average fruit weight, number of fruits per plant, vine length, number of primary branches, fruit length and seed length in ridge gourd. On the other hand, fruit yield had negative and significant correlation with number of node at first female/hermaphrodite flower, days of first female flower anthesis and days of first fruit harvesting.

In an correlation experiment conducted by Mitu *et al.* (2018) with twenty nine genotypes of ridge gourd and observed that, yield per plant had highly significant positive relationship with fruit length and fruit weight at both genotypic and phenotypic

levels. While, plant height, fruit diameter and fruit thickness exhibited negative association with fruit yield.

The scientist Ramesh *et al.* (2018c) conducted the correlation coefficient analysis in 14 genotypes of ridge gourd and reported that fruit yield was positively and significantly correlated with per cent fruit, number of fruits per plant, fruit length, average weight of fruit, diameter of fruit, sex ratio, rind thickness and vine length at 90 days.

Divyaraj *et al.* (2019) evaluated fifteen genotypes of ridge gourd for genotypic and phenotypic correlation coefficient analysis and revealed that fruit yield per plant had positive significant association with vine length at 90 DAS, fruit diameter and number of fruits. While the negative significant association was observed for days to first female flower, days to first male flower, node to first male flower, node to first female flower, days to first harvest, days to last harvest and fruit length.

A correlation co-efficient analysis was performed by Harshitha *et al.* (2019b) in 25 genotypes of ridge gourd and showed positive and significant association for number of primary branches/plant, vine length, number of nodes/vine, nodes to first female flower, days to first and last harvest, per cent fruit set, number of fruits/plant, fruit weight and fruit length with fruit yield/plant both at genotypic and phenotypic level. Since, these association characters are in the desirable direction, selection of these traits may improve the yield/plant whereas, negative correlation was observed for sex ratio which is also in desirable direction.

Ahmed *et al.* (2020) analyzed both genotypic and phenotypic correlation coefficients and reported that number of secondary branches, number of female flowers/plant, fresh weight/fruit, number of male flowers, primary branches and fruits/plant had significant and positively correlation with yield per plant at both genotypic and phenotypic level. This analysis indicated that if these characters were improved then the yield/plant will also improve. Similarly, Akhila and Singh (2020) also noticed that fruit yield per plant in ridge gourd had positive significant association with fruit length, fruit diameter, rind thickness, flash thickness, number of fruit per plant, vine length at 90 DAS and average fruit weight in both genotypic and phenotypic levels. While, negative and significant association was observed for days to first male

flowering, node to first female flowering, days to 50 per cent flowering and first harvest and TSS.

Gowda (2020) conducted correlation analysis for 18 traits in thirty genotypes of ridge gourd. The values of genotypic correlation co-efficient were greater than the phenotypic correlation co-efficient. Fruit yield per plant was highly significant and positively correlated with vine length at 45 and 90 DAS, number of branches at 90 DAS, node to first female and male flowering, days to last harvest, sex ratio, number of fruits per plant, fruit yield per plot, average fruit weight and fruit length at both genotypic and phenotypic level. Whereas, days to first female flowering, 50 per cent flowering, first male flowering and first harvest were negative and highly significant correlation with fruit yield per plant. Krishnamoorthy (2020a) also evaluated twenty four F₁ hybrids of ridge gourd and observed that higher fruit yield per hectare was significantly and positively associated with fruit weight and yield per plant.

Kumar and Singh (2020) conducted correlation studies with 32 genotypes of ridge gourd. They found that highly significant and positive correlation with fruit yield per plant was observed with number of fruits per plant followed by average fruit weight, days to first fruit harvest, days to anthesis of first pistillate flower, node number to anthesis of first pistillate flower and fruit diameter only at phenotypic level.

Vijayakumar *et al.* (2020) studied on F₆ generation of ridge gourd (*Luffa acutangla* (Roxb) L.). They found that fruit yield was significantly and positively correlated with fruit weight and sex ratio. This indicated that fruit yield can be improved by making selection on the bases of yield attributing characters.

An experiment was conducted with 57 genotypes of ridge gourd and observed that, days to first fruit harvest, number of fruits per vine, fruit diameter, fruit length, fruit flesh thickness and average fruit weight had significant positive correlation with fruit yield per plant, which indicated that selecting these characters helps in enhancing the yield of ridge gourd (Srikanth *et al.*, 2021).

Vinitha *et al.* (2021) assessed thirty recombinant inbred lines (RILs) of ridge gourd derived from a cross between Arka Sujeet (monoecious) x Kashi Kushi (hermaphrodite) for correlation analysis. The results showed that, the fruit yield had

significant and positive correlation with number of fruits per plant followed by vine length and fruit weight.

2.5 Path co-efficient analysis

Path coefficient analysis is an important tool for partitioning the correlation coefficients into direct and indirect effects of an independent variable on a dependent variable or it simply measures direct and indirect contribution of various independent characters on a dependent character. The degree of influence of one variable on the other can be expressed in quantitative terms with the help of path analysis. The concept of path analysis was originally developed by Wright (1921) but the technique was first used for plant selection by Dewey and Lu (1959). The available literature on path analysis on yield per plant with other component traits in sponge gourd and related cucurbits are briefly reviewed below

2.5.1 Sponge gourd

Khule *et al.* (2011) observed that, number of fruit per plant had highest positive direct effect on marketable fruit yield per plant followed by days to appearance of first female flower, fruit length, fruit diameter, number of seeds per fruit and 100-seed weight. The data further revealed that days to appearance of first female flower and number of fruit per plant showed maximum positive indirect effects through days to appearance of first male flower and fruit length, respectively on marketable fruit yield per plant in sponge gourd.

Pandey *et al.* (2012a) noticed average fruit weight, number of fruit per plant and days to first marketable fruit harvest exhibited positive direct effects on marketable fruit yield per plant in sponge gourd. While, the vine length, days to anthesis of first male flower, node number of first female flower and days to anthesis of first female flower exhibited negative direct effect on fruit yield per plant. Similarly, Dubey *et al.* (2013) also noticed that the number of fruit per plant made the most direct contribution and exerted an indirect influence on fruit yield per plant *via* fruit diameter in sponge gourd. Fruit weight was another important trait that positively affected fruit yield per plant and had indirect effects through a number of branches per plant at the genotypic level. Later,

days to first male flower anthesis had the most negative direct effect on fruit yield per plant.

In twenty genotypes of sponge gourd, Kumar *et al.* (2013) observed that average diameter of fruit, total soluble solids, number of primary branches, average weight of fruits and number of fruits per vine exhibited positive direct effect on fruit yield per vine. Whereas, days to maturity, number of seeds per fruit, node number at which first female flower appeared and days to anthesis of first female flower 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.

A path analysis study was conducted in twenty two genotypes of sponge gourd and they reported that per fruit weight, number of primary branches per plant, number of fruits per plant and number of seeds per fruit had a direct, strong and positive effect on fruit yield per plant at both phenotypic and genotypic levels. Whereas, the characters number of days to first male flower anthesis, number of node to first female flower appearance, number of days to first fruit harvest, fruit diameter and vine length were exhibited direct, strong and negative effect on fruit yield per plant (Patidar, 2014).

Sharma *et al.* (2017) used fifteen sponge gourd genotypes for path analysis studies and reported that substantial positive and direct effect on fruit yield per vine which was exerted by traits like days to first harvest after sowing, number of fruits/vine, days to first pistillate flowering, number of branches/vine at 45 DAS, vine length at 45 DAS, number of nodes at which first appearance of staminate flower, number of leaves per vine at 45 DAS, sex ratio and number of nodes at which first appearance of pistillate flower in path analysis. Similarly, Yadav *et al.* (2017) also conducted path analysis experiment with thirty genotypes in sponge gourd and reported that average fruit weight followed by number of fruit per plant and fruit diameter had positive direct effect with fruit yield per plant.

Singh and Tiwari (2018) experimented with twenty one germplasm of sponge gourd for path analysis in order to quantify the contribution of explanatory characters towards yield in sponge gourd. They found that average fruit weight had the highest positive direct effect on fruit yield per plant. Kumar *et al.* (2019) also observed that

number of fruits per plant and number of seeds per fruit had the highest positive and direct effect on fruit yield per plant in sponge gourd.

Similar to above studies, Parveen *et al.* (2019) also noticed that the maximum positive direct effects on yield per plant were exerted by single fruit weight and number of fruits per plant in sponge gourd genotypes.

Singh *et al.* (2019a) studied path analysis in twenty eight genotypes of sponge gourd and indicated that number of fruits per plant had significantly positive and direct effect on fruit yield per plant at both genotypic and phenotypic levels. The high direct effect of these traits appeared to be the main factors for their strong association with fruit yield. Therefore, maximum weightage should be given to these characters for improvement of yield in sponge gourd.

The characters number of fruits per vine, node at first female flowering and days to first harvest had recorded maximum positive direct effect on fruit yield per plant in sponge gourd. Whereas, number of leaves per vine, average fruit yield per hectare, total soluble solids, number of branches and fruit width exhibited negative direct effect on fruit yield per plant (Annigeri, 2020).

Som *et al.* (2020b) observed direct effect of fruit yield per plot with number of fruit per plant followed by duration of crop, fruit girth, days to female flower appears, node number in male flower, number of branch per plant, node number of female flower and 50 per cent flowering in sponge gourd. Whereas, vine length, average fruit weight, fruit length, days to first fruit harvest, days to first male flower were found to be negatively associated with fruit yield per plot but in desirable direction.

In 16 genotypes of sponge gourd, Yadav (2020) observed that number of fruits per plant had positive and direct effect on fruit yield per plant at both genotypic and phenotypic levels. Similarly, specific gravity of fruits and node number of first female flower exhibited high positive and direct effect only at phenotypic level. However, fruit weight showed positive and direct effect on fruit yield per plant only at genotypic level.

An experiment was conducted with fourteen genotypes of sponge gourd for path analysis and they revealed that maximum direct effect on total fruit yield per plant was

noticed with average fruit weight followed by number of fruits per plant and fruit weight. The characters like fruit girth, internodal length and vine length had also exhibited direct effect on yield per plant. While, the negative direct effect on total fruit yield in sponge gourd was observed primarily with characters like days to first female flower and days to first male flower (Ray, 2021).

Purushottama (2022) conducted path co-efficient analysis with twenty two genotypes of sponge gourd. Among all the characters studied, yield per vine had positive direct effect with vine length, number of primary branches per vine, internodal length, number of nodes on the main vine, days to appearance of first female flower, fruit length, fruit weight, number of fruits per vine, fruit firmness, flesh thickness and number of seeds per fruit. Therefore, the higher magnitude of positive direct effect of these traits explained the higher value of association between these traits with yield per vine. However, direct selection of these traits would reward yield improvement in sponge gourd.

2.5.2 Ridge gourd

Rabbani *et al.* (2012) evaluated sixty landraces of ridge gourd for path co-efficient analysis and showed that number of fruits per plant exhibited the highest positive direct effect on fruit yield followed by average fruit weight. Similarly, Varalakshmi *et al.* (2015) also noticed that fruit weight had the highest direct effect on fruit yield/ha followed by fruit yield/plant, number of fruits/plant, peduncle length and number of branches in 51 genotypes of ridge gourd. Indirect effects of most other parameters through these stated parameters were also positive. Therefore, for yield improvement in ridge gourd, emphasis might be laid on direct selection of fruit parameters like fruit weight, number of fruits/plant and fruit yield/plant.

The scientist Koppad *et al.* (2016) conducted an experiment with eighteen genotypes of ridge gourd for path coefficient analysis and stated that number of leaves per vine, tendril length, number of fruits per vine and fruit diameter showed positive direct effect on total yield per vine at both phenotypic and genotypic levels.

Ananthan and Krishnamoorthy (2017) examined twenty ridge gourd genotypes and they reported that number of fruits per plant exhibited significant and positive direct

effect on yield per plant in ridge gourd followed by fruit weight directly and indirectly. Similarly, Mitu *et al.* (2018) observed similar results that individual fruit weight had exhibited highest positive direct effect on fruit yield followed by number of fruits per plant in ridge gourd. Therefore, emphasis should be given on these characters for enhancing the yield of ridge gourd.

A path analysis study conducted with 14 genotypes of ridge gourd for 16 important yield and quality parameters. They observed fruit yield per plot had high positive and direct effect on yield. While they noticed positive and indirect effect with node to first male flower appearance, days to last harvest, number of fruits/plant, average fruit weight, fruit length and fruit diameter. The negative and indirect effect were also observed in vine length at 90 DAS, days to first female and male flowering, node to first female flowering, days to 50 per cent flowering, days to first harvest and sex ratio with fruit yield per plot (Ramesh *et al.*, 2018d).

Divyaraj *et al.* (2019) evaluated fifteen genotypes of ridge gourd for path analysis and reported that highest positive direct effect on fruit yield/ha was exhibited by node to first male flower, number of fruits per plant, average fruit weight and fruit yield per plant. However, characters like vine length at 90 DAS, days to first male flower, days to first harvest, days to last harvest and fruit length showed direct negative effect on fruit yield/ha at both genotypic and phenotypic levels.

An experiment was conducted by Harshitha *et al.* (2019b) with twenty five genotypes of ridge gourd and reported that number of primary branches/plant, vine length, days to anthesis of first female flower, days to last harvest, sex ratio, number of fruits/plant, fruit weight and fruit length had exhibited positive direct effect indicating their true positive and significant positive association with yield. Therefore, direct selection for these traits would be rewarding for improvement of yield. Similarly, Ahmed *et al.* (2020) investigated on 15 ridge gourd genotypes for path analysis and they revealed that length of main vine, number of male flower/plant, days to first male flowering, number of fruits/plant and fresh weight/fruit have direct effect on yield/plant in both genotypic and phenotypic level. However, direct selection of plants based on these traits would be effective to increase fruit yield. While, the number of seeds/fruit had direct negative effect on fruit yield/plant.

Gowda (2020) evaluated thirty genotypes of ridge gourd for eighteen traits. Path co-efficient analysis for these characters with yield and revealed that the number of fruits per plant had the direct positive effect on yield, followed by average fruit weight and fruit length both at phenotypic and genotypic levels. Thus, selection for these characters will improve the yield in ridge gourd genotypes. Similarly, Krishnamoorthy (2020a) assessed path coefficient analysis on twenty four ridge gourd hybrids and reported that fruit weight, number of fruits per plant and yield per plant had highest direct effect on fruit yield per hectare.

A path coefficient study was conducted with 32 genotypes of ridge gourd and they reported that number of fruits per plant followed by average fruit weight and days to first fruit harvest had direct positive effect on fruit yield per plant whereas, the characters like days to anthesis of first male flower followed by average fruit length and node number to anthesis of first male flower showed direct negative effect on fruit yield per plant (Kumar and Singh, 2020).

Vijayakumar *et al.* (2020) also evaluated F₆ generation of ridge gourd (*Luffa acutangla* (Roxb) L.) for these traits. They noticed that vine length, days to first fruit harvest, fruit weight, fruit length, rind thickness and number of fruits per vine exhibited positive and direct effects on fruit yield at genotypic level indicating their true positive significant association with fruit yield per plant.

2.6 Magnitude of heterosis

The term heterosis refers to the phenomena in which the F₁ hybrid obtained through crossing the two genetically dissimilar homozygous individuals, shows increased or decreased vigour over the parents. Shull (1914) first suggested the term "heterosis" for hybrid vigour, heterozygosity or heterotic effect. Heterozygosity, allelic interaction such as dominance or over-dominance, non-allelic or epistasis and maternal interactions are the factors responsible for the expression of heterosis. The degree of heterosis depends upon the number of heterozygous alleles. Higher the number of heterozygous alleles, more is the heterosis expected (East and Hayes, 1912). Fonseca and Patterson (1968) coined the term heterobeltiosis which refers to the increased or

decreased vigour of F_1 over its better parent. Hays and Jones (1916) were the first investigators to report heterosis in cucurbits.

Hybrids offer an opportunity for increased yield, vigour, earliness, uniformity, fruitfulness and resistant to pest and diseases. A considerable degree of heterosis has been documented in cucurbits for various characters. The details of heterosis reported for various characters in sponge gourd and related cucurbits are presented in tabular form as under (Table 2).

2.7 General and specific combining ability studies

Combining ability is defined as the cultivars or parents ability to combine among each others during hybridization process such that, desirable genes or characters are transmitted to their progenies. In other words, it is an estimation of the value of genotypes on the basis of their offspring performance in some definite mating design. The combining ability is having the prime importance in crop breeding because it provides information for the selection of parents and as well as regarding the nature and magnitude of involved gene action. Therefore, it helps the breeder in identifying the best combiners which may be hybridized either to exploit heterosis or to combine the favorable fixable genes.

The concept of combining ability was introduced first by Sprague and Tatum (1942) and defined that general combining ability (GCA) as the comparative ability of the line that can combine with other lines. Then, it is the deviation of the mean performance of all the crosses involving a parent from overall mean. Whereas, specific combining ability (SCA) was defined as the deviation in the performance of the specific cross from the performance expected on the basis of general combining ability effects of the parents involved in the cross. The expression of heterosis is highly associated with specific combining ability of the crosses. The line $\times$ tester analysis design developed by Kempthorne (1957) is a powerful and commonly used tool for estimation of general and specific combining abilities of parents and hybrids, respectively. The genetic potential of parents is expressed in terms of combining ability. Among the parents involved in a large number of crosses, only few exhibits superiority and such parents producing good hybrids are considered as good general combiners.

The general combining ability is the measure of additive genetic factor whereas specific combining ability is due to non-additive genetic factors like dominance, over dominance and epistasis. For the successful breeding programme, knowledge on these aspects is of most important. So, review of literature on combining ability and gene action in sponge gourd and other related cucurbitaceous crops are presented below (Table 3).

Table 2. Review of literature on heterosis for different characters in sponge gourd and other related cucurbits

Sl. No.	Character	Crop	No. of hybrids and method	Heterobeltiosis (%)	Heterosis over best parent (%)	Standard Heterosis (%)	References
1.	Vine length at harvest time (m)	SG	36 HD	-	-50.50 to 29.06	-38.41 to 75.28	Naliyadhara <i>et al.</i> (2007)
		SG	28 HD	8.82 to 28.03	4.23 to 18.59	-	Patel and Desai (2008)
		SG	6 FD	-6.35 to 41.64	-31.31 to 8.66	-	Sanandia <i>et al.</i> (2008)
		SG	15 HD	8.73 to 18.46	11.68 to 19.41	10.10 to 24.35	Chauhan <i>et al.</i> (2018)
		SG	36 FD	-	-23.54 to 60.33	1.63 to 117.65	Rajneesh and Singh (2018a)
		SG	40 L × T	-	-26.97 to 171.83	-20.73 to 135.37	Singh and Singh (2018)
		SG	28 HD	9.92 to 55.09	-14.06 to 32.98	-27.22 to 69.02	Kumar and Pandit (2019)
		SG	32 L × T	-	-24.41 to 36.56	-30.77 to -21.36	Lakhnotra <i>et al.</i> (2019)
		SG	36 HD	-26.50 to 45.86	-29.63 to 33.35	-21.58 to 26.07	Reddy <i>et al.</i> (2019a)
		SG	45 FD	-40.47 to 43.54	-38.33 to 42.86	-56.76 to 4.05	Bhardwaj and Kumar (2021)
		RG	28 HD	-2.17 to -42.74	-1.08 to -22.55	-0.84 to -22.55	Karmakar <i>et al.</i> (2014)
		RG	28 HD	-	-	-51.53 to 34.09	Lodam <i>et al.</i> (2014)
		RG	51 L × T	-49.26 to 18.71	-49.36 to 9.11	-46.29 to 15.73	Narasannavar <i>et al.</i> (2014a)
		RG	36 HD	-	-49.37 to 45.60	-40.15 to 29.72	Poshiya <i>et al.</i> (2015)
		RG	28 HD	-	-29.75 to 59.01	-15.88 to 59.66	Sarkar <i>et al.</i> (2015)
		RG	33 L × T	-10.23 to 19.21	0.00 to 14.41	0.00 to 9.15	Chittora <i>et al.</i> (2018b)
		RG	21 L × T	-	-24.77 to 14.19	-13.86 To 16.63	Jadav and Sapovadiya (2018)
		RG	16 L × T	-	-	-4.82 to 8.67	Nandhini <i>et al.</i> (2018a)
		RG	21 HD	-	-5.88 to 30.70	1.11 to 39.86	Wakale <i>et al.</i> (2018)
		RG	12 L × T	-	-43.12 to 5.19	-35.22 to 23.32	Varalakshmi <i>et al.</i> (2019)
		RG	40 L × T	-16.26 to 34.65	-12.9 to 57.5	-16.26 to 43.58	Bhalerao <i>et al.</i> (2022)

Table 2. *Contd...*

Sl. No.	Character	Crop	No. of hybrids and method	Heterobeltiosis (%)	Heterosis over best parent (%)	Standard Heterosis (%)	References
2.	Number of primary branches per plant	SG	36 HD	-	-32.28 to 22.78	-27.43 to 30.38	Naliyadhara <i>et al.</i> (2007)
		SG	28 HD	1.39 to 19.44	-14.12 to 3.12	-	Patel and Desai (2008)
		SG	6 FD	-30.88 to 44.92	-50.00 to 32.15	-	Sanandia <i>et al.</i> (2008)
		SG	15 HD	11.77 to 27.27	9.58 to 28.14	12.87 to 37.54	Chauhan <i>et al.</i> (2018)
		SG	36 FD	-	-41.78 to 8.71	-59.36 to -19.85	Rajneesh and Singh (2018a)
		SG	40 L × T	-	-20.33 to 74.11	-10.99 to 53.11	Singh and Singh (2018)
		SG	32 L × T	-	11.80 to 59.73	-28.13 to 23.96	Lakhnotra <i>et al.</i> (2019)
		SG	28 HD	-46.09 to 63.35	-52.31 to 42.97	-61.73 to 72.84	Kumar and Pandit (2019)
		SG	36 HD	-48.73 to 68.90	-46.41 to 68.58	-46.16 to 41.71	Reddy <i>et al.</i> (2019a)
		SG	45 FD	-66.20 to 3.23	-69.23 to 5.88	-50 to 300	Bhardwaj and Kumar (2021)
		RG	28 HD	-	-	-47.28 to 58.33	Lodam <i>et al.</i> (2014)
		RG	51 L × T	-69.57 to 76.32	-78.26 to 1.45	-48.28 to 141.38	Narasannavar <i>et al.</i> (2014a)
		RG	36 HD	-	-40.63 to 24.44	-51.69 to 13.56	Poshiya <i>et al.</i> (2015)
		RG	26 HD	-	-33.33 to 70.00	-27.27 to 54.55	Sarkar <i>et al.</i> (2015)
		RG	33 L × T	-17.93 to 22.68	0 to 18.00	0.00 to 7.46	Chittora <i>et al.</i> (2018b)
		RG	21 L × T	-	-20.00 to 60.00	-1.33 to 38.67	Jadav and Sapovadiya (2018)
		RG	12 L × T	-	-47.83 to 19.05	-57.14 to -10.71	Varalakshmi <i>et al.</i> (2019)
		RG	40 L × T	-38.38 to 80.46	-50.98 to 75.66	-40.35 to 39.12	Bhalerao <i>et al.</i> (2022)
3.	Days to first male flower	SG	28 HD	6.37 to -17.11	-19.85 to 15.11	-	Patel and Desai (2008)
		SG	28 HD	-	-17.86 to 35.23	19.90 to 27.69	Sonavane <i>et al.</i> (2013b)
		SG	15 HD	-8.06 to -19.01	-6.21 to -18.81	-	Chauhan <i>et al.</i> (2018)

Table 2. *Contd...*

Sl. No.	Character	Crop	No. of hybrids and method	Heterobeltiosis (%)	Heterosis over best parent (%)	Standard Heterosis (%)	References
3.	Days to first male flower	SG	36 FD	-	-15.42 to 20.00	-2.94 to 23.53	Rajneesh and Singh (2018a)
		SG	40 L × T	-	-28.32 to 56.01	-28.88 to 20.35	Singh and Singh (2018)
		SG	28 HD	-23.91 to 8.11	-33.37 to 2.86	-26.36 to 17.80	Kumar and Pandit (2019)
		SG	32 L × T	-	-13.35 to 31.85	9.48 to 35.29	Lakhnotra <i>et al.</i> (2019)
		SG	45 FD	3.03 to 85.58	-10.29 to 74.47	-21.79 to 35.90	Bhardwaj and Kumar (2021)
		RG	51 L × T	-14.67 to 20.97	0.00 to 29.03	-19.48 to 3.90	Narasannavar <i>et al.</i> (2014a)
		RG	33 L × T	-15.06 to 2.83	-13.17 to 0	-10.65 to 0.00	Chittora <i>et al.</i> (2018b)
4.	Days to first female flower	SG	45 L × T	-	-22.37 to 6.21	-	Singh <i>et al.</i> (2009a)
		SG	28 HD	-16.30 to 16.78	-19.29 to 15.97	-	Patel and Desai (2008)
		SG	10 L × T	-	-18.6 to 12.08	-18.29 to 9.16	Islam <i>et al.</i> (2012)
		SG	28 HD	-	-14.72 to 32.17	-15.90 to 23.52	Sonavane <i>et al.</i> (2013b)
		SG	15 HD	-6.60 to -20.53	-7.54 to -18.55	-8.42 to -11.23	Chauhan <i>et al.</i> (2018)
		SG	36 FD	-	-9.30 to 24.31	-8.13 to 22.49	Rajneesh and Singh (2018a)
		SG	40 L × T		-22.82 to 42.38	-39.58 to 4.89	Singh and Singh (2018)
		SG	28 HD	-22.32 to 8.25	-31.06 to 4.39	-23.07 to 26.87	Kumar and Pandit (2019)
		SG	32 L × T	-	-9.16 to 34.03	-6.15 to 34.69	Lakhnotra <i>et al.</i> (2019)
		SG	36 HD	-7.29 to 22.68	-9.71 to 19.00	-14.42 to 14.42	Reddy <i>et al.</i> (2019b)
		SG	28 HD	-	-30.79 to 4.39	-23.07 to 26.87	Kumar and Pandit (2020)
		SG	45 FD	-3.89 to 105.17	-8.72 to 80.30	-19.05 to 41.68	Bhardwaj and Kumar (2021)
		RG	28 HD	-3.62 to -31.27	-1.17 to -21.05	-4.78 to -21.05	Karmakar <i>et al.</i> (2014)
		RG	51 L × T	-18.02 to 25.17	-1.23 to 66.67	-4.71 to 58.82	Narasannavar <i>et al.</i> (2014a)

Table 2. *Contd...*

Sl. No.	Character	Crop	No. of hybrids and method	Heterobeltiosis (%)	Heterosis over best parent (%)	Standard Heterosis (%)	References
4.	Days to first female flower	RG	36 HD	-	-14.29 to 17.08	-21.77 to 7.94	Poshiya <i>et al.</i> (2015)
		RG	28 HD	-	-17.97 to 8.73	-11.40 to 20.18	Sarkar <i>et al.</i> (2015)
		RG	28 HD	-24.20 to 26.90	-28.24 to 18.10	-	Bairwa <i>et al.</i> (2017)
		RG	28 HD	-9.50 to 8.86	-9.50 to 4.50	11.49 to 5.13	Muthaiah <i>et al.</i> (2017a)
		RG	21 HD	-23.25 to -0.88	-	16.10 to 3.29	Singh <i>et al.</i> (2017a)
		RG	33 L × T	-11.60 to 2.52	-11.01 to 0	-10.85 to 0.00	Chittora <i>et al.</i> (2018b)
		RG	16 L × T	-	-	-23.68 to 1.36	Nandhini <i>et al.</i> (2018a)
5.	Node at first male flower	RG	12 L × T	-	-40.27 to -5.57	-24.48 to 1.44	Varalakshmi <i>et al.</i> (2019)
		SG	28 HD	-1.45 to 32.14	-6.45 to 12.12	-	Patel and Desai (2008)
		SG	15 HD	-12.00 to -54.71	-19.23 to -53.84	-	Chauhan <i>et al.</i> (2018)
		SG	40 L × T	-	-63.28 to 59.22	-24.59 to 36.07	Singh and Singh (2018)
		SG	32 L × T	-	-6.85 to 61.29	-11.76 to 23.53	Lakhnotra <i>et al.</i> (2019)
		SG	45 FD	-62.32 to 144.44	-72.34 to 100	-67.86 to 64.29	Bhardwaj and Kumar (2021)
		RG	51 L × T	-28.85 to 173.33	-9.68 to 277.42	-56.92 to 80.00	Narasannavar <i>et al.</i> (2014a)
6.	Node at first female flower	RG	36 HD	-	-16.19 to 52.44	-29.59 to 27.55	Poshiya <i>et al.</i> (2015)
		RG	28 HD	-37.04 to 16.33	-37.04 to 9.26	20.93 to 37.21	Muthaiah <i>et al.</i> (2017a)
		SG	28 HD	-11.41 to 17.89	-11.41 to 7.32	-	Patel and Desai (2008)
		SG	45 L × T	-	-45.09 to 68.87	-	Singh <i>et al.</i> (2009a)
		SG	15 HD	-9.48 to -37.93	-19.44 to -30.43	-19.44 to -25.00	Chauhan <i>et al.</i> (2018)
		SG	40 L × T		-58.81 to 112.80	-26.57 to 68.60	Singh and Singh (2018)
		SG	28 HD	-32.00 to 10.49	-52.19 to -9.87	-46.82 to 54.55	Kumar and Pandit (2019)
		SG	32 L × T	-	-16.81 to 30.56	-27.91 to 9.30	Lakhnotra <i>et al.</i> (2019)

Table 2. *Contd..*

Sl. No.	Character	Crop	No. of hybrids and method	Heterobeltiosis (%)	Heterosis over best parent (%)	Standard Heterosis (%)	References
6.	Node at first female flower	SG	36 HD	-60.00 to 252.94	-74.07 to 233.33	-80.56 to 19.44	Reddy <i>et al.</i> (2019b)
		SG	45 FD	-52.54 to 69.23	-57.58 to 39.39	-60.6 to 8.45	Bhardwaj and Kumar (2021)
		RG	28 HD	-0.79 to -47.51	-1.05 to -44.31	-1.96 to -44.31	Karmakar <i>et al.</i> (2014)
		RG	28 HD	-	-	-23.78 to 23.56	Lodam <i>et al.</i> (2014)
		RG	51 L × T	-21.69 to 112.69	13.64 to 139.09	-19.35 to 83.87	Narasannavar <i>et al.</i> (2014a)
		RG	36 HD	-	-17.08 to 36.97	-28.42 to 24.10	Poshiya <i>et al.</i> (2015)
		RG	28 HD	-	-59.26 to 56.00	-59.26 to 44.44	Sarkar <i>et al.</i> (2015)
		RG	28 HD	-27.19 to 31.96	-33.37 to 23.67	-	Bairwa <i>et al.</i> (2017)
		RG	28 HD	-16.67 to 18.75	-18.89 to 6.67	11.49 to 20.00	Muthaiah <i>et al.</i> (2017a)
		RG	33 L × T	-19.03 to 15.84	-15.28 to 0	-14.59 to 0.00	Chittora <i>et al.</i> (2018b)
		RG	16 L × T	-	-	-15.03 to 5.59	Nandhini <i>et al.</i> (2018a)
		RG	12 L × T	-	-73.78 to 16.39	-70.61 to -11.82	Varalakshmi <i>et al.</i> (2019)
7.	Days to first harvest	SG	36 HD	-	-6.19 to 21.89	-17.56 to 5.6	Naliyadhara <i>et al.</i> (2007)
		SG	28 HD	-21.47 to 11.11	-24.71 to 4.23	-	Patel and Desai (2008)
		SG	10 L × T	-	-16.84 to 9.03	-17.59 to 6.03	Islam <i>et al.</i> (2012)
		SG	28 HD	-	-17.13 to 24.63	-18.51 to 20.84	Sonavane <i>et al.</i> (2013b)
		SG	36 FD	-	-7.34 to 20.00	-4.48 to 18.44	Rajneesh and Singh (2018a)
		SG	40 L × T	-	-21.82 to 42.38	-30.04 to 1.93	Singh and Singh (2018)
		SG	32 L × T	-	-12.10 to 24.20	-9.49 to 17.60	Lakhnotra <i>et al.</i> (2019)
		SG	36 HD	-6.25 to 18.03	-6.98 to 17.07	-10.45 to 8.21	Reddy <i>et al.</i> (2019b)
		SG	45 FD	-3.68 to 87.00	-7.10 to 67.10	-17.37 to 36.32	Bhardwaj and Kumar (2021)
		RG	28 HD	-3.55 to -28.69	-1.24 to -19.62	-2.08 to -19.62	Karmakar <i>et al.</i> (2014)
		RG	51 L × T	-4.63 to -8.70	-	-	Narasannavar <i>et al.</i> (2014a)

Table 2. *Contd..*

Sl. No.	Character	Crop	No. of hybrids and method	Heterobeltiosis (%)	Heterosis over best parent (%)	Standard Heterosis (%)	References
7.	Days to first harvest	RG	36 HD	-	-16.67 to 6.95	-18.12 to 5.08	Poshiya <i>et al.</i> (2015)
		RG	28 HD	-	-14.49 to 17.83	-9.30 to 17.83	Sarkar <i>et al.</i> (2015)
		RG	28 HD	-20.79 to 24.51	-24.12 to 15.74	-	Bairwa <i>et al.</i> (2017)
		RG	21 HD	-21.22 to 3.09	-	-10.39 to 6.56	Singh <i>et al.</i> (2017a)
		RG	33 L × T	-11.65 to 2.79	-10.93 to 0	-9.97 to 0.00	Chittora <i>et al.</i> (2018b)
		RG	16 L × T	-	-	-35.91 to -5.18	Nandhini <i>et al.</i> (2018a)
		RG	21 HD	-	0.17 to 3.76	-0.75 to 5.97	Wakale <i>et al.</i> (2018)
		RG	40 L × T	-18.27 to 14.80	-20.86 to 12.39	-7.58 to 17.83	Bhalerao <i>et al.</i> (2022)
8.	Days to last harvest	SG	36 HD	-	-5.44 to 2.78	-4.87 to 4.04	Naliyadhara <i>et al.</i> (2007)
		SG	36 HD	-17.67 to 20.27	-19.44 to 17.07	-17.92 to 11.01	Reddy <i>et al.</i> (2019b)
9.	Fruit length (cm)	SG	36 HD	-	-26.82 to 24.23	-22.25 to 35.25	Naliyadhara <i>et al.</i> (2007)
		SG	28 HD	12.72 to 21.68	7.55 to 20.58	-	Patel and Desai (2008)
		SG	6 FD	-	-12.24 to 48.29	-22.96 to 8.66	Sanandia <i>et al.</i> (2008)
		SG	45 L × T	-	-8.95 to 15.52	-	Singh <i>et al.</i> (2009a)
		SG	15 HD	6.87 to 34.61	12.15 to 24.37	13.56 to 25.93	Chauhan <i>et al.</i> (2018)
		SG	28 HD	-8.43 to 94.90	-6.04 to 48.74	-42.46 to 44.07	Kumar and Pandit (2019)
		SG	32 L × T	-	-30.52 to 29.32	-25.74 to 23.95	Lakhnotra <i>et al.</i> (2019)
		SG	36 FD	-	-24.29 to 11.47	-21.59 to 20.30	Rajneesh and Singh (2018a)
		SG	40 L × T	-	-12.43 to 55.88	-28.40 to 20.58	Singh and Singh (2018)
		SG	36 HD	-28.99 to 45.39	-33.29 to 20.66	-26.63 to 19.44	Reddy <i>et al.</i> (2019a)
		SG	45 FD	-44.30 to 40.00	-44.30 to 29.63	-43.59 to 7.69	Bhardwaj and Kumar (2021)

Table 2. *Contd..*

Sl. No.	Character	Crop	No. of hybrids and method	Heterobeltiosis (%)	Heterosis over best parent (%)	Standard Heterosis (%)	References
9.	Fruit length (cm)	RG	28 HD	5.39 to 37.71	4.20 to 28.64	5.83 to 18.08	Karmakar <i>et al.</i> (2014)
		RG	28 HD	-	-	-33.05 to 27.41	Lodam <i>et al.</i> (2014)
		RG	51 L × T	-28.39 to 33.77	-33.63 to 60.53	-41.65 to 36.91	Narasannavar <i>et al.</i> (2014a)
		RG	45 L × T	-39.42 to 9.92	-33.92 to 19.23	9.84 to 40.57	Prakash <i>et al.</i> (2015)
		RG	36 HD	-	-23.23 to 6.92	-39.64 to 7.63	Poshiya <i>et al.</i> (2015)
		RG	28 HD	-24.82 to 76.10	-33.56 to 72.87	-	Bairwa <i>et al.</i> (2017)
		RG	21 HD	-24.41 to 10.60	-	-35.82 to 6.14	Singh <i>et al.</i> (2017a)
		RG	33 L × T	-17.40 to 19.37	0.00 to 15.95	0 to 12.73	Chittora <i>et al.</i> (2018b)
		RG	21 L × T	-	-6.67 to 27.80	-8.03 to 12.17	Jadav and Sapovadiya (2018)
		RG	16 L × T	-	-	-13.07 to 25.97	Nandhini <i>et al.</i> (2018a)
		RG	35 L × T	-	-31.43 to 50.61	-44.47 to -4.33	Narasannavar <i>et al.</i> (2018)
		RG	21 HD	-	1.40 to 45.88	0.28 to 52.36	Wakale <i>et al.</i> (2018)
		RG	12 L × T	-	-12.07 to 24.34	-22.8 to 5.94	Varalakshmi <i>et al.</i> (2019)
		RG	45 HD	-49.16 to 42.56	-50.76 to 26.58	-33.85 to 95.38	Srikanth <i>et al.</i> (2020a)
		RG	40 L × T	-35.96 to 68.12	-37.22 to 53.42	-49.54 to 22.29	Bhalerao <i>et al.</i> (2022)
10.	Fruit diameter (cm)	SG	36 HD		-8.57 to 6.63	-10.85 to 3.81	Naliyadhara <i>et al.</i> (2007)
		SG	28 HD	8.76 to 13.89	7.11 to 10.45	-	Patel and Desai (2008)
		SG	45 L × T	-	-20.48 to 10.91	-	Singh <i>et al.</i> (2009a)
		SG	36 FD	-	-23.9 to 3.82	-20.45 to 13.64	Rajneesh and Singh (2018a)
		SG	40 L × T	-	-17.88 to 23.50	-17.88 to 10.22	Singh and Singh (2018)
		SG	32 L × T	-	-14.80 to 29.89	-17.90 to 14.12	Lakhnotra <i>et al.</i> (2019)
		SG	28 HD	-36.06 to 73.58	-40.00 to 44.44	-22.51 to 148.72	Kumar and Pandit (2019)

Table 2. *Contd..*

Sl. No.	Character	Crop	No. of hybrids and method	Heterobeltiosis (%)	Heterosis over best parent (%)	Standard Heterosis (%)	References
10.	Fruit diameter (cm)	SG	36 HD	-11.48 to 16.08	-15.93 to 13.03	-21.13 to 3.44	Reddy <i>et al.</i> (2019a)
		SG	45 FD	-15.25 to 12.04	-19.51 to 9.91	-30.28 to 21.83	Bhardwaj and Kumar (2021)
		RG	28 HD	2.34 to 46.50	0.74 to 36.31	0.69 to 11.78	Karmakar <i>et al.</i> (2014)
		RG	28 HD	-	-	-22.13 to 43.44	Lodam <i>et al.</i> (2014)
		RG	51 L × T	-37.72 to 50.92	-56.29 to 6.80	-36.53 to 55.09	Narasannavar <i>et al.</i> (2014a)
		RG	36 HD	-	-9.33 to 12.00	-9.93 to 11.26	Poshiya <i>et al.</i> (2015)
		RG	45 L × T	-15.42 to 49.59	-50.49 to 0	-40.94 to 13.72	Prakash <i>et al.</i> (2015)
		RG	28 HD	-16.00 to 24.75	16.00 to 20.62	15.12 to 24.20	Muthaiah <i>et al.</i> (2017a)
		RG	33 L × T	-19.75 to 25.19	0 to 23.69	0 to 9.76	Chittora <i>et al.</i> (2018b)
		RG	21 L × T	-	4.65 to 48.15	-5.03 to 52.17	Jadav and Sapovadiya (2018)
		RG	16 L × T	-	-	-4.32 to 13.56	Nandhini <i>et al.</i> (2018a)
		RG	35 L × T	-	-28.95 to 52.43	-29.31 to 26.79	Narasannavar <i>et al.</i> (2018)
		RG	21 HD	-	0.18 to 9.17	0.38 to 24.76	Wakale <i>et al.</i> (2018)
		RG	12 L × T	-	-18.16 to 18.59	-16.24 to 0.86	Varalakshmi <i>et al.</i> (2019)
		RG	45 HD	-31.51 to 28.62	-35.33 to 17.03	-41.85 to -1.94	Srikanth <i>et al.</i> (2020a)
		RG	40 L × T	-18.67 to 51.54	-22.43 to 51.12	-29.88 to 12.66	Bhalerao <i>et al.</i> (2022)
11.	Average fruit weight (g)	SG	36 HD	-	-11.43 to 18.63	-14.63 to 10.74	Naliyadhara <i>et al.</i> (2007)
		SG	6 FD	-	-2.53 to 16.10	-15.11 to 0.89	Sanandia <i>et al.</i> (2008)
		SG	28 HD	15.34 to 34.47	9.46 to 26.27	-	Patel and Desai (2008)
		SG	15 HD	16.79 to 61.84	24.17 to 67.46	13.05 to 31.61	Chauhan <i>et al.</i> (2018)
		SG	36 FD	-	-18.93 to 17.47	-18.93 to 5.60	Rajneesh and Singh (2018a)
		SG	40 L × T	-	-12.77 to 34.97	-36.07 to 15.31	Singh and Singh (2018)

Table 2. *Contd..*

Sl. No.	Character	Crop	No. of hybrids and method	Heterobeltiosis (%)	Heterosis over best parent (%)	Standard Heterosis (%)	References
11.	Average fruit weight (g)	SG	28 HD	-16.82 to 40.94	-44.55 to 29.57	-28.12 to 110.09	Kumar and Pandit (2019)
		SG	32 L × T	-	-35.14 to 65.21	-40.45 to 21.96	Lakhnotra <i>et al.</i> (2019)
		SG	36 HD	-35.73 to 72.50	-39.39 to 62.41	-52.26 to 13.37	Reddy <i>et al.</i> (2019a)
		SG	45 FD	-41.06 to 59.69	-135.00 to 53.73	-54.69 to 53.13	Bhardwaj and Kumar (2021)
		RG	28 HD	2.20 to 28.18	1.67 to 8.52	1.51 to 8.52	Karmakar <i>et al.</i> (2014)
		RG	28 HD	-	-	-40.98 to 32.30	Lodam <i>et al.</i> (2014)
		RG	51 L × T	23.23 to 71.49	-	36.34 to 40.86	Narasannavar <i>et al.</i> (2014a)
		RG	36 HD		-21.83 to 13.57	-32.31 to 13.14	Poshiya <i>et al.</i> (2015)
		RG	45 L × T	-47.79 to 29.94	-43.34 to 3.19	-46.51 to 54.78	Prakash <i>et al.</i> (2015)
		RG	28 HD	-12.29 to 32.26	-21.50 to 30.28		Bairwa <i>et al.</i> (2017)
		RG	28 HD	-35.15 to 45.95	36.70 to 42.47	33.87 to 48.84	Muthaiah <i>et al.</i> (2017a)
		RG	21 HD	-0.68 to 21.92	-	-8.71 to 19.50	Singh <i>et al.</i> (2017a)
		RG	33 L × T	-15.21 to 13.00	0.00 to 12.55	0 to 10.50	Chittora <i>et al.</i> (2018b)
		RG	21 L × T	-	-23.52 to 23.09	-17.23 To 27.05	Jadav and Sapovadiya (2018)
		RG	35 L × T	-	-39.85 to 28.66	-35.82 to 0.36	Narasannavar <i>et al.</i> (2018)
		RG	21 HD	-	0.04 to 17.87	-3.74 to 33.06	Wakale <i>et al.</i> (2018)
		RG	12 L × T	-	-44.06 to 18.41	-17.02 to -2.29	Varalakshmi <i>et al.</i> (2019)
		RG	45 HD	-47.57 to 141.29	-58.93 to 126.03	-17.00 to 174.51	Srikanth <i>et al.</i> (2020a)

Table 2. *Contd..*

Sl. No.	Character	Crop	No. of hybrids and method	Heterobeltiosis (%)	Heterosis over best parent (%)	Standard Heterosis (%)	References
11.	Average fruit weight (g)	RG	40 L × T	0.54 to 50.98	-5.26 to 44.08	-17.23 to 25.41	Bhalerao <i>et al.</i> (2022)
12.	Number of fruits per vine	SG	36 HD	-	-27.54 to 112.58	-26.21 to 72.12	Naliyadhara <i>et al.</i> (2007)
		SG	28 HD	51.31 to 82.48	17.13 to 78.70	-	Patel and Desai (2008)
		SG	6 FD	-	-10.89 to 31.32	-17.82 to 20.62	Sanandia <i>et al.</i> (2008)
		SG	45 L × T	-	-36.67 to 44.70	-	Singh <i>et al.</i> (2009a)
		SG	15 HD	19.35 to 88.77	29.85 to 104.08	35.17 to 82.79	Chauhan <i>et al.</i> (2018)
		SG	36 FD	-	-40.46 to 19.69	-30.69 to 38.62	Rajneesh and Singh (2018a)
		SG	40 L × T	-	-14.83 to 115.16	-31.05 to 72.07	Singh and Singh (2018)
		SG	28 HD	-26.81 to 56.78	-37.54 to 25.86	-63.98 to 34.56	Kumar and Pandit (2019)
		SG	32 L × T	-	-19.35 to 58.06	-46.39 to 8.64	Lakhnotra <i>et al.</i> (2019)
		SG	36 HD	-41.54 to 55.70	-47.53 to 48.76	-14.01 to 66.04	Reddy <i>et al.</i> (2019a)
		SG	45 FD	-27.59 to 45.45	-32.26 to 40.74	-28.57 to 166.67	Bhardwaj and Kumar (2021)
		RG	28 HD	8.41 to 79.09	0.30 to 35.30	0.30 to 28.43	Karmakar <i>et al.</i> (2014)
		RG	51 L × T	-20.00 to 87.50	-46.51 to 39.53	-41.03 to 53.85	Narasannavar <i>et al.</i> (2014a)
		RG	45 L × T	-34.48 to 45.05	-47.37 to -5.26	-41.67 to 10.83	Prakash <i>et al.</i> (2015)
		RG	36 HD	-	-37.89 to 57.13	-28.81 to 99.60	Poshiya <i>et al.</i> (2015)
		RG	28 HD	-48.78 to 29.51	48.78 to 12.50	46.08 to 18.41	Muthaiah <i>et al.</i> (2017a)
		RG	21 HD	3.30 to 54.08	-	-24.65 to 54.08	Singh <i>et al.</i> (2017a)

Table 2. *Contd..*

Sl. No.	Character	Crop	No. of hybrids and method	Heterobeltiosis (%)	Heterosis over best parent (%)	Standard Heterosis (%)	References
12.	Number of fruits per vine	RG	33 L × T	-12.79 to 49.17	0.00 to 49.02	0.00 to 28.36	Chittora <i>et al.</i> (2018b)
		RG	21 L × T	-	-22.75 to 31.14	-18.35 to 38.61	Jadav and Sapovadiya (2018)
		RG	16 L × T	-	-	-4.50 to 22.48	Nandhini <i>et al.</i> (2018a)
		RG	35 L × T	-	-57.45 to 161.01	-75.37 to 29.66	Narasannavar <i>et al.</i> (2018)
		RG	21 HD	-	1.00 to 47.43	11.19 to 53.82	Wakale <i>et al.</i> (2018)
		RG	12 L × T	-	15.19 to 319.42	62.14 to 319.42	Varalakshmi <i>et al.</i> (2019)
		RG	45 HD	-47.26 to 57.14	-48.32 to 50.47	-14.44 to 107.78	Srikanth <i>et al.</i> (2020a)
		RG	40 L × T	-21.61 to 41.33	-22.96 to 39.47	-31.62 to 8.14	Bhalerao <i>et al.</i> (2022)
13.	Fruit yield per vine (kg)	SG	36 HD	-	-23.52 to 69.10	-25.26 to 53.56	Naliyadhara <i>et al.</i> (2007)
		SG	28 HD	33.87 to 58.13	23.70 to 51.55	-	Patel and Desai (2008)
		SG	6 FD	-	-8.46 to 37.99	-17.98 to 17.37	Sanandia <i>et al.</i> (2008)
		SG	45 L × T	-	-34.78 to 72.84	-	Singh <i>et al.</i> (2009a)
		SG	10 L × T	-	-50.58 to 74.90	-41.55 to 106.85	Islam <i>et al.</i> (2012)
		SG	28 HD	-	-18.12 to 50.49	-31.15 to 26.33	Sonavane <i>et al.</i> (2013b)
		SG	15 HD	16.94 to 125.74	21.05 to 113.43	21.05 to 81.58	Chauhan <i>et al.</i> (2018)
		SG	36 FD	-	-32.65 to 44.81	-29.15 to 44.81	Rajneesh and Singh (2018a)
		SG	40 L × T	-	-17.35 to 118.59	-34.47 to 36.73	Singh and Singh (2018)
		SG	28 HD	-42.93 to 66.01	-62.71 to 51.99	-76.02 to 127.74	Kumar and Pandit (2019)
		SG	32 L × T	-	-61.95 to 45.45	-61.98 to -12.47	Lakhnotra <i>et al.</i> (2019)
		SG	36 HD	-47.30 to 90.16	-57.50 to 78.27	-23.91 to 100.74	Reddy <i>et al.</i> (2019a)
		SG	28 HD	-	-47.79 to 51.99	-76.02 to 127.74	Kumar and Pandit (2020)
		SG	45 FD	-41.96 to 91.69	-48.52 to 62.72	-22.19 to 116.25	Bhardwaj and Kumar (2021)

Table 2. *Contd..*

Sl. No.	Character	Crop	No. of hybrids and method	Heterobeltiosis (%)	Heterosis over best parent (%)	Standard Heterosis (%)	References
13.	Fruit yield per vine (kg)	RG	18 L × T	-	-58.33 to 97.92	-74.09 to 24.04	Prabhakar (2008)
		RG	28 HD	20.00 to 186.2	8.30 to 177.76	8.30 to 91.36	Karmakar <i>et al.</i> (2014)
		RG	28 HD	-	-	-34.29 to 63.81	Lodam <i>et al.</i> (2014)
		RG	51 L × T	-56.46 to 185.71	-75.57 to 25.28	-75.90 to 23.61	Narasannavar <i>et al.</i> (2014a)
		RG	36 HD	-	-45.93 to 67.46	-52.12 to 80.51	Poshiya <i>et al.</i> (2015)
		RG	45 L × T	-75.47 to 77.52	-48.98 to 0	-75.70 to 75.70	Prakash <i>et al.</i> (2015)
		RG	28 HD	-54.60 to 54.82	-63.67 to 33.33	-	Bairwa <i>et al.</i> (2017)
		RG	21 HD	2.72 to 84.62	-	-18.57 to 84.38	Singh <i>et al.</i> (2017a)
		RG	33 L × T	-18.60 to 68.33	0.00 to 67.45	0.00 to 41.64	Chittora <i>et al.</i> (2018b)
		RG	21 L × T	-	-24.22 to 36.69	-17.23 To 26.55	Jadav and Sapovadiya (2018)
		RG	16 L × T	-	-	-14.92 to 24.74	Nandhini <i>et al.</i> (2018a)
		RG	35 L × T	-	-62.86 to 180.00	-83.46 to 25.95	Narasannavar <i>et al.</i> (2018)
		RG	21 HD	-	4.58 to 22.08	-0.39 to 64.96	Wakale <i>et al.</i> (2018)
		RG	12 L × T	-	34.48 to 133.33	44.44 to 177.78	Varalakshmi <i>et al.</i> (2019)
		RG	45 HD	-55.33 to 132.21	-57.47 to 68.51	-64.65 to 35.51	Srikanth <i>et al.</i> (2020a)
		RG	40 L × T	-4.22 to 110.24	-7.54 to 108.39	-32.61 to 28.99	Bhalerao <i>et al.</i> (2022)
14.	Fruit yield per plot (kg)	RG	51 L × T	-39.38 to 165.86	-56.60 to 34.45	-59.16 to 26.53	Narasannavar <i>et al.</i> (2014a)
		RG	45 L × T	-15.42 to 49.59	-50.49 to 0	-40.94 to 13.72	Prakash <i>et al.</i> (2015)
15.	Fruit yield per hectare (t/ha)	RG	51 L × T	-44.34 to 166.22	-56.61 to 34.65	-59.26 to 26.46	Narasannavar <i>et al.</i> (2014a)
		RG	21 HD	-	3.26 to 38.58	4.67 to 84.42	Wakale <i>et al.</i> (2018)
		RG	12 L × T	-	37.4 to 130.06	44.54 to 173.22	Varalakshmi <i>et al.</i> (2019)

Table 2. *Contd..*

Sl. No.	Character	Crop	No. of hybrids and method	Heterobeltiosis (%)	Heterosis over best parent (%)	Standard Heterosis (%)	References
16.	Number of seeds per fruit	SG	28 HD	-22.67 to 47.47	-36.44 to 27.04	-48.82 to 56.54	Kumar and Pandit (2019)
		SG	32 L × T	-	-23.10 to 48.55	-33.24 to 19.03	Lakhnotra <i>et al.</i> (2019)
		SG	36 HD	-34.13 to 50.06	-45.34 to 43.23	-42.66 to 14.27	Reddy <i>et al.</i> (2019b)
		RG	51 L × T	-62.50 to 456.05	-77.09 to 97.24	-60.66 to 238.80	Narasannavar <i>et al.</i> (2014a)
		RG	33 L × T	-24.36 to 21.61	-22.07 to 0.00	-10.09 to 0.00	Chittora <i>et al.</i> (2018b)
		RG	21 L × T	-	-4.63 to 47.49	-5.98 To 45.11	Jadav and Sapovadiya (2018)
		RG	16 L × T	-	-	-1.96 to 16.97	Nandhini <i>et al.</i> (2018a)
		RG	45 HD	-36.11 to 164.78	-40.26 to 121.64	-61.67 to 60.53	Srikanth <i>et al.</i> (2020a)
17.	TSS (⁰ Brix)	SG	36 HD	-28.16 to 4.04	-20.00 to 2.94	-16.92 to 12.82	Reddy <i>et al.</i> (2019b)
		RG	33 L × T	-13.85 to 21.12	0.00 to 19.20	0.00 to 1.77	Chittora <i>et al.</i> (2018b)
		RG	45 HD	-38.19 to 56.31	-45.94 to 36.43	-44.60 to 38.92	Srikanth <i>et al.</i> (2020a)
18.	Crude fiber (%)	RG	28 HD	-30.85 to 50.54	-34.28 to 44.00	-	Bairwa <i>et al.</i> (2017)
		RG	45 HD	-44.90 to 39.64	-43.64 to 17.86	-47.46 to 16.95	Srikanth <i>et al.</i> (2020a)
19.	Ascorbic acid (mg/100 gm)	RG	33 L × T	-27.32 to 20.58	8.52 to 0.00	-	Chittora <i>et al.</i> (2018b)
		RG	45 HD	-34.19 to 9.19	-40.69 to 0.30	-30.13 to 10.92	Srikanth <i>et al.</i> (2020a)
20.	Potassium (%)	RG	21 HD	-5.84 to 28.79	-	-8.51 to 30.30	Singh <i>et al.</i> (2017a)

Table 3. Review of literature on combining ability and gene action on various traits in sponge gourd and other related cucurbits

Sl. No.	Character	Crop	Material and method used	Combining ability		Gene action		References
				GCA	SCA	Additive	Non-additive	
1.	Vine length at harvest time (m)	SG	8 × 8 HD	-	Significant	-	+	Patel and Desai (2008)
		SG	9 × 9 HD	Significant	Significant	+	+	Naliyadhara <i>et al.</i> (2010)
		SG	8 × 8 HD	Significant	Significant	+	+	Sonavane <i>et al.</i> (2013a)
		SG	10 × 10 HD	Significant	Significant	+	+	Kumar <i>et al.</i> (2018)
		SG	9 × 9 HD	Significant	Significant	+	+	Rajneesh and Singh (2018b)
		SG	9 × 9 HD	Significant	Significant	+	+	Singh <i>et al.</i> (2018a)
		SG	10 × 4 L × T	Significant	Significant	+	+	Singh <i>et al.</i> (2018b)
		SG	8 × 8 HD	Significant	Significant	+	+	Chauhan <i>et al.</i> (2019)
		SG	6 × 6 HD	Significant	Significant	+	+	Chauhan <i>et al.</i> (2020)
		RG	8 × 8 HD	Significant	Significant	+	+	Purohit <i>et al.</i> (2007)
		RG	6 × 3 L × T	Significant	Significant	+	+	Prabhakar (2008)
		RG	8 × 8 HD	Significant	Significant	+	+	Lodam <i>et al.</i> (2009)
		RG	10 × 10 HD	Significant	Significant	+	+	Tyagi <i>et al.</i> (2010)
		RG	6 × 3 L × T	Significant	Significant	+	+	Reddy <i>et al.</i> (2013)
		RG	8 × 8 HD	Significant	Significant	+	+	Sarkar <i>et al.</i> (2015)
		RG	8 × 8 HD	Significant	Significant	+	+	Muthaiah <i>et al.</i> (2017b)
		RG	11 × 3 L × T	Significant	Significant	+	+	Chittora <i>et al.</i> (2018a)
		RG	10 × 3 L × T	Significant	Significant	+	+	Kamble <i>et al.</i> (2018)
		RG	5 × 5 FD	Significant	Significant	+	+	Chandan <i>et al.</i> (2019)
		RG	3 × 4 HD	Significant	Significant	+	+	Varalakshmi <i>et al.</i> (2019)
		RG	6 × 4 L × T	Significant	Significant	+	+	Krishnamoorthy (2020b)
		RG	8 × 8 HD	Significant	Significant	+	+	Malve <i>et al.</i> (2020)

Table 3. *Contd..*

Sl. No.	Character	Crop	Material and method used	Combining ability		Gene action		References
				GCA	SCA	Additive	Non-additive	
2.	Number of branches per vine	SG	10×10 FD	Significant	Significant	+	+	Ram <i>et al.</i> (2007)
		SG	8 × 8 HD	-	Significant	-	+	Patel and Desai (2008)
		SG	9 × 9 HD	Significant	Significant	+	+	Naliyadhara <i>et al.</i> (2010)
		SG	8 × 8 HD	Significant	Significant	+	+	Sonavane <i>et al.</i> (2013a)
		SG	10 × 10 HD	Significant	Significant	+	+	Kumar <i>et al.</i> (2018)
		SG	9 × 9 HD	Significant	Significant	+	+	Rajneesh and Singh (2018b)
		SG	9 × 9 HD	Significant	Significant	+	+	Singh <i>et al.</i> (2018a)
		SG	10 × 4 L × T	Significant	Significant	+	+	Singh <i>et al.</i> (2018b)
		SG	8 × 8 HD	Non-Significant	Significant	-	+	Chauhan <i>et al.</i> (2019)
		SG	6 × 6 HD	Significant	Significant	+	+	Chauhan <i>et al.</i> (2020)
		SG	8 × 8 HD	Significant	-	+	-	Kumar and Pandit (2020)
		RG	8 × 8 HD	Significant	Significant	+	+	Purohit <i>et al.</i> (2007)
		RG	6 × 3 L × T	Significant	Significant	+	+	Prabhakar (2008)
		RG	8 × 8 HD	Significant	Significant	+	+	Lodam <i>et al.</i> (2009)
		RG	6 × 3 L × T	Significant	Significant	+	+	Reddy <i>et al.</i> (2013)
		RG	20 × 3 L × T	Significant	Significant	+	+	Narasannavar <i>et al.</i> (2014b)
		RG	8 × 8 HD	Significant	Significant	+	+	Sarkar <i>et al.</i> (2015)
		RG	8 × 8 HD	Significant	Significant	+	+	Muthaiah <i>et al.</i> (2017b)
		RG	11 × 3 L × T	Significant	Significant	+	+	Chittora <i>et al.</i> (2018a)
		RG	8 × 4 L × T	Significant	Significant	+	+	Nandhini <i>et al.</i> (2018b)
		RG	3 × 4 HD	Non-Significant	Non-Significant	-	-	Varalakshmi <i>et al.</i> (2019)
3.	Days to first male flower	SG	8 × 8 HD	-	Significant	-	+	Patel and Desai (2008)
		SG	8 × 8 HD	Significant	Significant	+	+	Sonavane <i>et al.</i> (2013a)
		SG	9 × 9 HD	Significant	Significant	+	+	Rajneesh and Singh (2018b)
		SG	9 × 9 HD	Significant	Significant	+	+	Singh <i>et al.</i> (2018a)

Table 3. *Contd..*

Sl. No.	Character	Crop	Material and method used	Combining ability		Gene action		References
				GCA	SCA	Additive	Non-additive	
3.	Days to first male flower	SG	10 × 4 L × T	Significant	Significant	+	+	Singh <i>et al.</i> (2018b)
		SG	6 × 6 HD	Significant	Significant	+	+	Chauhan <i>et al.</i> (2020)
		SG	8 × 8 HD	Significant	-	+	-	Kumar and Pandit (2020)
		RG	10 × 10 HD	Significant	Significant	+	+	Tyagi <i>et al.</i> (2010)
		RG	6 × 3 L × T	Significant	Significant	+	+	Reddy <i>et al.</i> (2013)
		RG	11 × 3 L × T	Significant	Significant	+	+	Chittora <i>et al.</i> (2018a)
		RG	10 × 3 L × T	Significant	Significant	-	+	Kamble <i>et al.</i> (2018)
		RG	6 × 4 L × T	Significant	Significant	+	+	Krishnamoorthy (2020b)
4.	Days to first female flower	SG	10 × 10 FD	Significant	Significant	+	+	Ram <i>et al.</i> (2007)
		SG	8 × 8 HD	-	Significant	-	+	Patel and Desai (2008)
		SG	2 × 5 L × T	Significant	Non-Significant	+	-	Islam <i>et al.</i> (2012)
		SG	8 × 8 HD	Significant	Significant	+	+	Sonavane <i>et al.</i> (2013a)
		SG	10 × 10 HD	Significant	Significant	+	+	Kumar <i>et al.</i> (2018)
		SG	9 × 9 HD	Significant	Significant	+	+	Rajneesh and Singh (2018b)
		SG	9 × 9 HD	Significant	Significant	+	+	Singh <i>et al.</i> (2018a)
		SG	10 × 4 L × T	Significant	Significant	+	+	Singh <i>et al.</i> (2018b)
		SG	8 × 8 HD	Non-Significant	Significant	-	+	Chauhan <i>et al.</i> (2019)
		SG	6 × 6 HD	Significant	Significant	+	+	Chauhan <i>et al.</i> (2020)
		SG	8 × 8 HD	Significant	-	+	-	Kumar and Pandit (2020)
		RG	10 × 10 HD	Significant	Significant	+	+	Tyagi <i>et al.</i> (2010)
		RG	6 × 3 L × T	Significant	Significant	+	+	Reddy <i>et al.</i> (2013)

Table 3. *Contd..*

Sl. No.	Character	Crop	Material and method used	Combining ability		Gene action		References
				GCA	SCA	Additive	Non-additive	
4.	Days to first female flower	RG	20 × 3 L × T	Significant	Significant	+	+	Narasannavar <i>et al.</i> (2014b)
		RG	8 × 8 HD	Significant	Significant	+	+	Sarkar <i>et al.</i> (2015)
		RG	11 × 3 L × T	Significant	Significant	+	+	Chittora <i>et al.</i> (2018a)
		RG	8 × 4 L × T	Significant	Significant	+	+	Nandhini <i>et al.</i> (2018b)
		RG	5 × 5 HD	Significant	Significant	+	+	Chandan <i>et al.</i> (2019)
		RG	3 × 4 HD	Significant	Significant	+	+	Varalakshmi <i>et al.</i> (2019)
		RG	6 × 4 L × T	Significant	Significant	+	+	Krishnamoorthy (2020b)
5.	Node at first male flower	SG	8 × 8 HD	-	Significant	-	+	Patel and Desai (2008)
		SG	10 × 10 HD	Significant	Significant	+	+	Kumar <i>et al.</i> (2018)
		SG	9 × 9 HD	Significant	Significant	+	+	Rajneesh and Singh (2018b)
		SG	9 × 9 HD	Significant	Significant	+	+	Singh <i>et al.</i> (2018a)
		SG	10 × 4 L × T	Significant	Significant	+	+	Singh <i>et al.</i> (2018b)
		SG	6 × 6 HD	Significant	Significant	+	+	Chauhan <i>et al.</i> (2020)
		SG	8 × 8 HD	Significant	-	+	-	Kumar and Pandit (2020)
		RG	8 × 8	Significant	Significant	+	+	Lodam <i>et al.</i> (2009)
		RG	6 × 4 L × T	Significant	Significant	+	-	Krishnamoorthy (2020b)
6.	Node at first female flower	SG	8 × 8 HD	-	Significant	-	+	Patel and Desai (2008)
		SG	10 × 10 HD	Significant	Significant	+	+	Kumar <i>et al.</i> (2018)
		SG	9 × 9 HD	Significant	Significant	+	+	Rajneesh and Singh (2018b)
		SG	9 × 9 HD	Significant	Significant	+	+	Singh <i>et al.</i> (2018a)
		SG	10 × 4 L × T	Significant	Significant	+	+	Singh <i>et al.</i> (2018b)
		SG	8 × 8 HD	Significant	Significant	+	+	Chauhan <i>et al.</i> (2019)
		SG	6 × 6 HD	Significant	Significant	+	+	Chauhan <i>et al.</i> (2020)

Table 3. *Contd..*

Sl. No.	Character	Crop	Material and method used	Combining ability		Gene action		References
				GCA	SCA	Additive	Non-additive	
6.	Node at first female flower	RG	6 × 3 L × T	Significant	Significant	+	+	Prabhakar (2008)
		RG	8 × 8 HD	Significant	Significant	+	+	Lodam <i>et al.</i> (2009)
		RG	6 × 3 L × T	Significant	Significant	+	+	Reddy <i>et al.</i> (2013)
		RG	20 × 3 L × T	-	Significant	-	+	Narasannavar <i>et al.</i> (2014b)
		RG	8 × 8 HD	Significant	Significant	+	+	Sarkar <i>et al.</i> (2015)
		RG	11 × 3 L × T	Significant	Significant	+	+	Chittora <i>et al.</i> (2018a)
		RG	8 × 4 L × T	Significant	Significant	+	+	Nandhini <i>et al.</i> (2018b)
		RG	5 × 5 HD	Significant	Significant	+	+	Chandan <i>et al.</i> (2019)
		RG	3 × 4 HD	Significant	Non-Significant	+	-	Varalakshmi <i>et al.</i> (2019)
		RG	6 × 4 L × T	Significant	Significant	+	-	Krishnamoorthy (2020b)
7.	Days to first harvest	SG	8 × 8 HD	-	Significant	-	+	Patel and Desai (2008)
		SG	9 × 9 HD	Significant	Significant	+	+	Naliyadhara <i>et al.</i> (2010)
		SG	2 × 5 L × T	Significant	Non-Significant	+	-	Islam <i>et al.</i> (2012)
		SG	8 × 8 HD	Significant	Significant	+	+	Sonavane <i>et al.</i> (2013a)
		SG	10 × 10 HD	Significant	Significant	+	+	Kumar <i>et al.</i> (2018)
		SG	9 × 9 HD	Significant	Significant	+	+	Rajneesh and Singh (2018b)
		SG	9 × 9 HD	Significant	Significant	+	+	Singh <i>et al.</i> (2018a)
		SG	10 × 4 L × T	Significant	Significant	+	+	Singh <i>et al.</i> (2018b)
		SG	8 × 8 HD	Significant	Significant	+	+	Chauhan <i>et al.</i> (2019)
		RG	8 × 8 HD	Significant	Significant	+	+	Purohit <i>et al.</i> (2007)
		RG	10 × 10 HD	Significant	Significant	+	+	Tyagi <i>et al.</i> (2010)
		RG	20 × 3 L × T	Significant	Significant	+	+	Narasannavar <i>et al.</i> (2014b)
		RG	8 × 8 HD	Significant	Significant	+	+	Sarkar <i>et al.</i> (2015)
		RG	11 × 3 L × T	Significant	Significant	+	+	Chittora <i>et al.</i> (2018a)
		RG	10 × 3 L × T	Significant	Significant	-	+	Kamble <i>et al.</i> (2018)

Table 3. *Contd..*

Sl. No.	Character	Crop	Material and method used	Combining ability		Gene action		References
				GCA	SCA	Additive	Non-additive	
7.	Days to first harvest	RG	8 × 4 L × T	Significant	Significant	+	+	Nandhini <i>et al.</i> (2018b)
		RG	5 × 5 HD	Significant	Significant	+	+	Chandan <i>et al.</i> (2019)
		RG	6 × 4 L × T	Significant	Significant	+	+	Krishnamoorthy (2020b)
		RG	8 × 8 HD	Non-Significant	Significant	-	+	Malve <i>et al.</i> (2020)
8.	Days to last harvest	SG	9 × 9 HD	Significant	Significant	+	+	Naliyadhara <i>et al.</i> (2010)
		RG	8 × 8 HD	Significant	Significant	+	+	Purohit <i>et al.</i> (2007)
9.	Fruit length (cm)	SG	8 × 8 HD	-	Significant	-	+	Patel and Desai (2008)
		SG	9 × 9 HD	Significant	Significant	+	+	Naliyadhara <i>et al.</i> (2010)
		SG	8 × 8 HD	Significant	Significant	+	+	Sonavane <i>et al.</i> (2013a)
		SG	10 × 10 HD	Significant	Significant	+	+	Kumar <i>et al.</i> (2018)
		SG	9 × 9 HD	Significant	Significant	+	+	Rajneesh and Singh (2018b)
		SG	9 × 9 HD	Significant	Significant	+	+	Singh <i>et al.</i> (2018a)
		SG	10 × 4 L × T	Significant	Significant	+	+	Singh <i>et al.</i> (2018b)
		SG	8 × 8 HD	Significant	Significant	+	+	Chauhan <i>et al.</i> (2019)
		SG	6 × 6 HD	Significant	Significant	+	+	Chauhan <i>et al.</i> (2020)
		SG	8 × 8 HD	Significant	-	+	-	Kumar and Pandit (2020)
		RG	8 × 8 HD	Significant	Significant	+	+	Purohit <i>et al.</i> (2007)
		RG	8 × 8 HD	Significant	Significant	+	+	Lodam <i>et al.</i> (2009)
		RG	10 × 10 HD	Significant	Significant	+	+	Tyagi <i>et al.</i> (2010)
		RG	20 × 3 L × T	Significant	Significant	+	+	Narasannavar <i>et al.</i> (2014b)
		RG	8 × 8 HD	Significant	Significant	+	+	Muthaiah <i>et al.</i> (2017b)
		RG	11 × 3 L × T	Significant	Significant	+	+	Chittora <i>et al.</i> (2018a)
		RG	10 × 3 L × T	Significant	Significant	+	+	Kamble <i>et al.</i> (2018b)
		RG	8 × 4 L × T	Significant	Significant	+	+	Nandhini <i>et al.</i> (2018b)

Table 3. *Contd..*

Sl. No.	Character	Crop	Material and method used	Combining ability		Gene action		References
				GCA	SCA	Additive	Non-additive	
9.	Fruit length (cm)	RG	7 × 5 L × T	Significant	Significant	+	+	Narasannavar <i>et al.</i> (2018)
		RG	5 × 5 HD	Significant	Significant	+	+	Chandan <i>et al.</i> (2019)
		RG	8 × 8 HD	Significant	Significant	+	+	Sharma and Soni (2019)
		RG	3 × 4 HD	Significant	Significant	+	+	Varalakshmi <i>et al.</i> (2019)
		RG	6 × 4 L × T	Significant	Significant	+	+	Krishnamoorthy (2020b)
		RG	8 × 8 HD	Significant	Significant	+	+	Malve <i>et al.</i> (2020)
		RG	10 HD 45	Significant	Significant	+	+	Srikanth <i>et al.</i> (2020b)
10.	Fruit diameter (cm)	SG	8 × 8 HD	-	Significant	-	+	Patel and Desai (2008)
		SG	9 × 9 HD	Significant	Significant	+	+	Naliyadhara <i>et al.</i> (2010)
		SG	10 × 10 HD	Significant	Significant	+	+	Kumar <i>et al.</i> (2018)
		SG	9 × 9 HD	Significant	Significant	+	+	Rajneesh and Singh (2018b)
		SG	9 × 9 HD	Significant	Significant	+	+	Singh <i>et al.</i> (2018a)
		SG	10 × 4 L × T	Significant	Significant	+	+	Singh <i>et al.</i> (2018b)
		SG	8 HD 28	Significant	Significant	+	+	Chauhan <i>et al.</i> (2019)
		SG	8 × 8 HD	Significant	-	+	-	Kumar and Pandit (2020)
		RG	8 × 8 HD	Non-Significant	Significant	-	+	Purohit <i>et al.</i> (2007)
		RG	8 × 8 HD	Significant	Significant	+	+	Lodam <i>et al.</i> (2009)
		RG	10 × 10 HD	Significant	Significant	+	+	Tyagi <i>et al.</i> (2010)
		RG	20 × 3 L × T	Significant	Significant	+	+	Narasannavar <i>et al.</i> (2014b)
		RG	7 × 5 L × T	Non-Significant	Significant	-	+	Narasannavar <i>et al.</i> (2018)
		RG	11 × 3 L × T	Significant	Significant	+	+	Chittora <i>et al.</i> (2018a)
		RG	8 × 4 L × T	Significant	Significant	+	+	Nandhini <i>et al.</i> (2018b)
		RG	5 × 5 HD	Significant	Significant	+	+	Chandan <i>et al.</i> (2019)
		RG	8 × 8 HD	Significant	Significant	+	+	Sharma and Soni (2019)

Table 3. *Contd..*

Sl. No.	Character	Crop	Material and method used	Combining ability		Gene action		References
				GCA	SCA	Additive	Non-additive	
10.	Fruit diameter (cm)	RG	3 × 4 HD	Non-Significant	Non-Significant	-	-	Varalakshmi <i>et al.</i> (2019)
		RG	6 × 4 L × T	Significant	Significant	+	+	Krishnamoorthy (2020b)
		RG	8 × 8 HD	Significant	Significant	+	+	Malve <i>et al.</i> (2020)
		RG	10 × 10 HD	Significant	Significant	+	+	Srikanth <i>et al.</i> (2020b)
11.	Average fruit weight (g)	SG	10×10 HD	Significant	Significant	+	+	Ram <i>et al.</i> (2007)
		SG	8 × 8 HD	-	Significant	-	+	Patel and Desai (2008)
		SG	9 × 9 HD	Significant	Significant	+	+	Naliyadhara <i>et al.</i> (2010)
		SG	8 × 8 HD	Non-Significant	Significant	+	+	Sonavane <i>et al.</i> (2013a)
		SG	10 × 10 HD	Significant	Significant	+	+	Kumar <i>et al.</i> (2018)
		SG	9 × 9 HD	Significant	Significant	+	+	Rajneesh and Singh (2018b)
		SG	9 × 9 HD	Significant	Significant	+	+	Reddy <i>et al.</i> (2018)
		SG	9 × 9 HD	Significant	Significant	+	+	Singh <i>et al.</i> (2018a)
		SG	10 × 4 L × T	Significant	Significant	+	+	Singh <i>et al.</i> (2018b)
		SG	8 × 8 HD	Significant	Significant	+	+	Chauhan <i>et al.</i> (2019)
		SG	6 × 6 HD	Significant	Significant	+	+	Chauhan <i>et al.</i> (2020)
		SG	8 × 8 HD	Significant	-	+	-	Kumar and Pandit (2020)
		RG	8×8 FD	Significant	Significant	+	+	Purohit <i>et al.</i> (2007)
		RG	6×3 L×T	Significant	Significant	+	+	Prabhakar (2008)
		RG	18 L × T	Significant	Significant	+	+	Reddy <i>et al.</i> (2013)

Table 3. *Contd..*

Sl. No.	Character	Crop	Material and method used	Combining ability		Gene action		References
				GCA	SCA	Additive	Non-additive	
11.	Average fruit weight (g)	RG	20 × 3 L × T	Significant	Significant	+	+	Narasannavar <i>et al.</i> (2014b)
		RG	11 × 3 L × T	Significant	Significant	+	+	Chittora <i>et al.</i> (2018a)
		RG	10 × 3 L × T	Significant	Significant	+	+	Kamble <i>et al.</i> (2018)
		RG	8 × 4 L × T	Significant	Significant	+	+	Nandhini <i>et al.</i> (2018b)
		RG	7 × 5 L × T	Non-Significant	Non-Significant	-	-	Narasannavar <i>et al.</i> (2018)
		RG	5 × 5 HD	Significant	Significant	+	+	Chandan <i>et al.</i> (2019)
		RG	8 × 8 HD	Significant	Significant	+	+	Sharma and Soni (2019)
		RG	3 × 4 HD	Significant	Significant	+	+	Varalakshmi <i>et al.</i> (2019)
		RG	6 × 4 L × T	Significant	Significant	+	+	Krishnamoorthy (2020b)
		RG	8 × 8 HD	Significant	Significant	+	+	Malve <i>et al.</i> (2020)
		RG	10 × 10 HD	Significant	Significant	+	+	Srikanth <i>et al.</i> (2020b)
12.	Number of fruits per vine	SG	8 × 8 HD	-	Significant	-	+	Patel and Desai (2008)
		SG	9 × 9 HD	Significant	Significant	+	+	Naliyadhara <i>et al.</i> (2010)
		SG	8 × 8 HD	Significant	Significant	+	+	Sonavane <i>et al.</i> (2013a)
		SG	10 × 10 HD	Significant	Significant	+	+	Kumar <i>et al.</i> (2018)
		SG	9 × 9 HD	Significant	Significant	+	+	Rajneesh and Singh (2018b)
		SG	9 × 9 36 HD	Significant	Significant	+	+	Singh <i>et al.</i> (2018a)
		SG	10 × 4 L × T	Significant	Significant	+	+	Singh <i>et al.</i> (2018b)
		SG	8 HD	Significant	Significant	+	+	Chauhan <i>et al.</i> (2019)
		SG	6 × 6 HD	Significant	Significant	+	+	Chauhan <i>et al.</i> (2020)
		SG	8 × 8 HD	Significant	-	+	-	Kumar and Pandit (2020)

Table 3. *Contd..*

Sl. No.	Character	Crop	Material and method used	Combining ability		Gene action		References
				GCA	SCA	Additive	Non-additive	
12.	Number of fruits per vine	RG	8 × 8 FD	Significant	Significant	+	+	Purohit <i>et al.</i> (2007)
		RG	6×3 L×T	Significant	Significant	+	+	Prabhakar (2008)
		RG	10 × 10	Significant	Significant	+	+	Tyagi <i>et al.</i> (2010)
		RG	18 L × T	Significant	Significant	+	+	Reddy <i>et al.</i> (2013)
		RG	20 × 3 L × T	Significant	-	+	-	Narasannavar <i>et al.</i> (2014b)
		RG	7 × 5 L × T	Significant	Significant	+	+	Narasannavar <i>et al.</i> (2018)
		RG	11 × 3 L × T	Significant	Significant	+	+	Chittora <i>et al.</i> (2018a)
		RG	10 × 3 L × T	Significant	Significant	+	+	Kamble <i>et al.</i> (2018b)
		RG	8 × 4 L × T	Significant	Significant	+	+	Nandhini <i>et al.</i> (2018b)
		RG	5 × 5 HD	Significant	Significant	+	+	Chandan <i>et al.</i> (2019)
		RG	8 × 8 HD	Significant	Significant	+	+	Sharma and Soni (2019)
		RG	3 × 4 HD	Significant	Significant	+	+	Varalakshmi <i>et al.</i> (2019)
		RG	6 × 4 L × T	Significant	Significant	+	+	Krishnamoorthy (2020b)
		RG	8 × 8 HD	Significant	Significant	+	+	Malve <i>et al.</i> (2020)
		RG	10×10 HD	Significant	Significant	+	+	Srikanth <i>et al.</i> (2020b)
13.	Fruit yield per vine (kg)	SG	10×10 FD	Significant	Significant	+	+	Ram <i>et al.</i> (2007)
		SG	8 × 8 HD	-	Significant	-	+	Patel and Desai (2008)
		SG	9 × 9 HD	Significant	Significant	+	+	Naliyadhara <i>et al.</i> (2010)
		SG	2 × 5 L × T	Significant	Significant	+	+	Islam <i>et al.</i> (2012)
		SG	8 × 8 HD	-	Significant	-	+	Sonavane <i>et al.</i> (2013a)
		SG	10 × 10 HD	Significant	Significant	+	+	Kumar <i>et al.</i> (2018)
		SG	9 × 9 HD	Significant	Significant	+	+	Rajneesh and Singh (2018b)
		SG	9 × 9 HD	Significant	Significant	+	+	Reddy <i>et al.</i> (2018)
		SG	9 × 9 HD	Significant	Significant	+	+	Singh <i>et al.</i> (2018a)
		SG	10 × 4 L × T	Significant	Significant	+	+	Singh <i>et al.</i> (2018b)
		SG	8 × 8 HD	Significant	Significant	+	+	Chauhan <i>et al.</i> (2019)

Table 3. *Contd..*

Sl. No.	Character	Crop	Material and method used	Combining ability		Gene action		References
				GCA	SCA	Additive	Non-additive	
13.	Fruit yield per vine (kg)	SG	6 × 6 HD	Significant	Significant	+	+	Chauhan <i>et al.</i> (2020)
		SG	8 × 8 HD	Significant	-	+	-	Kumar and Pandit (2020)
		RG	8 × 8 FD	Significant	Significant	+	+	Purohit <i>et al.</i> (2007)
		RG	6×3 L×T	Significant	Significant	+	+	Prabhakar (2008)
		RG	8 × 8 D	Significant	Significant	+	+	Lodam <i>et al.</i> (2009)
		RG	10 × 10 HD	Significant	Significant	+	+	Tyagi <i>et al.</i> (2010)
		RG	6 × 3 L × T	Significant	Significant	+	+	Reddy <i>et al.</i> (2013)
		RG	20 × 3 L × T	Significant	Significant	+	+	Narasannavar <i>et al.</i> (2014b)
		RG	8 × 8 HD	Significant	Significant	+	+	Muthaiah <i>et al.</i> (2017b)
		RG	11 × 3 L × T	Significant	Significant	+	+	Chittora <i>et al.</i> (2018a)
		RG	8 × 4 L × T	Significant	Significant	+	+	Nandhini <i>et al.</i> (2018b)
		RG	7 × 5 L × T	Significant	Significant	+	+	Narasannavar <i>et al.</i> (2018)
		RG	5× 5 HD	Significant	Significant	+	+	Chandan <i>et al.</i> (2019)
		RG	8 × 8 HD	Significant	Significant	+	+	Sharma and Soni (2019)
		RG	6 × 4 L × T	Significant	Significant	+	+	Krishnamoorthy (2020b)
		RG	8 × 8 HD	Significant	Significant	+	+	Malve <i>et al.</i> (2020)
		RG	10 × 10 HD	Significant	Significant	+	+	Srikanth <i>et al.</i> (2020b)
14.	Fruit yield per plot (kg)	RG	20 × 3 L × T	Significant	Significant	+	+	Narasannavar <i>et al.</i> (2014b)
		RG	8 × 8 HD	Significant	Significant	+	+	Muthaiah <i>et al.</i> (2017b)
		RG	8 × 8 HD	Significant	Significant	+	+	Malve <i>et al.</i> (2020)

Table 3. *Contd..*

Sl. No.	Character	Crop	Material and method used	Combining ability		Gene action		References
				GCA	SCA	Additive	Non-additive	
15.	Fruit yield per hectare (t/ha)	RG	20 × 3 L × T	Significant	Significant	+	+	Narasannavar <i>et al.</i> (2014b)
		RG	8 × 8 HD	Significant	Significant	+	+	Muthaiah <i>et al.</i> (2017b)
		RG	8 × 4 L × T	Significant	Significant	+	+	Nandhini <i>et al.</i> (2018b)
		RG	5 × 5 HD	Significant	Significant	+	+	Chandan <i>et al.</i> (2019)
		RG	3 × 4 HD	Significant	Significant	+	+	Varalakshmi <i>et al.</i> (2019)
		RG	6 × 4 L × T	Significant	Significant	+	+	Krishnamoorthy (2020b)
		RG	8 × 8 HD	Significant	Significant	+	+	Malve <i>et al.</i> (2020)
16.	Number of seeds per fruit	SG	8 × 8 HD	Significant	-	+	-	Kumar and Pandit (2020)
		RG	10 × 10 HD	Significant	Significant	+	+	Tyagi <i>et al.</i> (2010)
		RG	11 × 3 L × T	Significant	Significant	+	+	Chittora <i>et al.</i> (2018a)
		RG	10 × 10 HD	Significant	Significant	+	+	Srikanth <i>et al.</i> (2020b)
17.	TSS (⁰ Brix)	SG	9 × 9 HD	Significant	Significant	+	+	Reddy <i>et al.</i> (2018)
		RG	11 × 3 L × T	Significant	Significant	+	+	Chittora <i>et al.</i> (2018a)
		RG	6 × 4 L × T	Significant	Significant	+	+	Krishnamoorthy (2020b)
		RG	10 × 10 HD	Significant	Significant	+	+	Srikanth <i>et al.</i> (2020b)
18.	Ascorbic acid (mg/100 g)	RG	11 × 3 L × T	Significant	Significant	+	+	Chittora <i>et al.</i> (2018a)
		RG	5 × 5 HD	Significant	Significant	+	+	Chandan <i>et al.</i> (2019)
		RG	10 × 10 HD	Significant	Significant	+	+	Srikanth <i>et al.</i> (2020b)
19.	Crude fiber (%)	RG	8 × 4 L × T	Significant	Significant	+	+	Nandhini <i>et al.</i> (2018b)
		RG	5 × 5 HD	Significant	Significant	+	+	Chandan <i>et al.</i> (2019)
		RG	6 × 4 L × T	Significant	Significant	+	+	Krishnamoorthy (2020b)
		RG	10 × 10 HD	Significant	Significant	+	+	Srikanth <i>et al.</i> (2020b)

GCA-General combining ability, SCA-specific combining ability, HD – Half diallel, FD – Full diallel, L×T – Line × tester

3. MATERIAL AND METHODS

The investigation on “Molecular diversity assessment and manifestation of heterosis for growth and yield in sponge gourd (*Luffa cylindrica* (L.) Roem.)” was carried out during the period from 2020 to 2022 at College of Horticulture, Bagalkot. The details of genotypes used, hybridization programme, experimental design, data collected on different quantitative and qualitative traits and statistical procedures adopted in the investigation are briefly presented in this chapter.

3.1 Experimental site

The experiment was conducted at the experimental block of Department of Vegetable Science, College of Horticulture, Bagalkot, Karnataka.

3.2 Location and Climate

Bagalkot comes under the zone-3 of region-2 among the Agro-climatic zones of Karnataka. It is situated in Northern Dry Zone of Karnataka with an altitude of 533 meters above the mean sea level and at a latitude and longitude of 16° 46' North and 74° 59' East, respectively. This zone has benefits of both South-West and North- East monsoons. The average rainfall of this area is 563 mm distributed over a period of six to eight months (March to October) with peak during August month. The meteorological data was taken from the Main Horticultural Research and Extension Centre (MHREC), Bagalkot which is adjacent to fields of COH, Bagalkot and is presented in Appendix-I.

3.3 Experimental details

3.3.1 Design

The experiment was laid out in a Randomized Complete Block Design (RCBD) with two replications. Each genotype consists of 10 plants per treatment and per replication.

3.3.2 Experimental material

The study was carried out with 40 diverse genotypes collected from different sources and are listed in Table 4.

Table 4. List of sponge gourd genotypes used in the experiment and their source of collection

Sl. No.	Field code	Varieties/ lines	Source of collection
1	G1	Bagalkot Local-1	Local Collection (Simikeri village)
2	G2	Bagalkot Local-2	Local Collection
3	G3	Bagalkot Local-3	Local Collection
4	G4	Basavana Bagewadi Local	Local Collection
5	G5	Chikni Turai	Private (New Rama Seed Corporation)
6	G6	COH Mandsaur-1	COH, Mandsaur (MP)
7	G7	COH Mandsaur-2	COH, Mandsaur (MP)
8	G8	Dharwad Local	Dharwad
9	G9	HUB-3	HRES, Hidkal
10	G10	Jaipur Long	Private (New Rama Seed Corporation)
11	G11	Jaunpari	Private (Shankar Seed Company)
12	G12	Kalyanpur Hari Chikani	CAUAT, Kanpur
13	G13	Komal	Private (Nath Seeds)
14	G14	KRCCH-1	KRCCH, Arabhavi
15	G15	KRCCH-3	KRCCH, Arabhavi
16	G16	KSG-2	CAUAT, Kanpur
17	G17	KSG-3	CAUAT, Kanpur
18	G18	KSG-12	CAUAT, Kanpur
19	G19	KSG-14	CAUAT, Kanpur
20	G20	KSG-32	CAUAT, Kanpur
21	G21	KSG-36	CAUAT, Kanpur
22	G22	KSG-44	CAUAT, Kanpur
23	G23	KSG-47	CAUAT, Kanpur
24	G24	KSG-63	CAUAT, Kanpur
25	G25	Lata	Private (Doctor Seeds Private Ltd)
26	G26	Mysore Local	Private (Sahaja Seeds)
27	G27	Pusa Chikni	IARI, New Delhi
28	G28	Pusa Sneha	IARI, New Delhi
29	G29	Sadhva	Private (S. R. Seeds)
30	G30	Samreen	Private (S. R. Seeds)
31	G31	SG-1	HRES, Hidkal
32	G32	SG-2	HRES, Hidkal
33	G33	SG-3	HRES, Hidkal
34	G34	SG-4	HRES, Hidkal
35	G35	SG-5	HRES, Hidkal
36	G36	SG-6	HRES, Hidkal
37	G37	Kashi Divya	IIVR, Varanasi
38	G38	Kashi Shreya	IIVR, Varanasi
39	G39	Konkan Ghosali	DBSKKV, Dapoli
40	G40	Yadgiri Local	Yadgiri

3.4 Experiment-I: Morphological characterization of sponge gourd genotypes

Forty sponge gourd genotypes were collected from different sources (Table 4) and are evaluated to know the performance in the *rabi* season of 2020-21.

Design	RCBD
Genotypes	40
Replications	02
Spacing	2 × 1 m
Plot size	10 m × 2 m=20 m ²

3.4.1 Preparation of experimental plot and planting

The experimental plot was thoroughly ploughed and brought into fine tilth. The raised beds were prepared at a distance of 2 meter apart. The recommended dose (20 t/ha) of FYM, half dose of N and full dose of P and K (50: 50: 50 kg NPK/ha) as per the package of practices of University of Horticultural Sciences, Bagalkot (Anon., 2016) were incorporated into the soil as a basal dose during the land preparation. At the centre of each bed, two inline lateral pipes were placed at 30 cm apart. The raised beds were covered with 30-micron thickness black polythene mulch with 1-2 m width by securing the both edges of sheet buried in the soil. After mulching at the centre of the bed, a 5 cm size hole was made on the mulch film at a distance of one meter spacing for planting. Then the beds were irrigated to a field capacity level a day before sowing. Further, 15 days old healthy, uniform, pest and disease free seedlings (which were raised in portrays) were transplanted in the field during the month of December 2020. The light irrigation was provided immediately after transplanting. Staking was provided before flowering as a support to the plants. Later, remaining half dose of nitrogen was top dressed in two split doses at 30 and 60 days after sowing, respectively. Irrigation and the other cultural practices were followed as per the POP of UHS, Bagalkot (Anon., 2016). The general view of the experimental plot is shown in Plate 1.

3.5 Experiment-II: Molecular characterization of sponge gourd genotypes

3.5.1 DNA extraction

Young leaves of two month old seedlings were collected from all the 40 cultivars for the isolation of plant genomic DNA, using cetyltrimethyl ammonium bromide (CTAB) method as explained by Briard *et al.* (2000).

The detailed procedure followed was as follows

1. The young leaves of sponge gourd were collected and ground into a fine powder of quantity 100 mg using a mortar and pestle which was later transferred into a two ml micro centrifuge tube and kept the sample in ice for immediate use or frozen at -20°C for further use.
2. To this 700 μl of freshly prepared 2 % CTAB buffer was added and vortexed for 15 seconds then incubated at 60°C for 30-45 minutes.
3. After cooling the tubes, equal volume (700 μl) of Phenol: Chloroform: Isoamyl Alcohol (25:24:1) were added and mixed by inverting them for 8-10 times then centrifuged (15000 rpm) for 15 minutes at room temperature (27°C).
4. Supernatant was transferred to a fresh 1.5 ml micro centrifuge tubes separately with proper labeling then added with equal volume of approximately 500 μl of chilled isopropanol for precipitation of DNA, mixed properly by inversion and incubated at -20°C for overnight. After incubation, it was centrifuged for 15 min at 15000 rpm at 4°C .
5. Then carefully decanted the supernatant and wash the pellet with 500 μl of 70 % ethanol then incubated and centrifuged at 15000 rpm for 15 min at 4°C .
6. Further, carefully removed all the traces of ethanol from the pellet and then air dried the pellet till the smell of ethanol goes off (3-4 hrs or overnight).
7. After complete drying of pellet, dissolve it in 200 μl of Tris-EDTA buffer (TE) and stored at -20°C as a stock.



Plate 1. General view of the experimental plot of experiment I

3.5.2 Qualitative and Quantitative determination of DNA

The stock of DNA was tested for its quality and quantity in nano-spectrophotometer (Eppendorf India Ltd.). DNA Absorbance was recorded at 260 nm and 280 nm. A ratio of in and around 1.8 represented pure DNA. Qualitative analysis of DNA was done by running the extracted DNA samples on 1 % agarose gel using 0.5X TAE buffer (10 mM Tris- HCl and 1mM EDTA, pH 8.0). The gel was stained with ethidium bromide and visualized under UV fluorescence in Gel Documentation system.

3.5.3 PCR Amplification, Electrophoresis and Marker scoring

1. The 30 microsatellite primers were diluted into 10 Picomoles from the stock primers of both forward and reverse. The detailed information about the list of molecular markers utilized in the study is presented in the Table 5.
2. PCR was done for 10 µl reaction by using the components with respective concentration and the protocol is presented in the Table 6a and 6b.
3. PCR amplified products were size separated in 4.0 % agarose gel electrophoresis for SSR markers which showed co-dominant banding pattern. The co-dominant markers were screened based on the allele size using the standard marker ladder of 100 bp (Takara Life Sciences).

3.5.4 Statistical analysis of SSR profiles

Amplified DNA fragments were scored as 1 for presence of bands and 0 for absence of bands. Cluster analysis was performed by means of Darwin's procedure of NTSYSpc via unweighted pair-group method using arithmetic average (UPGMA) to develop dendrograms. Primer banding characteristics such as number of scored bands (NSB), number of polymorphic bands (NPB) and percentage of polymorphic bands (PPB) and Polymorphism information content (PIC) of bands were calculated according to Anderson *et al.* (1993) as follow.

$$PIC_i = \sum f_{ij}^2$$

Where, f_{ij} is the frequency of the j^{th} pattern of the i^{th} band (Powell *et al.*, 1996).

Table 5. Details of SSR primers used for molecular characterization of sponge gourd genotypes

Sl. No.	Primer code	Forward sequence (5'-3')	Reverse sequence (3'-5')
1	SG_La_1	GAAC TTATCTACACGGCGATCC	AGGTCAAAGGTTCAAATCTCAACC
2	SG_La_2	CGCGAATCTGGAAATTTTGCC	TTCGGGACATGAAAAAGGGC
3	SG_La_3	CCATGGCTTTTCATCATTGAAACC	GGACCCCATTTGATAATCATTTGG
4	SG_La_4	TGGAGAACC AAAAGTGAGAATAGG	AGTACAAGCTTCAATTCCCCC
5	SG_La_5	ATCTCTGACCTCTTAGTCGACG	GTGAACTTCACA ACTAGTGCTAGC
6	SG_La_6	AATTGTACTACTCGACCAGGAGG	ACGTGGCTCTTTTGCTTTGG
7	SG_La_7	TGGCTTCCAACATGATGATTTCC	ACTCCTACATGTAATTGCCCTACC
8	SG_La_8	ACGACAGGAAGTAACCATAGC	AGAACTTGCAAGATTTCGATGC
9	SG_La_9	TCAGAATAGTCAACCCTCTCCC	CTCTGACTAACAACACTTTTTCACC
10	SG_La_10	CTGGGTTTTGATGAGTGGTTCC	AGGGAAGGGGAGAGAATATTTAGC
11	SG_La_11	ATTGGCATGCACTCTTGACC	AGTTCGGCCTTTCTTTGTGG
12	SG_La_12	ACAGAAGAAGAAGAAGTGGG	AAATTTTCGGGTTGGGTCGG
13	SG_La_13	TGTCATGAGTTCGAATCTCCC	TTCAATTCTCCTCCACACG
14	SG_La_14	TTCAATTCTCCTCCACACG	TGTCATGAGTTCGAATCTCCC
15	SG_La_15	GTTCCATGGTATCTTCGTTGGG	TGGTTAAGTTGTTTTTCCCCTCC
16	SG_La_16	ACACAAACTCTTTGACATGCCC	GGCATTTAAGATTATACGCTGTGC
17	SG_La_17	AAAGTAGGGTTTTGGTGCGC	TGGGTAAGATTTGGAGTCTGAGG
18	SG_La_18	GATGATAACATCGGAGTGACCC	AGGATAAGTCACGTGCAAAGC
19	SG_La_19	CAATACCCAAAGGCTTCATCGG	TGACCAAAAGAAATGTCTGTGTGG
20	SG_La_20	ATTTTCCCTTG TCCCGATCG	ATTTTGCAAGGTCCCACTCG
21	SG_La_21	ATAGCGTCAGAGTCACACATCC	CTTAAAGCAAAGGCACACATCC
22	SG_La_22	TCTTCTTGCTGTGCACTTTCG	TTCAGTACCTGCAACAACCG
23	SG_La_23	ACTTTGTTAACCAAAAAGTTGATGG	ACATAGACATGACATTTTCGGC
24	SG_La_24	GGTCTGCCTATCTAATATGGTTGG	TTTCTTCACCCTCCACCTAAGC
25	SG_La_25	AAATACACTCCGTTGGCTGC	TCCAAAGGAAGTTGTTGTTCAAC
26	SG_La_26	ACTCAACTGGCATAA CACTCG	AGTAGGTGTAACAATTCGATTCCC
27	SG_La_27	TCAAGGGAATGTGGTAAATGGC	TCGTACAAAATCACGGTAGCC
28	SG_La_28	TCCCTTCCTTTAGTCAA ACTCCC	TGCCTGTCACAAAATTCAGCC
29	SG_La_29	TTTAATTTCCGACACGCGGG	AGATTTTGGA AAAAGCGGCGG
30	SG_La_30	TGGCCATTTCTGAAGATT TCCC	TCAGGGCAGTGATTTTTCACG

Table 6a. PCR reactions for microsatellite primers

Components	Concentration	PCR reaction (10 µl)
Primers (F + R)	10 pM	1
PCR master mix (Takara)	2X	3
Template	50 ng/µl	1
Deionizer water		5
Total		10 µl

Table 6b. PCR protocol followed for microsatellite primers of 40 sponge gourd genotypes

Stage	Steps	Temperature (°C)	Time	Cycles
1	Initial denaturation	95	5 min	40 cycles
2	Denaturation	94	30 sec	
3	Annealing	60*	30 sec	
4	Extention	72	45 sec	
5	Final extention	72	5 min	
6	Hold	4	∞	

*Specific annealing temperature as per the Primers

3.6 Experiment-III: Development of F₁ hybrids and their evaluation

3.6.1 Selection of parents for hybridization

The best ten lines were selected from the experiment-1 based on the *per se* performance for fruit length, number of fruits per vine, fruit yield per vine, variability and diversity analysis. Four testers which are having broad genetic base were chosen for crossing with lines (Plate 2a and 2b). The details of ten lines, four testers and one commercial check (hybrid) are given in Table 7.

Table 7. Details of lines, tester and standard checks used in this study

Sl. No.	Entry	Genotypes	Source
Lines			
1	L1	Bagalkot Local-2	Bagalkot
2	L2	HUB-3	HRES, Hidkal
3	L3	KSG-2	CAUAT, Kanpur
4	L4	KSG-36	CAUAT, Kanpur
5	L5	KSG-44	CAUAT, Kanpur
6	L6	KSG-63	CAUAT, Kanpur
7	L7	SG-1	HRES, Hidkal
8	L8	SG-3	HRES, Hidkal
9	L9	SG-4	HRES, Hidkal
10	L10	SG-6	HRES, Hidkal
Testers			
1	T1	Kashi Divya	IIVR, Varanasi
2	T2	Kashi Shreya	IIVR, Varanasi
3	T3	Konkan Ghosali	DBSKKV, Dapoli
4	T4	Pusa Sneha	IARI, New Delhi
Commercial check			
1	H1	Kashi Rakshita	IIVR, Varanasi

3.6.2 Hybridization programme

The seeds of all the lines (10) and testers (04) were sown during the month of September 2021 for attempting crosses in line $\times$ tester fashion as suggested by Kempthorne (1957) to produce 40 hybrids. To carry out hybridization work, the male and female parent's flower buds were selected on the previous day evening prior to their opening. The selected flower buds of male and female parents were then covered with



Plate 2a. Fruits of parents (lines and testers) and commercial check used in the experiment

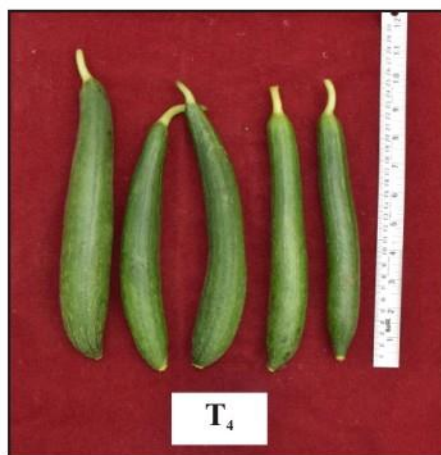
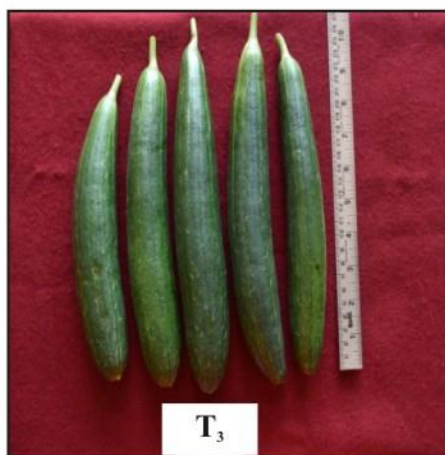
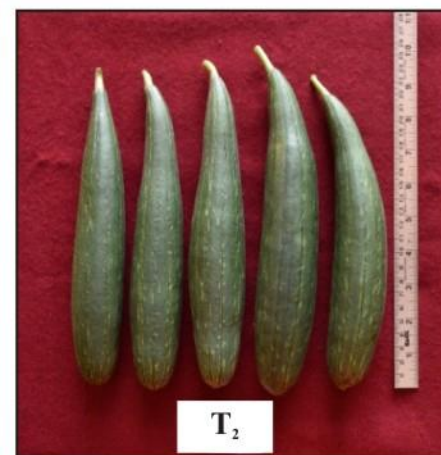


Plate 2b. Fruits of parents (lines and testers) and commercial check used in the experiment

butter paper bags to avoid contamination of pollens by other parents. Then the pollination was done on the next day morning by using pollens of respective male parent. After pollination, the pollinated female flowers were again covered with butter paper bags to avoid contamination and are tagged with the details of male parent and date of pollination. Further, at the same time the male and female parents were selfed by bagging the flower buds with butter paper bags prior to the day of flower opening then pollinated in the next day. Both crossed and selfed fruits were harvested separately at full maturity stage. After drying of fruits, seeds were hand extracted and then they were preserved in separate bags. These bags were labeled with details of cross or self with genotype name or parents and other details. The general view of the crossing block is presented in Plate 3.

3.6.3 Evaluation of F₁ hybrids

Design	RCBD
Lines	10
Testers	4
F ₁ hybrids	40
Commercial check (hybrid)	1 (Kashi Rakshita)
Total genotypes	55 (40 +10+4+1)
Replications	2
Spacing	2 × 1 m

All the 40 hybrids, 14 parents (Lines + testers) and one commercial check were evaluated in a Randomized Complete Block Design (RCBD) with two replications during summer, 2022. All the cultural practices were followed as per POP of UHS, Bagalkot. The fruits were harvested from the five tagged plants at tender marketable stage to record the observations for yield and yield attributing characters. The general view of the hybrids and parents evaluation block during summer 2022 shown in Plate 4.

3.7 Observations recorded

Five randomly chosen plants from each genotype and replication were labeled and used for recording the observations. The mean of five plants was taken for analysis. The characters studied and techniques adopted to record the observations are given below.

3.7.1 Growth parameters

3.7.1.1 Vine length (m)

The length of the vine was measured at 45 and 90 days after sowing from the ground level to the tip of the vine using meter scale and was expressed in meters. The mean values were used for analysis.

3.7.1.2 Number of branches per vine

The number of branches on main stem at the base of the vine were counted at 90 days after sowing. The mean was calculated using these values and taken for analysis.

3.7.1.3 Node at first male flower

Number of nodes from ground level to the node at which the first male flower appeared was counted and recorded.

3.7.1.4 Node at first female flower

Number of nodes from ground level to the node at which the first female flower appeared was counted and recorded.

3.7.1.5 Days to first male flower

Number of days taken from the date of sowing to the onset of first male flower opening in each genotype was counted, recorded and expressed in days.

3.7.1.6 Days to first female flower

Number of days taken from the date of sowing to the onset of first female flower opening in each genotype was counted, recorded and expressed in days.



Plate 3. General view of the crossing block



Plate 4. General view of the hybrids and parents evaluation block during summer 2022

3.7.1.7 Days to first harvest

Number of days taken from date of sowing to the date on which fruits attained edible maturity was recorded as days to first fruit harvest.

3.7.1.8 Days to last harvest

Number of days taken from the date of sowing to the date of last harvest was recorded as days to last fruit harvest.

3.7.2 Yield parameters

3.7.2.1 Fruit length (cm)

In each treatment, five fruits from tagged plants were randomly selected at edible maturity stage and then length was measured in centimeter from the base to apex of fruit using scale. The average fruit length was calculated and expressed in centimeter.

3.7.2.2 Fruit diameter (cm)

The five fruits taken for recording fruit length were also used to record diameter of fruit with the help of digital vernier callipers at the middle point of fruit and then average diameter of five fruits was worked out and expressed in centimeter.

3.7.2.3 Average fruit weight (g)

The fruits which were used to record fruit length and fruit diameter were initially weighed for recording this observation and it is expressed in grams.

3.7.2.4 Number of fruits per vine

Fruits from each selected and tagged vines were harvested and recorded as and when they attained marketable edible maturity. The total numbers of fruits produced by these vines from all the harvest were pooled and mean was calculated as number of fruits per vine.

3.7.2.5 Fruit yield per vine (kg)

Total weight of fruits harvested from five labelled plants from all the harvests were added and average yield per plant was computed and was expressed in kilogram.

3.7.2.6 Fruit yield per plot (kg)

The weight of fruits harvested from each picking was recorded from each plot and the total yield per plot was obtained by adding the yields of all the harvests from each plot and was expressed in kilogram.

3.7.2.7 Fruit yield per hectare (t/ha)

The yield per hectare was calculated by multiplying the yield per plot (kg) with the number of plots per hectare and expressed in tonnes per hectare.

3.7.2.8 Number of seeds per fruit

The number of seeds from five randomly selected matured fruits were dried, counted and then averaged to obtain number of seeds per fruit.

3.7.2.9 Sponge yield (g/fruit)

The five randomly selected dry fruits from each treatment were taken and weighted. Then outer coat was manually removed. The sponge was separated from the fruits then weight was taken again. The average sponge yield was computed by dividing with number of fruits and expressed in grams.

3.7.3 Quality parameters

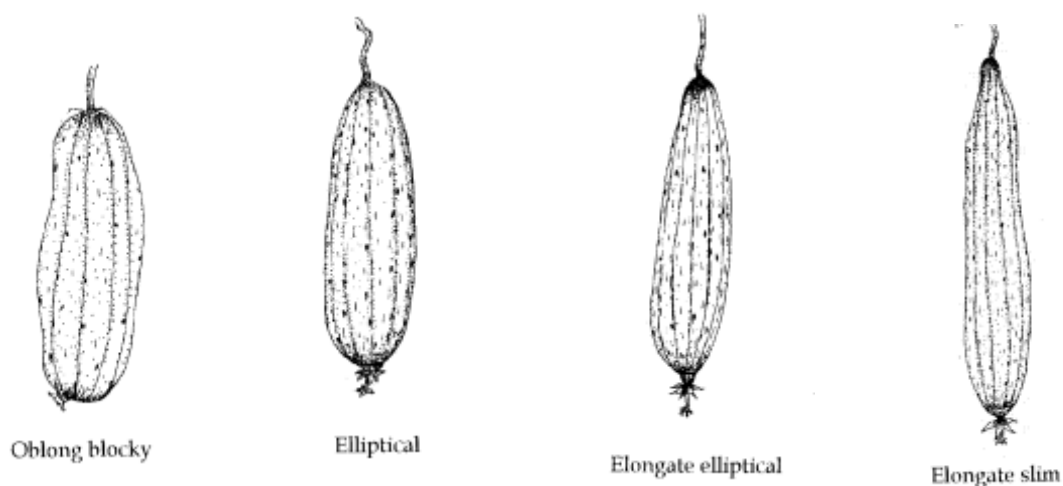
3.7.3.1 Fruit colour (L*, a*, b*)

The colour of the sample was measured using Colour Flex EZ colorimeter fitted with 45 mm diameter aperture. Calibration of the instrument was carried out using black and white tiles provided. The colour was measured and expressed as L* (lightness/darkness), a* (redness/greenness) and b* (yellowness and blueness) values. The measurements were performed on five randomly selected fruits and the mean was

recorded. The different fruit color like whitish, light green, green and dark green fruit color were observed visually and individual genotype was classified.

3.7.3.2 Fruit shape

The different fruit shapes viz., oblong, elliptical, elongate elliptical, elongate slim and elongate tapered was observed visually and individual genotype was classified according to the IPGRI descriptor, Rome, Italy.

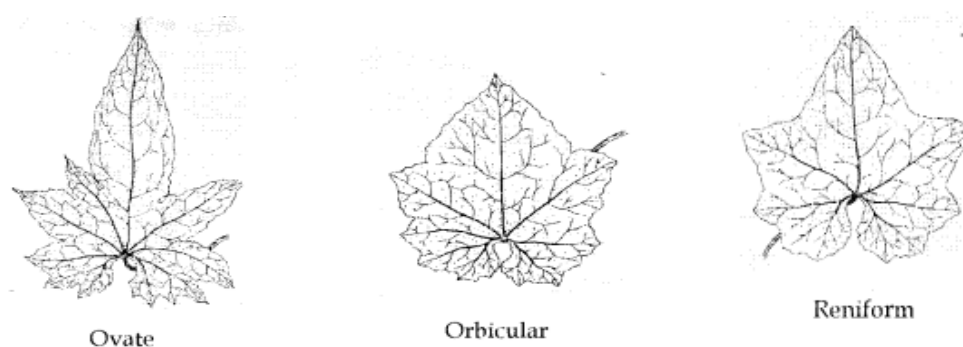


3.7.3.3 Leaf color

The different leaf color viz., green color and green with patches on its surface was observed visually and individual genotype were classified.

3.7.3.4 Leaf shape

The different leaf shapes like ovate, orbicular and reniform was observed visually and individual genotype was classified.



3.7.3.5 Leaf lobe shape

The different leaf lobe shapes like shallow, intermediate and deep leaf lobe shapes were observed.

3.7.3.6 Flower color

Two different flower colors light yellow and yellow were observed.

3.7.3.6 Flesh color

Two different flesh color like cream and white color were observed and recorded.

3.7.3.7 Fruit firmness (N)

Fruit texture analyser model FT011 (Stable Micro System) was used to measure the fruit firmness using shearing blade thickness of 1.016mm. Tender marketable edible stage fruits were randomly picked and pressure was applied with shear probe and reading was recorded as Newton force at surface area.

3.7.3.8 Total soluble solids (°Brix)

Total soluble solids of fruits was determined by using digital refractometer at room temperature by placing drop of sponge gourd fruit juice on absolutely dry digital refractometer and the reading was recorded in degree brix. The mean of five fruits readings was averaged in each replication for all the treatments.

3.7.3.9 Potassium content (%)

Potassium content in fruits was estimated by using flame photometric method. taking tissue samples and were wet digested with a diacid mixture of concentrated nitric acid and perchloric acid (10:4). Further, 10 ml of diacid mixture was added to 0.5 g of the prepared samples and pre-digested at a temperature of 100 °C for an hour and at 250 °C until the solution turned colourless. Then the total volume was reduced to 2-3 ml.

The digested material was diluted and filtered through Whatman No. 1 filter paper and volume was made up to 50 ml. The filtrate obtained was used for the estimation of potassium. Later, the potassium was determined by the Flame Photometer method (Jackson, 1973).

The concentration of K present in the test samples were calculated and expressed as per cent K according to the formula as given below:

$$\text{Potassium (\%)} = \frac{\text{Graph ppm}}{10^6} \times \frac{\text{Volume of digested sample}}{\text{Weight of sample}} \times 100$$

3.7.3.10 Phenol content (mg GAE/ 100 g)

Total phenol content of sponge gourd was estimated by using Folin Ciocalteu Reagent (FCR) method using gallic acid as a standard. Methanol extract of sample (0.1 ml) was diluted to 2 ml by adding 1.90 ml of distilled water. Then 0.5 ml of 1 N FCR reagent was added. After three minutes, 2 ml of 10 % of Na₂CO₃ was added to it and then the prepared samples were kept in a hot water bath at a temperature of 60 °C for 10 minutes and immediately placed in a ice-cold water for cooling. Finally the absorbance was recorded at 650 nm by using spectrophotometer against blank. Total phenol content was calculated using the formula mentioned below and expressed as mg of gallic acid equivalents (GAE) per 100 g of sample (Madaan *et al.*, 2011).

$$\text{Phenol content (mg GAE/100 g)} = \frac{\text{Absorbance} \times \text{Volume made up} \times \text{Dilution} \times 100}{\text{Aliquot taken} \times \text{Sample weight (g)} \times 1000}$$

3.7.3.11 Crude fiber (%)

Crude fiber estimation was done by using Fibra plus-FES-6 instrument. For estimation of fiber, one g of the sample was weighed in the crucibles and fixed to the fibraplus instrument, then 100 ml of 1.25 % H₂SO₄ was added to all the samples by closing the knobs. Later, the temperature was set to 370 °C and run the sample for 40 minutes. After 40 minutes, the temperature was reduced to 200 °C and the knobs were opened to remove all H₂SO₄ by suctioning and washed with distilled water. This distilled water was also removed by suctioning. The same procedure was repeated by adding 100 ml of 1.25 % of NaOH to all the samples. The crucibles were taken and kept in an oven at 100 °C for 3 hours. Then, these crucibles were cooled in a desiccator and weight was

taken (W_1). After weighing, the crucibles were kept in a muffle furnace at 500 °C for 1 hour, allowed to cool and reweighed (W_2). Per cent of crude fiber in sponge gourd powder was calculated by using the following formula.

$$\text{Crude fiber (\%)} = \frac{W_1 \text{ (g)} - W_2 \text{ (g)}}{\text{Weight of the sample (g)}} \times 100$$

Where,

W_1 -Weight of the crucibles after drying in an oven

W_2 -Weight of the crucibles after ashing in muffle furnace

3.7.3.12 Ash content (%)

The total ash content was estimated by burning the sponge gourd dried fruit powder in pre weighed crucible in a muffle furnace at 500 °C for six hours (Rao and Xiang, 2009). After burning, the residue ash weight was recorded. Finally, the ash content was calculated by using the following formula.

$$\text{Total ash (\%)} = \frac{\text{Weight of the ash (g)}}{\text{Weight of the sample (g)}} \times 100$$

3.7.3.13 Ascorbic acid (mg/100 gm)

Ascorbic acid content was estimated by using 2, 6,-dichlorophenol indophenol dye by volumetric method. Two grams of sample was taken then, 5-20 ml of 4 % oxalic acid was added and crushed it. Then it was filtered through muslin cloth or centrifuge to collect the supernatant and made up to a known volume of about 25 ml of oxalic acid solutions. Pipette out known 10 ml of filtrates in a conical flask and then 90 ml of oxalic acid solution was added to it to titrate against 2, 6-dichlorophenol indophenol dye till the pink end point which persisted for at least few seconds. The amount of ascorbic acid was calculated in terms of mg/100 gm of sample using the formula given below and expressed per 100 g of edible part (Tauber and Kleiner, 1934).

$$\text{Ascorbic acid (mg/100g)} = \frac{\text{Content in standard}}{\text{Aliquot taken}} \times \frac{V_2}{V_1} \times \frac{\text{Volume made}}{\text{Weight of the sample (g)}} \times 100$$

Where,

V_1 -Dye factor value

V_2 -Titration value

3.7.3.14 Protein content (%)

Estimation of protein content was carried out by micro Kjeldhal method which consists of wet digestion, distillation and titration. The protein content was determined by weighing one g sponge gourd powder and transfer to a 250 ml Kjeldhal flask and care should be taken to see that no portion of the sample clings to the neck of the flask. For this add two g of catalyst mixture (Potassium Sulphate 100 g and Copper Sulphate 20 g) and 10 ml of concentrated Sulphuric acid. Later, flasks were placed on the stand in the digestion chamber and the process of digestion was continued until the colour of the digest become clear. After digestion transfer the digested fruit sample into Kjeldahl distillation assembly and place 20 ml of 2 % Boric acid and mixed indicator solution at the receiving end. Then add 20 ml of 40 % NaOH to Kjeldahl flask. Then carry out the distillation till color changes from bluish purple to bluish green. Finally, it is titrated against 0.1 N H_2SO_4 till color changes to pink. The nitrogen content was calculated as follows.

$$\text{Nitrogen (\%)} = \frac{\text{Titrate value} \times N \text{ } H_2SO_4 \times 0.014}{\text{Weight of the sample (g)}} \times 100$$

Then protein content was obtained by converting nitrogen to protein by using conversion factor of 6.25 %.

$$\text{Protein (\%)} = 6.25 \times \text{Nitrogen (T)}$$

3.7.3.15 Total antioxidants (mg AAE/100 g)

The determination of antioxidant activity was done through FRAP reagent method, where 100 ml of acetate buffer, 10 ml of TPTZ (2, 4, 6- tris (2-pyridyl)-s-triazine) and 10 ml of $FeCl_3.H_2O$ stock was prepared from these stock. These were

mixed in the ratio of 10:1:1 to form working FRAP solution. About 1.5 ml of FRAP reagent was added to 0.5 ml of sponge gourd fruit extracts and the absorbance was taken at 593 nm wavelength with the spectrophotometer after 30 minutes of incubation. The calibration curve of ascorbic acid was set up to estimate the activity capacity of samples. The result was expressed as mg of ascorbic acid equivalents per 100 g of dried sample (Benzie and Strain, 1996).

$$\text{Total antioxidants (mg AAE / 100 g)} = \frac{A \times B \times C \times D}{1.67 \times 10^4 \times E \times F}$$

Where,

A-Absorbance

B- Final volume made up

C-Total volume of sample made with methanol

D-Dilution

E-Volume of sample taken for estimation

F-Weight of sample

3.7.3.16 Total flavonoids (mg QE/ 100 g)

Estimation of total flavonoid content in the sponge gourd extracts was determined using spectrophotometer where, 0.5 ml of aliquot was taken in a test tube to which 0.5 ml of distilled water and 0.3 ml of 5 % NaNO₂ (5 g in 100 ml DW) were added. Further, after 5 min 0.3 ml of 10 % Al₂Cl₃ was added. Then after sometime 2 ml of 1 N NaOH (4 g in 100 ml DW) was added to it and then the absorbance was measured at 510 nm. The flavonoid content was expressed as mg of quercetin equivalents (QE) per g of dried extract by using a standard graph (Maciel *et al.*, 2011).

$$\text{Total flavonoids (mg QE/ 100 g)} = \frac{\text{Absorbance} \times \text{Volume made up} \times \text{dilution} \times 100}{\text{Aliquot taken} \times \text{sample weight} \times 100}$$

3.7.4 Pest and disease incidence

3.7.4.1 Fruit fly infestation (%)

After each harvest the number of fruits infested by fruit fly were counted and all the values of all the harvest were added to get total number of infested fruits for each plot. The per cent incidence of fruit fly under natural epiphytotic condition was calculated by using following given formula

$$\text{Per cent fruit fly incidence (\%)} = \frac{\text{Number of fruits infested}}{\text{Total number of fruits}} \times 100$$

Genotypes were grouped into different categories based on per cent fruit infestation as given below (Nath, 1966).

Sl. No.	Per cent fruit infestation	Reaction categories
1	0 – 10	Resistant (R)
2	11 – 25	Moderately resistant (MR)
3	26 – 50	Moderately susceptible (MS)
4	51 – 75	Susceptible (S)
5	> 75	Highly susceptible (HS)

3.7.4.2 Leaf miner infestation (%)

The leaf mining intensity (%) of the pest under natural epiphytotic conditions was assessed by categorizing the sponge gourd plants into different groups on the basis of their per cent leaf mining intensity. The observations were taken on five tagged plants in each treatment and average was worked out.

$$\text{Per cent leaf miner incidence (\%)} = \frac{\text{Number of leaves infested}}{\text{Total number of leaves per vine}} \times 100$$

Scoring was done from 1-5 scale given by Oliveria *et al.* (2017) as described below.

Sl. No.	Symptoms	Scoring	Reaction categories
1	Plant without mines in the leaves	1	Resistant (R)
2	1-25 % of the leaves attacked	2	Moderately resistant (MR)
3	26-50 % of the leaves attacked	3	Moderately susceptible (MS)
4	51-75 % of the leaves attacked	4	Susceptible (S)
5	76-100 % of the leaves attacked	5	Highly susceptible (HS)

3.7.4.3 Powdery mildew

The per cent powdery mildew incidence was recorded in genotypes as per cent leaf area infected which were scored using zero to four disease rating scale (Girisha, 1989) as given below.

Sl. No.	Symptoms	Scoring	Reaction categories
1	No symptoms	0	Immune (I)
2	1 to 25 % foliage infected	1	Resistant (R)
3	26 to 50 % foliage infected	2	Moderately resistant (MR)
4	51 to 75 % foliage infected	3	Susceptible (S)
5	>75 % foliage infected	4	Highly susceptible (S)

PDI was calculated by using given formula.

$$\text{PDI (\%)} = \frac{\text{Summation of total numerical ratings}}{\text{Total plants observed} \times \text{Maximum grade used}} \times 100$$

3.7.4.4 Downy mildew

The per cent downy mildew incidence was recorded in genotypes as per cent leaf area infected which were scored using zero to five disease rating scale Singh *et al.* (1996) and Dhillon *et al.* (1999) as given below.

Sl. No.	Per cent leaf area affected	Scoring	Reaction categories
1	0	0	Immune (I)
2	1-10	1	Resistant (R)
3	11-25	2	Moderately resistant (MR)
4	26-50	3	Moderately susceptible (MS)
5	51-75	4	Susceptible (S)
6	76-100	5	Highly susceptible (HS)

PDI was calculated by using given formula.

$$\text{PDI (\%)} = \frac{\text{Summation of total numerical ratings}}{\text{Total plants observed} \times \text{Maximum grade used}} \times 100$$

3.8 Statistical analysis

3.8.1 Analysis of variance

Analysis of variance was carried out as per the procedure given by Panse and Sukhatme (1967) using the mean values of different traits in each replication from all the treatments to find out significance of treatment effects.

Source of variation	Degrees of freedom (df)	Sum of square	Mean sum of square	Cal. F
Replication	(r-1)	RSS	RSS/(r-1)	RMSS/EMSS
Treatments	(t-1)	TrSS	TrSS/(t-1)	TrMSS/EMSS
Error	(r-1) (t-1)	ESS	ESS/(t-1) (r-1)	
Total	(rt-1)	TSS		

Where,

r = number of replications

t = number of genotypes

RSS = Mean sum of square of replication

TrMSS = Mean sum of square of genotypes

EMSS = Mean sum of square of error

The significance of treatment mean squares and replication mean squares were tested by comparing Cal. F with table 'F' values at 5 and 1 per cent level of probability.

3.8.2 Genetic divergence

Mahalanobis (1936) D^2 statistics was used for assessing the genetic divergence between different populations. The D^2 analysis was carried out using the data recorded on germplasm. Mahalanobis generalized distance (D^2) between any two populations is given by the formula

$$D^2 = \sum \lambda^{ij} \sigma^i \sigma^j$$

Where,

D^2 = Square of generalized distance

λ^{ij} = Reciprocal of the common dispersal index

$\sigma^i = \mu_{i1} - \mu_{i2}$

$\sigma^j = \mu_{j1} - \mu_{j2}$

μ = General mean

Since, the formula for computation requires inversion of higher order determinants, transformation of the original correlated unstandardized character mean (Xs) to standardise uncorrelated variable (Ys) was done to simplify the computational procedure. The D^2 values were obtained as the corresponding uncorrelated (Ys) values of any two uncorrelated genotypes (Rao, 1952).

3.8.2.1 Clustering D^2 values

$$\frac{n(n-1)}{2} \times D^2$$

All the values were clustered by using Toucher's method (Rao, 1952).

3.8.2.2 Intra and inter-cluster distance

The intra and inter-cluster distances were calculated by following the formula described by Singh and Choudhary (1977).

$$\text{Intra cluster distance} = \frac{\sum D_{ij}^2}{n}$$

Where,

$\sum D_{ij}^2$ = Sum of distances between all possible combinations of the entries included in the cluster

n = Number of all possible combinations

$$\text{Inter cluster distance} = \frac{\sum D_{ij}^2}{n_i n_j}$$

Similarly,

$\sum D_{ij}^2$ = Sum of distances between all possible combinations ($n_i n_j$) of the entries included in the cluster

n_i = Number of genotypes in the cluster i

n_j = Number of genotypes in the cluster j

3.8.3 Estimates of genetic variability parameters

3.8.3.1 Phenotypic variance and genotypic variance

The genotypic and phenotypic variances were computed based on the mean sum of squares as follows

$$\text{Genotypic variance } (\sigma_g^2) = \frac{\text{Treatment MSS} - \text{Error MSS}}{r}$$

$$\text{Phenotypic variance } (\sigma_p^2) = (\sigma_g^2 + \sigma_e^2)$$

Where,

$$\sigma_g^2 = \text{Genotypic variance}$$

$$r = \text{Number of replications}$$

$$\sigma_p^2 = \text{Phenotypic variance}$$

$$\sigma_e^2 = \text{Environmental variance}$$

3.8.3.2 Phenotypic and genotypic coefficient of variation

Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) for all the characters was calculated according to the formula provided by Burton and Devane (1953).

$$\text{a) PCV (\%)} = \frac{\frac{\sqrt{\sigma_p^2}}{\bar{X}}}{100} \times 100$$

$$\text{b) GCV (\%)} = \frac{\frac{\sqrt{\sigma_g^2}}{\bar{X}}}{100} \times 100$$

Where,

$$\sigma_p^2 = \text{Phenotypic variance}$$

$$\sigma_g^2 = \text{Genotypic variance}$$

$$\bar{X} = \text{Grand mean}$$

PCV and GCV were classified as suggested by Sivasubramanian and Madhavamenon (1973).

0-10 % = Low

10-20 % = Moderate

> 20 % = High

3.8.3.3 Heritability (h^2 broadsense)

Broad-sense heritability was estimated for all the traits using the following formula which was given by Johnson *et al.* (1955).

$$h^2 (\%) = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Where,

σ_p^2 = Phenotypic variance

σ_g^2 = Genotypic variance

The heritability percentage was categorized as suggested by Robinson *et al.* (1949)

0-30 % = Low

30-60 % = Moderate

> 60 % = High

3.8.3.4 Genetic advance (GA)

The extent of genetic advance expected for each character was estimated by using the following formula as suggested by Johnson *et al.* (1955).

$$GA = h^2 \times k \times \sigma_p$$

Where,

h^2 = Heritability in broad sense

k = Selection differential (2.06) at 5 per cent selection intensity

σ_p = Phenotypic standard deviation

3.8.3.5 Genetic advance as per cent over mean

Genetic advance as percentage over mean (GAM) was worked out as suggested by Johnson *et al.* (1955).

$$GAM = \frac{GA}{\bar{X}} \times 100$$

Where,

GA= Genetic advance

$\bar{X}$ = Grand mean

The genetic advance as per cent over mean was categorized as follows (Johnson *et al.*, 1955).

0 to 10 % = Low

10 to 20 % = Moderate

> 20 % = High

3.8.4 Correlation analysis

The correlation coefficients were calculated to determine the degree of association of characters with yield, quality and its components. Phenotypic and genotypic correlation coefficients were estimates employing following formulas (Al-Jibouri *et al.*, 1958).

$$\text{Phenotypic correlation} = Co_{vxy} (p) = \frac{Co_{vxy} (p)}{\sqrt{V_x (p) + V_y (p)}}$$

$$\text{Genotypic correlation} = Co_{vxy} (g) = \frac{Co_{vxy} (g)}{\sqrt{V_x (g) + V_y (g)}}$$

Where,

$Cov_{xy}(g)$ = Genotypic covariance between x and y

$Cov_{xy}(p)$ = Phenotypic covariance between x and y

$V_x(g)$ = Genotypic variance of character 'x'

$V_x(p)$ = Phenotypic variance of character 'x'

$V_y(g)$ = Genotypic variance of character 'y'

$V_y(p)$ = Phenotypic variance of character 'y'

The test of significance for association between characters was done by comparing table 'r' values at n-2 error degrees of freedom for phenotypic and genotypic correlations with estimated values, respectively.

3.8.5 Path analysis

The path co-efficient analysis was performed as given by Wright (1921) and Dewey and Lu (1959). The following set of simultaneous equations were formed and solved for estimating direct and indirect effects.

$$r_{1y} = a + r_{12}b + r_{13}c + \dots + r_{11i}$$

$$r_{2y} = r_{21}a + b + r_{23}c + \dots + r_{21i}$$

$$r_{3y} = r_{31}a + r_{32}b + c + \dots + r_{31i}$$

$$r_{1y} = r_{11}a + r_{12}b + r_{13}c + \dots + I$$

Where,

r_{1y} to r_{iy} = Correlation co-efficients between causal factors 1 to I with dependent character Y

r_{12} to r_{1I} = Correlation co-efficient among the causal factor

a, b, c,.....i = Direct effects of characters 'a' to 'I' on dependent character Y

Residual effect (R) was computed as follows.

$$\text{Residual effect (\%)} = 1 - \sqrt{a^2 + b^2 + c^2 + \dots i^2 + 2abr_{12} + 2acr_{13} + \dots}$$

3.8.6 Estimation of heterosis

The mean value of all parents and hybrids for each character was calculated and used in the estimation of heterosis. The magnitude of heterosis was calculated as per cent increase or decrease of F_1 means over the mean of better parent (BP), best parent (BTP) and the standard check (SC) by using the methods of Turner (1953) and Hayes *et al.* (1956).

$$\text{a) Heterosis over better parent (\%)} = \frac{\overline{F_1} - \overline{BP}}{\overline{BP}} \times 100$$

(Heterobeltosis)

$$\text{b) Heterosis over best parent (\%)} = \frac{\overline{F_1} - \overline{BTP}}{\overline{BTP}} \times 100$$

$$\text{c) Heterosis over standard check (\%)} = \frac{\overline{F_1} - \overline{SC}}{\overline{SC}} \times 100$$

(Standard heterosis)

Where,

$\overline{F_1}$ = Mean value of F_1 hybrid

$\overline{BP}$ = Mean of superior parent in the cross

$\overline{BTP}$ = Mean of best parent among 14 parents

$\overline{SC}$ = Mean of standard check

3.8.7 Estimation of combining ability

Variance due to general combining ability (*gca*) of parents and specific combining ability (*sca*) of hybrids were worked out based on procedure developed by Kempthorne (1957) using means of each replication for the above characters recorded

for 40 hybrids, 10 lines and four testers. The mathematical model for combining ability estimation is given below:

$$X_{ijk} = \mu + g_i + g_j + s_{ij} + e_{ijk}$$

Where,

X_{ijk} = Value of the ijk^{th} observation of the cross involving i^{th} line and j^{th} tester in k^{th} replication

μ = General mean (an effect common to all hybrids in all replications)

g_i = gca effect of i^{th} line (Female parent)

g_j = gca effect of j^{th} tester (Male parent)

s_{ij} = sca effect of the cross involving i^{th} line and j^{th} tester

e_{ijk} = environmental effect particular to ijk^{th} individual

3.8.7.1 ANOVA for Line $\times$ Tester analysis

Source	Degree of freedom	Mean sum of squares	Expected sum of squares
Replications	$(r-1)$	M_r	
Genotype	$(l + t + lt - 1)$	M_g	
Parents	$(l + t - 1)$	M_p	
Parents Vs crosses	1	M_{pc}	
Crosses	$(lt - 1)$	M_c	
Lines	$(l - 1)$	M_l	$\sigma^2_e + r [\text{Cov. FS} - 2 \text{Cov. HS}] + rt [\text{Cov. HS}]$
Testers	$(t - 1)$	M_t	$\sigma^2_e + r [\text{Cov. FS} - 2 \text{Cov. HS}] + rl [\text{Cov. HS}]$
Line $\times$ Testers	$(l - 1) \times (t - 1)$	M_{lt}	$\sigma^2_e + r [\text{Cov. FS} - 2 \text{Cov. HS}]$
Error	$(l + t + lt - 1)(r - 1)$	M_e	σ^2_e
Total	$(ltr-1)$		

Where,

f = number of lines.

m = number of testers.

r = number of replications

M_l = Mean squares due to lines

M_t = Mean squares due to testers

M_{lt} = Mean squares due to Line tester interactions

M_e = Error mean squares

Cov. FS = Covariance of full sibs

Cov. HS = Covariance of half sibs

3.8.7.2 Estimation of variance

From the expected mean sum of squares, Covariance of full sib (FS) and Covariance of half sib (HS) were estimated as follows:

$$\text{Covariance of half sib (H.S.)} = M_1 + M_2 - 2M_3 / r(l+t)$$

$$\text{Covariance of full sib (FS)} = (M_1 - M_4) + (M_2 - M_4) + (M_3 - M_4) / 3r + 6r + \text{Cov H.S.} \\ r(l+t) \text{ Cov H.S.} / 3r$$

After estimating Cov (HS) and Cov (FS) the GCA variance of lines and testers and SCA variance for the hybrids were estimated under

$$\text{GCA Variance for lines} = M_1 - M_3 / l \times T$$

$$\text{GCA Variance for testers} = M_2 - M_3 / r \times l$$

$$\text{SCA Variance for hybrids} = M_3 - M_4 / r = \sigma^2_{lt}$$

3.8.7.3 Estimation of general and specific combining ability effects

The GCA and SCA effects were obtained from the two-way table of female parents vs. male parents. The individual effect was estimated as follow:

a) GCA effects of i^{th} line

$$g_i = \frac{x_i}{t \times r} - \frac{x_{...}}{l \times t \times r}$$

b) GCA effects of j^{th} tester

$$g_j = \frac{x_j}{l \times r} - \frac{x_{...}}{l \times t \times r}$$

c) SCA effects of ij^{th} cross

$$s_{ij} = \frac{x_{ij}}{r} - \frac{x_{i..}}{t \times r} - \frac{x_{.j.}}{l \times r} + \frac{x_{...}}{l \times t \times r}$$

Where,

$X_{...}$ = sum total of all crosses

X_i = total of i^{th} female parents over all males and replications

X_j = total of j^{th} male parents over all females and replications

X_{ij} = ij^{th} combination total over all replications

r = number of replications

l = number of lines/female parents

t = number of testers/male parents

3.8.7.4 Estimation of standard errors for combining ability effects

The standard error pertaining to *gca* effect of lines and testers and *sca* effects of different cross combinations were calculated as shown below.

$$SE \text{ (CAG of lines)} = \sqrt{\frac{\text{Error variance}}{t \times r}}$$

$$SE \text{ (CAG of testers)} = \sqrt{\frac{\text{Error variance}}{l \times r}}$$

$$SE \text{ (CAG of hybrids)} = \sqrt{\frac{\text{Error variance}}{r}}$$

Where,

t = Number of testers

l = Number of lines

r = Number of replications

Significance was tested by student 't' test.

4. EXPERIMENTAL RESULTS

The present investigation on “Molecular diversity assessment and manifestation of heterosis for growth and yield in sponge gourd (*Luffa cylindrica* (L.) Roem.)” was carried out in the Department of Vegetable Science, College of Horticulture, Bagalkot (Karnataka) with a view to study the extent of genetic variability, character association, path analysis, morphological and molecular diversity, heterosis and combining ability in different genotypes of sponge gourd during 2020 to 2022. The results obtained from the study are presented under the following sub-headings.

- 4.1 Analysis of variance
- 4.2 Morphological characterization
- 4.3 Genetic variability
- 4.4 Genetic diversity studies
- 4.5 Molecular characterization
- 4.6 Correlation co-efficient analysis
- 4.7 Path co-efficient analysis
- 4.8 Magnitude of heterosis
- 4.9 Combining ability effects and variances

4.1 Analysis of variance

The results from analysis of variance revealed that highly significant differences among the genotypes for all the characters under studied viz., vine length at 45 and 90 DAS, number of branches at 45 and 90 DAS, days to first male and female flower, node at first male and female flower, days to first and last harvest, fruit length, fruit diameter, average fruit weight, number of fruits per vine, fruit yield per vine, fruit yield per plot, fruit yield per hectare, number of seeds per fruit, sponge yield, total soluble solids, fruit firmness, fruit color (L^* , a^* , b^*), protein, ascorbic acid, potassium content, phenol content, total antioxidants, total flavonoids, crude fiber and ash content (Table 8).

Table 8. Analysis of variance (ANOVA) for growth, yield and quality parameters in sponge gourd

Sl. No.	Source	Replication	Treatment	Error
	Degrees of freedom	1	39	39
1	Vine length at 45 DAS	0.051	0.445 ^{**}	0.025
2	Vine length at 90 DAS	0.354	0.536 ^{**}	0.179
3	Number of branches at 45 DAS	0.032	0.368 ^{**}	0.016
4	Number of branches at 90 DAS	0.480	1.497 ^{**}	0.282
5	Days to first male flower	26.609	59.823 ^{**}	8.871
6	Days to first female flower	16.325	58.77 ^{**}	10.378
7	Node at first male flower	1.152	2.197 ^{**}	0.291
8	Node at first female flower	2.125	9.355 ^{**}	1.066
9	Days to first harvest	49.880	57.006 ^{**}	24.953
10	Days to last harvest	58.940	62.962 [*]	29.626
11	Fruit length	3.276	24.707 ^{**}	2.346
12	Fruit diameter	8.919	22.799 ^{**}	5.907
13	Average fruit weight	66.104	654.880 ^{**}	67.573
14	Number of fruits per vine	3.172	25.889 ^{**}	4.429
15	Fruit yield per vine	0.057	0.589 ^{**}	0.049
16	Fruit yield per plot	22.642	57.950 ^{**}	4.077
17	Fruit yield per hectare	0.086	12.318 ^{**}	1.258
18	Number of seeds per fruit	1050.781	11513.684 ^{**}	527.415
19	Sponge yield	2.350	13.152 ^{**}	0.893
20	Total soluble solids	0.4470	0.269 ^{**}	0.111
21	Fruit firmness	3.321	73.803 ^{**}	3.017
22	Fruit color (L [*])	0.090	59.877 ^{**}	1.972
23	Fruit color (a [*])	0.156	1.667 ^{**}	0.058
24	Fruit color (b [*])	0.158	44.588 ^{**}	0.372
25	Protein content	0.365	5.253 [*]	0.181
26	Ascorbic acid	0.245	2.227 [*]	0.534
27	Potassium content	0.012	0.338 ^{**}	0.006
28	Phenol content	0.005	1470.532 ^{**}	2.454
29	Total antioxidants	0.192	2089.989 ^{**}	4.492
30	Total flavonoids	3.499	57.443 ^{**}	0.902
31	Crude fiber	0.289	7.249 ^{**}	0.280
32	Ash content	0.199	1.859 [*]	0.583

^{**} and ^{*} indicates significant at 1% and 5 % respectively DAS-Days after sowing

4.2 Morphological characterization

4.2.1 Leaf shape

The genotypes G1, G2, G5, G7, G9, G14, G28 and G32 showed ovate leaf shape. Similarly, the genotypes G3, G16, G15, G17, G18, G19, G20, G21, G22, G23, G25, G39 and G40 were expressed for renformi shape of leaf whereas remaining all the other genotypes resulted in orbicular leaf shape (Table 9 and Plate 5).

4.2.2 Leaf lobe

The genotype G7, G11, G14, G28, G29 and G30 recorded deep leaf lobe shape whereas, G6, G8, G10, G12, G13, G18, G19, G20, G21, G22, G23, G25, G26, G31, G32, G35, G36, G38 and G40 showed shallow leaf lobe and remaining all the other genotypes showed intermediate shape of leaf lobe (Table 9 and Plate 6).

4.2.3 Leaf color

Among the 40 genotypes studied for morphology, the genotype G29 and G30 showed green leaf color with patches on its surface whereas, remaining all the other genotypes showed green color for leaves (Table 9 and Plate 7).

4.2.4 Flower color

The genotypes G7, G8, G15, G21, G22, G30, G31, G36 and G40 were recorded light yellow color of flowers and remaining all the other genotypes showed yellow flower colour (Table 9 and Plate 8).

4.2.5 Flesh color

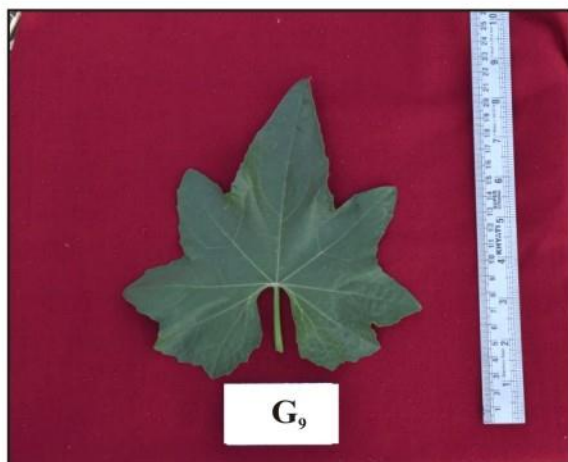
The genotypes like G8, G9, G11, G12, G16, G20, G22, G28, G31, G33 and G37 recorded cream flesh color whereas remaining all the other genotypes exhibited whitish flesh color (Table 10 and Plate 9).

4.2.6 Fruit shape

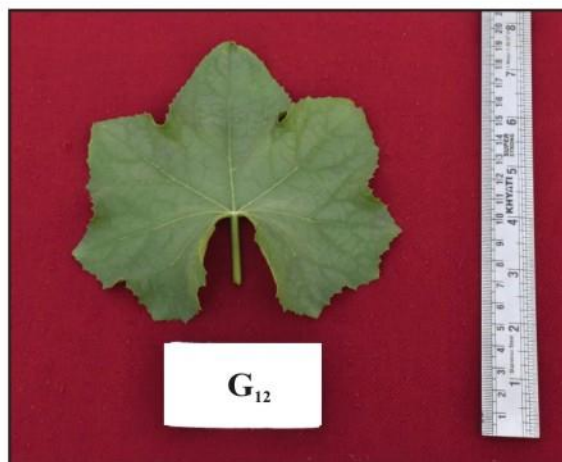
The genotypes G5 and G18 recorded oblong blocky fruit shape whereas G7, G12, G14, G15, G17, G20, G23, G36, G37 and G40 showed elliptical fruit shape.

Table 9. Morphological characterization of sponge gourd genotypes for leaf color, leaf shape, leaf lobe and flower color

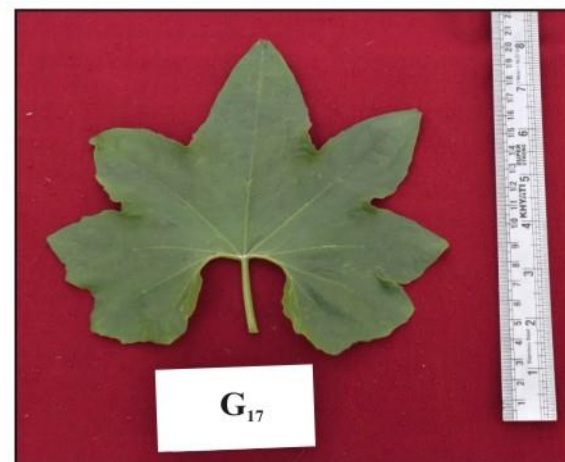
Sl. No.	Genotypes	Leaf color	Leaf shape	Leaf lobe	Flower color
1	G1	Green	Ovate	Intermediate	Yellow
2	G2	Green	Ovate	Intermediate	Yellow
3	G3	Green	Renformi	Intermediate	Yellow
4	G4	Green	Orbicular	Intermediate	Yellow
5	G5	Green	Ovate	Intermediate	Yellow
6	G6	Green	Renformi	Shallow	Yellow
7	G7	Green	Ovate	Deep	Light yellow
8	G8	Green	Orbicular	Shallow	Light yellow
9	G9	Green	Ovate	Intermediate	Yellow
10	G10	Green	Orbicular	Shallow	Yellow
11	G11	Green	Orbicular	Deep	Yellow
12	G12	Green	Orbicular	Shallow	Yellow
13	G13	Green	Orbicular	Shallow	Yellow
14	G14	Green	Ovate	Deep	Yellow
15	G15	Green	Renformi	Intermediate	Light yellow
16	G16	Green	Orbicular	Intermediate	Yellow
17	G17	Green	Renformi	Intermediate	Yellow
18	G18	Green	Renformi	Shallow	Yellow
19	G19	Green	Renformi	Shallow	Yellow
20	G20	Green	Renformi	Shallow	Yellow
21	G21	Green	Renformi	Shallow	Light yellow
22	G22	Green	Renformi	Shallow	Light yellow
23	G23	Green	Renformi	Shallow	Yellow
24	G24	Green	Orbicular	Intermediate	Yellow
25	G25	Green	Renformi	Shallow	Yellow
26	G26	Green	Orbicular	Shallow	Yellow
27	G27	Green	Orbicular	Intermediate	Yellow
28	G28	Green	Ovate	Deep	Yellow
29	G29	Green with patches	Orbicular	Deep	Yellow
30	G30	Green with patches	Orbicular	Deep	Light yellow
31	G31	Green	Orbicular	Shallow	Light yellow
32	G32	Green	Ovate	Shallow	Yellow
33	G33	Green	Orbicular	Intermediate	Yellow
34	G34	Green	Orbicular	Intermediate	Yellow
35	G35	Green	Orbicular	Shallow	Yellow
36	G36	Green	Orbicular	Shallow	Light yellow
37	G37	Green	Orbicular	Intermediate	Yellow
38	G38	Green	Orbicular	Shallow	Yellow
39	G39	Green	Renformi	Intermediate	Yellow
40	G40	Green	Renformi	Shallow	Light yellow



Ovate



Orbicular

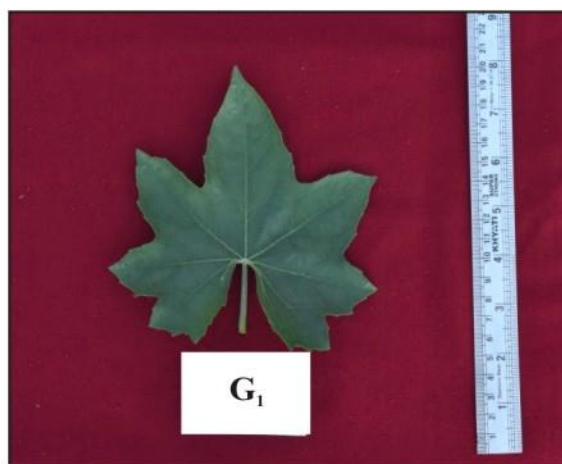


Reniform

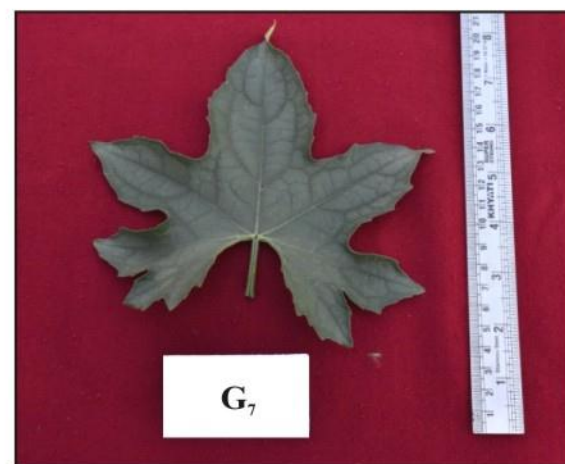
Plate 5. Morphological characterization of sponge gourd genotypes for leaf shape



Shallow

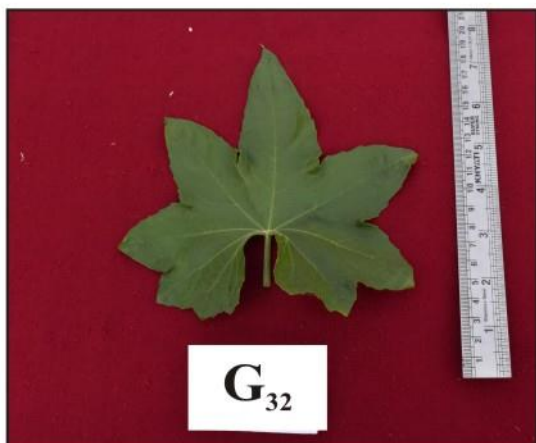


Intermediate



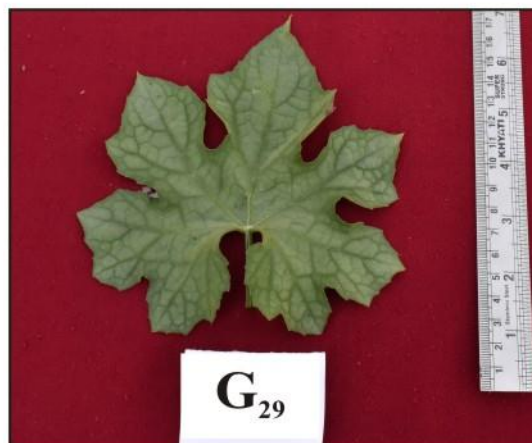
Deep

Plate 6. Morphological characterization of sponge gourd genotypes for leaf lobe



G₃₂

Green



G₂₉

Green with patches

Plate 7. Morphological characterization of sponge gourd genotypes for leaf color



Light yellow



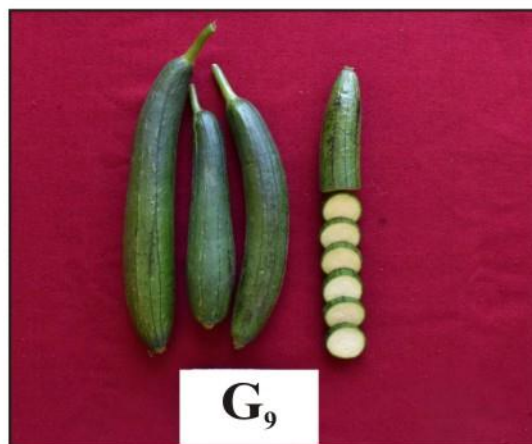
Yellow

Plate 8. Morphological characterization of sponge gourd genotypes for fruit flower color



G₄

White



G₉

Cream

Plate 9. Morphological characterization of sponge gourd genotypes for flesh color

Table 10. Morphological characterization of sponge gourd genotypes for fruit shape, fruit color and flesh color

Sl. No.	Genotypes	Fruit shape	Fruit color	Flesh color
1	G1	Elongate slim	Dark geen	White
2	G2	Elongate elliptical	Dark geen	White
3	G3	Elongate slim	Green	White
4	G4	Elongate slim	Green	White
5	G5	Oblong blocky	Green	White
6	G6	Elongate slim	Green	White
7	G7	Elliptical	Green	White
8	G8	Elongate slim	Green	Cream
9	G9	Elongate elliptical	Dark geen	Cream
10	G10	Elongate elliptical	Dark geen	White
11	G11	Elongate slim	Green	Cream
12	G12	Elliptical	Green	Cream
13	G13	Elongate slim	Dark geen	White
14	G14	Elliptical	Green	White
15	G15	Elliptical	Green	White
16	G16	Elongate elliptical	Green	Cream
17	G17	Elliptical	Dark geen	White
18	G18	Oblong blocky	Dark geen	White
19	G19	Elongate slim	Dark geen	White
20	G20	Elliptical	Dark geen	Cream
21	G21	Elongate elliptical	Green	White
22	G22	Elongate slim	Green	Cream
23	G23	Elliptical	Light geen	White
24	G24	Elongate slim	Green	White
25	G25	Elongate elliptical	Dark geen	White
26	G26	Elongate elliptical	Light geen	White
27	G27	Elongate slim	Dark geen	White
28	G28	Elongate slim	Dark geen	Cream
29	G29	Elongate slim	Light geen	White
30	G30	Elongate slim	Dark geen	White
31	G31	Elongate slim	Whitish	Cream
32	G32	Elongate slim	Dark geen	White
33	G33	Elongate elliptical	Dark geen	Cream
34	G34	Elongate elliptical	Dark geen	White
35	G35	Elongate slim	Dark geen	White
36	G36	Elliptical	Whitish	White
37	G37	Elliptical	Light geen	Cream
38	G38	Elongate elliptical	Dark geen	White
39	G39	Elongate slim	Dark geen	White
40	G40	Elliptical	Light geen	White

Similarly, the genotypes G2, G9, G10, G16, G21, G25, G26, G33, G34 and G38 were expressed for elongate elliptical shape of fruit whereas remaining all the other genotypes resulted in elongate slim leaf shape (Table 10 and Plate 10).

4.2.7 Fruit colour

The genotype varied from whitish to dark green for fruit color. The genotypes G31 and G36 recorded whitish fruit color whereas G23, G26, G29, G37 and G40 genotypes showed light green colour fruit. The genotypes G3, G4, G5, G6, G7, G8, G11, G12, G14, G15, G16, G21, G22 and G24 recorded green fruit color whereas, remaining all the other genotypes exhibited dark green colour for fruit (Table 10 and Plate 11).

4.3 Genetic variability

The mean and parameters of genetic variability, heritability (h^2) and GAM are presented in Table 11. *Per se* performance of forty sponge gourd genotypes for different quantitative and qualitative parameters are presented in Tables 12 to 16.

4.3.1 Vine length at 45 DAS (m)

Among all the 40 genotypes studied maximum vine length at 45 DAS was observed in G9 (2.86 m) and minimum was observed in G8 (1.39 m) with mean of 2.21 m (Table 12). This trait has exhibited low GV (0.21) and PV (0.24) with high GCV (20.74 %) and high PCV (22.17 %). Further, the estimate of broad sense heritability (87.50 %) was high coupled with high genetic advance as per cent of mean (40.27 %) were observed for this trait (Table 11).

4.3.2 Vine length at 90 DAS (m)

Maximum vine length (7.07 m) at 90 DAS was observed in genotype G9 and minimum was observed in G8 (4.76 m) with mean value of 5.99 m (Table 12). The GV



Oblong blocky



Elliptical



Elongate slim



Elongate elliptical

Plate 10. Morphological characterization of sponge gourd genotypes for fruit shape



Light green



Green



Dark green



Whitish

Plate 11. Morphological characterization of sponge gourd genotypes for fruit color

and PV were 0.37 and 0.63, respectively. The trait exhibited moderate values of genotypic coefficient of variation (10.15 %), phenotypic coefficient of variation (13.25 %), along with moderate heritability (58.73 %) and genetic advance over per cent of mean (10.35 %) (Table 11).

4.3.3 Number of branches at 45 DAS

The number of branches per vine at 45 DAS ranged from 1.30 (G8) to 2.90 (G9) with an average of 1.91 branches per vine (Table 12). The GV and PV were 0.18 and 0.19, respectively. The estimates of GCV and PCV were high with 21.99 % and 23.04 %, respectively. Similarly, both heritability estimate (94.74 %) and GAM (43.46 %) were found to be high (Table 11).

4.3.4 Number of branches at 90 DAS

The number of branches per vine at 90 DAS ranged from 3.10 (G8) to 6.20 (G9) with a mean of 4.31 (Table 12). The GV and PV were 0.61 and 0.89, respectively. The calculated genotypic coefficient of variation was moderate (18.12 %) with little more phenotypic coefficient of variation (21.88 %). However, estimates of heritability (68.34 %) and genetic advance as per cent over mean (30.86 %) were found to be high for this trait (Table 11).

4.3.5 Days to first male flower

Number of days taken for first male flower appearance was minimum in genotype G9 and G24 (38.10) while it was maximum in genotype G4 (62.30) with an average of 46.47 days (Table 12). The high genotypic (25.48) and phenotypic variance (34.35) was observed for this trait. However, estimate of GCV and PCV were moderate with 10.86 % and 12.61 %, respectively. A high heritability 74.18 % coupled with low genetic advance 8.96 with moderate genetic advance as per cent over mean (19.28 %) was noticed for this trait (Table 11).

Table 11. Estimates of genetic variability parameters for growth, yield and quality traits in sponge gourd genotypes

Sl. No.	Characters	Mean	Range		GV	PV	GCV (%)	PCV (%)	h^2 (%)	GA	GAM (%)
1	Vine length at 45 DAS (m)	2.21	1.39	2.86	0.21	0.24	20.74	22.17	87.50	0.89	40.27
2	Vine length at 90 DAS (m)	5.99	4.76	7.07	0.37	0.63	10.15	13.25	58.73	0.62	10.35
3	Number of branches at 45 DAS	1.91	1.30	2.90	0.18	0.19	21.99	23.04	94.74	0.83	43.46
4	Number of branches at 90 DAS	4.31	3.10	6.20	0.61	0.89	18.12	21.88	68.54	1.33	30.86
5	Days to first male flower	46.47	38.10	62.30	25.48	34.35	10.86	12.61	74.18	8.96	19.28
6	Days to first female flower	49.56	42.80	64.40	24.20	34.57	9.93	11.86	70.00	8.48	17.11
7	Node at first male flower	5.38	3.50	7.30	0.95	1.24	18.03	20.63	76.61	1.76	32.71
8	Node at first female flower	13.18	9.30	18.00	4.14	5.21	15.40	17.30	79.46	3.74	28.38
9	Days to first harvest	59.29	51.80	74.10	16.03	40.98	6.75	10.79	39.12	5.16	8.70
10	Days to last harvest	118.29	111.80	134.00	16.67	46.29	3.45	5.75	36.01	5.05	4.27
11	Fruit length (cm)	21.17	13.54	27.12	11.18	13.53	15.78	17.38	82.63	6.26	29.57
12	Fruit diameter (mm)	31.28	25.76	37.43	8.45	14.35	9.30	12.12	58.89	4.59	14.67
13	Average fruit weight (g)	145.44	116.74	170.25	293.66	361.23	11.78	13.07	81.29	31.83	21.89
14	Number of fruits per vine	19.00	11.60	24.80	10.73	15.16	17.26	20.47	70.78	5.68	29.89
15	Fruit yield per vine (kg)	2.62	1.26	3.85	0.30	0.35	20.91	22.58	85.71	0.98	37.40
16	Fruit yield per plot (kg)	24.74	12.56	36.66	26.94	31.01	20.98	22.51	86.88	9.97	40.30
17	Fruit yield per hectare (t)	11.72	6.17	18.17	5.53	6.79	20.05	22.27	81.44	4.37	37.29

Table 11. *Contd...*

Sl. No.	Characters	Mean	Range		GV	PV	GCV (%)	PCV (%)	h ² (%)	GA	GAM (%)
18	Number of seeds per fruit	193.30	63.70	338.00	5493.13	6198.95	38.34	40.73	88.61	145.84	75.45
19	Sponge yield (g/fruit)	13.32	8.83	18.09	6.13	7.02	18.62	19.89	87.32	4.77	35.81
20	Total soluble solids (⁰ Brix)	4.78	3.58	6.14	0.23	0.40	10.04	13.18	57.50	0.62	12.97
21	Fruit firmness (N)	34.37	23.10	45.82	35.40	38.41	17.31	18.04	92.16	11.76	34.22
22	Fruit color (L [*])	36.13	25.01	52.37	28.95	30.93	14.89	15.39	93.60	10.73	29.70
23	Fruit color (a [*])	7.39	5.32	9.47	0.80	0.86	12.04	12.58	93.02	1.78	24.09
24	Fruit color (b [*])	21.97	12.59	29.91	22.11	22.88	21.39	21.76	96.63	9.61	43.74
25	Protein content (%)	11.82	8.11	15.91	2.54	2.72	13.45	13.96	93.38	3.17	26.82
26	Ascorbic acid (mg/100 g)	7.06	5.38	9.72	0.85	1.12	13.03	14.87	75.89	1.48	20.96
27	Potassium content (%)	2.22	1.41	2.88	0.17	0.18	18.47	18.92	94.44	0.83	37.39
28	Phenol content (mg GAE/100 g)	288.24	225.17	344.40	734.04	755.12	9.40	9.53	97.21	55.72	19.33
29	Total antioxidants (mg AAE/100 g)	778.01	712.61	841.95	1042.75	1085.24	4.15	4.23	96.08	78.14	10.04
30	Total flavonoids (mg QE/100 g)	37.52	25.56	48.29	28.27	29.17	14.18	14.39	96.91	10.78	28.73
31	Crude fiber (%)	9.34	6.23	14.96	3.08	3.34	18.79	19.57	92.22	3.69	39.51
32	Ash content (%)	7.91	6.19	10.44	0.64	1.22	10.11	13.91	52.46	1.19	15.04

GV: Genotypic Variance

GCV: Genotypic co-efficient of variance

h²: heritability (broad sense)

GAM: Genetic advance as per cent of mean

PV: Phenotypic variance

PCV: Phenotypic co-efficient of variance

GA: Genetic advance

DAS: Days after sowing

4.3.6 Days to first female flower

Minimum number of days taken for first female flower appearance was noticed in genotype G9 (42.80) while it was maximum in G4 (64.40) with a grand mean of 49.56 days (Table 12). There was not much variability found for this trait in the genotypes evaluated. It was confirmed with low genotypic coefficient of variation (9.93 %) with moderate phenotypic coefficient of variation (11.86 %). However the heritability for this trait was high 70.00 % coupled with low genetic advance 8.48 and moderate (17.11 %) genetic advance as per cent over mean (Table 11).

4.3.7 Node at first male flower

Node at which first male flower appear was minimum (3.50) in G24 and it was maximum in G4 (7.30) with a mean value of 5.38 (Table 13). This trait has exhibited low GV (0.95) and PV (1.24), moderate GCV (18.03 %) and high PCV (20.63 %). Further, the estimates of heritability (76.61 %) and genetic advance as per cent of mean (32.71 %) were found to be high for this trait (Table 11).

4.3.8 Node at first female flower

The genotype G9 recorded early node (9.30) to first female flower while it was later node in G4 (18.00) while it was maximum in G4 (18.00) with a mean value of 13.18 (Table 13). The GV and PV were 4.14 and 5.21 respectively (Table 11). This trait has shown moderate GCV and PCV (15.40 and 17.30 respectively) with high heritability (79.46 %) and GAM (28.38 %).

4.3.9 Days to first harvest

Early first harvest (51.80 days) was noticed in the genotype G9 and it was very late in G4 (74.10 days) with mean value of 59.29 days (Table 13). This trait had shown genotypic and phenotypic variance of 16.03 and 40.98, respectively. Low GCV (6.75 %) and moderate PCV (10.79 %) and heritability (39.12 %) coupled with low genetic advance as per cent of mean (8.70 %) were observed for this trait (Table 11).

Table 12. *Per se* performance of sponge gourd genotypes for growth and earliness parameters

Sl. No.	Genotypes	Vine length (m)		Number of branches		Days to first male flower	Days to first female flower
		45 DAS	90 DAS	45 DAS	90 DAS		
1	G1	1.56	5.91	1.50	4.60	54.20	57.00
2	G2	2.58	6.57	2.40	5.70	43.20	45.20
3	G3	1.42	6.27	2.00	4.10	49.20	52.20
4	G4	1.51	5.96	1.50	3.20	62.30	64.40
5	G5	2.36	5.54	2.00	3.60	48.40	52.40
6	G6	2.51	5.74	1.70	4.20	61.20	64.40
7	G7	1.81	5.37	1.60	4.00	46.60	50.70
8	G8	1.39	4.76	1.30	3.10	55.80	56.80
9	G9	2.86	7.07	2.90	6.20	38.10	42.80
10	G10	2.51	5.24	1.30	4.50	48.80	51.50
11	G11	1.62	5.18	1.70	4.20	50.00	55.20
12	G12	2.09	4.90	1.60	3.50	47.00	51.60
13	G13	1.59	5.92	2.00	3.10	48.20	52.40
14	G14	2.10	6.11	1.40	4.00	47.00	50.20
15	G15	1.58	5.13	1.30	3.50	49.50	52.60
16	G16	2.62	6.41	2.60	5.90	41.70	43.30
17	G17	2.54	6.05	1.60	3.60	46.80	51.00
18	G18	1.94	6.12	1.40	3.40	45.70	47.80
19	G19	2.47	6.31	1.50	3.80	47.20	51.10
20	G20	2.40	5.92	2.00	3.90	46.80	48.40
21	G21	2.71	6.45	2.40	5.70	42.80	46.40
22	G22	2.73	6.42	2.60	5.30	42.40	44.60
23	G23	2.54	5.25	1.40	4.10	46.80	47.60
24	G24	2.80	6.86	2.80	6.10	38.10	43.50
25	G25	1.53	5.74	1.80	3.30	45.40	47.90
26	G26	2.38	6.11	1.60	3.70	47.40	49.40
27	G27	2.54	6.21	1.70	4.10	45.40	47.20
28	G28	2.01	5.44	1.80	3.40	44.70	46.20
29	G29	2.46	6.07	2.00	3.80	46.00	50.20
30	G30	1.78	6.01	1.70	4.20	47.20	49.30
31	G31	2.76	6.55	2.30	4.40	42.60	44.80
32	G32	1.43	5.51	1.60	4.20	46.20	52.90
33	G33	2.66	6.81	2.60	6.00	41.00	43.70
34	G34	2.59	6.72	2.50	5.00	43.20	44.20
35	G35	2.35	6.34	1.60	4.10	43.60	48.40
36	G36	2.58	6.58	2.20	5.10	41.10	43.80
37	G37	2.50	6.39	2.60	4.80	42.60	46.50
38	G38	2.28	5.95	2.30	4.60	44.20	47.00
39	G39	2.06	5.94	1.60	4.40	45.30	51.00
40	G40	2.33	5.95	1.80	3.80	45.10	46.90
Mean		2.21	5.99	1.91	4.31	46.47	49.56
S.Em±		0.11	0.30	0.09	0.38	2.11	2.28
CD at 5%		0.32	0.86	0.26	1.07	6.02	6.52
CD at 1%		0.43	1.15	0.34	1.44	8.07	8.72

Table 13. *Per se* performance of sponge gourd genotypes for earliness and yield parameters

Sl. No.	Genotypes	Node at first male flower	Node at first female flower	Days to first harvest	Days to last harvest	Fruit length (cm)	Fruit diameter (mm)
1	G1	6.80	12.00	66.80	125.40	23.71	28.36
2	G2	4.60	11.90	54.80	114.00	25.95	33.69
3	G3	5.90	12.50	62.30	120.40	16.05	26.89
4	G4	7.30	18.00	74.10	134.00	22.27	30.67
5	G5	5.30	13.20	63.20	120.20	16.06	31.63
6	G6	6.20	13.10	72.30	132.40	22.52	30.45
7	G7	5.20	14.70	66.80	126.40	15.84	29.84
8	G8	7.10	17.60	60.20	120.50	22.15	25.76
9	G9	3.80	9.30	51.80	111.80	27.12	37.43
10	G10	6.60	13.60	62.50	122.60	18.70	30.55
11	G11	5.80	12.20	66.60	124.60	19.88	29.53
12	G12	6.20	13.10	60.30	118.80	18.40	30.45
13	G13	5.20	12.30	61.40	120.20	22.23	29.42
14	G14	5.20	13.20	61.90	120.40	20.62	31.58
15	G15	6.50	15.50	63.10	120.60	21.40	31.87
16	G16	4.50	10.80	54.30	114.20	24.65	35.11
17	G17	6.50	14.90	59.80	116.40	16.97	32.63
18	G18	5.70	15.20	56.70	115.20	16.87	30.89
19	G19	5.40	12.80	61.40	118.90	18.80	29.28
20	G20	5.80	16.80	57.70	117.40	13.54	30.98
21	G21	4.60	11.10	56.00	114.60	25.29	33.20
22	G22	4.20	11.20	53.30	113.40	25.07	34.60
23	G23	5.40	18.00	58.70	117.00	17.51	31.34
24	G24	3.50	9.30	52.50	113.20	26.06	36.17
25	G25	5.20	12.10	56.40	118.60	19.45	31.85
26	G26	5.50	13.90	56.40	116.70	18.92	29.85
27	G27	5.40	15.20	57.70	115.60	21.07	28.69
28	G28	4.80	16.70	56.10	116.20	25.01	28.70
29	G29	5.80	13.00	59.20	118.80	22.18	31.78
30	G30	5.20	14.60	57.50	115.80	20.58	30.85
31	G31	4.60	11.40	54.40	112.40	24.67	33.45
32	G32	5.00	13.70	63.40	120.40	20.04	31.62
33	G33	4.20	9.60	53.20	112.40	25.70	35.14
34	G34	4.00	10.80	53.70	114.60	25.29	34.45
35	G35	5.10	14.70	57.50	115.40	18.77	31.93
36	G36	4.40	11.00	55.10	114.20	23.87	33.31
37	G37	4.80	11.40	55.80	115.70	22.76	32.70
38	G38	5.70	11.50	56.80	116.40	24.55	31.34
39	G39	5.50	12.60	60.40	119.20	20.08	27.06
40	G40	6.70	12.80	59.40	116.40	16.43	26.29
Mean		5.38	13.18	59.29	118.29	21.17	31.28
S.Em±		0.38	0.73	3.53	3.85	1.08	1.72
CD at 5%		1.09	2.09	10.10	11.01	3.10	4.92
CD at 1%		1.46	2.80	13.53	14.74	4.15	6.58

4.3.10 Days to last harvest

Among the 40 sponge gourd genotypes evaluated, the fruits of genotype G4 can be harvested upto 134.00 days. However, the genotype G9 produces fruits upto 111.80 days with mean of 118.29 days (Table 13). The trait had shown moderate to high genotypic and phenotypic variance of 16.67 and 46.29, respectively. The trait exhibited very low genotypic coefficient variation (3.45 %) and phenotypic coefficient variation (5.75 %). The moderate heritability (36.01 %) along with low GAM (4.27 %) was observed for this trait (Table 11).

4.3.11 Fruit length (cm)

It indicated the presence of very low variability for this trait in the evaluated genotypes. The genotype G9 produces more lengthiest fruit (27.12 cm) among 40 sponge gourd genotypes whereas, the genotype G20 produced small fruits (13.54 cm) with average length of 21.17 cm (Table 13). Moderate GCV (15.78 %) and PCV (17.38 %) were observed for this trait with high estimates of heritability (82.63 %) and genetic advance as per cent of mean (29.57 %) for this trait (Table 11).

4.3.12 Fruit diameter (mm)

Fruit diameter was maximum in the genotype G9 (37.43 mm) and it was minimum in G8 (25.76 mm) with a mean diameter value of 31.28 mm (Table 13). This trait has exhibited low GCV (9.30 %) and moderate PCV (12.12 %). The estimates of heritability (58.89 %) and genetic advance as per cent of mean (14.67 %) were also recorded moderate value for this trait (Table 11).

4.3.13 Average fruit weight (g)

The highest average fruit weight was observed in the genotype G9 (170.25 g) and it was lowest in G8 (116.74 g) with over all mean of 145.44 g (Table 14). The GV and PV for the trait were 293.66 and 361.23, respectively (Table 11). The moderate values of GCV (11.78 %), PCV (13.07 %) and high heritability (81.29 %) coupled with high GAM (27.89 %) was observed for this trait.

4.3.14 Number of fruits per vine

The genotype G9 recorded more number of fruits per vine (24.80) among 40 genotypes whereas, it was least (11.60) in the genotype G8 with an average of 19.00 fruits per vine (Table 14). The GV and PV for the trait were 10.73 and 15.16, respectively. Moderate GCV (17.26 %) to little high PCV (20.47 %) with high estimates of heritability (70.78 %) and GAM (29.89 %) were observed for this trait (Table 11).

4.3.15 Fruit yield per vine (kg)

Among the 40 sponge gourd genotypes evaluated the highest fruit yield per vine was observed in the genotype G9 (3.85 kg) and it was lowest in G8 (1.26 kg) with a mean value of 2.62 kg per vine (Table 14). The low GV and PV (0.30 and 0.35 respectively) were recorded for this trait. The estimated values of GCV (20.91 %), PCV (22.58 %), heritability (85.71 %) and GAM (37.40 %) were found to be high for this character (Table 11).

4.3.16 Fruit yield per plot (kg)

The total fruit yield per plot was recorded highest (36.66 kg) in the genotype G9 and it was lowest in G8 (12.56 kg) with an average plot yield of 24.74 kg (Table 14). This trait has exhibited high GV and PV (26.94 and 31.01), high GCV and PCV (20.98 % and 22.51 %) along with high heritability (86.88 %) and genetic advance over per cent of mean (40.30 %) (Table 11).

4.3.17 Fruit yield per hectare (t)

The estimates of fruit yield per hectare was more (18.17 t) in the genotype G9 and it was least in G8 (6.15 t) with a mean of 11.72 t per hectare (Table 14). This trait has shown low GV (5.53) and PV (6.79) but high GCV (20.05 %) and PCV (22.27 %). The high heritability (81.44 %) along with low genetic advance (4.37) and high genetic advance as per cent of mean (37.29 %) were observed for this character (Table 11).

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Table 14. *Per se* performance of sponge gourd genotypes for yield and yield parameters

Sl. No.	Genotypes	Average fruit weight (g)	Number of fruits/ vine	Fruit yield/ vine (kg)	Fruit yield/ plot (kg)	Fruit yield/ hectare (t)	No. of seeds/ fruit
1	G1	143.86	14.10	1.98	18.11	8.97	109.20
2	G2	160.97	22.80	3.44	33.84	15.82	279.60
3	G3	137.93	17.20	2.14	19.59	9.58	188.60
4	G4	159.26	15.60	2.39	23.73	10.70	83.80
5	G5	158.53	17.30	2.51	24.38	11.46	128.70
6	G6	158.56	19.20	2.84	27.52	12.70	137.10
7	G7	156.25	18.40	2.66	24.71	11.28	81.00
8	G8	116.74	11.60	1.26	12.56	6.15	187.90
9	G9	170.25	24.80	3.85	36.66	18.17	338.00
10	G10	127.01	14.40	1.73	16.29	7.89	125.50
11	G11	132.77	18.20	2.37	21.72	9.25	150.40
12	G12	135.19	13.60	1.78	15.49	7.36	245.50
13	G13	157.28	13.50	2.01	19.34	9.54	166.20
14	G14	146.68	19.20	2.66	24.42	11.59	114.70
15	G15	152.15	17.90	2.68	25.56	12.54	207.70
16	G16	161.42	23.40	3.64	34.24	15.71	276.40
17	G17	134.95	20.00	2.40	23.01	10.70	217.10
18	G18	117.36	21.30	2.34	21.41	9.91	132.00
19	G19	119.57	20.70	2.35	22.61	11.12	152.60
20	G20	122.01	19.40	2.16	20.22	9.69	63.70
21	G21	162.45	23.00	3.65	34.41	16.12	277.90
22	G22	163.65	22.80	3.45	32.07	15.68	275.20
23	G23	124.03	17.30	1.92	17.94	8.58	150.50
24	G24	165.50	23.80	3.69	34.85	17.29	322.20
25	G25	138.50	16.20	1.93	16.21	7.98	153.10
26	G26	143.32	15.40	2.15	19.23	9.25	123.50
27	G27	141.32	18.80	2.49	22.12	10.79	236.50
28	G28	147.16	17.90	2.48	23.19	10.56	153.60
29	G29	117.48	21.80	2.51	24.65	11.48	208.10
30	G30	145.81	19.50	2.65	25.23	12.27	126.60
31	G31	161.72	22.50	3.48	32.19	14.49	265.30
32	G32	151.86	22.00	2.89	27.58	13.01	213.60
33	G33	163.15	23.60	3.67	34.79	16.34	289.10
34	G34	161.42	23.30	3.56	33.21	14.91	282.70
35	G35	124.22	20.70	2.39	22.29	10.59	217.90
36	G36	160.6	22.40	3.32	32.97	14.60	281.80
37	G37	156.16	18.50	2.72	26.83	13.24	250.10
38	G38	152.35	17.40	2.61	25.75	12.70	252.00
39	G39	134.72	17.10	2.28	21.05	10.27	163.70
40	G40	133.55	14.30	1.88	17.69	8.69	103.00
Mean		145.44	19.00	2.62	24.74	11.72	193.30
S.Em±		5.81	1.49	0.16	1.43	0.79	16.24
CD at 5%		16.63	4.26	0.45	2.02	2.27	36.45
CD at 1%		22.26	5.70	0.60	10.78	3.04	42.19

4.3.18 Number of seeds per fruit

Highest number of seeds per fruit were noticed in genotype G9 (338.00) and lowest was observed in G20 (63.70) with mean of 193.30 (Table 14). This trait has recorded high GV (5493.13), PV (6198.95), GCV (38.34 %) and PCV (40.73 %). Similarly, the trait also recorded high heritability (88.61 %) and genetic advance as per cent of mean (75.45 %) (Table 11).

4.3.19 Sponge yield (g/fruit)

The sponge yield was recorded highest in the genotype G9 (18.09 g) and it was least in the genotype G20 (8.83g) with mean of 13.32 g (Table 15). The low GV (6.13) and PV (7.02), moderate GCV (18.62 %) and PCV (19.89 %), high heritability (87.32 %) and genetic advance as per cent of mean (35.81 %) were observed for this trait (Table 11).

4.3.20 Total soluble solids (⁰Brix)

Total soluble solids ranged between 3.58 (G33) to 6.14 ⁰Brix (G4) in the sponge gourd genotypes with mean of 4.78 ⁰Brix (Table 15). The low GV and PV (0.23 and 0.40 respectively) were observed for this trait (Table 11). The estimated values for GCV (10.04 %), PCV (13.18 %), heritability (57.50 %) and GAM (12.97 %) were found to be moderate for this trait.

4.3.21 Fruit firmness (N)

Fruit firmness ranged from 23.10 N (G24) to 45.82 N (G8) with average of 34.37 N, the GV and PV found were 35.40 and 38.41 respectively (Table 15). The value of GCV and PCV observed were moderate with 17.31 % and 18.04 % respectively (Table 11) with high heritability (92.16 %) and GAM (34.22 %).

4.3.22 Fruit color (L*, a*, b*)

Per se value for fruit color (L*) varied from 25.01 (G11) to 52.37 (G7) in the sponge gourd genotypes with average mean of 36.13 (Table 15). The high GV and PV observed for the trait were 28.95 and 30.93 respectively (Table 11). Moderate GCV and PCV (14.89 and 15.39 % respectively), high heritability (93.60 %) and GAM (29.70 %) were observed for this trait.

Table 15. *Per se* performance of sponge gourd genotypes for sponge yield and quality parameters

Sl. No.	Genotypes	Sponge yield (g/fruit)	TSS (^o Brix)	Fruit firmness (N)	Fruit color (L [*])	Fruit color (a [*])	Fruit color (b [*])	Protein (%)
1	G1	12.77	5.26	33.12	36.38	7.90	26.17	12.81
2	G2	15.06	3.84	24.11	31.00	7.08	23.42	11.17
3	G3	12.55	4.94	33.68	34.50	8.89	25.88	13.89
4	G4	12.16	6.14	40.77	43.81	6.88	26.20	15.91
5	G5	11.67	4.80	34.72	40.83	8.23	28.23	12.02
6	G6	10.79	4.90	42.55	46.40	7.72	28.02	11.64
7	G7	10.45	5.34	37.10	52.37	9.47	29.91	12.79
8	G8	12.81	5.75	45.82	39.15	9.14	29.50	15.82
9	G9	18.09	4.45	24.59	38.45	6.87	16.91	10.23
10	G10	13.97	5.21	34.82	29.44	7.87	22.83	15.13
11	G11	11.48	4.76	30.34	25.01	5.32	12.59	12.97
12	G12	9.01	5.29	30.84	34.71	8.09	22.15	13.96
13	G13	11.55	4.75	31.34	29.79	7.04	16.02	11.57
14	G14	12.06	5.34	34.32	40.33	8.47	26.20	12.67
15	G15	10.94	5.11	37.40	43.55	8.61	28.51	13.65
16	G16	15.91	4.38	27.72	33.35	7.42	20.97	10.3
17	G17	11.83	5.23	41.66	39.49	8.12	25.12	13.57
18	G18	12.03	5.40	36.51	31.34	7.59	17.74	11.76
19	G19	12.84	4.64	36.28	31.20	6.24	20.98	12.16
20	G20	8.83	5.29	41.78	37.02	7.95	23.88	12.11
21	G21	15.89	4.33	26.72	32.01	6.99	19.86	10.76
22	G22	17.06	4.29	25.32	33.18	7.63	17.89	11.09
23	G23	12.32	5.23	37.26	32.03	6.83	17.37	13.78
24	G24	17.84	4.42	23.10	31.90	6.63	16.63	10.79
25	G25	13.81	4.83	37.82	31.73	6.80	17.47	12.32
26	G26	12.16	5.12	30.88	36.38	6.33	29.09	11.01
27	G27	13.68	5.33	34.96	37.43	7.38	23.89	12.67
28	G28	11.78	4.77	34.88	38.75	7.03	20.79	9.76
29	G29	11.78	4.75	41.02	36.23	7.99	23.97	11.20
30	G30	13.56	4.96	44.83	29.22	5.99	13.69	12.22
31	G31	16.39	4.71	27.93	34.54	6.42	17.41	9.21
32	G32	14.32	4.96	38.09	30.49	6.19	16.90	12.22
33	G33	17.18	3.58	27.38	31.31	6.13	17.55	8.11
34	G34	16.19	4.12	28.37	42.79	8.14	25.06	9.45
35	G35	13.69	4.86	33.37	33.41	6.96	18.86	11.62
36	G36	15.48	3.78	28.16	38.85	7.91	23.74	10.03
37	G37	14.87	4.32	38.67	43.32	7.34	24.05	9.63
38	G38	14.23	3.86	39.11	36.19	7.16	17.87	8.76
39	G39	13.22	3.68	36.87	36.84	6.78	17.84	8.45
40	G40	10.63	4.42	40.77	40.44	8.24	27.58	13.54
Mean		13.32	4.78	34.37	36.13	7.39	21.97	11.82
S.Em±		0.67	0.24	1.23	0.99	0.17	0.43	0.30
CD at 5%		1.91	0.70	3.51	2.84	0.49	1.23	0.86
CD at 1%		2.56	0.94	4.70	3.80	0.65	1.65	1.15

Among the 40 genotypes evaluated fruit color (a^*) value was maximum in the genotype G7 (9.47) and it was least in the genotype G11 (5.32) with mean value of 7.39 (Table 15). GV and PV recorded for this trait were 0.80 and 0.86 respectively (Table 11). Moderate GCV and PCV (12.04 % and 12.58 % respectively) and high heritability (93.02 %) and GAM (24.09 %) were observed for this trait.

Fruit color value (b^*) varied from 12.59 (G11) to 29.91 (G7) with an average mean of 21.97 (Table 15). This trait has recorded high GV (22.11), (PV 22.88), GCV (21.39 %) and PCV (21.76 %). Similarly the trait also recorded high heritability (96.63 %) and GAM (43.74 %).

4.3.23 Protein content (%)

Among the 40 genotypes, protein content was highest in the genotype G4 (15.91 %) and it was lowest in the genotype G33 (8.11 %) with mean value 11.82 % (Table 15). This trait exhibited low GV and PV (2.54 and 2.72), moderate GCV and PCV (13.45 % and 13.96 %) with high heritability (93.38 %) and GAM (26.82 %) (Table 11).

4.3.24 Ascorbic acid (mg/100g)

The genotype G25 recorded highest value for ascorbic acid (9.72 mg) and lowest in the genotype G9 with 5.38 mg with a mean of 7.06 mg per 100 g (Table 16). The genotypic variance observed was low 0.85 with low phenotypic variance 1.12 (Table 11). This trait has shown moderate GCV (13.03 %) and PCV (14.87 %) with high heritability (75.89 %) coupled with high GAM (20.96 %).

4.3.25 Potassium content in fruit (%)

Fruit potassium content was maximum in the genotypes G4 and G8 (2.88 %) and it was lowest minimum in G24 (1.41 %) with a mean value of 2.22 % (Table 16). The observed GV and PV for this trait were 0.17 and 0.18 respectively. The calculated GCV and PCV were moderate (18.47 % and 18.92 %) with high heritability (94.44 %) and genetic advance over per cent of mean (37.39 %) were recorded for this trait (Table 11).

4.3.26 Fruit phenol content (mg GAE/100 g)

Among 40 genotypes studied, the fruit phenol content was highest in G8 with 344.40 mg GAE and lowest in G33 with 225.17 mg GAE with a mean observed was 288.24 mg GAE per 100 g (Table 16). The GV and PV observed were 734.04 and 755.12 respectively (Table 11). The observed GCV (9.40 %) and PCV (9.53 %) estimates were found to be low with high heritability (97.21 %) and moderate GAM (19.33 %).

4.3.27 Total antioxidants in fruit (mg AAE/100 g)

The total antioxidant value in fruit was maximum in the genotype G8 (841.95 mg AAE) while it was minimum in the genotype G33 (712.61 mg AAE) with a mean value of 778.01 mg AAE per 100 g (Table 16). The GV and PV observed were 1042.75 and 1085.24 respectively. There was less variability was seen for this trait as evidenced by low estimates of GCV and PCV (4.15 % and 4.23 % respectively) with high heritability (96.08 %) and GAM (10.04 %) were observed for total antioxidants in the fruit (Table 11).

4.3.28 Total flavonoids in fruit (mg QE/100g)

The genotypes varied significantly for fruit flavonoid content and it was maximum in the genotype G33 (25.56 mg QE) and least in the genotype G8 (48.29 mg QE) with a mean of 37.52 mg QE (Table 16). The GV and PV observed were 28.27 and 29.17 respectively (Table 11). GCV and PCV were moderate with 14.18 and 14.39 % respectively and high heritability (96.91 %) coupled with high GAM (28.73 %) was observed for this trait.

4.3.29 Crude fiber (%)

Crude fiber content was highest in the genotype G4 (14.96 %) and lowest in the genotype G24 (6.23 %) with mean value of 9.34 (Table 16). GV and PV observed were 3.08 and 3.34 respectively (Table 11). The GCV observed was moderate (18.79 %) along with moderate PCV (19.57 %), high heritability (92.22 %), low GA (3.69) and high GAM (39.51 %).

Table 16. Nutritional composition and antioxidant properties of sponge gourd genotypes

Sl. No.	Genotypes	Ascorbic acid (mg/100g)	Potassium (%)	Phenol (mg GAE/100g)	Anti-oxidants (mg AAE/100g)	Flavonoids (mg QE/100g)	Fiber (%)	Ash (%)
1	G1	6.94	2.42	323.01	814.00	47.95	10.84	9.23
2	G2	5.76	1.68	268.14	719.86	34.80	7.37	7.21
3	G3	8.20	2.44	320.23	813.06	42.50	14.53	10.07
4	G4	7.17	2.88	333.64	828.40	44.49	14.96	10.44
5	G5	8.50	2.76	324.56	815.29	39.45	10.88	8.38
6	G6	6.86	2.60	342.69	820.12	42.34	8.85	8.27
7	G7	6.91	2.43	290.32	775.54	37.72	11.23	9.34
8	G8	8.91	2.88	344.40	841.95	48.29	10.56	8.01
9	G9	5.38	1.62	256.34	754.98	29.79	6.46	7.05
10	G10	6.74	2.87	299.90	821.90	44.05	7.96	8.11
11	G11	7.31	2.21	286.80	782.66	39.54	9.02	9.55
12	G12	9.17	2.44	296.29	811.06	38.33	11.34	8.52
13	G13	7.11	2.30	279.56	785.14	36.16	8.23	8.06
14	G14	7.51	2.61	292.24	791.50	39.06	10.06	7.89
15	G15	6.57	2.23	311.16	802.84	41.29	12.06	7.56
16	G16	6.34	1.66	245.16	778.11	35.23	7.17	7.23
17	G17	7.06	2.76	284.66	764.05	27.11	10.51	8.05
18	G18	8.44	2.44	277.01	769.44	38.56	13.23	8.17
19	G19	7.63	2.64	321.27	776.51	42.52	9.09	7.16
20	G20	6.65	2.56	310.15	804.62	39.45	13.23	7.77
21	G21	6.01	1.73	253.89	719.85	34.67	6.84	7.11
22	G22	6.11	1.61	266.14	768.23	32.06	7.44	7.05
23	G23	8.18	2.67	286.16	722.09	37.34	9.11	9.16
24	G24	6.03	1.41	262.66	733.66	36.29	6.23	6.19
25	G25	9.72	2.56	313.41	766.43	37.59	9.32	8.34
26	G26	7.11	2.25	323.70	824.31	37.61	9.93	7.83
27	G27	6.89	2.54	276.15	802.74	44.15	10.81	8.20
28	G28	6.45	1.69	286.31	754.45	36.67	7.02	7.21
29	G29	8.40	2.77	320.16	811.01	44.83	11.23	8.56
30	G30	7.51	2.64	284.85	784.16	38.70	11.54	7.56
31	G31	6.34	1.68	254.65	756.51	32.66	7.45	7.01
32	G32	6.89	2.59	287.90	790.12	37.84	9.12	8.56
33	G33	5.66	1.52	225.17	712.61	25.56	7.23	7.42
34	G34	6.45	1.56	255.66	746.86	30.41	6.96	7.44
35	G35	8.56	2.48	290.67	782.01	37.50	9.56	7.60
36	G36	6.11	1.54	255.21	747.11	30.61	7.29	6.83
37	G37	6.16	1.45	268.45	759.14	33.90	7.12	7.44
38	G38	5.61	1.71	255.7	744.05	36.06	7.08	6.98
39	G39	6.35	1.46	269.97	755.11	27.67	6.69	6.34
40	G40	6.78	2.44	285.36	769.00	39.87	8.12	7.65
Mean		7.06	2.22	288.24	778.01	37.52	9.34	7.91
S.Em±		0.52	0.05	1.11	1.50	0.67	0.37	0.54
CD at 5%		1.48	0.16	3.17	4.29	1.92	1.07	1.54
CD at 1%		1.98	0.21	4.24	5.74	2.57	1.43	2.07



Plate 12a. Variation in fruit characters of sponge gourd genotypes



Plate 12b. Variation in fruit characters of sponge gourd genotypes

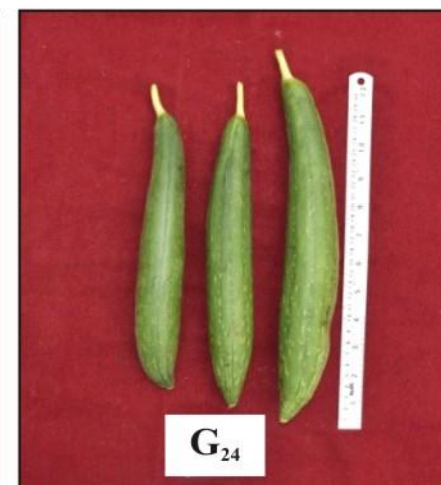


Plate 12c. Variation in fruit characters of sponge gourd genotypes



Plate 12d. Variation in fruit characters of sponge gourd genotypes



Plate 12e. Variation in fruit characters of sponge gourd genotypes

4.3.30 Ash content (%)

The values of ash content in fruits of sponge gourd were varied among the genotypes from 6.19 % (G24) to 10.44 % (G4) with average mean of 7.91 % (Table 16). The GV and PV observed were 0.64 and 1.22 respectively (Table 11). Moderate GCV and PCV estimates observed were 10.11 % and 13.91 %, respectively with moderate heritability (52.46 %), low GA (1.19) and moderate GAM (15.04 %).

The variation in fruit characteristics of 40 sponge gourd genotypes were shown in Plate 12a to 12e.

4.4 Genetic diversity study

The success of a breeding programme depends upon the selection of parents. It has been found that the progenies derived from crossing of diverse parents gives divergent and useful progenies. The D^2 analysis proposed by Mahalanobis (1936) has been reported to be an effective tool to assess the genetic divergence. This analysis eventually helps to choose desirable parents for crop improvement programme, which results in the development of high heterotic hybrids. The genetic diversity among 40 genotypes of sponge gourd was measured in this experiment by using Mahalanobis D^2 statistics for seventeen important yield attributing characters and all the genotypes were grouped into seven clusters using Tocher's method.

4.4.1 Relative contribution of different characters towards divergence

The relative contribution of different characters for genetic diversity is given in Table 17. Among all the characters studied, average fruit weight contributed maximum (14.54 %) to the genetic diversity by taking first rank in 114 times out of 783 combinations, followed by fruit yield per vine (13.25 % with 104 times ranked first), number of seeds per fruit (11.20 % with 88 times ranked first), phenol content (8.59 % with 67 times ranked first), sponge yield (8.54 % with 67 times ranked first), potassium content (7.69 % with 60 times ranked first), days to first harvest (6.25 % with 49 times ranked first), fruit diameter (5.22 % with 41 times ranked first), total soluble solids (4.65 % with 36 times ranked first), number of branches per vine (4.00 % with 31 times ranked first), ascorbic acid (3.65 % with 29 times ranked first), days to first female

flower (3.00 % with 23 times ranked first), number of fruits per vine (2.41 % with 19 times ranked first), node at first female flower (2.36 % with 18 times ranked first), vine length at harvest time (2.00 % with 16 times ranked first), fruit length (1.50 % with 12 times ranked first) and crude fiber content (1.15 % with nine times ranked first).

4.4.2 Classification of sponge gourd genotypes

Based on estimated Mahalanobis D^2 value forty sponge gourd genotypes were grouped into seven clusters by following Tocher's method. Cluster I had maximum number of nineteen genotypes followed by cluster II with ten genotypes, cluster III with seven genotypes while, cluster IV, cluster V, cluster VI and cluster VII were with one genotype each and is presented in Table 18. Dendrogram of clustering pattern of forty genotypes of sponge gourd was shown in Fig. 1.

4.4.3 Intra and inter-cluster distance

The intra and inter-cluster D^2 values among seven clusters were furnished in the Table 19. Intra-cluster D^2 values ranged from 0 to 667.55. Among the clusters, cluster III had the maximum intra-cluster distance ($D^2 = 667.55$) followed by cluster II ($D^2 = 665.10$) and cluster I ($D^2 = 466.27$). The clusters IV, V, VI and VII had no inter cluster distance (zero) as they had single genotypes in each cluster.

The inter cluster D^2 value ranged from 629.38 to 10081.40. The maximum inter cluster D^2 value was found between cluster IV and VI ($D^2 = 10081.40$) followed by cluster IV and VII ($D^2 = 8163.44$), cluster III and IV ($D^2 = 5374.53$), cluster II and cluster VI ($D^2 = 4944.16$), cluster IV and cluster V ($D^2 = 4643.08$), cluster II and cluster VII ($D^2 = 4498.17$), cluster I and IV ($D^2 = 3771.80$), cluster II and V ($D^2 = 2847.72$), cluster III and V ($D^2 = 2807.09$), cluster III and VII ($D^2 = 2594.97$), cluster I and VI ($D^2 = 2326.49$), cluster V and VI ($D^2 = 2186.73$), cluster III and VI ($D^2 = 2022.75$), cluster I and VII ($D^2 = 1898.12$), cluster II and IV ($D^2 = 1785.74$), cluster II and III ($D^2 = 1732.32$), cluster I and II ($D^2 = 1317.70$), cluster I and V ($D^2 = 1157.31$) and cluster I and III ($D^2 = 1151.48$). The minimum inter-cluster D^2 values were observed between cluster VI and VII ($D^2 = 629.38$) followed by cluster V and VII ($D^2 = 897.04$).

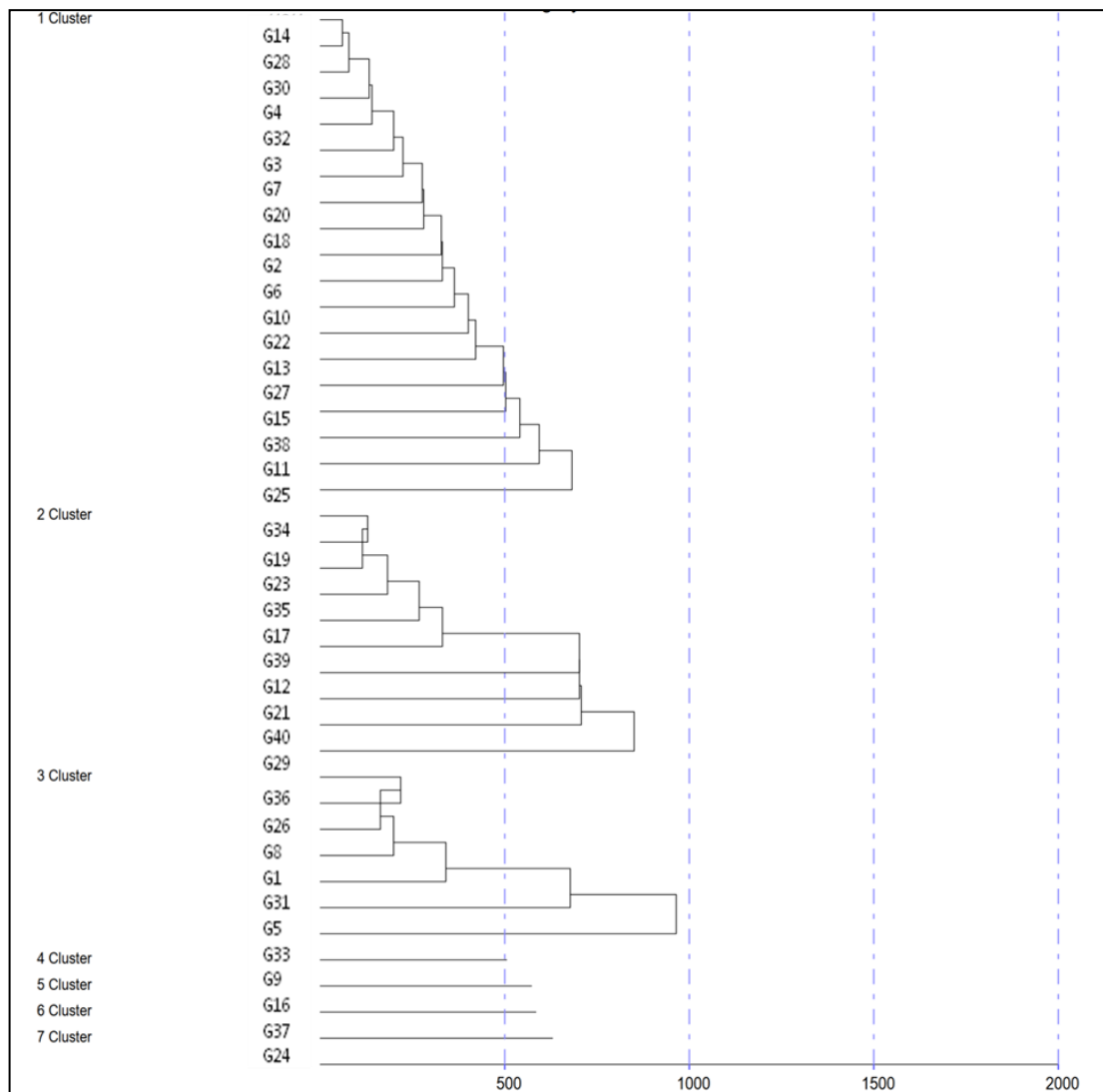


Fig. 1. Dendrogram of clustering pattern of fourty genotypes of sponge gourd

Table 17. Per cent contribution of seventeen characters towards total divergence in sponge gourd genotypes

Sl. No.	Character	Number of times ranked first	Per cent contribution
1	Vine length at harvest time	16	2.00
2	Number of branches at harvest time	31	4.00
3	Days to first female flower	23	3.00
4	Node at first female flowering	18	2.36
5	Days to first harvest	49	6.25
6	Fruit length	12	1.50
7	Fruit diameter	41	5.22
8	Average fruit weight	114	14.54
9	Number of fruits per vine	19	2.41
10	Fruit yield per vine	104	13.25
11	Number of seeds per fruit	88	11.20
12	Sponge yield	67	8.54
13	Total soluble solids	36	4.65
14	Ascorbic acid	29	3.65
15	Potassium content	60	7.69
16	Phenol content	67	8.59
17	Crude fiber	9	1.15
	Total	783	100.00

Table 18. Classification of sponge gourd genotypes into different clusters based on D^2 statistics

Cluster	Number of genotypes	Genotypes included in the cluster
I	19	G14, G28, G30, G4, G32, G3, G7, G20, G18, G2, G6, G10, G22, G13, G27, G15, G38, G11, G25
II	10	G34, G19, G23, G35, G17, G39, G12, G21, G40, G29
III	7	G36, G26, G8, G1, G31, G5, G33
IV	1	G9
V	1	G16
VI	1	G37
VII	1	G24

Table 19. Average intra-cluster (diagonal) and inter-cluster D^2 value in sponge gourd genotypes

Clusters	I	II	III	IV	V	VI	VII
I	466.27	1317.70	1151.48	3771.80	1157.31	2326.49	1898.12
II		665.10	1732.32	1785.74	2847.72	4944.16	4498.17
III			667.55	5374.53	2807.09	2022.75	2594.97
IV				0.00	4643.08	10081.40	8163.44
V					0.00	2186.73	897.04
VI						0.00	629.38
VII							0.00

4.4.4 Cluster means analysis

The mean values of 17 characters for seven clusters are summarized as follows (Table 20).

4.4.4.1 Vine length at harvest time

The highest cluster mean was recorded in cluster IV (7.07 m) for vine length accompanied by cluster VII (6.86 m) and cluster V (6.41 m). Whereas, lowest was found in cluster I (5.83 m) and second lowest was in cluster II (6.00 m) for vine length.

4.4.4.2 Number of branches per vine

The mean number of branches per vine was highest in cluster IV (6.20) followed by cluster VII (6.10) and cluster V (5.90). However, lowest cluster mean was observed in cluster I (4.05) followed by cluster II (4.18).

4.4.4.3 Days to first female flower

The cluster IV showed lowest cluster mean (42.80 days) for days to first female flower appearance succeeded by cluster V (43.30 days) and cluster VII (43.50 days). The highest mean was observed in cluster I (51.06 days) accompanied by cluster III (49.70 days).

4.4.4.4 Node at first female flower appearance

The cluster IV and cluster VII (9.30) exhibited lowest cluster mean for node at first female flowering followed by cluster V (10.80) and cluster VI (11.40). The highest mean was observed in the cluster I (13.89) and cluster II (13.38).

4.4.4.5 Days to first harvest

The cluster mean for days to first fruit picking was maximum in cluster IV (51.80 days) succeeded by cluster VII (52.50 days) and cluster V (54.30 days). Whereas, highest cluster mean was noticed in cluster I (61.13 days) accompanied by cluster II (58.64 days).

Table 20. Cluster mean values for yield and its components in sponge gourd genotypes

Sl. No.	Character	Cluster mean						
		I	II	III	IV	V	VI	VII
1	Vine length at harvest time	5.83	6.00	6.04	7.07	6.41	6.39	6.86
2	Number of branches	4.05	4.18	4.36	6.20	5.90	4.80	6.10
3	Days to first female flower	51.06	48.84	49.70	42.80	43.30	46.50	43.50
4	Node at first female flower	13.89	13.38	12.67	9.30	10.80	11.40	9.30
5	Days to first harvest	61.13	58.64	58.47	51.80	54.30	55.80	52.50
6	Fruit length	20.52	19.96	22.42	27.12	24.65	22.76	26.06
7	Fruit diameter	30.74	30.84	31.07	37.43	35.11	32.70	36.17
8	Average fruit weight	145.73	134.76	149.70	170.25	161.42	156.16	165.50
9	Number of fruits per vine	18.46	19.18	18.13	24.80	23.40	18.50	23.80
10	Fruit yield per vine	2.52	2.47	2.62	3.85	3.68	2.72	3.69
11	Number of seeds per fruit	165.31	201.90	197.93	338.00	276.40	250.10	322.20
12	Sponge yield	12.65	12.74	14.07	18.09	15.91	14.87	17.84
13	Total soluble solids	4.95	4.66	4.71	4.45	4.38	4.32	4.42
14	Ascorbic acid	7.07	7.46	7.08	5.38	6.34	6.16	6.03
15	Potassium content	2.33	2.30	2.15	1.62	1.66	1.71	1.41
16	Phenol content	293.81	286.41	292.96	256.34	245.16	268.45	262.66
17	Crude fiber	10.16	8.95	9.17	6.46	7.17	7.12	6.23

4.4.4.6 Fruit length

The highest cluster mean was recorded in cluster IV (27.12 cm) for fruit length followed by cluster VII (26.06 cm) and cluster V (24.65 cm). While, lowest was found in cluster II (19.96 cm) and second lowest was noticed in cluster I (20.52 cm).

4.4.4.7 Fruit diameter

The highest cluster mean for fruit diameter was observed in cluster IV (37.43 mm) followed by cluster VII (36.17 mm) and cluster V (35.11 mm). The least was observed in cluster I (30.74 mm) and cluster II (30.84 mm).

4.4.4.8 Average fruit weight

The character average fruit weight had highest cluster mean in cluster IV (170.25 g) followed by cluster VII (165.50 g) and cluster V (161.42 g). While, the lowest cluster mean was noticed in cluster II (134.76 g) and cluster I (145.73 g).

4.4.4.9 Number of fruits per vine

The cluster IV recorded highest mean (24.80) for number of fruits per vine followed by cluster VII (23.80) and cluster V (23.40) whereas, lowest cluster mean was observed in cluster III (18.13) and cluster I (18.46).

4.4.4.10 Fruit yield per vine

The cluster IV showed highest cluster mean (3.85 kg) for fruit yield per vine followed by cluster VII (3.69 kg) and cluster V (3.68 kg). The lowest cluster mean was observed in cluster II (2.47 kg) and cluster I (2.52 kg).

4.4.4.11 Number of seeds per fruit

Number of seeds per fruit showed highest cluster means in cluster IV (338.00) followed by cluster VII (322.20) and cluster V (276.40). The lowest cluster mean was observed in cluster I (165.31) and cluster III (197.93).

4.4.4.12 Sponge yield

The highest cluster mean for sponge yield was observed in cluster IV (18.09 g) followed by cluster VII (15.91 g) and cluster V (17.84 g). The lowest cluster mean was observed in cluster I (12.65 g) and cluster II (12.74 g).

4.4.4.13 Total soluble solids

The cluster I (4.95 °Brix) showed highest cluster mean for total soluble solids followed by cluster III (4.71 °Brix) and cluster II (4.66 °Brix). The lowest cluster mean was observed in cluster VI (4.32 °Brix) and cluster V (4.38 °Brix).

4.4.4.14 Ascorbic acid

The highest cluster mean for ascorbic acid content was observed in cluster II (7.46 mg) followed by cluster III (7.08 mg) and cluster I (7.07 mg). The lowest cluster mean was recorded in cluster IV (5.38 mg) and cluster VII (6.03 mg).

4.4.4.15 Fruit potassium content

Cluster I recorded highest mean (2.33 %) for fruit potassium content followed by cluster II (2.30 %) and cluster III (2.15 %) with lowest cluster mean in cluster VII (1.41 %) and cluster IV (1.62 %).

4.4.4.16 Fruit phenol content

Highest cluster mean for this character was noted in the cluster I (293.81 mg GAE) followed by cluster III (292.96 mg GAE) and cluster II (286.41 mg GAE). The lowest cluster mean was observed in cluster V (245.16 mg GAE) and cluster IV (256.34 mg GAE).

4.4.4.17 Fruit crude fiber

The cluster I observed highest cluster mean (10.16 %) for crude fiber content in fruit, followed by cluster III (9.17 %) and cluster II (8.95 %), while, it was lowest in cluster VII (6.23 %) and cluster IV (6.46 %).

4.5 Molecular characterization

The assessment of genetic diversity using molecular markers has been generally superior to morphological markers. The genetic diversity is commonly assessed by genetic distance with comparison of genetic similarity. Hence, an attempt has been made to assess the genetic diversity in 40 genotypes of sponge gourd using 20 SSR marker. For analysis at molecular level, 30 SSR primers were used, out of which five were found to be monomorphic, 5 primers has not shown any bands and twenty primers were polymorphic. Hence they were further used for genetic diversity analysis on the basis of scorable amplified bands.

The number of alleles per each locus (N_a), number of effective alleles (N_e), Major allele frequency (MAF), Shanon's information Index (I), observed heterozygosity (H_o), expected heterozygosity (H_e), fixation index (F) and polymorphic information content (PIC) were determined by using the software package GENALEX 6.50 version and is presented in Table 21.

The number of alleles per locus (N_a) ranged from 2 to 6 with an average of 3.65. The highest number of alleles (6) was detected in primer SG_La_28. The number of effective alleles per locus (N_e) ranged from 1.34 to 3.36 with an average of 2.17. The major allele frequency ranged from 0.12 to 0.50 with a mean of 0.30. Shanon's information index (I) ranged from 0.51 to 1.31 with an average of 0.89. Fixation index ranged from -0.15 to 1.00 with a mean value of 0.62.

PIC (polymorphic information content) value is a reflection of allele diversity and frequency among varieties it ranged from 0.24 to 0.65 with an average of 0.44. The high polymorphism information content (PIC) value was found by the marker SG_La_28 (0.65) followed by the marker SG_La_11, SG_La_15 (0.61), SG_La_27 (0.59), SG_La_13 (0.56), SG_La_25 (0.51) and SG_La_8 (0.50). Banding profile of SSR markers obtained on agarose gel of sponge gourd genotypes were shown in the Plate 13.

Table 21. Details of the genetic parameters of molecular markers used for characterizing sponge gourd genotypes

Sl. No.	Markers	Genetic parameters								
		Na	Ne	MAF	I	Ho	He	uHe	F	PIC
1	SG_La_1	2.00	1.60	0.50	0.56	0.00	0.38	0.38	1.00	0.31
2	SG_La_4	5.00	1.52	0.20	0.72	0.00	0.34	0.35	1.00	0.32
3	SG_La_7	3.00	2.11	0.33	0.80	0.61	0.53	0.53	-0.15	0.41
4	SG_La_8	3.00	2.35	0.33	0.96	0.35	0.57	0.58	0.39	0.50
5	SG_La_10	2.00	1.90	0.50	0.67	0.78	0.47	0.48	-0.63	0.36
6	SG_La_11	5.00	3.03	0.20	1.24	0.41	0.67	0.68	0.39	0.61
7	SG_La_12	2.00	1.98	0.50	0.69	0.90	0.50	0.50	-0.82	0.37
8	SG_La_13	4.00	2.59	0.25	1.13	0.00	0.61	0.62	1.00	0.56
9	SG_La_14	3.00	2.18	0.33	0.85	0.00	0.54	0.55	1.00	0.44
10	SG_La_15	5.00	2.84	0.20	1.27	0.17	0.65	0.66	0.73	0.61
11	SG_La_19	4.00	1.99	0.25	0.92	0.00	0.50	0.50	1.00	0.45
12	SG_La_20	3.00	1.73	0.33	0.73	0.00	0.42	0.43	1.00	0.37
13	SG_La_21	2.00	1.70	0.50	0.60	0.00	0.41	0.42	1.00	0.33
14	SG_La_23	3.00	1.71	0.33	0.75	0.26	0.42	0.42	0.38	0.38
15	SG_La_24	3.00	1.34	0.33	0.51	0.00	0.26	0.26	1.00	0.24
16	SG_La_25	5.00	2.72	0.12	1.16	0.16	0.24	0.24	0.37	0.51
17	SG_La_27	5.00	3.36	0.20	1.31	0.00	0.70	0.71	1.00	0.59
18	SG_La_28	6.00	2.89	0.17	1.27	0.03	0.65	0.66	0.96	0.65
19	SG_La_29	4.00	2.31	0.25	0.97	0.13	0.57	0.58	0.77	0.49
20	SG_La_30	4.00	1.54	0.25	0.71	0.00	0.35	0.36	1.00	0.33
	Mean	3.65	2.17	0.30	0.89	0.19	0.49	0.50	0.62	0.44

Na-Number of alleles

MAF-Major allele frequency

Ho-Observed heterozygosity

uHe-unbiased expected heterozygosity

PIC-Polymorphic information content

Ne-No of effective alleles

I-Shanon's Information index

He-Expected heterozygosity

F-Fixation index

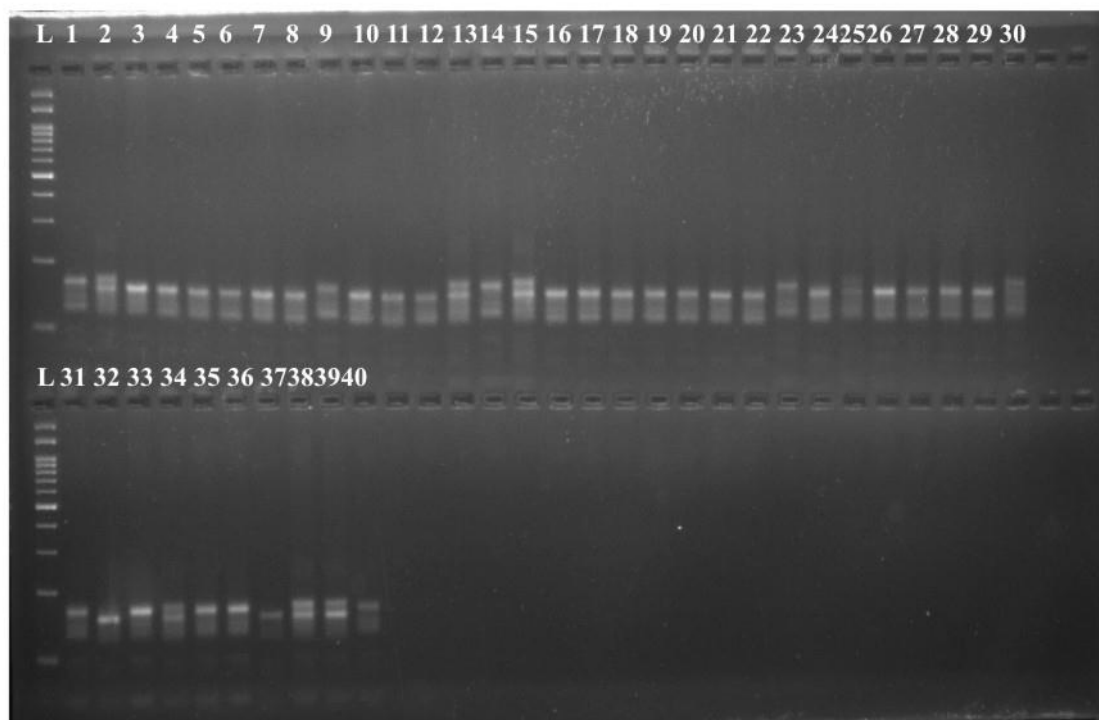


Plate 13a. Banding profile of SSR marker (SG_La_1) obtained on agarose gel of sponge gourd genotypes

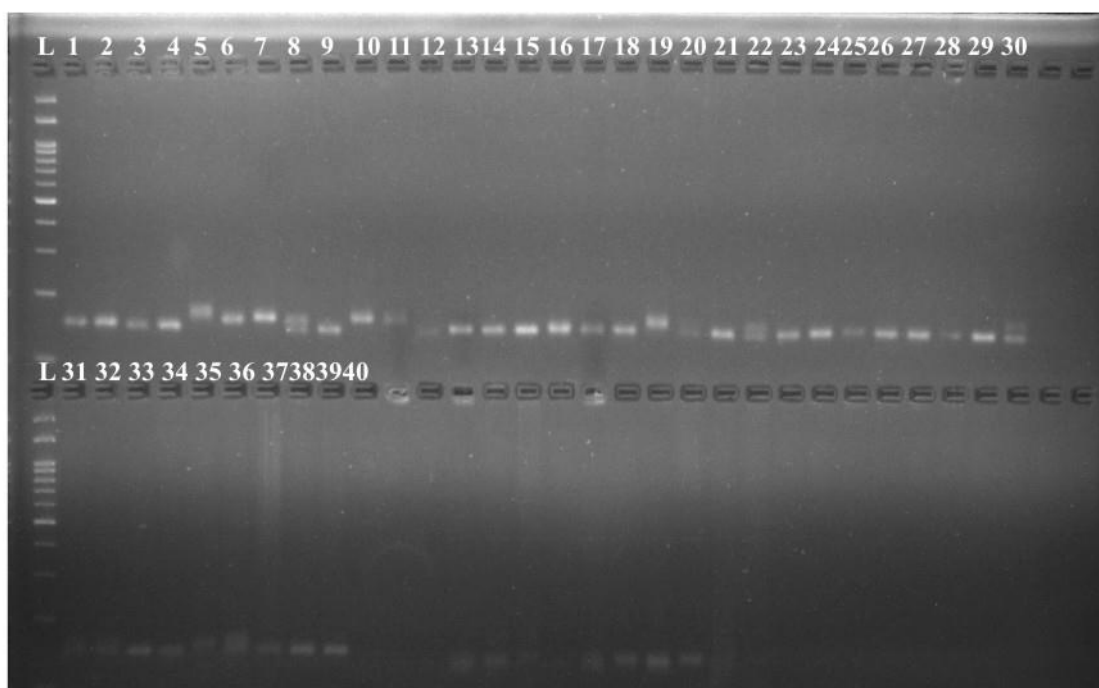


Plate 13b. Banding profile of SSR marker (SG_La_4) obtained on agarose gel of sponge gourd genotypes

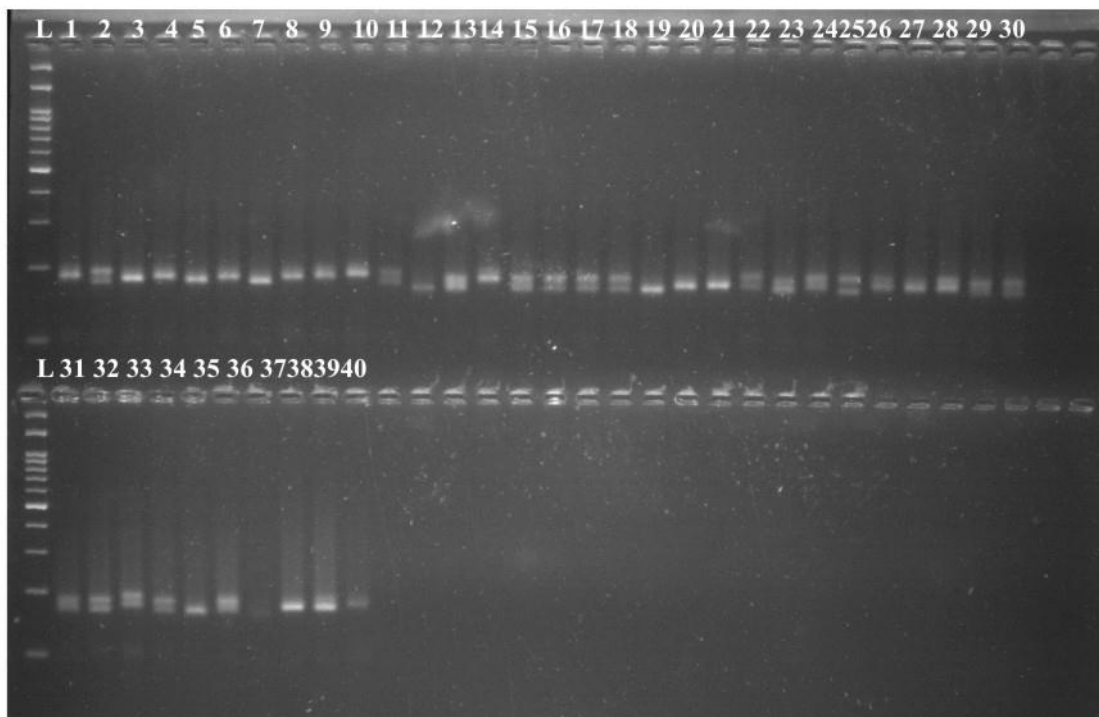


Plate 13c. Banding profile of SSR marker (SG_La_11) obtained on agarose gel of sponge gourd genotypes

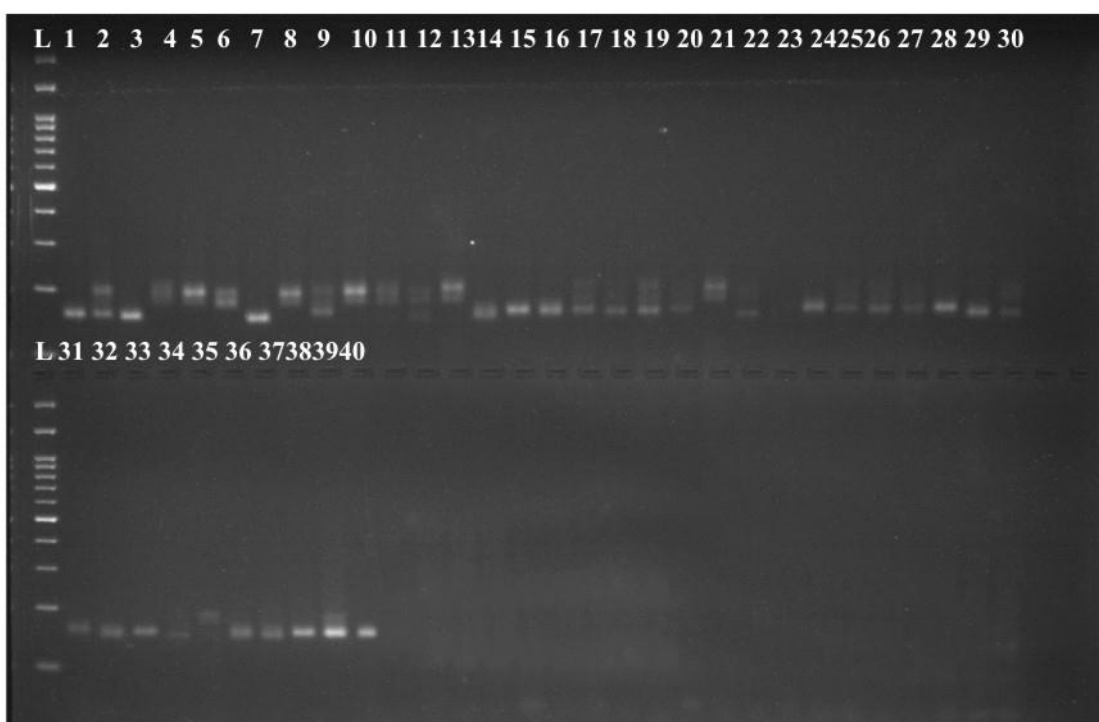


Plate 13d. Banding profile of SSR marker (SG_La_28) obtained on agarose gel of sponge gourd genotypes

Heterozygosity is an important measurement depicts the gene diversity. In general, the observed heterozygosity (0.19) in the total sample was much lesser when compared with the expected heterozygosity (0.49) in the genotypes for almost all the loci indicating the deficiency of heterozygote's at these loci. The superior genotypes of this germplasm panel are suitable for hybridization.

To study the molecular diversity of 40 sponge gourd genotypes they were subjected to cluster analysis with unweighted neighbour joining tree using a software package DARwin 6.0. All the 40 genotypes were grouped into three main clusters, cluster II had maximum number of twenty one genotypes followed by cluster III with fourteen genotypes, cluster I with five genotypes and is presented in Fig. 2 and Table 22.

4.6 Correlation co-efficient analysis

Correlation coefficient at both genotypic and phenotypic levels shows the mutual relationship between yield and its component traits on which selection can be done for improvement of dependent character. The yield improvement in sponge gourd can be achieved by indirect selection through other easily observable characters. But this needs a good understanding of the association of different traits with yield and other possible associations among themselves. In general, the genotypic correlation coefficients were higher than phenotypic correlation coefficients which might be due to the masking effect of the environment in the total expression of the genotypes resulting in reduced phenotypic association.

4.6.1 Phenotypic correlation co-efficient analysis

The phenotypic correlation co-efficients for different characters in sponge gourd are presented in Table 23.

The fruit yield per vine in the present study had highly significant (at $p=0.01$) and positive correlation with number of fruits per vine (0.784), vine length (0.532) and fruit length (0.508). While, it is positive and significantly (at $p=0.05$) correlated with sponge yield (0.484), number of branches per vine (0.453) and average fruit weight

(0.434). It also had a positive but non-significant correlation with crude fiber content (0.133), TSS (0.097), number of seeds per vine (0.033) and potassium content (0.011). However, the traits such as phenol content (-0.250), days to first fruit harvest (-0.210), days to first female flower (-0.206), node at first female flower (-0.178), ascorbic acid (-0.146) and fruit diameter (-0.096) were negatively and non-significantly associated with fruit yield per vine at phenotypic level.

The vine length had highly significant and positive association with number of fruits per vine (0.533) and fruit yield per vine (0.532) at phenotypic level. While, positive significant (at $p=0.05$) association was observed for fruit length (0.458) and sponge yield (0.449). The trait, number of branches per vine showed highly significant (at $p=0.01$) positive association with sponge yield (0.503) while, it exhibited positive significant association with fruit yield per vine (0.453), number of fruits per vine (0.407) and fruit length (0.365).

Days to first female flowering had manifested negative and significant correlation with sponge yield (-0.431) and number of fruits per vine (-0.387). But it was exhibited positive and highly significant correlation with days to first harvest (0.738) and it also exhibited significant positive association with average fruit weight (0.370).

The trait node at which first female flower appear had shown negative but non-significant association with fruit yield per vine (-0.178), number of seeds per fruit (-0.119), fruit diameter (-0.088), phenol content (-0.080) and TSS (-0.029). Days taken for first fruit harvest had significant and negative association with sponge yield (-0.398) and number of fruits per vine (-0.390).

Fruit length had recorded positive and highly significant (at $p=0.01$) correlation with fruit yield per vine (0.508). While, it exhibited significant and positive association with sponge yield (0.439) and number of fruits per vine (0.317).

The parameter fruit diameter had exhibited positive and non-significant correlation with crude fiber content (0.299), ascorbic acid (0.205), TSS (0.192), potassium content (0.160), number of seeds per fruit (0.148) and number of fruits per vine (0.016).

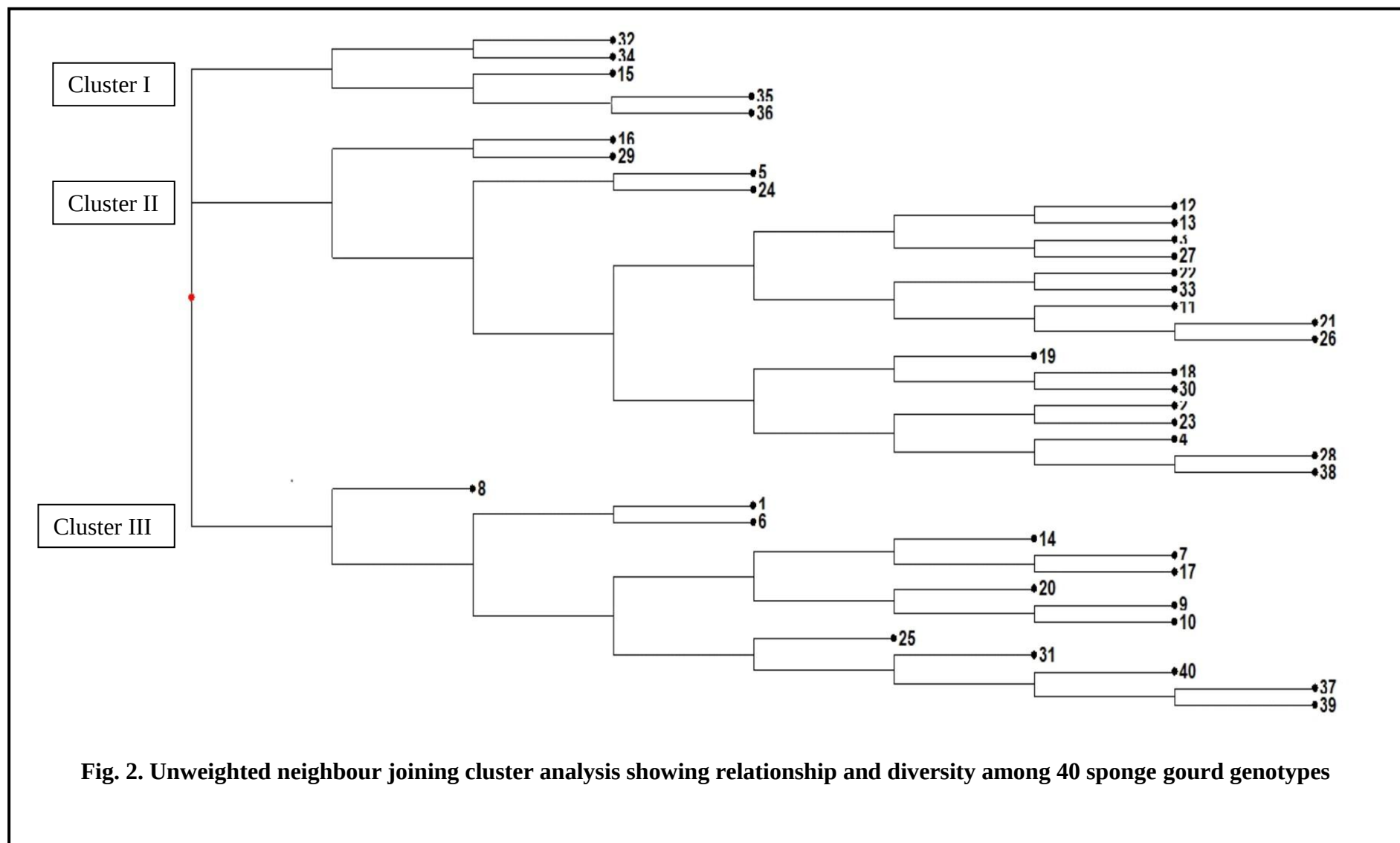


Fig. 2. Unweighted neighbour joining cluster analysis showing relationship and diversity among 40 sponge gourd genotypes

Table 22. Clustering pattern of forty genotypes of sponge gourd on the basis of molecular marker analysis

Sl. No.	Cluster	Number of genotypes	Genotypes
1.	Cluster I	5	G32, G34, G15, G35, G36
2.	Cluster II	21	G16, G29, G5, G24, G12, G13, G3, G27, G22, G33, G11, G21, G26, G19, G18, G30, G2, G23, G4, G28, G38
3.	Cluster III	14	G8, G1, G6, G14, G7, G17, G20, G9, G10, G25, G31, G40, G37, G39

Table 23. Estimates of phenotypic correlation coefficients for yield and its attributing traits in sponge gourd genotypes

	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉	X ₁₀	X ₁₁	X ₁₂	X ₁₃	X ₁₄	X ₁₅	X ₁₆	X ₁₇
X ₁	1.000	0.287	-0.296	0.025	-0.397*	0.458*	-0.192	0.067	0.533**	0.133	0.449*	0.165	-0.095	0.080	-0.123	-0.036	0.532**
X ₂		1.000	-0.254	0.240	-0.149	0.365*	-0.118	0.043	0.407*	0.067	0.503**	0.056	-0.212	0.093	-0.120	-0.061	0.453*
X ₃			1.000	-0.181	0.738**	-0.292	0.090	0.370*	-0.387*	-0.157	-0.431*	-0.087	0.075	-0.124	0.147	-0.110	-0.206
X ₄				1.000	0.022	0.140	-0.088	0.060	0.112	-0.119	0.187	-0.029	0.145	0.184	-0.080	0.077	-0.178
X ₅					1.000	-0.217	0.035	0.300	-0.390*	-0.184	-0.398*	-0.110	0.130	-0.190	0.169	-0.077	-0.210
X ₆						1.000	-0.309	0.230	0.317*	0.074	0.439*	-0.084	-0.032	-0.068	0.064	-0.051	0.508**
X ₇							1.000	-0.108	0.016	0.148	-0.133	0.192	0.205	0.160	-0.169	0.299	-0.096
X ₈								1.000	-0.090	-0.222	-0.035	-0.216	-0.212	-0.300	0.053	0.021	0.434*
X ₉									1.000	0.084	0.456*	0.272	-0.005	0.208	-0.296	0.159	0.784**
X ₁₀										1.000	0.190	0.171	-0.138	0.199	-0.115	0.152	0.033
X ₁₁											1.000	0.186	-0.220	0.093	-0.281	-0.116	0.484*
X ₁₂												1.000	0.087	0.168	-0.233	0.208	0.097
X ₁₃													1.000	0.160	0.244	0.030	-0.146
X ₁₄														1.000	-0.023	0.071	0.011
X ₁₅															1.000	-0.160	-0.250
X ₁₆																1.000	0.133
X ₁₇																	1.000

Critical r value at 5 % = 0.312, Critical r value at 1 % = 0.500

*Indicates significant at 5 %

**Indicates significant at 1 %

X₁= Vine length at harvestX₂= Number of branches per vineX₃= Days to first female flowerX₄= Node at first female flowerX₅= Days to first harvestX₆= Fruit lengthX₇= Fruit diameterX₈= Average fruit weightX₉= Number of fruits per vineX₁₀= No. of seeds per fruitX₁₁= Sponge yieldX₁₂= TSSX₁₃= Ascorbic acidX₁₄=Potassium contentX₁₅= Phenol contentX₁₆= Crude fiberX₁₇= Fruit yield per vine

Phenotypic correlation co-efficient for average fruit weight had exhibited significant and positive correlation with fruit yield per vine (0.434). The character number of fruits per vine had positive and highly significant ($p=0.01$) correlation with fruit yield per vine (0.784) while, it showed positive and significant association with sponge yield (0.456).

The trait number of seeds per fruit had positive but non-significant correlation with sponge yield (0.190), potassium content (0.199), TSS (0.171), crude fiber content (0.152) and fruit yield per vine (0.033). Whereas, sponge yield had manifested positive and significant correlation with fruit yield per vine (0.484).

The total soluble solids had positive association with crude fiber content (0.208), potassium (0.168), fruit yield per vine (0.097) and ascorbic acid content (0.087). The ascorbic acid content in fruit has a positive correlation with phenol (0.244), potassium content (0.160) and crude fiber content (0.030). Whereas, potassium content in fruits had positive association with crude fiber content (0.071) and fruit yield per vine (0.011).

Phenol content had exhibited negative association with fruit yield per vine (-0.250) and crude fiber content (-0.160). Whereas, crude fiber content in fruit had exhibited positive association with fruit yield per vine (0.133)

4.6.2 Genotypic correlation co-efficient

The data pertaining to genotypic correlation co-efficients for different characters in sponge gourd are presented in Table 24.

At genotypic level fruit yield per vine had highly positive and significant ($p=0.01$) association with number of fruits per vine (0.914), vine length (0.769), number of branches per vine (0.564), fruit length (0.555) and sponge yield (0.531). While, it had positive and significant correlation with average fruit weight (0.439). However, the trait exhibited negative and significant correlation with node at first female flower (-0.437) and days to first harvest (-0.328) which is desirable. It also similarly exhibited positive but non-significant association with crude fiber content (0.147), TSS (0.130), number of seeds per vine (0.048) and potassium content. Further, negative and non-significant association was noticed with days to first female flower (-0.248), fruit diameter (-0.127), ascorbic acid (-0.213) and phenol (-0.250) content.

Table 24. Estimates of genotypic correlation coefficients for yield and its attributing traits in sponge gourd genotypes

	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉	X ₁₀	X ₁₁	X ₁₂	X ₁₃	X ₁₄	X ₁₅	X ₁₆	X ₁₇
X ₁	1.000	0.622**	-0.372*	-0.099	-0.525**	0.589**	-0.068	0.093	0.856**	0.176	0.773**	0.319*	-0.088	0.097	-0.175	-0.062	0.769**
X ₂		1.000	-0.491*	0.745**	-0.529**	0.517**	-0.233	0.055	0.555**	0.051	0.650**	-0.010	-0.203	0.085	-0.151	-0.114	0.564**
X ₃			1.000	-0.387*	0.821**	-0.388*	0.173	0.449*	-0.586**	-0.198	-0.539**	-0.276	0.017	-0.187	0.176	-0.112	-0.248
X ₄				1.000	-0.095	0.197	-0.251	0.129	0.519**	-0.214	0.332*	0.070	0.260	0.429*	-0.204	0.050	-0.437*
X ₅					1.000	-0.414*	0.030	0.464*	-0.644**	-0.288	-0.651**	-0.443*	0.174	-0.287	0.262	-0.167	-0.328*
X ₆						1.000	-0.363*	0.252	0.448*	0.121	0.539**	-0.127	-0.084	-0.111	0.065	-0.055	0.555**
X ₇							1.000	-0.144	-0.044	0.240	-0.193	0.292	0.237	0.278	-0.214	0.364*	-0.127
X ₈								1.000	-0.103	-0.231	-0.035	-0.286	-0.264	-0.305	0.054	0.021	0.439*
X ₉									1.000	0.172	0.626**	0.321*	0.020	0.270	-0.350*	0.173	0.914**
X ₁₀										1.000	0.218	0.276	-0.149	0.214	-0.120	0.180	0.048
X ₁₁											1.000	0.260	-0.372*	0.107	-0.298	-0.146	0.531**
X ₁₂												1.000	0.129	0.196	-0.298	0.226	0.130
X ₁₃													1.000	0.221	0.320*	0.102	-0.213
X ₁₄														1.000	-0.024	0.079	0.012
X ₁₅															1.000	-0.166	-0.250
X ₁₆																1.000	0.147
X ₁₇																	1.000

Critical r value at 5 % = 0.312, Critical r value at 1 % = 0.500

* Indicates significant at 5 %

** Indicates significant at 1 %

X₁= Vine length at harvestX₂= Number of branches per vineX₃= Days to first female flowerX₄= Node at first female flowerX₅= Days to first harvestX₆= Fruit lengthX₇= Fruit diameterX₈= Average fruit weightX₉= Number of fruits per vineX₁₀= No. of seeds per fruitX₁₁= Sponge yieldX₁₂= TSSX₁₃= Ascorbic acidX₁₄= Potassium contentX₁₅= Phenol contentX₁₆= Crude fiberX₁₇= Fruit yield per vine

The vine length had showed highly significant ($p=0.01$) and positive association with number of fruits per vine (0.856), sponge yield (0.773), fruit yield per vine (0.769), number of branches per vine (0.622) and fruit length (0.589). While, it had positive significant correlation with TSS (0.319). However, negative and highly significant association was observed for days to first fruit harvest (-0.525) and negative significant association with days to first female flower (-0.372).

The number of branches per vine had exhibited highly significant ($p=0.01$) and positive association with node at first female flower (0.745), sponge yield (0.650), fruit yield per vine (0.564), number of fruits per vine (0.555) and fruit length (0.517). Whereas, it exhibited negative and highly significant association ($p=0.01$) with days to first harvest (-0.529) and negative significant association with days to first female flower (-0.491).

Days to first female flower appearance had showed negative and highly significant correlation with number of fruits per vine (-0.586) and sponge yield (-0.539). It had negative and significant association with fruit length (-0.388) and node at first female flower (-0.387). While it had positive and highly significant ($p=0.01$) correlation with days to first harvest (0.821) and it exhibited significant at $p=0.05$ and positive association with average fruit weight (0.449).

The parameter, node at first female flower appearance had shown negative and significant association with fruit yield per vine (-0.437). While it exhibited positive and highly significant ($p=0.01$) association with number of fruits per vine (0.519) and it showed positive and significant association with potassium content (0.429) and sponge yield (0.332).

It was noticed that days to first fruit harvest had exhibited highly significant and negative association with sponge yield (-0.651) and number of fruits per vine (-0.644). Whereas, significant and negative association was observed for TSS (-0.443), fruit length (-0.414) and fruit yield per vine (-0.328). While it exhibited positive and significant association with average fruit weight (0.464).

Fruit length had positive and highly significant ($p=0.01$) correlation with fruit yield per vine (0.555) and sponge yield (0.539). While, it exhibited significant and

positive association with number of fruits per vine (0.448). Whereas, significant and negative association between fruit length and fruit diameter (-0.363) was seen.

The trait fruit diameter had exhibited positive and significant correlation with crude fiber content (0.364). The average fruit weight was recorded significant and positive association with fruit yield per vine (0.439).

The character number of fruits per vine had exhibited positive and highly significant correlation with fruit yield per vine (0.914) and sponge yield (0.626) while, it recorded positive and significant association with TSS content (0.321). It also exhibited significant negative association with phenol content (-0.350).

Number of seeds per fruit had exhibited positive and non-significant correlation with TSS (0.276), sponge yield (0.218), potassium content (0.214), crude fiber content (0.180) and fruit yield per vine (0.048).

The fruit sponge yield had recorded positive and highly significant correlation with fruit yield per vine (0.531). However, it has negative significant correlation with ascorbic acid content (-0.372). The total soluble solids had positive association with crude fiber (0.226), potassium content (0.196), fruit yield per vine (0.130) and ascorbic acid content (0.129).

Ascorbic acid content in the fruit has a positive significant correlation with phenol content (0.320). Whereas, potassium content had positive association with crude fiber content (0.079) and fruit yield per vine (0.012). Besides that, crude fiber content had showed positive association with fruit yield per vine (0.147).

4.7 Path co-efficient analysis

The correlation would only indicate the overall relationship of independent trait with dependent trait but does not provide cause and effect relationship. Using path analysis, it is possible to resolve the correlations, which provide clue about such relationship. In sponge gourd seventeen important growth, yield and quality parameters were subjected to genotypic and phenotypic path coefficient analysis by considering total yield as dependent variable on sixteen other are independent variables.

4.7.1 Phenotypic path co-efficient analysis

The data pertaining to the phenotypic path co-efficient for different characters of sponge gourd are presented in Table 25.

Among all characters studied yield per vine had exhibited positive direct effect through number of fruits per vine (0.721), average fruit weight (0.487), fruit length (0.092), sponge yield (0.080), number of seeds per fruit (0.060), number of branches per vine (0.047), crude fiber content (0.019), ascorbic acid (0.015) and vine length (0.014). While, node at first female flower (-0.098), phenol content (-0.040), days to first female flower (-0.029), TSS (-0.024), fruit diameter (-0.022), days to first harvest (-0.021) and potassium content (-0.011) had negative direct effect on fruit yield per vine.

The vine length had positive and direct effect on fruit yield per vine (0.014) but it also had indirect and positive effect via through number of fruits per vine (0.007), fruit length (0.006), sponge yield (0.006), number of branches per vine (0.004), node at first female flower (0.003), number of seeds per fruit (0.002), TSS (0.002), average fruit weight (0.001) and potassium content (0.001).

Number of branches per vine showed positive direct effect (0.047) on yield per vine via sponge yield (0.023), number of fruits per vine (0.019), fruit length (0.017), vine length (0.013), potassium content (0.004), number of seeds per fruit (0.003), TSS (0.003) and average fruit weight (0.002).

Days to appearance of first female flower had negative direct impact (-0.029) on yield per vine through indirect effect of average fruit weight (-0.011), phenol content (-0.004), fruit diameter (-0.003) and ascorbic acid (-0.002).

The character, node at first female flower appearance had exerted negative direct effect on yield per vine (-0.098) but it also had negative and indirect effect (which is desirable) via days to first female flower (-0.004), number of seeds per fruit (-0.003), fruit diameter (-0.002), phenol content (-0.002) and TSS (-0.001).

Days to first harvest had negative direct impact (-0.021) on yield per vine through indirect negative effect of vine length (-0.009), number of fruits per vine (-0.009), sponge yield (-0.009), fruit length (-0.005), number of branches per vine (-0.004), number of seeds per fruit (-0.004), TSS (-0.003), potassium content (-0.004) and crude fiber content (-0.002).

Table 25. Phenotypic path coefficient analysis for yield and its attributing characters in sponge gourd genotypes

	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉	X ₁₀	X ₁₁	X ₁₂	X ₁₃	X ₁₄	X ₁₅	X ₁₆	rP
X ₁	0.014	0.004	-0.004	-0.063	-0.005	0.006	-0.003	0.001	0.007	0.002	0.006	0.002	-0.001	0.001	-0.002	-0.001	0.532**
X ₂	0.013	0.047	-0.012	-0.161	-0.007	0.017	-0.006	0.002	0.019	0.003	0.023	0.003	-0.010	0.004	-0.006	-0.003	0.453*
X ₃	0.009	0.007	-0.029	0.005	0.023	0.008	-0.003	-0.011	0.011	0.005	0.012	0.003	-0.002	0.004	-0.004	0.003	-0.206
X ₄	0.001	0.005	-0.004	-0.098	0.001	0.003	-0.002	0.001	0.003	-0.003	0.004	-0.001	0.003	0.004	-0.002	0.002	-0.178
X ₅	-0.009	-0.004	0.017	0.001	-0.021	-0.005	0.001	0.007	-0.009	-0.004	-0.009	-0.003	0.003	-0.004	0.004	-0.002	-0.210
X ₆	0.042	0.034	-0.027	0.013	-0.020	0.092	-0.028	0.021	0.029	0.007	0.040	-0.008	-0.003	-0.006	0.006	-0.005	0.508**
X ₇	0.004	0.003	-0.002	0.002	-0.001	0.007	-0.022	0.002	0.000	-0.003	0.003	-0.004	-0.005	-0.004	0.004	-0.007	-0.096
X ₈	0.033	0.021	0.180	0.029	0.146	0.112	-0.052	0.487	-0.044	-0.108	-0.017	-0.105	-0.103	-0.146	0.026	0.010	0.434*
X ₉	0.384	0.293	-0.279	0.081	-0.281	0.228	0.012	-0.065	0.721	0.061	0.329	0.196	-0.004	0.150	-0.213	0.115	0.784**
X ₁₀	0.008	0.004	-0.009	-0.007	-0.011	0.004	0.009	-0.013	0.005	0.060	0.011	0.010	-0.008	0.012	-0.007	0.009	0.033
X ₁₁	0.036	0.040	-0.035	0.015	-0.032	0.035	-0.011	-0.003	0.037	0.015	0.080	0.015	-0.018	0.007	-0.023	-0.009	0.484*
X ₁₂	-0.004	-0.001	0.002	0.001	0.003	0.002	-0.005	0.005	-0.007	-0.004	-0.004	-0.024	-0.002	-0.004	0.006	-0.005	0.097
X ₁₃	-0.001	-0.003	0.001	0.002	0.002	-0.001	0.003	-0.003	0.000	-0.002	-0.003	0.001	0.015	0.002	0.004	0.001	-0.146
X ₁₄	-0.001	-0.001	0.001	-0.002	0.002	0.001	-0.002	0.003	-0.002	-0.002	-0.001	-0.002	-0.002	-0.011	0.000	-0.001	0.011
X ₁₅	0.005	0.005	-0.006	0.003	-0.007	-0.003	0.007	-0.002	0.012	0.005	0.011	0.009	-0.010	0.001	-0.040	0.006	-0.250
X ₁₆	-0.001	-0.001	-0.002	0.001	-0.001	-0.001	0.006	0.000	0.003	0.003	-0.002	0.004	0.001	0.001	-0.003	0.019	0.133

rP = dependent character Diagonal values indicates direct effect Residual effect=0.305 *Indicates significant at p=0.05 **Indicates significant at p=0.01

X₁= Vine length at harvest

X₂= Number of branches per vine

X₃= Days to first female flower

X₄= Node at first female flower

X₅= Days to first harvest

X₆= Fruit length

X₇= Fruit diameter

X₈= Average fruit weight

X₉= Number of fruits per vine

X₁₀= No. of seeds per fruit

X₁₁= Sponge yield

X₁₂= TSS

X₁₃= Ascorbic acid

X₁₄=Potassium content

X₁₅= Phenol content

X₁₆= Crude fiber

Fruit length recorded positive direct effect on fruit yield per vine (0.092) via indirect effect through vine length (0.042), sponge yield (0.040), number of branches per vine (0.034), number of fruits per vine (0.029), average fruit weight (0.021), node at first female flower (0.013), number of seeds per fruit (0.007) and phenol content (0.006).

Fruit diameter observed negative direct effect on fruit yield per vine (-0.022) but it had very little positive indirect effect via fruit length (0.007), vine length (0.004), phenol content (0.004), number of branches per vine (0.003), sponge yield (0.003), node at first female flower (0.002) and average fruit weight (0.002).

The trait average fruit weight had high positive direct effect (0.487) on fruit yield per vine through its indirect effect of days to first harvest (0.146), days to first female flower (0.180), fruit length (0.112), vine length (0.033), node at first female flower (0.029), phenol content (0.026), number of branches per vine (0.021) and crude fiber content (0.010).

Number of fruits per vine shown positive direct effect on fruit yield per vine (0.721). It also exhibited positive and indirect effect through vine length (0.384), sponge yield (0.329), number of branches per vine (0.293), fruit length (0.228), TSS (0.196), node at first female flower (0.081), number of seeds per fruit (0.061), potassium content (0.026), fruit diameter (0.012) and crude fiber content (0.010).

The character number of seeds per fruit exhibited positive direct effect (0.721) on fruit yield per vine through its positive indirect effect of potassium content (0.012), sponge yield (0.011), TSS (0.010), fruit diameter (0.009), crude fiber content (0.009), vine length (0.008), number of fruits per vine (0.005), number of branches per vine (0.004) and fruit length (0.004).

Sponge yield observed positive direct effect (0.080) on fruit yield per vine, while it had positive indirect effect via number of branches per vine (0.040), number of fruits per vine (0.037), vine length (0.036), fruit length (0.035), node at first female flower (0.015), number of seeds per fruit (0.015), TSS (0.015) and potassium content (0.007).

The TSS even though reported to had negative direct effect (-0.024) on fruit yield per vine but it had positive indirect effect through phenol content (0.006), average fruit weight (0.005), days to first fruit harvest (0.003), days to first female flower (0.002), fruit length (0.002) and node at first female flower (0.001).

Ascorbic acid value in fruits reported to had positive but less direct effect (0.015) on fruit yield per vine through its indirect effect of phenol (0.004), fruit diameter (0.003), node at first female flower (0.002), days to first fruit harvest (0.002), potassium content (0.002), days to first female flower (0.001), TSS (0.001) and crude fiber content (0.001).

Percentage of potassium content in fruits had negative direct effect on fruit yield per vine (-0.011) but it had very negligible indirect effects (positively / negatively) through average fruit weight (0.003), node at first female flower (0.002), fruit length (0.001), days to first female flower (0.001), node at first female flower (-0.002), fruit diameter (-0.002), number of fruits per vine (-0.002), number of seeds per fruit (-0.002), TSS (-0.002), ascorbic acid (-0.002), vine length (-0.001), number of branches per vine (-0.001), sponge yield (-0.001), and crude fiber content (-0.001).

The amount of phenol content in the fruits exhibited negative direct effect (-0.040) on fruit yield per vine. While, the trait also exhibited positive and indirect association with number of fruits per vine (0.012), sponge yield (0.011), TSS (0.009), fruit diameter (0.007), crude fiber content (0.006), vine length (0.005), number of branches per vine (0.005), number of seeds per fruit (0.005), node at first female flower (0.003) and potassium content (0.001).

Crude fiber content in fruits had positive direct association with fruit yield per vine (0.019) through its positive indirect effects of fruit diameter (0.006), TSS (0.004), number of fruits per vine (0.003), number of seeds per fruit (0.003), node at first female flower (0.001), ascorbic acid (0.001) and potassium content (0.001).

4.7.2 Genotypic path co-efficient analysis

Genotypic path coefficient of fruit yield per vine had positive direct effect through number of fruits per vine (1.295) followed by phenol content (0.291), fruit diameter (0.271), average fruit weight (0.258), fruit length (0.219), number of branches

per vine (0.159), TSS (0.110) and vine length (0.035). While, ascorbic acid (-0.515), node at first female flower (-0.405), sponge yield (-0.305), potassium content (-0.210), crude fiber content (-0.121), days to first harvest (-0.091), number of seeds per fruit (-0.027) and days to first female flower (-0.005) had exhibited negative direct effect on fruit yield per vine (Table 26).

The vine length had positive and direct effect on fruit yield per vine (0.035) but it had indirect positive effect through days to first harvest (0.019), days to first female flower (0.014), phenol content (0.006), node at first female flower (0.004), fruit diameter (0.003), ascorbic acid (0.003) and crude fiber content (0.002).

The trait, number of branches per vine showed positive direct effect on fruit yield per vine (0.196) via days to first harvest (0.084), days to first female flower (0.078), fruit diameter (0.037), ascorbic acid (0.032), phenol content (0.024), crude fiber content (0.018) and TSS (0.002).

Days to appearance of first female flower indicated negative direct effect on fruit yield per vine (-0.005) through indirect effect of days to first harvest (-0.006), average fruit weight (-0.002), fruit diameter (-0.001) and phenol content (-0.001).

Node at first female flower appear exhibits negative direct effect on fruit yield per vine (-0.405) but it also had negative and indirect effect (which is desirable) via number of branches per vine (-0.159), days to first female flower (-0.102), fruit diameter (-0.066), number of seeds per fruit (-0.056), phenol content (-0.054), vine length (-0.026) and days to first harvest (-0.025).

The character days to first fruit harvest reported to have negative direct effect on yield per vine (-0.091) through indirect effects of sponge yield (-0.112), number of fruits per vine (-0.110), number of branches per vine (-0.091), vine length (-0.090), TSS (-0.076), number of seeds per fruit (-0.049), potassium content (-0.049), crude fiber content (-0.029) and node at first female flower (-0.016).

Fruit length showed positive direct effect on fruit yield per vine (0.219) via indirect effect of vine length (0.129), number of seeds per fruit (0.118), number of branches per vine (0.113), number of fruits per vine (0.098), average fruit weight (0.055), node at first female flower (0.043) and phenol content (0.014).

Table 26. Genotypic path coefficient analysis for yield and its attributing characters in sponge gourd genotypes

	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉	X ₁₀	X ₁₁	X ₁₂	X ₁₃	X ₁₄	X ₁₅	X ₁₆	rG
X ₁	0.035	-0.023	0.014	0.004	0.019	-0.022	0.003	-0.003	-0.031	-0.007	-0.028	-0.012	0.003	-0.004	0.006	0.002	0.769**
X ₂	-0.099	-0.159	0.078	-0.119	0.084	-0.082	0.037	-0.009	-0.088	-0.008	-0.104	0.002	0.032	-0.014	0.024	0.018	0.564**
X ₃	0.002	0.002	-0.005	0.002	-0.006	0.002	-0.001	-0.002	0.003	0.001	0.003	0.001	0.000	0.001	-0.001	0.001	-0.248*
X ₄	-0.026	0.196	-0.102	-0.405	-0.025	0.052	-0.066	0.034	0.136	-0.056	0.087	0.018	0.068	0.113	-0.054	0.013	-0.437*
X ₅	-0.090	-0.091	0.213	-0.016	-0.091	-0.071	0.005	0.080	-0.110	-0.049	-0.112	-0.076	0.030	-0.049	0.045	-0.029	-0.328*
X ₆	0.129	0.113	-0.085	0.043	0.171	0.219	-0.079	0.055	0.098	0.027	0.118	-0.028	-0.018	-0.024	0.014	-0.012	0.555**
X ₇	-0.019	-0.063	0.047	-0.068	0.008	-0.098	0.271	-0.039	-0.012	0.065	-0.052	0.079	0.064	0.075	-0.058	0.099	-0.127
X ₈	0.024	0.014	0.116	0.033	0.120	0.065	-0.037	0.258	-0.027	-0.060	-0.009	-0.074	-0.068	-0.079	0.014	0.005	0.439*
X ₉	1.109	0.718	-0.759	0.466	-0.834	0.580	-0.057	-0.133	1.295	0.223	0.811	0.416	0.025	0.350	-0.454	0.223	0.914**
X ₁₀	-0.005	-0.001	0.005	0.006	0.008	-0.003	-0.007	0.006	-0.005	-0.027	-0.006	-0.008	0.004	-0.006	0.003	-0.005	0.048
X ₁₁	-0.236	-0.198	0.164	-0.101	0.199	-0.164	0.059	0.011	-0.191	-0.066	-0.305	-0.079	0.113	-0.033	0.091	0.045	0.531**
X ₁₂	-0.037	-0.001	-0.030	0.008	-0.049	-0.014	0.032	-0.032	0.036	0.030	0.029	0.110	0.014	0.022	-0.033	0.025	0.130
X ₁₃	0.045	0.105	-0.009	-0.134	-0.090	0.043	-0.122	0.136	-0.010	0.077	0.192	-0.066	-0.515	-0.114	-0.165	-0.052	-0.213*
X ₁₄	-0.021	-0.018	0.039	-0.090	0.060	0.023	-0.058	0.064	-0.057	-0.045	-0.022	-0.041	-0.046	-0.210	0.005	-0.017	0.012
X ₁₅	-0.051	-0.044	0.051	-0.059	0.076	0.019	-0.062	0.016	-0.102	-0.035	-0.087	-0.087	0.093	-0.007	0.291	-0.048	-0.250*
X ₁₆	0.008	0.014	0.014	-0.006	0.020	0.007	-0.044	-0.003	-0.021	-0.022	0.018	-0.027	-0.012	-0.010	0.020	-0.121	0.147

rG = dependent character Diagonal values indicates direct effect Residual effect=0.209 *Indicates significant at p=0.05 **Indicates significant at p=0.01

X₁= Vine length at harvest

X₂= Number of branches per vine

X₃= Days to first female flower

X₄= Node at first female flower

X₅= Days to first harvest

X₆= Fruit length

X₇= Fruit diameter

X₈= Average fruit weight

X₉= Number of fruits per vine

X₁₀= No. of seeds per fruit

X₁₁= Sponge yield

X₁₂= TSS

X₁₃= Ascorbic acid

X₁₄=Potassium content

X₁₅= Phenol content

X₁₆= Crude fiber

Fruit diameter had positive direct impact on fruit yield per vine (0.271) but it had indirect positive effects through via crude fiber content (0.099), TSS (0.079), potassium content (0.075) number of seeds per fruit (0.065), ascorbic acid (0.064), days to first female flower (0.047) and days to first harvest (0.008).

Average fruit weight had positive direct effect on fruit yield per vine (0.258) through its indirect effects of days to first harvest (0.120), days to first female flower (0.116), fruit length (0.065), node at first female flower (0.033), vine length (0.024), number of branches per vine (0.014), phenol content (0.014) and crude fiber content (0.005).

The character number of fruits per vine exhibited positive direct effect on fruit yield per vine (1.295). It also exhibited positive and indirect effects through vine length (1.109), sponge yield (0.811), number of branches per vine (0.718), fruit length (0.580), node at first female flower (0.466), TSS (0.416), potassium content (0.350), number of seeds per fruit (0.223), ascorbic acid (0.025) and crude fiber content (0.010).

Number of seeds per fruit indicated negative direct effect on fruit yield per vine (-0.027) while it had positive indirect effects through days to first harvest (0.008), node at first female flower (0.006), average fruit weight (0.006), days to first female flower (0.005), ascorbic acid (0.004) and phenol content (0.003).

The sponge yield reported to have negative direct effect on fruit yield per vine (-0.305) but it had positive indirect effect through days to first harvest (0.199), days to first female flower (0.164), ascorbic acid (0.113), phenol content (0.091), fruit diameter (0.059), crude fiber content (0.045) and average fruit weight (0.011).

TSS reported positive direct effect on fruit yield per vine (0.110) through its indirect effect via number of fruits per vine (0.036), fruit diameter (0.032), number of seeds per fruit (0.030), sponge yield (0.029), crude fiber content (0.025), potassium content (0.022), ascorbic acid (0.014) and node at first female flower (0.008).

Ascorbic acid content in fruits had negative direct effect (-0.515) on fruit yield per vine while it had positive indirect effects through sponge yield (0.192), average fruit

weight (0.136), number of branches per vine (0.105), number of seeds per fruit (0.077), vine length (0.045) and fruit length (0.043).

The amount of potassium content in fruits exhibited negative direct effect on fruit yield per vine (-0.210) but it had very negligible positive indirect effects through average fruit weight (0.064), days to first harvest (0.060), days to first female flower (0.039), fruit length (0.023) and phenol content (0.005).

Phenol content in fruits noticed to have positive direct effect (0.291) on fruit yield per vine while it had positive indirect effect through ascorbic acid content (0.093), days to first harvest (0.076), days to first female flower (0.051), fruit length (0.019) and average fruit weight (0.016).

The crude fiber content in fruits had negative direct effect on fruit yield per vine (-0.121) while the trait also exhibited positive and indirect association with days to first harvest (0.020), phenol content (0.020), sponge yield (0.018), number of branches per vine (0.014), days to first female flower (0.014), vine length (0.008) and fruit length (0.007).

4.8 Analysis of variance and magnitude of heterosis

4.8.1 Analysis of variance

The results of analysis of variance for 32 characters under study are summarised in Table 27 and presented under different headings as components of variance.

4.8.1.1 Genotypes

The variance due to genotypes (crosses and parents) was highly significant both at $p=0.01$ and $p=0.05$ for vine length at 45 and 90 DAS, number of branches at 45 and 90 DAS, days to first male and first female flower, node at first male and female flower,

days to first and last harvest, fruit length, fruit diameter, average fruit weight, number of fruits per vine, fruit yield per vine, fruit yield per plot and hectare, number of seeds per fruit, sponge yield, total soluble solids, fruit firmness, fruit color (L^* , a^* , b^*), protein,

ascorbic acid, potassium content, phenol content, total antioxidants, total flavonoids, crude fiber and ash content.

4.8.1.2 Parents (Lines + Testers)

Parents differed highly significantly (at $p=0.01$) for all the growth, earliness, yield and quality parameters studied.

4.8.1.3 Parent V/s Crosses

Variance due to parents versus crosses were found to be significant at $p=0.01$ for all the 32 parameters studied.

4.8.1.4 Crosses

There was highly significant (at $p=0.01$) difference among the crosses for all the growth, earliness, yield and quality parameters studied.

4.8.1.5 Lines

Lines differed highly significantly (at $p=0.01$) among themselves for vine length at 45 and 90 DAS, number of branches at 45 and 90 DAS, days to first male and female flower, node at first male flower, days to first harvest and last harvest, fruit length, fruit diameter, average fruit weight, fruit yield per vine, fruit yield per plot and hectare, number of seeds per fruit, sponge yield, total soluble solids, fruit firmness, ascorbic acid, phenol content, total anti-oxidants, total flavonoids and crude fiber content. For node at first female flower, number of fruits per vine, fruit color (a^*) and protein content, the variance due to lines was significant at $p=0.05$. Whereas, variance due to lines were not significant for fruit firmness, fruit color (L^*), Protein, phenol and total antioxidant content.

4.8.1.6 Testers

Variance due to testers was not significant for all the parameters studied.

4.8.1.7 Line $\times$ tester

Variance due to line $\times$ Tester interaction was highly significant (at $p=0.01$) for all the growth, earliness, yield and quality parameters studied.

Table 27. Analysis of variance (mean sum of squares) of line × tester analysis for various characters in sponge gourd

Sl. No.	Character	Replications	Genotypes	Parents	Parents vs. Crosses	Crosses	Lines	Testers	Line × Tester	Error
	Degrees of freedom	1	53	13	1	39	9	3	27	53
	Growth parameters									
1	Vine length at 45 DAS	0.073	0.198 **	0.136 **	0.528 **	0.210 **	0.465 **	0.138	0.133 **	0.013
2	Vine length at 90 DAS	0.001	0.927 **	0.355 **	0.684 **	1.124 **	2.871 **	0.451	0.617 **	0.081
3	Number of branches at 45 DAS	0.037	0.553 **	0.214 **	3.384 **	0.594 **	1.336 **	0.381	0.371 **	0.074
4	Number of branches at 90 DAS	0.454	2.502 **	1.249 **	27.345 **	2.283 **	4.859 **	2.523	1.397 **	0.229
5	Days to first male flower	0.001	28.386 **	9.092 **	151.120 **	31.670 **	84.585 **	7.543	16.713 **	2.897
6	Days to first female flower	0.018	28.296 **	8.831 **	134.716 **	32.056 **	86.209 **	8.877	16.579 **	2.165
7	Node at first male flower	0.623	1.754 **	0.680 **	4.3412 **	2.045 **	5.259 **	1.913	0.988 **	0.240
8	Node at first female flower	1.613	8.659 **	6.263 **	12.991 **	9.347 **	17.959 *	6.343	6.809 **	1.114
9	Days to first harvest	0.685	37.059 **	8.876 **	314.139 **	39.348 **	105.579 **	20.741	19.339 **	1.750
10	Days to last harvest	29.037 *	40.352 **	7.557 **	141.946 **	48.679 **	117.066 **	19.825	29.089 **	2.695
	Yield parameters									
11	Fruit length	1.320	16.209 **	5.774 **	21.747 **	19.545 **	45.637 **	21.920	10.584 **	1.037
12	Fruit diameter	1.003	25.376 **	14.521 **	1.104 **	29.617 **	71.320 **	37.124	14.883 **	1.156
13	Average fruit weight	2449.878	493.379 **	162.657 **	4.349 **	616.159 **	1166.925 *	202.829	478.495 **	1.656
14	Number of fruits per vine	4.400	35.348 **	14.004 **	154.174 **	39.415 **	71.438 *	23.170	30.546 **	0.480
15	Fruit yield per vine	0.103	1.334 **	0.545 **	4.220 **	1.523 **	3.510 **	1.012	0.918 **	0.031
16	Fruit yield per plot	13.975	126.163 **	46.758 **	313.281 **	147.834 **	344.659 **	95.374	88.054 **	1.086
17	Fruit yield per hectare	3.396	28.639 **	10.746 **	60.810 **	33.778 **	79.748 **	14.849	20.558 **	0.381

Table 27. *Contd...*

Sl. No.	Character	Replications	Genotypes	Parents	Parents vs. Crosses	Crosses	Lines	Testers	Line× Tester	Error
	Degrees of freedom	1	53	13	1	39	9	3	27	53
18	Number of seeds per fruit	11.343	5865.789**	4607.221**	75798.933**	4492.154**	10427.89**	2569.155	2727.241**	26.217
19	Sponge yield	0.097	14.107 **	5.902 **	50.262 **	15.915 **	39.150 **	6.770	9.186 **	0.556
	Quality parameters									
20	Total soluble solids	2.607 *	0.461 **	0.333 **	0.510 **	0.503 **	1.214 **	0.531	0.263 **	0.039
21	Fruit firmness	0.900	53.018 **	59.354 **	305.456 **	44.434 **	40.376 **	39.695	46.313 **	1.419
22	Fruit color (L*)	0.550	27.878 **	34.260 **	230.046 **	20.566 **	22.800 *	12.237	20.747 **	0.855
23	Fruit color (a*)	1.153 *	0.995 **	0.631 **	19.024 **	0.655 **	0.754	0.395	0.650 **	0.196
24	Fruit color (b*)	1.246	20.475 **	18.524 **	79.577 **	19.610 **	13.588	12.837	22.369 **	0.582
25	Protein content	0.347	5.369 **	1.787 **	84.800 **	4.527 **	4.226 *	0.463	5.078 **	0.367
26	Ascorbic acid	0.012	1.851 **	0.218 **	18.022 **	1.980 **	5.849 **	0.614	0.843 **	0.064
27	Potassium content	0.194 *	0.231 **	0.024 *	4.806 **	0.182 **	0.313	0.128	0.145 **	0.023
28	Phenol content	7754.792	761.035 **	387.240 **	1956.773 **	854.974 **	674.965 **	268.698	980.119 **	2.231
29	Total antioxidants	62272.827	1494.399 **	723.721 **	2111.468 **	1735.469 **	2892.775 **	445.391	1493.043 **	1.669
30	Total flavonoids	2.153	64.873 **	25.691 **	525.986 **	66.111 **	188.814 **	26.795	29.578 **	2.146
31	Crude fiber	0.184	4.082 **	0.280	53.700 **	4.077 **	9.818 **	4.674	2.097 **	0.274
32	Ash content	0.407	2.518 **	0.324	33.858 **	2.446 **	4.322	1.114	1.968 **	0.203

* and ** indicates significant of values at p=0.05 and p=0.01, respectively DAS-Days after sowing

4.8.2 *Per se* performance and magnitude of heterosis

The *per se* performance of parents and F_1 's and heterosis was worked out over better parent, best parent and the commercial check hybrid (Kashi Rakshita) and presented in Tables 26-46. The hybrid 'Kashi Rakshita' was selected as a commercial check, released from IIVR, Varanasi.

4.8.2.1 Vine length (Table 28 and 29)

The genotypes used in the experiment were differed significantly among themselves for vine length at 45 and 90 DAS. Vine length at 45 DAS varied from 2.01 (T4) to 2.50 m (T1) among testers, 2.58 (L1 and L10) to 2.86 m (L2) among lines and 1.96 (L10 $\times$ T3) to 3.41 m (L2 $\times$ T1) among the crosses. The magnitude of heterosis over better parent, best parent and commercial check in the crosses was highly significant in both the directions. The maximum heterosis over better parent (20.71 %) was observed in the cross L6 $\times$ T1. Whereas, the cross L2 $\times$ T1 exhibited higher heterosis over best parent (19.23 %) and commercial check (31.15 %). Among the 40 crosses, 22 crosses over better parent, 13 crosses over best parent and 24 crosses over commercial check exhibited significantly positive heterosis for vine length at 45 DAS.

Vine length at 90 DAS ranged from 5.40 m (T4) to 6.34 m (T1) among the testers, 6.37 m (L4) to 7.00 m (L2) among the lines and 5.40 m (L10 $\times$ T3) to 8.12 m (L2 $\times$ T1) among the crosses. Heterosis over better parent, best parent and commercial check were highly significant in both the directions. The maximum positive heterosis over the better parent was observed in the cross L4 $\times$ T3 (24.33 %). Further, the cross L2 $\times$ T1 exhibited significant positive heterosis over best parent (16.00 %) and commercial check (37.63 %). Out of 40 crosses, 15 crosses showed positive and significant heterosis over better parent, eleven crosses over the best parent and 32 crosses over the commercial check.

Table 28. *Per se* performance of crosses and parents for growth and earliness parameters in sponge gourd

Sl. No.	Crosses	Vine length (m)		Number of branches		Days to first male flower	Days to first female flower
		45 DAS	90 DAS	45 DAS	90 DAS		
1	L1 × T1	2.84	6.47	2.50	5.90	37.30	41.20
2	L1 × T2	2.81	6.73	3.20	6.80	38.40	43.20
3	L1 × T3	2.90	7.29	3.10	4.70	38.60	41.40
4	L1 × T4	2.50	6.33	2.50	6.00	36.20	39.60
5	L2 × T1	3.41	8.12	3.70	7.90	31.20	33.60
6	L2 × T2	3.29	7.96	3.60	7.60	33.20	35.20
7	L2 × T3	3.04	7.13	3.20	6.80	35.90	36.40
8	L2 × T4	2.99	7.44	3.30	7.40	36.10	39.60
9	L3 × T1	3.00	5.75	2.50	5.40	43.30	46.20
10	L3 × T2	2.15	5.73	3.30	5.00	42.30	45.20
11	L3 × T3	2.95	6.91	1.80	6.00	45.60	48.20
12	L3 × T4	2.84	5.52	2.30	7.50	41.60	44.20
13	L4 × T1	2.39	6.87	3.30	6.90	44.00	47.00
14	L4 × T2	2.80	6.01	2.90	6.80	36.20	39.20
15	L4 × T3	2.79	7.92	2.80	7.30	38.40	41.60
16	L4 × T4	2.52	6.28	2.40	5.00	37.20	40.40
17	L5 × T1	2.39	6.37	2.10	7.20	43.60	46.40
18	L5 × T2	2.66	5.58	2.90	4.80	42.80	45.60
19	L5 × T3	2.53	6.53	1.90	4.40	38.90	42.00
20	L5 × T4	2.00	5.45	2.10	5.60	40.90	43.60
21	L6 × T1	3.38	8.06	3.60	7.80	31.20	34.60
22	L6 × T2	2.89	7.83	3.30	7.50	35.70	38.20
23	L6 × T3	3.02	7.12	3.40	7.20	36.60	39.20
24	L6 × T4	2.80	6.69	2.90	6.70	37.00	40.80
25	L7 × T1	2.50	6.32	2.50	7.40	43.90	46.80
26	L7 × T2	2.84	6.28	1.90	6.50	43.20	46.20
27	L7 × T3	2.92	6.45	2.50	6.60	39.80	41.23
28	L7 × T4	2.73	7.15	3.00	7.40	43.90	46.80
29	L8 × T1	2.49	5.67	2.70	6.00	42.90	45.60
30	L8 × T2	2.80	6.22	2.50	4.60	41.60	44.40
31	L8 × T3	2.32	6.30	3.30	6.50	38.50	41.40
32	L8 × T4	2.59	6.57	3.00	6.80	45.60	48.40
33	L9 × T1	2.56	6.44	2.60	6.40	34.00	37.60

Table 28. *Contd...*

Sl. No.	Crosses	Vine length (m)		Number of branches		Days to first male flower	Days to first female flower
		45 DAS	90 DAS	45 DAS	90 DAS		
34	L9 × T2	2.66	7.43	2.70	4.60	43.10	46.40
35	L9 × T3	2.90	6.43	2.50	6.40	45.80	48.60
36	L9 × T4	2.52	6.35	2.50	7.00	44.40	47.20
37	L10 × T1	2.90	6.45	3.30	5.80	38.10	41.00
38	L10 × T2	2.51	5.70	1.90	4.80	35.80	38.60
39	L10 × T3	1.96	5.40	1.70	4.50	37.00	40.80
40	L10 × T4	2.45	6.20	2.10	5.00	40.80	43.60
	Lines						
41	L1	2.58	6.54	2.30	5.60	43.20	44.80
42	L2	2.86	7.00	2.80	6.10	38.10	42.40
43	L3	2.62	6.38	2.50	6.00	41.70	43.20
44	L4	2.71	6.37	2.30	5.60	42.80	46.20
45	L5	2.73	6.38	2.50	5.20	42.40	44.50
46	L6	2.80	6.83	2.70	6.00	38.10	43.20
47	L7	2.66	6.50	2.20	4.50	42.60	44.40
48	L8	2.76	6.79	2.50	5.90	41.00	43.60
49	L9	2.59	6.71	2.40	4.90	43.20	44.00
50	L10	2.58	6.56	2.30	5.00	41.10	43.40
	Testers						
51	T1	2.50	6.34	2.50	4.60	42.60	46.40
52	T2	2.28	5.93	2.20	4.40	44.20	46.80
53	T3	2.06	5.92	1.50	4.30	45.30	50.60
54	T4	2.01	5.40	1.90	3.50	44.70	46.00
55	SC	2.60	5.90	2.40	5.20	39.20	42.60
S.Em±		0.08	0.20	0.19	0.34	1.20	1.05
CD at 5%		0.23	0.57	0.55	0.96	3.40	2.97
CD at 1%		0.31	0.75	0.73	1.28	4.53	3.96

SC : Standard check (Kashi Rakshita) DAS:Days after sowing

Table 29. Heterosis (%) over better parent, best parent and standard check for vine length in sponge gourd

Sl. No.	Crosses	Vine length at 45 DAS			Vine length at 90 DAS		
		BP	BTP	SC	BP	BTP	SC
1	L1 × T1	10.08 **	-0.70 **	9.23 **	-1.07 **	-7.57 **	9.66 **
2	L1 × T2	8.91 **	-1.75 **	8.08 **	2.91 **	-3.86 **	14.07 **
3	L1 × T3	12.40 **	1.40 **	11.54 **	11.47 **	4.14 **	23.56 **
4	L1 × T4	-3.10 **	-12.59 **	-3.85 **	-3.21 **	-9.57 **	7.29 **
5	L2 × T1	19.23 **	19.23 **	31.15 **	16.00 **	16.00 **	37.63 **
6	L2 × T2	15.03 **	15.03 **	26.54 **	13.71 **	13.71 **	34.92 **
7	L2 × T3	6.29 **	6.29 **	16.92 **	1.86 **	1.86 **	20.85 **
8	L2 × T4	4.55 **	4.55 **	15.00 **	6.29 **	6.29 **	26.10 **
9	L3 × T1	14.50 **	4.90 **	15.38 **	-9.87 **	-17.86 **	-2.54 **
10	L3 × T2	-17.94 **	-24.83 **	-17.31 **	-10.19 **	-18.14 **	-2.88 **
11	L3 × T3	12.60 **	3.15 **	13.46 **	8.31 **	-1.29 **	17.12 **
12	L3 × T4	8.40 **	-0.70 **	9.23 **	-13.48 **	-21.14 **	-6.44 **
13	L4 × T1	-11.81 **	-16.43 **	-8.08 **	7.85 **	-1.86 **	16.44 **
14	L4 × T2	3.32 **	-2.10 **	7.69 **	-5.65 **	-14.14 **	1.86 **
15	L4 × T3	2.95 **	-2.45 **	7.31 **	24.33 **	13.14 **	34.24 **
16	L4 × T4	-7.01 **	-11.89 **	-3.08 **	-1.41 **	-10.29 **	6.44 **
17	L5 × T1	-12.45 **	-16.43 **	-8.08 **	-0.16 **	-9.00 **	7.97 **
18	L5 × T2	-2.56 **	-6.99 **	2.31 **	-12.54 **	-20.29 **	-5.42 **
19	L5 × T3	-7.33 **	-11.54 **	-2.69 **	2.35 **	-6.71 **	10.68 **
20	L5 × T4	-26.74 **	-30.07 **	-23.08 **	-14.58 **	-22.14 **	-7.63 **
21	L6 × T1	20.71 **	18.18 **	30.00 **	18.01 **	15.14 **	36.61 **
22	L6 × T2	3.21 **	1.05 **	11.15 **	14.64 **	11.86 **	32.71 **
23	L6 × T3	7.86 **	5.59 **	16.15 **	4.25 **	1.71 **	20.68 **
24	L6 × T4	0.00 **	-2.10 **	7.69 **	-2.05 **	-4.43 **	13.39 **
25	L7 × T1	-6.02 **	-12.59 **	-3.85 **	-2.77 **	-9.71 **	7.12 **
26	L7 × T2	6.77 **	-0.70 **	9.23 **	-3.38 **	-10.29 **	6.44 **
27	L7 × T3	9.77 **	2.10 **	12.31 **	-0.77 **	-7.86 **	9.32 **
28	L7 × T4	2.63 **	-4.55 **	5.00 **	10.00 **	2.14 **	21.19 **
29	L8 × T1	-9.78 **	-12.94 **	-4.23 **	-16.49 **	-19.00 **	-3.90 **
30	L8 × T2	1.45 **	-2.10 **	7.69 **	-8.39 **	-11.14 **	5.42 **
31	L8 × T3	-15.94 **	-18.88 **	-10.77 **	-7.22 **	-10.00 **	6.78 **
32	L8 × T4	-6.16 **	-9.44 **	-0.38 **	-3.24 **	-6.14 **	11.36 **
33	L9 × T1	-1.16 **	-10.49 **	-1.54 **	-4.02 **	-8.00 **	9.15 **
34	L9 × T2	2.70 **	-6.99 **	2.31 **	10.73 **	6.14 **	25.93 **
35	L9 × T3	11.97 **	1.40 **	11.54 **	-4.17 **	-8.14 **	8.98 **
36	L9 × T4	-2.70 **	-11.89 **	-3.08 **	-5.37 **	-9.29 **	7.63 **
37	L10 × T1	12.40 **	1.40 **	11.54 **	-1.68 **	-7.86 **	9.32 **
38	L10 × T2	-2.71 **	-12.24 **	-3.46 **	-13.11 **	-18.57 **	-3.39 **
39	L10 × T3	-24.03 **	-31.47 **	-24.62 **	-17.68 **	-22.86 **	-8.47 **
40	L10 × T4	-5.04 **	-14.34 **	-5.77 **	-5.49 **	-11.43 **	5.08 **
	S.Em±	0.08	0.08	0.08	0.20	0.20	0.20
	CD at 5%	0.23	0.23	0.23	0.57	0.57	0.57
	CD at 1%	0.31	0.31	0.31	0.75	0.75	0.75

* and ** indicate significance of values at p= 0.05 and p= 0.01, respectively. BP, BTP and SC: Heterosis over better parent, best parent and standard check (Kashi Rakshita), respectively. DAS: Days after sowing

4.8.2.2 Number of branches per vine (Table 28 and 30)

There was significant differences were observed among the genotypes for the character number of branches per vine at 45 DAS. Number of branches per vine ranged from 1.50 (T4) to 2.50 (T1) among testers, 2.20 (L7) to 2.80 (L2) among lines and 1.70 (L10 $\times$ T3) to 3.70 (L2 $\times$ T1) among crosses. Maximum positive and significant heterobeltiosis was observed in the cross L1 $\times$ T2 (39.13 %). The cross L2 $\times$ T1 exhibited maximum heterosis over the best parent (32.14 %) and commercial check (54.17 %). Among the crosses, 27 crosses over better parent, 18 crosses over the best parent and 30 crosses over commercial check exhibited positive and significant heterosis.

The trait number of branches per vine at 90 DAS varied from 3.50 (T4) to 4.60 (T1) among testers, 4.50 (L7) to 6.10 (L2) among lines and 4.50 (L10 $\times$ T3) to 7.90 (L2 $\times$ T1) among the crosses. Maximum positive and significant heterosis was observed in the cross L7 $\times$ T4 (64.44 %). While, maximum heterosis over best parent (29.51 %) and commercial check (8.12%) was recorded by the cross L2 $\times$ T1. Among all the 40 crosses studied, 28 crosses over better parent, 23 crosses over best parent and 30 crosses over the commercial check exhibited positive and significant heterosis.

4.8.2.3 Days to first male flower (Table 28 and 31)

Minimum number of days taken for first male flower production in sponge gourd differs significantly among the genotypes and it varied from 42.60 (T1) to 45.30 (T3) among testers, 38.10 (L2 and L6) to 43.20 days (L1 & L10) among lines and 31.20 (L2 $\times$ T1 and L6 $\times$ T1) to 45.80 days (L9 $\times$ T3) among crosses. Heterosis over better parent, best parent and commercial check was significant in both the directions. Negative heterosis for this trait indicates earliness and is desirable. Maximum and significant negative heterosis over better parent was observed in the cross L9 $\times$ T1 (-20.19 %), whereas, the crosses L2 $\times$ T1 and L6 $\times$ T1 were exhibited significant negative heterosis over best parent (-18.11%) and commercial check (-20.41 %). Out of 40 crosses, 22 crosses showed negative and significant heterosis over better parent, 11 crosses over best parent and 15 crosses over commercial check.

Table 30. Heterosis (%) over better parent, best parent and standard check for number of branches in sponge gourd

Sl. No.	Crosses	Number of branches at 45 DAS			Number of branches at 90 DAS		
		BP	BTP	SC	BP	BTP	SC
1	L1 × T1	0.00	-10.71 **	4.17 **	5.36 **	-3.28 **	13.46 **
2	L1 × T2	39.13 **	14.29 **	33.33 **	21.43 **	11.48 **	30.77 **
3	L1 × T3	34.78 **	10.71 **	29.17 **	-16.07 **	-22.95 **	-9.62 **
4	L1 × T4	8.70 **	-10.71 **	4.17 **	7.14 **	-1.64 **	15.38 **
5	L2 × T1	32.14 **	32.14 **	54.17 **	29.51 **	29.51 **	51.92 **
6	L2 × T2	28.57 **	28.57 **	50.00 **	24.59 **	24.59 **	46.15 **
7	L2 × T3	14.29 **	14.29 **	33.33 **	11.48 **	11.48 **	30.77 **
8	L2 × T4	17.86 **	17.86 **	37.50 **	21.31 **	21.31 **	42.31 **
9	L3 × T1	0.00	-10.71 **	4.17 **	-10.00 **	-11.48 **	3.85 **
10	L3 × T2	32.00 **	17.86 **	37.50 **	-16.67 **	-18.03 **	-3.85 **
11	L3 × T3	-28.00 **	-35.71 **	-25.00 **	0.00	-1.64 **	15.38 **
12	L3 × T4	-8.00 **	-17.86 **	-4.17 **	25.00 **	22.95 **	44.23 **
13	L4 × T1	32.00 **	17.86 **	37.50 **	23.21 **	13.11 **	32.69 **
14	L4 × T2	26.09 **	3.57 **	20.83 **	21.43 **	11.48 **	30.77 **
15	L4 × T3	21.74 **	0.00	16.67 **	30.36 **	19.67 **	40.38 **
16	L4 × T4	4.35 **	-14.29 **	0.00	-10.71 **	-18.03 **	-3.85 **
17	L5 × T1	-16.00 **	-25.00 **	-12.50 **	38.46 **	18.03 **	38.46 **
18	L5 × T2	16.00 **	3.57 **	20.83 **	-7.69 **	-21.31 **	-7.69 **
19	L5 × T3	-24.00 **	-32.14 **	-20.83 **	-15.38 **	-27.87 **	-15.38 **
20	L5 × T4	-16.00 **	-25.00 **	-12.50 **	7.69 **	-8.20 **	7.69 **
21	L6 × T1	33.33 **	28.57 **	50.00 **	30.00 **	27.87 **	50.00 **
22	L6 × T2	22.22 **	17.86 **	37.50 **	25.00 **	22.95 **	44.23 **
23	L6 × T3	25.93 **	21.43 **	41.67 **	20.00 **	18.03 **	38.46 **
24	L6 × T4	7.41 **	3.57 **	20.83 **	11.67 **	9.84 **	28.85 **
25	L7 × T1	0.00	-10.71 **	4.17 **	60.87 **	21.31 **	42.31 **
26	L7 × T2	-13.64 **	-32.14 **	-20.83 **	44.44 **	6.56 **	25.00 **
27	L7 × T3	13.64 **	-10.71 **	4.17 **	46.67 **	8.20 **	26.92 **
28	L7 × T4	36.36 **	7.14 **	25.00 **	64.44 **	21.31 **	42.31 **
29	L8 × T1	8.00 **	-3.57 **	12.50 **	1.69 **	-1.64 **	15.38 **
30	L8 × T2	0.00	-10.71 **	4.17 **	-22.03 **	-24.59 **	-11.54 **
31	L8 × T3	32.00 **	17.86 **	37.50 **	10.17 **	6.56 **	25.00 **
32	L8 × T4	20.00 **	7.14 **	25.00 **	15.25 **	11.48 **	30.77 **
33	L9 × T1	4.00 **	-7.14 **	8.33 **	30.61 **	4.92 **	23.08 **
34	L9 × T2	12.50 **	-3.57 **	12.50 **	-6.12 **	-24.59 **	-11.54 **
35	L9 × T3	4.17 **	-10.71 **	4.17 **	30.61 **	4.92 **	23.08 **
36	L9 × T4	4.17 **	-10.71v	4.17 **	42.86 **	14.75 **	34.62 **
37	L10 × T1	32.00 **	17.8 **	37.50 **	16.00 **	-4.92 **	11.54 **
38	L10 × T2	-17.39 **	-32.14 **	-20.83 **	-4.00 **	-21.31 **	-7.69 **
39	L10 × T3	-26.09 **	-39.29 **	-29.17 **	-10.00 **	-26.23 **	-13.46 **
40	L10 × T4	-8.70 **	-25.00 **	-12.50 **	0.00	-18.03 **	-3.85 **
	S.Em±	0.19	0.19	0.19	0.34	0.34	0.34
	CD at 5%	0.55	0.55	0.55	0.96	0.96	0.96
	CD at 1%	0.73	0.73	0.73	1.28	1.28	1.28

* and ** indicate significance of values at p= 0.05 and p= 0.01, respectively. BP, BTP and SC: Heterosis over better parent, best parent and standard check (Kashi Rakshita), respectively. DAS: Days after sowing

Table 31. Heterosis (%) over better parent, best parent and standard check for days to first male and female flower in sponge gourd

Sl. No.	Crosses	Days to first male flower			Days to first female flower		
		BP	BTP	SC	BP	BTP	SC
1	L1 × T1	-12.44 **	-2.10	-4.85 **	-8.04 **	-2.83	-3.29 *
2	L1 × T2	-11.11 **	0.79	-2.04	-3.57 *	1.89	1.41
3	L1 × T3	-10.65 **	1.31	-1.53	-7.59 **	-2.36	-2.82
4	L1 × T4	-16.20 **	-4.99 **	-7.65 **	-11.61 **	-6.60 **	-7.04 **
5	L2 × T1	-18.11 **	-18.11 **	-20.41 **	-20.75 **	-20.75 **	-21.13 **
6	L2 × T2	-12.86 **	-12.86 **	-15.31 **	-16.98 **	-16.98 **	-17.37 **
7	L2 × T3	-5.77 **	-5.77 **	-8.42 **	-14.15 **	-14.15 **	-14.55 **
8	L2 × T4	-5.25 **	-5.25 **	-7.91 **	-6.60 **	-6.60 **	-7.04 **
9	L3 × T1	3.84 *	13.65 **	10.46 **	6.94 **	8.96 **	8.45 **
10	L3 × T2	1.44	11.02 **	7.91 **	4.63 **	6.60 **	6.10 **
11	L3 × T3	9.35 **	19.69 **	16.33 **	11.57 **	13.68 **	13.15 **
12	L3 × T4	-0.24	9.19 **	6.12 **	2.31	4.25 **	3.76 *
13	L4 × T1	3.29	15.49 **	12.24 **	1.73	10.85 **	10.33 **
14	L4 × T2	-15.42 **	-4.99 **	-7.65 **	-15.15 **	-7.55 **	-7.98 **
15	L4 × T3	-10.28 **	0.79	-2.04	-9.96 **	-1.89	-2.35
16	L4 × T4	-13.08 **	-2.36	-5.10 **	-12.55 **	-4.72 **	-5.16 **
17	L5 × T1	2.83	14.44 **	11.22 **	4.27 **	9.43 **	8.92 **
18	L5 × T2	0.94	12.34 **	9.18	2.47	7.55 **	7.04 **
19	L5 × T3	-8.25 **	2.10	-0.77	-5.62 **	-0.94	-1.41
20	L5 × T4	-3.54 *	7.35 **	4.34 *	-2.02	2.83	2.35
21	L6 × T1	-18.11 **	-18.11 **	-20.41 **	-19.91 **	-18.40 **	-18.78 **
22	L6 × T2	-6.30 **	-6.30 **	-8.93 **	-11.57 **	-9.91 **	-10.33 **
23	L6 × T3	-3.94 *	-3.94 *	-6.63 **	-9.26 **	-7.55 **	-7.98 **
24	L6 × T4	-2.89	-2.89	-5.61 **	-5.56 **	-3.77 *	-4.23 **
25	L7 × T1	3.05	15.22 **	11.99 **	5.41 **	10.38 **	9.86 **
26	L7 × T2	1.41	13.39 **	10.20 **	4.05 **	8.96 **	8.45 **
27	L7 × T3	-6.57 **	4.46 *	1.53	-7.14 **	-2.76	-3.22 *
28	L7 × T4	3.05	15.22 **	11.99 **	5.41 **	10.38 **	9.86 **
29	L8 × T1	4.63 **	12.60 **	9.44 **	4.59 **	7.55 **	7.04 **
30	L8 × T2	1.46	9.19 **	6.12 **	1.83	4.72 **	4.23 **
31	L8 × T3	-6.10 **	1.05	-1.79	-5.05 **	-2.36	-2.82
32	L8 × T4	11.22 **	19.69 **	16.33 **	11.01 **	14.15 **	13.62 **
33	L9 × T1	-20.19 **	-10.76 **	-13.27 **	-14.55 **	-11.32 **	-11.74 **
34	L9 × T2	-0.23	13.12 **	9.95 **	5.45 **	9.43 **	8.92 **
35	L9 × T3	6.02 **	20.21 **	16.84 **	10.45 **	14.62 **	14.08 **
36	L9 × T4	2.78	16.54 **	13.27 **	7.27 **	11.32 **	10.80 **
37	L10 × T1	-7.30 **	0.00	-2.81	-5.53 **	-3.30 *	-3.76 *
38	L10 × T2	-12.90 **	-6.04 **	-8.67 **	-11.06 **	-8.96 **	-9.39 **
39	L10 × T3	-9.98 **	-2.89	-5.61 **	-5.99 **	-3.77 *	-4.23 **
40	L10 × T4	-0.73	7.09 **	4.08 *	0.46	2.83	2.35
	S.Em±	1.20	1.20	1.20	1.05	1.05	1.05
	CD at 5%	3.40	3.40	3.40	2.97	2.97	2.97
	CD at 1%	4.53	4.53	4.53	3.96	3.96	3.96

* and ** indicate significance of values at p= 0.05 and p= 0.01, respectively. BP, BTP and SC: Heterosis over better parent, best parent and standard check (Kashi Rakshita), respectively

4.8.2.4 Days to first female flower (Table 28 and 31)

The results from per se performance of parents and hybrids revealed that testers took 46.00 (T4) to 50.60 days (T3) and lines took 42.40 (L2) to 46.20 days (L4) for appearance of first female flower. However, the crosses took 33.60 (L2 $\times$ T1) to 48.60 (L9 $\times$ T3) days for first female flower production. Negative heterosis over better parent, best parent and commercial check was desirable for this trait, as it indicates earliness. The maximum and significant negative heterosis over better parent (-20.75 %), best parent (-20.75 %) and the commercial check (-21.13 %) was observed in the cross L2 $\times$ T1. Out of 40 crosses, 22 crosses over better parent, 13 crosses over best parent and 17 crosses over commercial check had exhibited significant and negative heterosis.

4.8.2.5 Node at first male flower (Table 32 and 33)

Node at first male flower appearance varied among the genotypes which ranged between 4.70 (T1) to 5.50 (T2) among testers, 3.80 (L2 and L6) to 4.50 (L7) among lines and 3.00 (L2 $\times$ T1 and L6 $\times$ T1) to 6.10 (10 $\times$ T2) among the crosses. The magnitude of heterosis was significant in both the directions over better parent, best parent and the commercial check. The maximum and significantly negative heterosis over better parent was registered in the cross L3 $\times$ T4 (-22.73 %). However, the crosses L2 $\times$ T1 and L6 $\times$ T1 exhibited the significant and negative heterosis over the best parent (-21.05 %) and over commercial check (-42.31 %). Out of 40 crosses, 18 crosses over better parent, seven crosses over best parent and 28 crosses over commercial check exhibited significant and negative heterosis.

4.8.2.6 Node at first female flower (Table 32 and 33)

The sponge gourd genotypes differed significantly among themselves for node at which first female flower emergence and it ranged from 11.20 (T1) to 16.40 (T4) nodes among testers, 9.20 (L2 and L6) to 11.80 (L1) among lines and 8.50 (L2 $\times$ T1) to 16.70 node (L9 $\times$ T3) among crosses. The magnitude of heterosis was significant in both directions over better parent, best parent and the commercial check. However, negative heterosis indicates early flowering. The maximum and significantly negative heterosis over the better parent was observed in the cross L5 $\times$ T1 (-20.00 %) and the cross L2 $\times$ T1 exhibited significant and negative heterosis over the best parent (-7.61 %).

Table 32. *Per se* performance of crosses and parents for earliness and yield parameters in sponge gourd

Sl. No.	Crosses	Node at first male flower	Node at first female flower	Days to first harvest	Days to last harvest	Fruit length (cm)	Fruit diameter (mm)
1	L1 × T1	3.90	14.20	49.20	110.80	20.54	32.14
2	L1 × T2	5.00	10.40	50.20	108.10	26.79	34.39
3	L1 × T3	4.00	11.90	48.60	108.20	21.23	30.12
4	L1 × T4	4.20	14.20	49.20	111.20	24.42	35.29
5	L2 × T1	3.00	8.50	40.40	106.20	29.98	43.65
6	L2 × T2	3.20	8.80	42.10	104.80	28.88	41.78
7	L2 × T3	3.90	11.90	46.00	104.20	27.80	34.83
8	L2 × T4	5.60	13.30	45.90	107.20	25.79	33.62
9	L3 × T1	3.80	9.80	54.60	114.60	23.56	32.71
10	L3 × T2	4.00	10.40	54.40	115.20	24.05	33.03
11	L3 × T3	4.10	9.90	56.80	116.40	22.12	33.82
12	L3 × T4	3.40	11.20	53.60	112.80	19.82	28.56
13	L4 × T1	4.20	13.00	55.80	115.20	25.31	31.23
14	L4 × T2	3.90	14.70	47.20	107.20	25.08	31.29
15	L4 × T3	5.40	13.70	48.90	109.20	24.40	29.34
16	L4 × T4	4.10	11.20	49.20	110.80	20.94	28.22
17	L5 × T1	3.40	10.80	55.60	115.20	19.34	33.23
18	L5 × T2	5.80	14.30	55.20	115.60	24.17	34.42
19	L5 × T3	5.50	11.00	51.20	110.80	19.63	28.43
20	L5 × T4	5.90	14.10	53.20	113.60	26.80	33.66
21	L6 × T1	3.00	8.60	41.60	105.60	29.56	42.98
22	L6 × T2	3.40	9.90	48.20	109.40	26.79	37.10
23	L6 × T3	4.50	10.40	46.20	106.20	24.88	35.57
24	L6 × T4	3.60	10.20	49.40	111.20	29.18	36.63
25	L7 × T1	5.00	11.10	54.20	114.60	20.12	29.71
26	L7 × T2	5.80	13.10	53.80	113.20	22.21	33.20
27	L7 × T3	5.50	14.10	49.40	109.20	20.34	34.72
28	L7 × T4	5.20	12.30	54.60	114.20	21.49	29.40
29	L8 × T1	5.10	13.00	54.40	114.80	23.73	35.40
30	L8 × T2	4.90	9.50	53.20	112.80	21.09	30.51
31	L8 × T3	4.40	8.90	50.40	114.20	20.34	28.62
32	L8 × T4	5.20	10.70	57.60	124.60	22.38	30.12

Table 32. *Contd...*

Sl. No.	Crosses	Node at first male flower	Node at first female flower	Days to first harvest	Days to last harvest	Fruit length (cm)	Fruit diameter (mm)
33	L9 × T1	5.20	9.40	47.20	106.80	18.45	29.45
34	L9 × T2	4.80	15.80	54.40	114.20	26.04	35.51
35	L9 × T3	4.00	16.70	58.40	127.60	25.11	34.40
36	L9 × T4	3.80	15.60	56.40	116.20	24.28	35.23
37	L10 × T1	3.90	13.20	48.60	108.60	20.13	32.65
38	L10 × T2	6.10	13.90	47.60	107.20	24.25	30.13
39	L10 × T3	4.80	10.80	47.20	106.20	19.56	26.98
40	L10 × T4	5.40	12.30	49.10	108.40	24.16	30.16
	Lines						
41	L1	4.40	11.80	54.40	113.50	25.90	33.44
42	L2	3.80	9.20	51.60	111.60	27.05	37.12
43	L3	4.40	10.60	53.90	114.00	24.59	35.02
44	L4	4.50	10.90	55.60	114.20	25.16	33.13
45	L5	4.20	11.00	52.80	113.20	25.08	34.56
46	L6	3.80	9.20	52.20	113.00	26.03	36.12
47	L7	4.50	11.20	54.20	112.00	24.56	33.35
48	L8	4.00	9.40	52.80	112.20	25.62	35.04
49	L9	4.00	10.70	53.50	114.40	25.21	34.39
50	L10	4.20	10.60	54.80	113.80	23.76	33.29
	Testers						
51	T1	4.70	11.20	55.60	115.60	22.67	32.67
52	T2	5.50	11.40	56.60	116.20	24.48	32.28
53	T3	5.30	12.20	59.80	118.80	19.98	27.05
54	T4	4.90	16.40	56.00	116.00	24.89	28.55
55	SC	5.20	11.60	49.80	110.20	21.32	30.56
S.Em±		0.34	0.75	0.96	1.15	0.71	0.75
CD at 5%		0.97	2.11	2.71	3.26	2.02	2.14
CD at 1%		1.30	2.82	3.61	4.35	2.69	2.85

SC : Standard check (Kashi Rakshita) DAS:Days after sowing

Table 33. Heterosis (%) over better parent, best parent and standard check for node at first male and female flower in sponge gourd

Sl. No.	Crosses	Node at first male flower			Node at first female flower		
		BP	BTP	SC	BP	BTP	SC
1	L1 × T1	-11.36 **	2.63 **	-25.00 **	26.79 **	54.35 **	22.41 **
2	L1 × T2	13.64 **	31.58 **	-3.85 **	-8.77 **	13.04 **	-10.34 **
3	L1 × T3	-9.09 **	5.26 **	-23.08 **	0.85	29.35 **	2.59 *
4	L1 × T4	-4.55 **	10.53 **	-19.23 **	27.12 **	63.04 **	29.31 **
5	L2 × T1	-21.05 **	-21.05 **	-42.31 **	-7.61 **	-7.61 **	-26.72 **
6	L2 × T2	-15.79 **	-15.79 **	-38.46 **	-4.35 **	-4.35 **	-24.14 **
7	L2 × T3	2.63 **	2.63 **	-25.00 **	29.35 **	29.35 **	2.59 *
8	L2 × T4	47.37 **	47.37 **	7.69 **	44.57 **	44.57 **	14.66 **
9	L3 × T1	-13.64 **	0.00	-26.92 **	-16.04 **	-3.26 **	-23.28 **
10	L3 × T2	-9.09 **	5.26 **	-23.08 **	-1.89	13.04 **	-10.34 **
11	L3 × T3	-6.82 **	7.89 **	-21.15 **	-6.60 **	7.61 **	-14.66 **
12	L3 × T4	-22.73 **	-10.53 **	-34.62 **	-15.09 **	-2.17 *	-22.41 **
13	L4 × T1	-6.67 **	10.53 **	-19.23 **	13.76 **	34.78 **	6.90 **
14	L4 × T2	-13.33 **	2.63 **	-25.00 **	34.86 **	59.78 **	26.72 **
15	L4 × T3	20.00 **	42.11 **	3.85 **	25.69 **	48.91 **	18.10 **
16	L4 × T4	-8.89 **	7.89 **	-21.15 **	2.75 **	21.74 **	-3.45 **
17	L5 × T1	-19.05 **	-10.53 **	-34.62 **	-20.00 **	-4.35 **	-24.14 **
18	L5 × T2	38.10 **	52.63 **	11.54 **	30.00 **	55.43 **	23.28 **
19	L5 × T3	30.95 **	44.74 **	5.77 **	0.00	19.57 **	-5.17 **
20	L5 × T4	40.48 **	55.26 **	13.46 **	28.18 **	53.26 **	21.55 **
21	L6 × T1	-21.05 **	-21.05 **	-42.31 **	-6.52 **	-6.52 **	-25.86 **
22	L6 × T2	-10.53 **	-10.53 **	-34.62 **	-1.09	-1.09	-21.55 **
23	L6 × T3	18.42 **	18.42 **	-13.46 **	13.04 **	13.04 **	-10.34 **
24	L6 × T4	-5.26 **	-5.26 **	-30.77 **	-3.26 **	-3.26 **	-23.28 **
25	L7 × T1	11.11 **	31.58 **	-3.85 **	-0.89	20.65 **	-4.31 **
26	L7 × T2	28.89 **	52.63 **	11.54 **	16.96 **	42.39 **	12.93 **
27	L7 × T3	22.22 **	44.74 **	5.77 **	23.21 **	50.00 **	18.97 **
28	L7 × T4	15.56 **	36.84 **	0.00	9.82 **	33.70 **	6.03 **
29	L8 × T1	27.50 **	34.21 **	-1.92 **	38.30 **	41.30 **	12.07 **
30	L8 × T2	22.50 **	28.95 **	-5.77 **	1.06	3.26 **	-18.10 **
31	L8 × T3	10.00 **	15.79 **	-15.38 **	-5.32 **	-3.26 **	-23.28 **
32	L8 × T4	30.00 **	36.84 **	0.00	13.83 **	16.30 **	-7.76 **
33	L9 × T1	30.00 **	36.84 **	0.00	-12.15 **	2.17 *	-18.97 **
34	L9 × T2	20.00 **	26.32 **	-7.69 **	30.84 **	52.17 **	20.69 **
35	L9 × T3	0.00	5.26 **	-23.08 **	34.58 **	56.52 **	24.14 **
36	L9 × T4	-5.00 **	0.00	-26.92 **	-15.89 **	-2.17 *	-22.41 **
37	L10 × T1	-7.14 **	2.63 **	-25.00 **	24.53 **	43.48 **	13.79 **
38	L10 × T2	45.24 **	60.53 **	17.31 **	24.53 **	43.48 **	13.79 **
39	L10 × T3	14.29 **	26.32 **	-7.69 **	1.89	17.39 **	-6.90 **
40	L10 × T4	28.57 **	42.11 **	3.85 **	16.04 **	33.70 **	6.03 **
	S.Em±	0.34	0.34	0.34	0.75	0.75	0.75
	CD at 5%	0.97	0.97	0.97	2.11	2.11	2.11
	CD at 1%	1.30	1.30	1.30	2.82	2.82	2.82

* and ** indicate significance of values at p= 0.05 and p= 0.01, respectively. BP, BTP and SC: Heterosis over better parent, best parent and standard check (Kashi Rakshita), respectively.

and commercial check (-26.72 %). Out of 40 crosses 12 crosses over better parent, nine crosses each over best parent and 21 crosses over commercial check exhibited significant and negative heterosis.

4.8.2.7 Days to first harvest (Table 32 and 34)

Days to first harvest varied significantly among the genotypes. It ranged from 55.60 (T1) to 59.80 days (T3) among testers, 51.60 (L2) to 54.80 days (L10) among lines and 40.40 (L2 × T1) to 58.40 days (L9 × T3) among crosses. The trait with negative heterosis is desirable as it indicates earliness. Maximum negative and significant heterosis was observed in the cross L2 × T1 over better parent (-21.71 %), best parent (-21.71 %) and commercial check (-18.88 %). Many of the crosses exhibited negative and significant heterosis over better parent (23 crosses), best parent (21 crosses) and commercial check (11 crosses).

4.8.2.8 Days to last harvest (Table 32 and 34)

The genotypes used in the experiment were varied significantly from 115.60 (T1) to 118.80 days (T3) among testers, 111.60 (L2) to 114.40 days (L9) among lines and 104.20 (L2 × T3) to 127.60 days (L9 × T3) among the crosses for days to last harvest. Heterosis over the better parent, best parent and commercial check was significant in both the directions. The significant positive heterosis was observed in the cross L8 × T3 and L9 × T3 over better parent (7.41 %) and maximum positive heterosis over best parent (7.41 %) and over commercial check (15.79 %) was observed in the cross L9 × T3. Out of 40 crosses, only two crosses each over better parent and best parent and 14 crosses over commercial check exhibited significant and positive heterosis.

4.8.2.9 Fruit length (Table 32 and 35)

The significant differences were observed among the sponge gourd genotypes for the character fruit length and it varied from 19.98 cm (T3) to 24.89 cm (T4) among testers, 23.76 cm (L10) to 27.05 cm (L2) among lines and 18.45 cm (L9 × T1) to 29.98 cm (L2 × T1) among crosses. Among the crosses, L6 × T1 showed maximum and positive significant heterosis over better parent (13.56 %), whereas, the cross L2 × T1

Table 34. Heterosis (%) over better parent, best parent and standard check for days to first harvest and last harvest in sponge gourd

Sl. No.	Crosses	Days to first harvest			Days to last harvest		
		BP	BTP	SC	BP	BTP	SC
1	L1 × T1	-9.56 **	-4.65 **	-1.20	-4.15 *	-6.73 **	0.36
2	L1 × T2	-7.72 **	-2.71 *	0.80	-6.97 **	-9.01 **	-1.91
3	L1 × T3	-10.66 **	-5.81 **	-2.41	-8.92 **	-8.92 **	-1.81
4	L1 × T4	-9.56 **	-4.65 **	-1.20	-4.14 *	-6.40 **	0.91
5	L2 × T1	-21.71 **	-21.71 **	-18.88 **	-8.13 **	-10.61 **	-3.63 *
6	L2 × T2	-18.41 **	-18.41 **	-15.46 **	-9.81 **	-11.78 **	-4.90 **
7	L2 × T3	-10.85 **	-10.85 **	-7.63 **	-12.29 **	-12.29 **	-5.44 **
8	L2 × T4	-11.05 **	-11.05 **	-7.83 **	-7.59 **	-9.76 **	-2.72
9	L3 × T1	1.30	5.81 **	9.64 **	-0.87	-3.54 *	3.99 *
10	L3 × T2	0.93	5.43 **	9.24 **	-0.86	-3.03	4.54 **
11	L3 × T3	5.38 **	10.08 **	14.06 **	-2.02	-2.02	5.63 **
12	L3 × T4	-0.56	3.88 **	7.63 **	-2.76	-5.05 **	2.36
13	L4 × T1	0.36	8.14 **	12.05 **	-0.35	-3.03	4.54 **
14	L4 × T2	-15.11 **	-8.53 **	-5.22 **	-7.75 **	-9.76 **	-2.72
15	L4 × T3	-12.05 **	-5.23 **	-1.81	-8.08 **	-8.08 **	-0.91
16	L4 × T4	-11.51 **	-4.65 **	-1.20	-4.48 **	-6.73 **	0.54
17	L5 × T1	5.30	7.75 **	11.65 **	-0.35	-3.03	4.54 **
18	L5 × T2	4.55 **	6.98 **	10.84 **	-0.52	-2.69	4.90 **
19	L5 × T3	-3.03 *	-0.78	2.81 *	-6.73 **	-6.73 **	0.54
20	L5 × T4	0.76	3.10 *	6.83 **	-2.07	-4.38 **	3.09
21	L6 × T1	-20.31 **	-19.38 **	-16.47 **	-8.65 **	-11.11 **	-4.17 *
22	L6 × T2	-7.66 **	-6.59 **	-3.21 *	-5.85 **	-7.91 **	-0.73
23	L6 × T3	-11.49 **	-10.47 **	-7.23 **	-10.61 **	-10.61 **	-3.63 *
24	L6 × T4	-5.36 **	-4.26 **	-0.80	-4.14 *	-6.40 **	0.91
25	L7 × T1	0.00	5.04 **	8.84 **	-0.87	-3.54 *	3.99 *
26	L7 × T2	-0.74	4.26 **	8.03 **	-2.58	-4.71 **	2.72
27	L7 × T3	-8.86 **	-4.26 **	-0.80	-8.08 **	-8.08 **	-0.91
28	L7 × T4	0.74	5.81 **	9.64 **	-1.55	-3.87 *	3.63 *
29	L8 × T1	3.03 *	5.43 **	9.24 **	-0.69	-3.37 *	4.17 *
30	L8 × T2	0.76	3.10 *	6.83 **	-2.93	-5.05 **	2.36
31	L8 × T3	-4.55 **	-2.33	1.20	-3.87 *	-3.87 *	3.63 *
32	L8 × T4	9.09 **	11.63 **	15.66 **	7.41 **	4.88 **	13.07 **
33	L9 × T1	-11.78 **	-8.53 **	-5.22 **	-7.61 **	-10.10 **	-3.09
34	L9 × T2	1.68	5.43 **	9.24 **	-1.72	-3.87 *	3.63 *
35	L9 × T3	9.16 **	13.18 **	17.27 **	7.41 **	7.41 **	15.79 **
36	L9 × T4	5.42 **	9.30 **	13.25 **	0.17	-2.19	5.44 **
37	L10 × T1	-11.31 **	-5.81 **	-2.41	-6.06 **	-8.59 **	-1.45
38	L10 × T2	-13.14 **	-7.75 **	-4.42 **	-7.75 **	-9.76 **	-2.72
39	L10 × T3	-13.87 **	-8.53 **	-5.22 **	-10.61 **	-10.61 **	-3.63 *
40	L10 × T4	-10.40 **	-4.84 **	-1.41	-6.55 **	-8.75 **	-1.63
	S.Em±	0.96	0.96	0.96	1.15	1.15	1.15
	CD at 5%	2.71	2.71	2.71	3.26	3.26	3.26
	CD at 1%	3.61	3.61	3.61	4.35	4.35	4.35

* and ** indicate significance of values at p= 0.05 and p= 0.01, respectively. BP, BTP and SC: Heterosis over better parent, best parent and standard check (Kashi Rakshita), respectively.

Table 35. Heterosis (%) over better parent, best parent and standard check for fruit length and fruit diameter in sponge gourd

Sl. No.	Crosses	Fruit length (cm)			Fruit diameter (mm)		
		BP	BTP	SC	BP	BTP	SC
1	L1 × T1	-20.69 **	-24.07 **	-3.66 **	-3.89 **	-13.42 **	5.17 **
2	L1 × T2	3.44 **	-0.96	25.66 **	2.84 *	-7.35 **	12.53 **
3	L1 × T3	-18.03 **	-21.52 **	-0.42	-9.93 **	-18.86 **	-1.44
4	L1 × T4	-5.71 **	-9.72 **	14.54 **	5.53 **	-4.93 **	15.48 **
5	L2 × T1	10.83 **	10.83 **	40.62 **	17.59 **	17.59 **	42.83 **
6	L2 × T2	6.77 **	6.77 **	35.46 **	12.55 **	12.55 **	36.71 **
7	L2 × T3	2.77 **	2.77 **	30.39 **	-6.17 **	-6.17 **	13.97 **
8	L2 × T4	-4.66 **	-4.66 **	20.97 **	-9.43 **	-9.43 **	10.01 **
9	L3 × T1	-4.19 **	-12.90 **	10.51 **	-6.60 **	-11.88 **	7.04 **
10	L3 × T2	-2.20 *	-11.09 **	12.80 **	-5.68 **	-11.02 **	8.08 **
11	L3 × T3	-10.04 **	-18.23 **	3.75 **	-3.43 **	-8.89 **	10.67 **
12	L3 × T4	-20.37 **	-26.73 **	-7.04 **	-18.45 **	-23.06 **	-6.54 **
13	L4 × T1	0.60	-6.43 **	18.71 **	-5.73 **	-15.87 **	2.19 *
14	L4 × T2	-0.32	-7.28 **	17.64 **	-5.55 **	-15.71 **	2.39 *
15	L4 × T3	-3.02 **	-9.80 **	14.45 **	-11.44 **	-20.96 **	-3.99 **
16	L4 × T4	-16.77 **	-22.59 **	-1.78	-14.82 **	-23.98 **	-7.66 **
17	L5 × T1	-22.89 **	-28.50 **	-9.29 **	-3.85	-10.48 **	8.74
18	L5 × T2	-3.63 **	-10.65 **	13.37 **	-0.41	-7.27 **	12.63 **
19	L5 × T3	-21.73 **	-27.43 **	-7.93 **	-17.74 **	-23.41 **	-6.97 **
20	L5 × T4	6.86 **	-0.92	25.70 **	-2.60 *	-9.32 **	10.14 **
21	L6 × T1	13.56 **	9.28 **	38.65 **	18.99 **	15.79 **	40.64 **
22	L6 × T2	2.92 **	-0.96	25.66 **	2.71 *	-0.05	21.40 **
23	L6 × T3	-4.42 **	-8.02 **	16.70 **	-1.52	-4.18 **	16.39 **
24	L6 × T4	12.10 **	7.87 **	36.87 **	1.41	-1.32	19.86 **
25	L7 × T1	-17.74 **	-25.62 **	-5.63 **	-10.91 **	-19.96 **	-2.78 *
26	L7 × T2	-9.20 **	-17.89 **	4.17 **	-0.45	-10.56 **	8.64 **
27	L7 × T3	-16.84 **	-24.81 **	-4.60 **	4.11 **	-6.47 **	13.61 **
28	L7 × T4	-13.66 **	-20.55 **	0.80	-11.84 **	-20.80 **	-3.80 **
29	L8 × T1	-7.38 **	-12.27 **	11.30 **	1.03	-4.63 **	15.84 **
30	L8 × T2	-17.68 **	-22.03 **	-1.08	-12.93 **	-17.81 **	-0.16
31	L8 × T3	-20.61 **	-24.81 **	-4.60 **	-18.32 **	-22.90 **	-6.35 **
32	L8 × T4	-12.65 **	-17.26 **	4.97 **	-14.04 **	-18.86 **	-1.44
33	L9 × T1	-26.81 **	-31.79 **	-13.46 **	-14.36 **	-20.66 **	-3.63 **
34	L9 × T2	3.29 **	-3.73 **	22.14 **	3.26 **	-4.34 **	16.20 **
35	L9 × T3	-0.40	-7.17 **	17.78 **	0.03	-7.33 **	12.57 **
36	L9 × T4	-3.69 **	-10.24 **	13.88 **	2.44 *	-5.09 **	15.28 **
37	L10 × T1	-15.28 **	-25.58 **	-5.58 **	-1.92	-12.04 **	6.84 **
38	L10 × T2	-0.94	-10.35 **	13.74 **	-9.49 **	-18.83 **	-1.41
39	L10 × T3	-17.68 **	-27.69 **	-8.26 **	-18.95 **	-27.32 **	-11.71 **
40	L10 × T4	-2.93 **	-10.68 **	13.32 **	-9.40 **	-18.75 **	-1.31
	S.Em±	0.71	0.71	0.71	0.75	0.75	0.75
	CD at 5%	2.02	2.02	2.02	2.14	2.14	2.14
	CD at 1%	2.69	2.69	2.69	2.85	2.85	2.85

* and ** indicate significance of values at p= 0.05 and p= 0.01, respectively. BP, BTP and SC: Heterosis over better parent, best parent and standard check (Kashi Rakshita), respectively.

showed highest positive significant heterosis over both best parent (10.83 %) and commercial check (40.62 %). Out of 40 crosses, 10 crosses over better parent, five crosses over best parent and 26 crosses over commercial check recorded positive and significant heterosis for this trait.

4.8.2.10 Fruit diameter (Table 32 and 35)

The genotypes differed significantly among themselves for fruit diameter which ranged from 27.05 (T3) to 32.67 mm (T1) among testers, 33.13 mm (L4) to 37.12 mm (L2) among lines and 26.98 mm (L10 × T3) to 43.65 mm (L2 × T1) among crosses. The cross L6 × T1 exhibited positive and highly significant heterosis over better parent (18.99 %), while the cross L2 XT1 recorded highest positive and significant heterosis over best parent (17.59 %) and commercial check (42.83 %). Out of 40 crosses, eight crosses over better parent, only three crosses over the best parent and 26 crosses over the commercial check showed positive and significant heterosis for fruit diameter.

4.8.2.11 Average fruit weight (Table 36 and 37)

Mean value among the testers varied from 133.58 (T3) to 155.35 g (T1), among lines from 159.78 (L10) to 170.11 g (L2) and among crosses from 130 (L7 × T2) to 190.56 g (L2 × T1) for average fruit weight. Maximum positive and significant heterosis over better parent was observed in the cross L5 × T3 (13.57 %). Whereas, the cross L2 × T1 recorded maximum positive and significant heterosis over best parent (12.02 %) and commercial check (20.11 %). Among 40 crosses, nine crosses over better parent, four crosses over best parent and twelve crosses over commercial check manifested positive and significant heterosis for this trait.

4.8.2.12 Number of fruits per vine (Table 36 and 37)

Number of fruits per vine varied significantly among the sponge gourd genotypes which ranged from 17.00 (T3) to 18.30 (T1) among testers, 22.10 (L10) to 24.60 (L2) among lines and 16 (L10 × T3) to 32.40 (L2 XT1) among crosses. Heterosis over better parent, best parent and the commercial check were highly significant in both the directions. The highest positive and significant heterosis (34.75 %) was observed in the cross L6 × T1 over better parent. While, the cross L2 × T1 exhibited positive and

significant heterosis over both best parent (31.71 %) and commercial check (43.36 %). Out of 40 crosses, 24 crosses over better parent, 19 crosses over best parent and 26 crosses over the commercial check recorded positive and significant heterosis for this trait.

4.8.2.13 Fruit yield per vine (Table 36 and 38)

The sponge gourd genotypes differed significantly among themselves for fruit yield per vine and it ranged from 2.21 (T3) to 2.68 kg (T1) among testers, 3.31 (L10) to 3.76 kg (L2) among lines and 2.03 (L10 × T3) to 5.91 kg (L2 × T1) among crosses. Crosses exhibited heterosis over better parent, best parent and the commercial check significantly in both the directions. The highest positive and significant heterosis over better parent was exhibited by the cross L6 × T1 (60.99 %) followed by the crosses L2 × T1 (57.18 %) and L2 × T3 (53.19 %). Whereas, the crosses L2 × T1 (57.18 %), L6 × T1 (55.85 %) and L2 × T2 (53.19 %) exhibited positive and significant heterosis over the best parent. Similarly, the crosses L2 × T1 (67.90 %), L6 × T1 (66.48 %) and L2 × T2 (63.64 %) also recorded more significant positive heterosis over the commercial check in order of merit. Among 40 crosses, 24 crosses over better parent, 18 crosses over the best parent and 23 crosses over commercial check recorded positive and significant heterosis for fruit yield per vine.

4.8.2.14 Fruit yield per plot (Table 36 and 38)

The significant differences were observed among the sponge gourd genotypes for fruit yield per plot. It varied from 21.02 (T3) to 26.83 kg (T1) among testers, 32.00 (L10) to 36.61 kg (L2) among lines and 19.66 (L10 × T3) to 57.66 kg (L2 × T1) among crosses. The heterosis was observed over better parent, the best parent and the commercial check in both the directions. The highest positive and significant heterosis over better parent was recorded in the cross L6 × T1 (62.07 %) which was followed by the cross L2 × T1 (54.77 %) and L2 × T2 (51.87 %). Maximum positive and significant heterosis over the best parent was recorded in the cross L2 × T1 (54.77 %) followed by L6 × T1 (54.19 %) and L2 × T2 (51.87 %), whereas, high positive and significant heterosis over the commercial check was exhibited by the cross L2 × T1 (65.24 %)

Table 36. *Per se* performance of crosses and parents for yield and yield parameters in sponge gourd

Sl. No.	Crosses	Average fruit weight (g)	Number of fruits/ vine	Fruit yield/ vine (kg)	Fruit yield/ plot (kg)	Fruit yield/ hectare (t)	No. of seeds/ fruit
1	L1 × T1	166.87	22.20	3.62	35.26	16.67	143.80
2	L1 × T2	153.58	24.60	3.74	36.11	17.35	155.20
3	L1 × T3	160.74	23.60	3.65	35.54	16.32	240.40
4	L1 × T4	146.52	29.40	4.12	39.23	18.66	197.80
5	L2 × T1	190.56	32.40	5.91	57.66	27.12	264.60
6	L2 × T2	188.97	31.60	5.76	55.60	25.76	260.20
7	L2 × T3	156.07	26.80	4.12	39.43	18.57	176.60
8	L2 × T4	162.68	24.40	3.78	36.17	17.46	245.20
9	L3 × T1	152.67	21.20	3.12	29.62	13.35	255.60
10	L3 × T2	165.45	27.80	4.47	43.39	20.15	254.10
11	L3 × T3	143.80	28.60	3.87	36.00	17.88	213.00
12	L3 × T4	163.86	28.00	4.46	42.65	18.88	226.50
13	L4 × T1	127.17	27.00	3.22	30.36	13.77	128.70
14	L4 × T2	160.94	27.00	4.21	40.28	18.72	154.40
15	L4 × T3	133.75	20.40	2.65	24.55	11.51	170.30
16	L4 × T4	148.33	29.20	4.21	39.44	18.47	181.40
17	L5 × T1	161.64	22.00	3.23	31.20	13.83	175.40
18	L5 × T2	169.15	25.80	4.22	40.61	19.55	179.40
19	L5 × T3	185.37	18.80	3.39	33.11	15.62	106.60
20	L5 × T4	177.33	20.40	3.45	32.38	15.07	207.90
21	L6 × T1	189.12	31.80	5.86	56.45	26.87	262.40
22	L6 × T2	138.57	27.20	3.56	33.65	15.90	194.10
23	L6 × T3	167.49	25.40	4.12	40.12	19.33	154.40
24	L6 × T4	173.58	25.20	4.21	39.66	18.96	177.50
25	L7 × T1	140.58	23.60	3.23	30.43	14.25	192.80
26	L7 × T2	130.00	19.60	2.67	24.66	10.44	162.60
27	L7 × T3	179.05	16.40	2.86	26.84	12.62	152.80
28	L7 × T4	143.95	26.80	3.76	35.78	16.44	254.20
29	L8 × T1	176.09	23.80	3.98	37.82	17.56	260.20
30	L8 × T2	172.99	23.60	3.89	37.07	17.57	270.20
31	L8 × T3	143.21	28.40	3.81	36.55	17.34	257.80
32	L8 × T4	138.63	20.00	2.65	24.62	11.53	254.20
33	L9 × T1	176.11	16.20	2.76	25.72	11.66	140.20

Table 36. *Contd...*

Sl. No.	Crosses	Average fruit weight (g)	Number of fruits/ vine	Fruit yield/ vine (kg)	Fruit yield/ plot (kg)	Fruit yield/ hectare (t)	No. of seeds/ fruit
34	L9 × T2	144.56	28.60	3.87	36.77	17.40	252.40
35	L9 × T3	146.63	24.20	3.43	32.37	15.63	221.00
36	L9 × T4	164.45	18.20	2.87	26.62	12.84	231.80
37	L10 × T1	140.20	25.00	3.34	31.07	14.65	128.90
38	L10 × T2	135.55	18.60	2.42	22.63	10.10	150.70
39	L10 × T3	133.00	16.00	2.03	19.66	9.78	178.20
40	L10 × T4	140.59	18.40	2.43	22.43	10.33	159.80
	Lines						
41	L1	160.26	22.60	3.34	33.80	15.78	278.60
42	L2	170.11	24.60	3.76	36.61	18.14	336.20
43	L3	160.22	23.20	3.62	34.13	15.69	276.00
44	L4	161.31	22.80	3.59	34.22	16.11	275.60
45	L5	163.22	22.60	3.43	32.87	15.66	274.40
46	L6	165.14	23.60	3.64	34.83	17.23	274.20
47	L7	161.21	22.40	3.42	32.06	14.57	264.20
48	L8	162.32	23.40	3.63	34.72	16.33	288.40
49	L9	160.27	23.10	3.52	33.12	14.83	282.00
50	L10	159.78	22.10	3.31	32.00	14.42	280.20
	Testers						
51	T1	155.35	18.30	2.68	26.83	13.22	248.20
52	T2	152.32	17.20	2.56	25.73	12.64	250.40
53	T3	133.58	17.00	2.21	21.02	10.23	162.80
54	T4	146.25	17.80	2.42	23.17	10.53	152.80
55	SC	158.65	22.60	3.52	34.29	16.32	192.20
S.Em±		1.90	0.49	0.16	0.73	0.43	3.34
CD at 5%		5.39	1.38	0.45	2.08	1.23	9.47
CD at 1%		7.18	1.83	0.59	2.77	1.64	12.61

SC : Standard check (Kashi Rakshita) DAS:Days after sowing

Table 37. Heterosis (%) over better parent, best parent and standard check for average fruit weight and number of fruits per vine in sponge gourd

Sl. No.	Crosses	Average fruit weight (g)			Number of fruits per vine		
		BP	BTP	SC	BP	BTP	SC
1	L1 × T1	4.12	-1.90	5.18	-1.77 *	-9.76 **	-1.77 *
2	L1 × T2	-4.17	-9.72 **	-3.20	8.85 **	0.00	8.85 **
3	L1 × T3	0.30	-5.51 *	1.32	4.42 **	-4.07 **	4.42 **
4	L1 × T4	-8.57 **	-13.87 **	-7.65 **	30.09 **	19.51 **	30.09 **
5	L2 × T1	12.02 **	12.02 **	20.11 **	31.71 **	31.71 **	43.36 **
6	L2 × T2	11.09 **	11.09 **	19.11 **	28.46 **	28.46 **	39.82 **
7	L2 × T3	-8.25 **	-8.25 **	-1.63	8.94 **	8.94 **	18.58 **
8	L2 × T4	-4.37	-4.37	2.54	-0.81	-0.81	7.96 **
9	L3 × T1	-4.71	-10.25 **	-3.77	-8.62 **	-13.82 **	-6.19 **
10	L3 × T2	3.26	-2.74	4.29	19.83 **	13.01 **	23.01 **
11	L3 × T3	-10.25 **	-15.47 **	-9.36 **	23.28 **	16.26 **	26.55 **
12	L3 × T4	2.27	-3.67	3.28	20.69 **	13.82 **	23.89 **
13	L4 × T1	-21.16 **	-25.24 **	-19.84 **	18.42 **	9.76 **	19.47 **
14	L4 × T2	-0.23	-5.39 *	1.44	18.42 **	9.76 **	19.47 **
15	L4 × T3	-17.09 **	-21.37 **	-15.69 **	-10.53 **	-17.07 **	-9.73 **
16	L4 × T4	-8.05 **	-12.80 **	-6.50 *	28.07 **	18.70 **	29.20 **
17	L5 × T1	-0.97	-4.98	1.88	-2.65 **	-10.57 **	-2.65 **
18	L5 × T2	3.63	-0.56	6.62 *	14.16 **	4.88 **	14.16 **
19	L5 × T3	13.57 **	8.97 **	16.84 **	-16.81 **	-23.58 **	-16.81 **
20	L5 × T4	8.64 **	4.24	11.77 **	-9.73 **	-17.07 **	-9.73 **
21	L6 × T1	14.52 **	11.18 **	19.21 **	34.75 **	29.27 **	40.71 **
22	L6 × T2	-16.09 **	-18.54 **	-12.66 **	15.25 **	10.57 **	20.35 **
23	L6 × T3	1.42	-1.54	5.57 *	7.63 **	3.25 **	12.39 **
24	L6 × T4	5.11	2.04	9.41 **	6.78 **	2.44 **	11.50 **
25	L7 × T1	-12.80 **	-17.36 **	-11.39 **	5.36 **	-4.07 **	4.42 **
26	L7 × T2	-19.36 **	-23.58 **	-18.06 **	-12.50 **	-20.33 **	-13.27 **
27	L7 × T3	11.07 **	5.26	12.86 **	-26.79 **	-33.33 **	-27.43 **
28	L7 × T4	-10.71 **	-15.38 **	-9.27 **	19.64 **	8.94 **	18.58 **
29	L8 × T1	8.48 **	3.52	10.99 **	1.71 *	-3.25 **	5.31 **
30	L8 × T2	6.57 *	1.69	9.04 **	0.85	-4.07 **	4.42 **
31	L8 × T3	-11.77 **	-15.81 **	-9.73 **	21.37 **	15.45 **	25.66 **
32	L8 × T4	-14.59 **	-18.51 **	-12.62 **	-14.53 **	-18.70 **	-11.50 **
33	L9 × T1	9.88 **	3.53	11.01 **	-29.87 **	-34.15 **	-28.32 **
34	L9 × T2	-9.80 **	-15.02 **	-8.88 **	23.81 **	16.26 **	26.55 **
35	L9 × T3	-8.51 **	-13.80 **	-7.58 **	4.76 **	-1.63 *	7.08 **
36	L9 × T4	2.61	-3.33	3.66	-21.21 **	-26.02 **	-19.47 **
37	L10 × T1	-12.25 **	-17.58 **	-11.63 **	13.12 **	1.63 *	10.62 **
38	L10 × T2	-15.16 **	-20.32 **	-14.56 **	-15.84 **	-24.39 **	-17.70 **
39	L10 × T3	-16.76 **	-21.82 **	-16.17 **	-27.60 **	-34.96 **	-29.20 **
40	L10 × T4	-12.01 **	-17.35 **	-11.38 **	-16.74 **	-25.20 **	-18.58 **
	S.Em±	1.90	1.90	1.90	0.49	0.49	0.49
	CD at 5%	5.39	5.39	5.39	1.38	1.38	1.38
	CD at 1%	7.18	7.18	7.18	1.83	1.83	1.83

* and ** indicate significance of values at p= 0.05 and p= 0.01, respectively. BP, BTP and SC: Heterosis over better parent, best parent and standard check (Kashi Rakshita), respectively.

Table 38. Heterosis (%) over better parent, best parent and standard check for fruit yield per vine and fruit yield per plot in sponge gourd

Sl. No.	Crosses	Fruit yield per vine (kg)			Fruit yield per plot (kg)		
		BP	BTP	SC	BP	BTP	SC
1	L1 × T1	8.38 **	-3.72 **	2.84 **	4.32 **	-3.69 **	2.83 **
2	L1 × T2	11.98 **	-0.53 *	6.25 **	6.83 **	-1.37	5.31 **
3	L1 × T3	9.28 **	-2.93 **	3.69 **	5.15 **	-2.92 **	3.65 **
4	L1 × T4	23.35 **	9.57 **	17.05 **	16.07 **	7.16 **	14.41 **
5	L2 × T1	57.18 **	57.18 **	67.90 **	54.77 **	54.77 **	65.24 **
6	L2 × T2	53.19 **	53.19 **	63.64 **	51.87 **	51.87 **	62.15 **
7	L2 × T3	9.57 **	9.57 **	17.05 **	7.70 **	7.70 **	14.99 **
8	L2 × T4	0.53 *	0.53 *	7.39 **	-1.20	-1.20	5.48 **
9	L3 × T1	-13.81 **	-17.02 **	-11.36 **	-13.21 **	-19.09 **	-13.62 **
10	L3 × T2	23.48 **	18.88 **	26.99 **	27.13 **	18.52 **	26.54 **
11	L3 × T3	6.91 **	2.93 **	9.94 **	5.48 **	-1.67	4.99 **
12	L3 × T4	23.20 **	18.62 **	26.70 **	24.96 **	16.50 **	24.38 **
13	L4 × T1	-10.31 **	-14.36 **	-8.52 **	-11.28 **	-17.07 **	-11.46 **
14	L4 × T2	17.27 **	11.97 **	19.60 **	17.71 **	10.02 **	17.47 **
15	L4 × T3	-26.18 **	-29.52 **	-24.72 **	-28.26 **	-32.94 **	-28.40 **
16	L4 × T4	17.27 **	11.97 **	19.60 **	15.25 **	7.73 **	15.02 **
17	L5 × T1	-5.83 **	-14.10 **	-8.24 **	-5.08 **	-14.78 **	-9.01 **
18	L5 × T2	23.03 **	12.23 **	19.89 **	23.55 **	10.93 **	18.43 **
19	L5 × T3	-1.17 **	-9.84 **	-3.69 **	0.73	-9.56 **	-3.44 **
20	L5 × T4	0.58 *	-8.24 **	-1.99 **	-1.49	-11.55 **	-5.57 **
21	L6 × T1	60.99 **	55.85 **	66.48 **	62.07 **	54.19 **	64.63 **
22	L6 × T2	-2.20 **	-5.32 **	1.14 **	-3.39 **	-8.09 **	-1.87
23	L6 × T3	13.19 **	9.57 **	17.05 **	15.19 **	9.59 **	17.00 **
24	L6 × T4	15.66 **	11.97 **	19.60 **	13.87 **	8.33 **	15.66 **
25	L7 × T1	-5.56 **	-14.10 **	-8.24 **	-5.08 **	-16.88 **	-11.26 **
26	L7 × T2	-21.93 **	-28.99 **	-24.15 **	-23.08 **	-32.64 **	-28.08 **
27	L7 × T3	-16.37 **	-23.94 **	-18.75 **	-16.28 **	-26.69 **	-21.73 **
28	L7 × T4	9.94 **	0.00	6.82 **	11.60 **	-2.27 *	4.35
29	L8 × T1	9.64 **	5.85 **	13.07 **	8.93 **	3.31 **	10.29 **
30	L8 × T2	7.16 **	3.46 **	10.51 **	6.77 **	1.26	8.11
31	L8 × T3	4.96 **	1.33 **	8.24 **	5.27 **	-0.16	6.59 **
32	L8 × T4	-27.00 **	-29.52 **	-24.72 **	-29.09 **	-32.75 **	-28.20 **
33	L9 × T1	-21.59 **	-26.60 **	-21.59 **	-22.34 **	-29.75 **	-24.99 **
34	L9 × T2	9.94 **	2.93 **	9.94 **	11.02 **	0.44	7.23 **
35	L9 × T3	-2.56 **	-8.78 **	-2.56 **	-2.26 *	-11.58 **	-5.60 **
36	L9 × T4	-18.47 **	-23.67 **	-18.47 **	-19.63 **	-27.29 **	-22.37 **
37	L10 × T1	0.91 **	-11.17 **	-5.11 **	-2.91 **	-15.13 **	-9.39 **
38	L10 × T2	-26.89 **	-35.64 **	-31.25 **	-29.28 **	-38.19 **	-34.00 **
39	L10 × T3	-38.67 **	-46.01 **	-42.33 **	-38.56 **	-46.30 **	-42.67 **
40	L10 × T4	-26.59 **	-35.37 **	-30.97 **	-29.91 **	-38.73 **	-34.59 **
	S.Em±	0.16	0.16	0.16	0.73	0.73	0.73
	CD at 5%	0.45	0.45	0.45	2.08	2.08	2.08
	CD at 1%	0.59	0.59	0.59	2.77	2.77	2.77

* and ** indicate significance of values at p= 0.05 and p= 0.01, respectively. BP, BTP and SC: Heterosis over better parent, best parent and standard check (Kashi Rakshita), respectively.

followed by L6 × T1 (64.63 %) and L2 × T2 (62.15 %). Among the 40 crosses, 21 crosses over better parent, 13 crosses over the best parent and 22 crosses over the commercial check manifested positive and significant heterosis for the character fruit yield per plot.

4.8.2.15 Fruit yield per hectare (Table 36 and 39)

Fruit yield per hectare varied significantly among the 40 genotypes which varied between 10.23 (T3) to 13.22 t (T1) among testers, 14.42 (L10) to 18.14 t (L2) among lines and 9.78 (L10 × T3) to 27.12 t (L2 × T1) among crosses. The top three hybrids which recorded maximum positive and significant heterosis over better parent were L6 × T1 (55.95 %), L2 × T1 (49.50 %) and cross L2 × T2 (42.01 %). Highest positive and significant heterosis over the best parent was noticed in the cross L2 × T1 (49.50 %) followed by L6 × T1 (48.13 %) and L2 × T2 (42.01 %), whereas, for heterosis over the commercial check, the cross L2 × T1 (66.18 %) followed by L6 × T1 (64.64 %) and L2 × T2 (57.84 %) were registered maximum positive and significant heterosis. Out of 40 crosses, 22 crosses over better parent, 12 crosses over the best parent and 20 crosses over the commercial check had recorded positive and significant heterosis.

4.8.2.16 Number of seeds per fruit (Table 36 and 39)

The number of seeds per fruit ranged from 152.80 (T4) to 250.40 (T2) among testers, 264.20 (L7) to 336.20 (L2) among lines and 106.60 (L5 × T3) to 264.60 (L2 × T1) among crosses. Magnitude of heterosis over better parent and best parent was highly significant in negative direction only whereas, heterosis over commercial was significant in both the directions. The cross L8 × T2 showed highest heterosis over commercial check (40.58 %) followed by L6 × T1 (36.52 %). Out of 40 crosses, no crosses had exhibited positive heterosis over best and better parent however, 13 crosses exhibited positive and significant heterosis over commercial check.

4.8.2.17 Sponge yield (g/fruit) (Table 40 and 41)

The sponge gourd genotypes differed significantly among themselves for sponge yield which ranged from 11.55 (T4) to 14.62 g (T1) among testers, 14.88 (L1) to 17.65 g (L2) among lines and 8.78 (L9 × T1) to 19.45 g (L2 × T1) among crosses. Maximum

Table 39. Heterosis (%) over better parent, best parent and standard check for fruit yield per hectare and number of seeds per fruit in sponge gourd

Sl. No.	Crosses	Fruit yield per hectare (t/ha)			Number of seeds per fruit		
		BP	BTP	SC	BP	BTP	SC
1	L1 × T1	5.64 **	-8.10 **	2.14 **	-48.38 **	-57.23 **	-25.18 **
2	L1 × T2	9.95 **	-4.36 **	6.31 **	-44.29 **	-53.84 **	-19.25 **
3	L1 × T3	3.42 **	-10.03 **	0.00	-13.71 **	-28.49 **	25.08 **
4	L1 × T4	18.25 **	2.87 **	14.34 **	-29.00 **	-41.17 **	2.91
5	L2 × T1	49.50 **	49.50 **	66.18 **	-21.30 **	-21.30 **	37.67 **
6	L2 × T2	42.01 **	42.01 **	57.84 **	-22.61 **	-22.61 **	35.38 **
7	L2 × T3	2.37 **	2.37 **	13.79 **	-47.47 **	-47.47 **	-8.12
8	L2 × T4	-3.75 **	-3.75 **	6.99 **	-27.07 **	-27.07 **	27.58 **
9	L3 × T1	-14.91 **	-26.41 **	-18.20 **	-7.39	-23.97 **	32.99 **
10	L3 × T2	28.43 **	11.08 **	23.47 **	-7.93	-24.42 **	32.21 **
11	L3 × T3	13.96 **	-1.43 *	9.56 **	-22.83 **	-36.64 **	10.82 *
12	L3 × T4	20.33 **	4.08 **	15.69 **	-17.93 **	-32.63 **	17.85 **
13	L4 × T1	-14.53 **	-24.09 **	-15.63 **	-53.30 **	-61.72 **	-33.04 **
14	L4 × T2	16.20 **	3.20 **	14.71 **	-43.98 **	-54.07 **	-19.67 **
15	L4 × T3	-28.55 **	-36.55 **	-29.47 **	-38.21 **	-49.35 **	-11.39 *
16	L4 × T4	14.65 **	1.82 **	13.17 **	-34.18 **	-46.04 **	-5.62
17	L5 × T1	-11.69 **	-23.76 **	-15.26 **	-36.08 **	-47.83 **	-8.74
18	L5 × T2	24.84 **	7.77 **	19.79 **	-34.62 **	-46.64 **	-6.66
19	L5 × T3	-0.26	-13.89 **	-4.29 **	-61.15 **	-68.29 **	-44.54 **
20	L5 × T4	-3.77 **	-16.92 **	-7.66 **	-24.23 **	-38.16 **	8.17
21	L6 × T1	55.95 **	48.13 **	64.64 **	-4.30	-21.95 **	36.52 **
22	L6 × T2	-7.72 **	-12.35 **	-2.57 **	-29.21 **	-42.27 **	0.99
23	L6 × T3	12.19 **	6.56 **	18.44 **	-43.69 **	-54.07 **	-19.67 **
24	L6 × T4	10.04 **	4.52 **	16.18 **	-35.27 **	-47.20 **	-7.65
25	L7 × T1	-2.20 **	-21.44 **	-12.68 **	-27.02 **	-42.65 **	0.31
26	L7 × T2	-28.35 **	-42.45 **	-36.03 **	-38.46 **	-51.64 **	-15.40 **
27	L7 × T3	-13.38 **	-30.43 **	-22.67 **	-42.17 **	-54.55 **	-20.50 **
28	L7 × T4	12.83 **	-9.37 **	0.74	-3.79	-24.39 **	32.26 **
29	L8 × T1	7.53 **	-3.20 **	7.60 **	-9.78 *	-22.61 **	35.38 **
30	L8 × T2	7.59 **	-3.14 **	7.66 **	-6.31	-19.63 **	40.58 **
31	L8 × T3	6.18 **	-4.41 **	6.25 **	-10.61 *	-23.32 **	34.13 **
32	L8 × T4	-29.39 **	-36.44 **	-29.35 **	-11.86 *	-24.39 **	32.26 **
33	L9 × T1	-21.38 **	-35.72 **	-28.55 **	-50.28 **	-58.30 **	-27.06 **
34	L9 × T2	17.33 **	-4.08 **	6.62 **	-10.50 *	-24.93 **	31.32 **
35	L9 × T3	5.39 **	-13.84 **	-4.23 **	-21.63 **	-34.27 **	14.98 **
36	L9 × T4	-13.42 **	-29.22 **	-21.32 **	-17.80 **	-31.05 **	20.60 **
37	L10 × T1	1.60 *	-19.24 **	-10.23 **	-54.00 **	-61.66 **	-32.93 **
38	L10 × T2	-29.96 **	-44.32 **	-38.11 **	-46.22 **	-55.18 **	-21.59 **
39	L10 × T3	-32.18 **	-46.09 **	-40.07 **	-36.40 **	-47.00 **	-7.28
40	L10 × T4	-28.36 **	-43.05 **	-36.70 **	-42.97 **	-52.47 **	-16.86 **
	S.Em±	0.43	0.43	0.43	3.34	3.34	3.34
	CD at 5%	1.23	1.23	1.23	9.47	9.47	9.47
	CD at 1%	1.64	1.64	1.64	12.61	12.61	12.61

* and ** indicate significance of values at p= 0.05 and p= 0.01, respectively. BP, BTP and SC: Heterosis over better parent, best parent and standard check (Kashi Rakshita), respectively.

Table 40. *Per se* performance of crosses and parents for sponge yield and quality parameters in sponge gourd

Sl. No.	Crosses	Sponge yield (g)	TSS (^o Brix)	Fruit firmness (N)	Fruit color (L [*])	Fruit color (a [*])	Fruit color (b [*])	Protein (%)
1	L1 × T1	11.88	4.26	25.43	44.24	7.38	23.86	12.12
2	L1 × T2	17.28	3.37	28.97	35.70	7.51	18.19	11.92
3	L1 × T3	14.11	3.69	30.22	40.05	8.80	20.27	9.67
4	L1 × T4	12.90	3.45	27.46	42.00	8.19	23.60	11.76
5	L2 × T1	19.45	4.39	44.67	35.04	8.09	18.03	9.80
6	L2 × T2	17.89	4.42	43.56	37.54	8.53	20.29	10.23
7	L2 × T3	17.45	4.18	26.61	36.31	7.35	24.10	12.32
8	L2 × T4	16.33	3.55	22.42	39.64	8.16	22.08	12.13
9	L3 × T1	9.64	3.90	33.18	37.19	7.78	20.43	12.89
10	L3 × T2	13.93	3.98	39.82	40.61	8.08	22.99	12.63
11	L3 × T3	14.22	4.01	30.90	36.13	7.91	16.94	11.97
12	L3 × T4	17.05	4.13	32.00	39.68	7.84	22.08	13.09
13	L4 × T1	11.89	4.09	31.01	37.04	8.04	26.06	10.23
14	L4 × T2	12.06	4.11	25.46	37.94	8.24	21.96	13.67
15	L4 × T3	12.12	4.50	28.44	37.80	7.90	18.88	13.77
16	L4 × T4	9.82	3.91	29.55	39.76	7.94	27.06	13.04
17	L5 × T1	15.95	4.03	33.21	34.67	7.62	18.27	13.87
18	L5 × T2	12.22	4.00	26.47	35.24	7.86	16.03	13.27
19	L5 × T3	16.99	3.61	27.87	35.96	7.66	27.98	9.85
20	L5 × T4	15.06	4.12	34.17	38.26	8.06	24.47	11.86
21	L6 × T1	18.67	4.53	46.45	38.97	7.45	22.78	11.72
22	L6 × T2	17.92	4.24	40.12	40.26	7.85	22.51	12.97
23	L6 × T3	14.51	4.04	25.87	41.40	8.47	17.93	12.92
24	L6 × T4	15.50	3.59	33.30	38.97	7.56	19.56	13.30
25	L7 × T1	12.09	4.66	35.60	40.96	8.76	18.38	12.87
26	L7 × T2	12.40	4.72	34.21	37.21	7.85	23.25	10.04
27	L7 × T3	10.84	5.70	30.22	41.00	7.63	20.01	13.61
28	L7 × T4	11.00	4.66	22.87	41.70	8.00	24.90	10.01
29	L8 × T1	13.21	3.83	33.66	45.09	5.74	28.00	12.03
30	L8 × T2	14.09	3.65	26.45	37.34	8.40	23.87	8.65
31	L8 × T3	11.89	4.32	35.23	37.27	7.99	23.21	12.91
32	L8 × T4	13.43	3.87	23.65	42.82	7.71	21.69	11.34

Table 40. Contd...

Sl. No.	Crosses	Sponge yield (g)	TSS (^o Brix)	Fruit firmness (N)	Fruit color(L*)	Fruit color (a*)	Fruit color (b*)	Protein (%)
33	L9 × T1	8.78	4.77	40.45	28.67	9.22	13.33	12.80
34	L9 × T2	13.24	4.42	42.68	43.81	8.74	22.64	12.98
35	L9 × T3	13.05	4.44	35.48	43.91	7.98	20.75	9.65
36	L9 × T4	9.06	4.62	35.39	38.55	8.33	21.91	7.86
37	L10 × T1	17.12	4.05	23.64	41.91	8.45	23.24	9.77
38	L10 × T2	14.98	4.68	29.17	40.42	8.78	24.02	10.72
39	L10 × T3	9.15	5.65	31.37	42.83	8.63	23.00	12.56
40	L10 × T4	13.02	4.34	32.65	39.84	7.69	19.56	11.24
	Lines							
41	L1	14.88	3.76	23.89	30.50	7.03	23.32	11.01
42	L2	17.65	4.34	24.12	38.35	6.82	16.71	10.13
43	L3	15.42	4.21	27.21	33.20	7.32	20.68	10.11
44	L4	15.68	4.24	26.46	31.91	6.93	19.38	10.21
45	L5	17.02	4.12	25.11	33.13	7.60	17.39	11.02
46	L6	17.45	4.38	23.77	31.80	6.59	16.38	10.73
47	L7	16.14	4.61	27.58	34.39	6.41	17.31	9.12
48	L8	16.77	3.21	27.12	31.26	8.08	17.30	8.04
49	L9	15.86	3.98	28.22	42.69	6.01	24.88	9.24
50	L10	15.11	3.67	27.89	38.80	7.88	23.89	9.89
	Testers							
51	T1	14.62	4.21	38.33	43.22	7.29	23.83	9.62
52	T2	13.87	3.76	38.88	36.09	7.05	17.72	8.57
53	T3	13.03	3.62	35.83	36.69	6.67	17.66	8.34
54	T4	11.55	4.65	34.43	38.65	6.98	19.55	9.67
55	SC	13.56	4.12	31.55	38.93	7.82	20.37	10.85
S.Em±		0.62	0.21	0.88	0.65	0.31	0.55	0.52
CD at 5%		1.74	0.60	2.50	1.85	0.88	1.57	1.47
CD at 1%		2.32	0.79	3.33	2.46	1.17	2.09	1.96

SC : Standard check (Kashi Rakshita) DAS : Days after sowing

Table 41. Heterosis (%) over better parent, best parent and standard check for sponge yield and total soluble solids in sponge gourd

Sl. No.	Crosses	Sponge yield (g/fruit)			Total soluble solids (°Brix)		
		BP	BTP	SC	BP	BTP	SC
1	L1 × T1	-20.16 **	-32.69 **	-12.39 **	1.19 **	-8.39 **	3.40 **
2	L1 × T2	16.13 **	-2.10 *	27.43 **	-10.37 **	-27.53 **	-18.20 **
3	L1 × T3	-5.17 **	-20.06 **	4.06 **	-1.86 **	-20.65 **	-10.44 **
4	L1 × T4	-13.31 **	-26.91 **	-4.87 **	-25.81 **	-25.81 **	-16.26 **
5	L2 × T1	10.20 **	10.20 **	43.44 **	1.15 **	-5.59 **	6.55 **
6	L2 × T2	1.36	1.36	31.93 **	1.84 **	-4.95 **	7.28 **
7	L2 × T3	-1.13	-1.13	28.69 **	-3.69 **	-10.11 **	1.46 **
8	L2 × T4	-7.48 **	-7.48 **	20.43 **	-23.66 **	-23.66 **	-13.83 **
9	L3 × T1	-37.48 **	-45.38 **	-28.91 **	-7.36 **	-16.13 **	-5.34 **
10	L3 × T2	-9.66 **	-21.08 **	2.73 *	-5.46 **	-14.41 **	-3.40 **
11	L3 × T3	-7.78 **	-19.43 **	4.87 **	-4.75 **	-13.76 **	-2.67 **
12	L3 × T4	10.57 **	-3.40 **	25.74 **	-11.18 **	-11.18 **	0.24
13	L4 × T1	-24.17 **	-32.63 **	-12.32 **	-3.54 **	-12.04 **	-0.73 *
14	L4 × T2	-23.09 **	-31.67 **	-11.06 **	-3.07 **	-11.61 **	-0.24
15	L4 × T3	-22.70 **	-31.33 **	-10.62 **	6.13 **	-3.23 **	9.22 **
16	L4 × T4	-37.37 **	-44.36 **	-27.58 **	-15.91 **	-15.91 **	-5.10 **
17	L5 × T1	-6.29 **	-9.63 **	17.63 **	-4.28 **	-13.33 **	-2.18 **
18	L5 × T2	-28.20 **	-30.76 **	-9.88 **	-2.91 **	-13.98 **	-2.91 **
19	L5 × T3	-0.18	-3.74 **	25.29 **	-12.38 **	-22.37 **	-12.38 **
20	L5 × T4	-11.52 **	-14.67 **	11.06 **	-11.40 **	-11.40 **	0.00
21	L6 × T1	6.99 **	5.78 **	37.68 **	3.42 **	-2.58 **	9.95 **
22	L6 × T2	2.69 **	1.53	32.15 **	-3.20 **	-8.82 **	2.91 **
23	L6 × T3	-16.85 **	-17.79 **	7.01 **	-7.76 **	-13.12 **	-1.94 **
24	L6 × T4	-11.17 **	-12.18 **	14.31 **	-22.80 **	-22.80 **	-12.86 **
25	L7 × T1	-25.09 **	-31.50 **	-10.84 **	1.08 **	0.22	13.11 **
26	L7 × T2	-23.17 **	-29.75 **	-8.55 **	2.39 **	1.51 **	14.56 **
27	L7 × T3	-32.84 **	-38.58 **	-20.06 **	23.64 **	22.58 **	38.35 **
28	L7 × T4	-31.85 **	-37.68 **	-18.88 **	0.22	0.22	13.11 **
29	L8 × T1	-21.23 **	-25.16 **	-2.58 **	-9.03 **	-17.63 **	-7.04 **
30	L8 × T2	-15.98 **	-20.17 **	3.91 **	-2.93 **	-21.51 **	-11.41 **
31	L8 × T3	-29.10 **	-32.63 **	-12.32 **	19.34 **	-7.10 **	4.85 **
32	L8 × T4	-19.92 **	-23.91 **	-0.96	-16.77 **	-16.77 **	-6.07 **
33	L9 × T1	-44.64 **	-50.25 **	-35.25 **	13.30 **	2.58 **	15.78 **
34	L9 × T2	-16.52 **	-24.99 **	-2.36 **	11.06 **	-4.95 **	7.28 **
35	L9 × T3	-17.72 **	-26.06 **	-3.76 **	11.56 **	-4.52 **	7.77 **
36	L9 × T4	-42.88 **	-48.67 **	-33.19 **	-0.65 *	-0.65 *	12.14 **
37	L10 × T1	13.30 **	-3.00 **	26.25 **	-3.80 **	-12.90 **	-1.70 **
38	L10 × T2	-0.86	-15.13 **	10.47 **	24.47 **	0.65 *	13.59 **
39	L10 × T3	-39.44 **	-48.16 **	-32.52 **	53.95 **	21.51 **	37.14 **
40	L10 × T4	-13.83 **	-26.23 **	-3.98 **	-6.67 **	-6.67 **	5.34 **
	S.Em±	0.62	0.62	0.62	0.21	0.21	0.21
	CD at 5%	1.74	1.74	1.74	0.60	0.60	0.60
	CD at 1%	2.32	2.32	2.32	0.79	0.79	0.79

* and ** indicate significance of values at p= 0.05 and p= 0.01, respectively. BP, BTP and SC: Heterosis over better parent, best parent and standard check (Kashi Rakshita), respectively.

positive and significant heterosis was observed in the cross $L1 \times T1$ over better parent (16.13 %) whereas, the cross $L2 \times T1$ exhibited heterosis of 10.20 per cent over best parent and 43.44 per cent over commercial check. Out of 40 crosses, only six crosses over better parent, two crosses over best parent and 19 crosses over commercial check showed positive and significant heterosis.

4.8.2.18 Total soluble solids of the fruit (Table 40 and 41)

Total soluble solids (TSS) of the fruit varied significantly among sponge gourd genotypes and it ranged from 3.62 (T3) to 4.65 °Brix (T4) among the testers, 3.21 (L8) to 4.61 °Brix (L7) among the lines and 3.37 ($L1 \times T2$) to 5.70 °Brix ($L7 \times T3$) among the crosses. Positive heterosis over better parent, best parent and commercial check was desirable for this trait. The trait recorded highest (53.95 %) positive and significant heterosis over better parent was observed in the cross $L10 \times T3$ whereas, the cross $L7 \times T3$ recorded 22.58 and 38.35 per cent heterosis over best parent and commercial check. Out of 40 crosses, 13 crosses over better parent, four crosses over best parent and 19 crosses over commercial check had exhibited positive and significant heterosis.

4.8.2.19 Fruit firmness (Table 40 and 42)

The *per se* performance for fruit firmness varied from 34.43 (T4) to 38.88 N (T2) among the testers, 23.77 (L6) to 28.22 N (L9) among the lines and 22.42 N ($L2 \times T4$) to 46.45 N ($L6 \times T1$) among the crosses. Positive heterosis over better parent, best parent and the commercial check is desirable for this trait. The cross $L6 \times T1$ recorded maximum positive and significant heterosis over the better parent (21.18 %), best parent (19.47 %) and commercial check (47.23 %). Among 40 crosses, only seven crosses over better parent, six crosses over best parent and as many as 18 crosses over the commercial check manifested significant negative heterosis.

4.8.2.20 Fruit color (Table 40, 42 and 43)

Sponge gourd genotypes differed significantly among themselves for this trait fruit color value (L^*). It varied from 36.69 (T3) to 43.22 (T1) among the testers, 30.50 (L1) to 42.69 (L9) among the lines and 28.67 ($L9 \times T1$) to 45.09 ($L8 \times T1$) among the

Table 42. Heterosis (%) over better parent, best parent and standard check for fruit firmness and fruit color (L*) in sponge gourd

Sl. No.	Crosses	Fruit firmness (N)			Fruit color (L*)		
		BP	BTP	SC	BP	BTP	SC
1	L1 × T1	-33.66 **	-34.59 **	-19.40 **	2.36 *	2.36 *	13.64 **
2	L1 × T2	-25.49 **	-25.49 **	-8.18 **	-1.08	-17.40 **	-8.30 **
3	L1 × T3	-15.66 **	-22.27 **	-4.22 **	9.16 **	-7.33 **	2.88 **
4	L1 × T4	-20.24 **	-29.37 **	-12.96 **	8.67 **	-2.82 **	7.89 **
5	L2 × T1	16.54 **	14.89 **	41.58 **	-18.93 **	-18.93 **	-9.99 **
6	L2 × T2	12.04 **	12.04 **	38.07 **	-2.11 *	-13.14 **	-3.57 **
7	L2 × T3	-25.73 **	-31.56 **	-15.66 **	-5.32 **	-15.99 **	-6.73 **
8	L2 × T4	-34.88 **	-42.34 **	-28.94 **	2.56 **	-8.28 **	1.82
9	L3 × T1	-13.44 **	-14.66 **	5.17 **	-13.95 **	-13.95 **	-4.47 **
10	L3 × T2	2.42	2.42	26.21 **	12.52 **	-6.04 **	4.32 **
11	L3 × T3	-13.76 **	-20.52 **	-2.06	-1.53	-16.40 **	-7.19 **
12	L3 × T4	-7.06 **	-17.70 **	1.43	2.66 **	-8.19 **	1.93 *
13	L4 × T1	-19.10 **	-20.24 **	-1.71	-14.30 **	-14.30 **	-4.85 **
14	L4 × T2	-34.52 **	-34.52 **	-19.30 **	5.13 **	-12.22 **	-2.54 **
15	L4 × T3	-20.63 **	-26.85 **	-9.86 **	3.03 **	-12.54 **	-2.90 **
16	L4 × T4	-14.17 **	-24.00 **	-6.34 **	2.87 **	-8.01 **	2.13 *
17	L5 × T1	-13.36 **	-14.58 **	5.26 **	-19.78 **	-19.78 **	-10.94 **
18	L5 × T2	-31.92 **	-31.92 **	-16.10 **	-2.36 *	-18.46 **	-9.48 **
19	L5 × T3	-22.22 **	-28.32 **	-11.66 **	-1.99 *	-16.80 **	-7.63 **
20	L5 × T4	-0.76	-12.11 **	8.30 **	-1.01	-11.48 **	-1.72
21	L6 × T1	21.18 **	19.47 **	47.23 **	-9.83 **	-9.83 **	0.10
22	L6 × T2	3.19 *	3.19 *	27.16 **	11.55 **	-6.85 **	3.42 **
23	L6 × T3	-27.80 **	-33.46 **	-18.00 **	12.84 **	-4.21 **	6.34 **
24	L6 × T4	-3.28 *	-14.35 **	5.55 **	0.83	-9.83 **	0.10
25	L7 × T1	-7.12 **	-8.44 **	12.84 **	-5.23 **	-5.23 **	5.21 **
26	L7 × T2	-12.01 **	-12.01 **	8.43 **	3.10 **	-13.91 **	-4.42 **
27	L7 × T3	-15.66 **	-22.27 **	-4.22 **	11.75 **	-5.14 **	5.32 **
28	L7 × T4	-33.58 **	-41.18 **	-27.51 **	7.89 **	-3.52 **	7.12 **
29	L8 × T1	-12.18 **	-13.43 **	6.69 **	4.33 **	4.33 **	15.82 **
30	L8 × T2	-31.97 **	-31.97 **	-16.16 **	3.46 **	-13.60 **	-4.08 **
31	L8 × T3	-1.67	-9.39 **	11.66 **	1.58	-13.77 **	-4.26 **
32	L8 × T4	-31.31 **	-39.17 **	-25.04 **	10.79 **	-0.93	9.99 **
33	L9 × T1	5.53 **	4.04 **	28.21 **	-33.66 **	-33.66 **	-26.35 **
34	L9 × T2	9.77 **	9.77 **	35.28 **	2.62 **	1.37	12.54 **
35	L9 × T3	-0.98	-8.74 **	12.46 **	2.86 **	1.60	12.79 **
36	L9 × T4	2.79 *	-8.98 **	12.17 **	-9.70 **	-10.81 **	-0.98
37	L10 × T1	-38.33 **	-39.20 **	-25.07 **	-3.03 **	-3.03 **	7.65 **
38	L10 × T2	-24.97 **	-24.97 **	-7.54 **	4.18 **	-6.48 **	3.83 **
39	L10 × T3	-12.45 **	-19.32 **	-0.57	10.39 **	-0.90	10.02 **
40	L10 × T4	-5.17 **	-16.02 **	3.49 **	2.68 **	-7.82 **	2.34 *
	S.Em±	0.88	0.88	0.88	0.65	0.65	0.65
	CD at 5%	2.50	2.50	2.50	1.85	1.85	1.85
	CD at 1%	3.33	3.33	3.33	2.46	2.46	2.46

* and ** indicate significance of values at p= 0.05 and p= 0.01, respectively. BP, BTP and SC: Heterosis over better parent, best parent and standard check (Kashi Rakshita), respectively.

Table 43. Heterosis (%) over better parent, best parent and standard check for fruit color (a^{*}) and fruit color (b^{*}) in sponge gourd

Sl. No.	Crosses	Fruit color (a [*])			Fruit color (b [*])		
		BP	BTP	SC	BP	BTP	SC
1	L1 × T1	1.23 **	-8.66 **	-5.63 **	-0.08	-4.10 **	17.13 **
2	L1 × T2	6.52 **	-7.05 **	-3.96 **	-22.00 **	-26.89 **	-10.70 **
3	L1 × T3	25.18 **	8.91 **	12.53 **	-13.08 **	-18.53 **	-0.49
4	L1 × T4	16.50 **	1.36 **	4.73 **	1.20	-5.14 **	15.86 **
5	L2 × T1	10.97 **	0.12	3.45 **	-24.34 **	-27.53 **	-11.49 **
6	L2 × T2	20.99 **	5.57 **	9.08 **	14.50 **	-18.45 **	-0.39
7	L2 × T3	7.77 **	-9.03 **	-6.01 **	36.47 **	-3.14 **	18.31 **
8	L2 × T4	16.91 **	0.99 *	4.35 **	12.94 **	-11.25 **	8.39 **
9	L3 × T1	6.28 **	-3.71 **	-0.51	-14.27 **	-17.89 **	0.29
10	L3 × T2	10.38 **	0.00	3.32 **	11.17 **	-7.60 **	12.86 **
11	L3 × T3	8.06 **	-2.10 **	1.15 *	-18.09 **	-31.91 **	-16.84 **
12	L3 × T4	7.10 **	-2.97 **	0.26	6.77 **	-11.25 **	8.39 **
13	L4 × T1	10.29 **	-0.50	2.81 **	9.36 **	4.74 **	27.93 **
14	L4 × T2	16.88 **	1.98 **	5.37 **	13.31 **	-11.74 **	7.81 **
15	L4 × T3	14.00 **	-2.23 **	1.02 *	-2.58 **	-24.12 **	-7.31 **
16	L4 × T4	13.75 **	-1.73 **	1.53 **	38.41 **	8.76 **	32.84 **
17	L5 × T1	0.26	-5.69 **	-2.56 **	-23.33 **	-26.57 **	-10.31 **
18	L5 × T2	3.42 **	-2.72 **	0.51	-9.54 **	-35.57 **	-21.31 **
19	L5 × T3	0.79	-5.20 **	-2.05 **	58.44 **	12.46 **	37.36 **
20	L5 × T4	6.05 **	-0.25	3.07 **	25.17 **	-1.65 *	20.13 **
21	L6 × T1	2.19 **	-7.80 **	-4.73 **	-4.41 **	-8.44 **	11.83 **
22	L6 × T2	11.35 **	-2.85 **	0.38	27.03 **	-9.53 **	10.51 **
23	L6 × T3	26.99 **	4.83 **	8.31 **	1.53	-27.93 **	-11.98 **
24	L6 × T4	8.31 **	-6.44 **	-3.32 **	0.05	-21.38 **	-3.98 **
25	L7 × T1	20.16 **	8.42 **	12.02 **	-22.87 **	-26.13 **	-9.77 **
26	L7 × T2	11.35 **	-2.85 **	0.38	31.21 **	-6.55 **	14.14 **
27	L7 × T3	14.39 **	-5.57 **	-2.43 **	13.31 **	-19.57 **	-1.77 *
28	L7 × T4	14.61 **	-0.99 *	2.30 **	27.37 **	0.08	22.24 **
29	L8 × T1	-28.96 **	-28.96 **	-26.60 **	17.50 **	12.54 **	37.46 **
30	L8 × T2	3.96 **	3.96 **	7.42 **	34.71 **	-4.06 **	17.18 **
31	L8 × T3	-1.11 *	-1.11 *	2.17 **	31.43 **	-6.71 **	13.94 **
32	L8 × T4	-4.58 **	-4.58 **	-1.41 **	10.95 **	-12.82 **	6.48 **
33	L9 × T1	26.47 **	14.11 **	17.90 **	-46.42 **	-46.42 **	-34.56 **
34	L9 × T2	23.97 **	8.17 **	11.76 **	-9.00 **	-9.00 **	11.14 **
35	L9 × T3	19.64 **	-1.24 **	2.05 **	-16.60 **	-16.60 **	1.87 *
36	L9 × T4	19.34 **	3.09 **	6.52 **	-11.94 **	-11.94 **	7.56 **
37	L10 × T1	7.23 **	4.58 **	8.06 **	-2.72 **	-6.59 **	14.09 **
38	L10 × T2	11.42 **	8.66 **	12.28 **	0.54	-3.46 **	17.92 **
39	L10 × T3	9.52 **	6.81 **	10.36 **	-3.73 **	-7.56 **	12.91 **
40	L10 × T4	-2.41 **	-4.83 **	-1.66 **	-18.12 **	-21.38 **	-3.98 **
	S.Em±	0.31	0.31	0.31	0.55	0.55	0.55
	CD at 5%	0.88	0.88	0.88	1.57	1.57	1.57
	CD at 1%	1.17	1.17	1.17	2.09	2.09	2.09

* and ** indicate significance of values at p= 0.05 and p= 0.01, respectively. BP, BTP and SC: Heterosis over better parent, best parent and standard check (Kashi Rakshita), respectively.

crosses. The cross L6 × T3 exhibited positive and significant heterosis over the better parent (12.84 %) while, the cross L8 × T1 exhibited positive and significant heterosis over the best parent (4.33 %) and over the commercial check (15.82 %). Among 40 crosses, 22 crosses over better parent, only two crosses over best parent and 19 crosses over the commercial check exhibited positive and significant heterosis.

Fruit color value (a^*) ranged from 6.67 (T3) to 7.29 (T1) among testers, 6.01 (L9) to 7.88 (L10) among lines and 5.74 (L8 × T1) to 9.22 (L9 × T1) among crosses. The cross L6 × T3 showed maximum positive and significant heterosis over the better parent (26.99) while, the cross L9 × T1 over best parent (14.11 %) and commercial check (17.90 %). Out of 40 crosses, 34 crosses over better parent, 14 over best parent and 24 crosses over the commercial check exhibited positive and significant heterosis.

Mean value for fruit color (b^*) ranged from 17.66 (T3) to 23.83 (T1) among the testers, 16.38 (L6) to 24.88 (L9) among lines and 13.33 (L9 × T1) to 28.00 (L8 × T1) among crosses. The cross L5 × T3 recorded highest positive and significant heterosis over the better parent (58.44 %) while, the cross L8 × T1 recorded highest positive and significant heterosis over the best parent (12.54 %) and commercial check (37.46 %). In the total 40 crosses, 17 crosses over better parent, only four crosses over best parent and as many as 25 crosses over the commercial check exhibited positive and significant heterosis.

4.8.2.21 Fruit protein content (%) (Table 40 and 44)

The sponge gourd genotypes varied significantly among themselves for protein content of the fruit. It ranged from 8.34 (T3) to 9.67 % (T4) among testers, 8.04 (L8) to 11.02 % (L5) among the lines and 7.86 (L9 × T4) to 13.87 % (L5 × T1) among the crosses. The maximum positive heterosis over better parent (54.80 %) was observed in the cross L8 × T3. Whereas, the cross L5 × T1 exhibited maximum positive heterosis over best parent (25.86 %) and commercial check (27.83 %). Among the 40 crosses, as many as 32 crosses over better parent, 28 crosses over the best parent and 28 crosses over commercial check has exhibited positive and significant heterosis for protein content.

Table 44. Heterosis (%) over better parent, best parent and standard check for protein and ascorbic acid content in sponge gourd

Sl. No.	Crosses	Protein (%)			Ascorbic acid (mg/100 g)		
		BP	BTP	SC	BP	BTP	SC
1	L1 × T1	10.08 **	9.98 **	11.71 **	-9.03 **	-12.76 **	-18.17 **
2	L1 × T2	8.27 **	8.17 **	9.86 **	16.16 **	2.99 **	-3.40 **
3	L1 × T3	-12.17 **	-12.25 **	-10.88 **	-1.92 **	-3.46 **	-9.45 **
4	L1 × T4	6.81 **	6.72 **	8.39 **	9.13 **	9.13 **	2.36 **
5	L2 × T1	-3.26 **	-11.07 **	-9.68 **	0.33	-3.78 **	-9.75 **
6	L2 × T2	0.99	-7.17 **	-5.71 **	24.82 **	9.29 **	2.51 **
7	L2 × T3	21.62 **	11.80 **	13.55 **	12.16 **	10.39 **	3.55 **
8	L2 × T4	19.74 **	10.07 **	11.80 **	8.19 **	8.19 **	1.48 **
9	L3 × T1	27.50 **	16.97 **	18.80 **	-0.33	-4.41 **	-10.34 **
10	L3 × T2	24.93 **	14.61 **	16.41 **	-7.06 **	-10.87 **	-16.40 **
11	L3 × T3	18.40 **	8.62 **	10.32 **	-4.32 **	-5.83 **	-11.67 **
12	L3 × T4	29.48 **	18.78 **	20.65 **	-6.77 **	-6.77 **	-12.56 **
13	L4 × T1	0.20	-7.17 **	-5.71 **	49.26 **	43.15 **	34.27 **
14	L4 × T2	33.89 **	24.05 **	25.99 **	24.70 **	15.28 **	8.12 **
15	L4 × T3	34.87 **	24.95 **	26.91 **	6.24 **	4.57 **	-1.92 **
16	L4 × T4	27.72 **	18.33 **	20.18 **	12.76 **	12.76 **	5.76 **
17	L5 × T1	25.86 **	25.86 **	27.83 **	6.24 **	1.89 **	-4.43 **
18	L5 × T2	20.42 **	20.42 **	22.30 **	-0.33	-5.51 **	-11.37 **
19	L5 × T3	-10.62 **	-10.62 **	-9.22 **	7.68 **	5.98 **	-0.59
20	L5 × T4	7.62 **	7.62 **	9.31 **	-6.77 **	-6.77 **	-12.56 **
21	L6 × T1	9.23 **	6.35 **	8.02 **	20.53 **	15.59 **	8.42 **
22	L6 × T2	20.88 **	17.70 **	19.54 **	23.58 **	16.38 **	9.16 **
23	L6 × T3	20.41 **	17.24 **	19.08 **	19.52 **	17.64 **	10.34 **
24	L6 × T4	23.95 **	20.69 **	22.58 **	34.17 **	34.17 **	25.85 **
25	L7 × T1	33.78 **	16.79 **	18.62 **	8.05 **	5.67 **	-0.89 **
26	L7 × T2	17.15 **	-8.89 **	-7.47 **	-6.44 **	-8.50 **	-14.18 **
27	L7 × T3	63.19 **	23.50 **	25.44 **	4.48 **	2.83 **	-3.55 **
28	L7 × T4	3.52 **	-9.17 **	-7.74 **	-5.67 **	-5.67 **	-11.52 **
29	L8 × T1	25.05 **	9.17 **	10.88 **	-9.20 **	-12.91 **	-18.32 **
30	L8 × T2	0.93	-21.51 **	-20.28 **	4.50 **	-8.50 **	-14.18 **
31	L8 × T3	54.80 **	17.15 **	18.99 **	17.44 **	15.59 **	8.42 **
32	L8 × T4	17.27 **	2.90 **	4.52 **	19.37 **	19.37 **	11.96 **
33	L9 × T1	33.06 **	16.15 **	17.97 **	-3.47 **	-3.62 **	-9.60 **
34	L9 × T2	40.48 **	17.79 **	19.63 **	3.63 **	3.46 **	-2.95 **
35	L9 × T3	4.44 **	-12.43 **	-11.06 **	19.24 **	19.06 **	11.67 **
36	L9 × T4	-18.72 **	-28.68 **	-27.56 **	44.41 **	44.41 **	35.45 **
37	L10 × T1	-1.21	-11.34 **	-9.95 **	37.77 **	32.13 **	23.93 **
38	L10 × T2	8.39 **	-2.72 **	-1.20	12.00 **	10.24 **	3.40 **
39	L10 × T3	27.00 **	13.97 **	15.76 **	46.72 **	44.41 **	35.45 **
40	L10 × T4	13.65 **	2.00 **	3.59 **	27.87 **	27.87 **	19.94 **
	S.Em±	0.52	0.52	0.52	0.23	0.23	0.23
	CD at 5%	1.47	1.47	1.47	0.65	0.65	0.65
	CD at 1%	1.96	1.96	1.96	0.87	0.87	0.87

* and ** indicate significance of values at p= 0.05 and p= 0.01, respectively. BP, BTP and SC: Heterosis over better parent, best parent and standard check (Kashi Rakshita), respectively.

4.8.2.22 Ascorbic acid of fruit (mg/100g) (Table 45 and 44)

The genotypes differed significantly among themselves for ascorbic acid content which ranged from 5.56 (T2) to 6.35 mg per 100 g (T4) among testers, 5.25 (L2) to 6.34 mg per 100 g (L9) among lines and 6.68 (L1 × T1) to 8.67 mg per 100 g (L9 × T4) among the crosses. Highest positive and significant heterosis over better parent was observed in the cross L8 × T3 (54.80 %). However, it was maximum positive and significant over best parent (44.41 %) and commercial check (35.45 %) in the cross L9 × T4. Among the 40 crosses, as many as 27 crosses over better parent, 26 crosses over best parent and 19 crosses over commercial check exhibited positive and significant heterosis.

4.8.2.23 Potassium content of fruit (%) (Table 45 and 46)

Potassium content of the fruit ranged from 1.41 % (T3) to 1.67 % (T1) among the testers, 1.38 (L6) to 1.72 % (L4) among the lines and 1.44 (L2 × T4) to 2.70 % (L10 × T3) among the crosses. Maximum positive and significant heterosis over better parent (65.56 %), best parent (45.35 %) and commercial check (37.36 %) were observed in the cross L10 × T3. Among 40 crosses tested, as many as 36 crosses over better parent, 33 crosses over best parent and 29 crosses over commercial check exhibited positive and significant heterosis.

4.8.2.24 Fruit phenol content (mg GAE/100g) (Table 45 and 46)

The amount of phenol content of the fruit varied significantly among genotypes and it ranged from 255.42 (T2) to 286.16 mg GAE per 100 g (T4) among the testers, 225.32 (L8) to 268.01 mg GAE per 100 g (L1) among the lines and from 308.85 (L1 × T4) to 207.79 mg GAE per 100 g (L6 × T4) among the crosses. The magnitude of heterosis was significant in both the directions over better parent, best parent and the commercial check. The cross L7 × T2 over better parent (10.66 %) and the cross L1 × T4 over best parent (7.93 %) and over commercial check (11.72 %) showed maximum and positive significant heterosis. Out of 40 crosses, 14 crosses over better parent, three crosses over best parent and six crosses over commercial check recorded positive and significant heterosis for phenol content of fruits.

Table 45. *Per se* performance of crosses and parents for quality parameters in sponge gourd genotypes

Sl. No.	Crosses	Ascorbic acid (mg)	Potassium (%)	Phenol (mg GAE)	Anti-oxidants (mg AAE)	Flavonoids (mg QE)	Crude fiber (%)	Ash (%)
1	L1 × T1	5.54	1.55	288.17	766.91	40.58	6.68	6.68
2	L1 × T2	6.54	1.67	262.14	744.39	35.27	8.25	7.07
3	L1 × T3	6.13	1.87	279.37	786.92	39.29	7.45	7.30
4	L1 × T4	6.93	1.89	308.85	792.43	41.72	8.83	9.02
5	L2 × T1	6.11	1.65	271.44	769.30	39.83	6.59	8.30
6	L2 × T2	6.94	1.89	254.15	775.44	38.71	6.23	7.92
7	L2 × T3	7.01	2.12	272.79	723.70	31.16	8.04	6.98
8	L2 × T4	6.87	1.44	303.48	751.33	42.33	6.84	6.91
9	L3 × T1	6.07	1.68	250.14	737.57	37.13	6.12	9.91
10	L3 × T2	5.66	2.27	278.16	820.36	45.32	9.45	8.95
11	L3 × T3	5.98	1.82	281.42	749.04	44.95	9.35	9.67
12	L3 × T4	5.92	1.60	252.92	801.06	43.66	9.40	7.04
13	L4 × T1	9.09	2.29	252.36	752.57	36.11	8.71	7.07
14	L4 × T2	7.32	2.28	260.72	756.03	37.17	8.37	8.14
15	L4 × T3	6.64	2.22	257.42	757.58	35.23	9.97	8.94
16	L4 × T4	7.16	2.34	277.58	712.84	31.24	8.56	6.69
17	L5 × T1	6.47	1.73	279.15	747.88	33.80	10.98	7.71
18	L5 × T2	6.00	2.26	268.12	813.46	44.33	10.45	7.94
19	L5 × T3	6.73	2.44	271.69	782.44	37.35	9.45	6.96
20	L5 × T4	5.92	2.28	285.04	756.91	35.28	7.04	7.66
21	L6 × T1	7.34	2.07	243.17	777.68	42.04	6.02	9.58
22	L6 × T2	7.39	2.04	237.10	768.20	39.56	7.81	7.36
23	L6 × T3	7.47	2.24	300.87	749.92	43.29	6.11	7.25
24	L6 × T4	8.52	2.03	207.79	756.73	42.73	6.23	9.69
25	L7 × T1	6.71	2.45	270.10	771.92	38.70	8.56	7.80
26	L7 × T2	5.81	2.31	282.66	730.65	35.43	9.23	6.87
27	L7 × T3	6.53	1.92	256.07	724.32	24.45	10.23	7.58
28	L7 × T4	5.99	1.74	272.36	713.23	24.56	10.90	8.64
29	L8 × T1	5.53	2.32	283.92	703.69	28.82	8.72	9.94
30	L8 × T2	5.81	1.67	289.10	710.51	31.03	9.68	9.24
31	L8 × T3	7.34	1.85	269.62	756.63	23.79	7.77	7.16
32	L8 × T4	7.58	2.12	215.50	703.39	27.89	10.12	8.36
33	L9 × T1	6.12	2.22	281.49	750.50	37.27	9.45	8.98

Table 45. *Contd...*

Sl. No.	Crosses	Ascorbic acid (mg)	Potassium (%)	Phenol (mg GAE)	Anti-oxidants (mg AAE)	Flavonoids (mg QE)	Fiber (%)	Ash (%)
34	L9 × T2	6.57	2.31	268.18	768.77	37.87	10.27	10.01
35	L9 × T3	7.56	1.88	256.31	780.19	34.23	9.73	9.23
36	L9 × T4	8.67	1.99	266.09	771.55	34.57	9.78	10.25
37	L10 × T1	8.39	1.78	289.15	735.01	40.92	7.15	7.73
38	L10 × T2	9.12	2.35	256.98	721.85	38.44	7.90	9.28
39	L10 × T3	9.17	2.50	272.69	796.06	42.59	9.65	8.20
40	L10 × T4	8.12	2.27	255.34	787.96	40.11	9.84	9.56
	Lines							
41	L1	5.63	1.64	268.01	720.16	34.27	7.21	7.12
42	L2	5.25	1.61	256.51	755.37	28.58	6.32	7.02
43	L3	6.09	1.63	244.37	778.56	34.68	7.12	7.16
44	L4	5.87	1.72	253.06	720.15	34.12	6.67	7.03
45	L5	6.02	1.58	266.53	768.65	31.78	7.34	6.98
46	L6	5.98	1.38	262.10	733.99	36.12	6.12	6.06
47	L7	6.21	1.65	254.19	756.90	31.33	7.34	6.87
48	L8	5.56	1.51	225.32	712.89	24.75	7.17	7.39
49	L9	6.34	1.45	255.76	747.23	29.58	6.78	7.43
50	L10	6.03	1.51	254.87	747.48	29.85	7.13	6.76
	Testers							
51	T1	6.09	1.67	268.53	759.54	33.54	7.02	7.43
52	T2	5.56	1.42	255.42	744.41	35.98	7.01	6.77
53	T3	6.25	1.41	268.53	755.50	26.55	6.56	6.28
54	T4	6.35	1.64	286.16	754.84	35.21	6.98	7.17
55	SC	6.77	1.82	276.45	738.54	35.12	7.52	7.87
S.Em±		0.23	0.11	1.09	0.91	1.03	0.39	0.32
CD at 5%		0.65	0.30	3.12	2.58	2.91	1.10	0.89
CD at 1%		0.87	0.40	4.11	3.43	3.88	1.46	1.19

SC : Standard check (Kashi Rakshita) DAS : Days after sowing

Table 46. Heterosis (%) over better parent, best parent and standard check for potassium and phenol content in sponge gourd

Sl. No.	Crosses	Potassium content (%)			Phenol content (mg GAE/100 g)		
		BP	BTP	SC	BP	BTP	SC
1	L1 × T1	-7.19 **	-9.88 **	-14.84 **	7.31 **	0.70	4.24 **
2	L1 × T2	1.83 **	-2.91 **	-8.24 **	-2.19	-8.39 **	-5.18 **
3	L1 × T3	14.02 **	8.72 **	2.75 **	4.04 *	-2.37	1.06
4	L1 × T4	15.24 **	9.88 **	3.85 **	7.93 **	7.93 **	11.72 **
5	L2 × T1	-1.20 **	-4.07 **	-9.34 **	1.08	-5.14 **	-1.81
6	L2 × T2	17.39 **	9.88 **	3.85 **	-0.92	-11.19 **	-8.07 **
7	L2 × T3	31.68 **	23.26 **	16.48 **	1.59	-4.67 **	-1.32
8	L2 × T4	-12.20 **	-16.28 **	-20.88 **	6.05 **	6.05 **	9.78 **
9	L3 × T1	0.60 **	-2.33 **	-7.69 **	-6.85 **	-12.59 **	-9.52 **
10	L3 × T2	39.26 **	31.98 **	24.73 **	8.90 **	-2.80	0.62
11	L3 × T3	11.66 **	5.81 **	0.00	4.80 **	-1.66	1.80
12	L3 × T4	-2.44 **	-6.98 **	-12.09 **	-11.62 **	-11.62 **	-8.51 **
13	L4 × T1	33.14 **	33.14 **	25.82 **	-6.02 **	-11.81 **	-8.71 **
14	L4 × T2	32.56 **	32.56 **	25.27 **	2.08	-8.89 **	-5.69 **
15	L4 × T3	29.07 **	29.07 **	21.98 **	-4.14 **	-10.04 **	-6.88 **
16	L4 × T4	36.05 **	36.05 **	28.57 **	-3.00	-3.00	0.41
17	L5 × T1	3.59 **	0.58 **	-4.95 **	3.95 *	-2.45	0.98
18	L5 × T2	43.04 **	31.40 **	24.18 **	0.60	-6.30 **	-3.01
19	L5 × T3	54.43 **	41.86 **	34.07 **	1.18	-5.06 **	-1.72
20	L5 × T4	39.02 **	32.56 **	25.27 **	-0.39	-0.39	3.11
21	L6 × T1	23.95 **	20.35 **	13.74 **	-9.44 **	-15.02 **	-12.04 **
22	L6 × T2	43.66 **	18.60 **	12.09 **	-9.54 **	-17.14 **	-14.23 **
23	L6 × T3	58.87 **	30.23 **	23.08 **	12.04 **	5.14 **	8.83 **
24	L6 × T4	23.78 **	18.02 **	11.54 **	-27.39 **	-27.39 **	-24.84 **
25	L7 × T1	46.71 **	42.44 **	34.62 **	0.58	-5.61 **	-2.30
26	L7 × T2	40.00 **	34.30 **	26.92 **	10.66 **	-1.22	2.25
27	L7 × T3	16.36 **	11.63 **	5.49 **	-4.64 **	-10.52 **	-7.37 **
28	L7 × T4	5.45 **	1.16 **	-4.40 **	-4.82 **	-4.82 **	-1.48
29	L8 × T1	38.92 **	34.88 **	27.47 **	5.73 **	-0.78	2.70
30	L8 × T2	10.60 **	-2.91 **	-8.24 **	13.19 **	1.03	4.58 **
31	L8 × T3	22.52 **	7.56 **	1.65 **	0.41	-5.78 **	-2.47
32	L8 × T4	26.95 **	23.26 **	16.48 **	-24.69 **	-24.69 **	-22.05 **
33	L9 × T1	53.10 **	29.07 **	21.98 **	4.83 **	-1.63	1.82
34	L9 × T2	59.31 **	34.30 **	26.92 **	4.86 **	-6.28 **	-2.99
35	L9 × T3	14.63 **	9.30 **	3.30 **	-4.55 **	-10.43 **	-7.29 **
36	L9 × T4	19.16 **	15.70 **	9.34 **	-7.01 **	-7.01 **	-3.75 *
37	L10 × T1	7.28 **	3.49 **	-2.20 **	7.68 **	1.04	4.59 **
38	L10 × T2	55.63 **	36.63 **	29.12 **	0.61	-10.20 **	-7.04 **
39	L10 × T3	65.56 **	45.35 **	37.36 **	1.55	-4.71 **	-1.36
40	L10 × T4	38.41 **	31.98 **	24.73 **	-10.77 **	-10.77 **	-7.64 **
	S.Em±	0.11	0.11	0.11	1.09	1.09	1.09
	CD at 5%	0.30	0.30	0.30	3.12	3.12	3.12
	CD at 1%	0.40	0.40	0.40	4.11	4.11	4.11

* and ** indicate significance of values at p= 0.05 and p= 0.01, respectively. BP, BTP and SC: Heterosis over better parent, best parent and standard check (Kashi Rakshita), respectively.

4.8.2.25 Total antioxidants (mg AAE/100g) (Table 43 and 45)

The antioxidants content of the fruit ranged from 744.41 (T2) to 759.54 mg AAE per 100 g (T1) among the testers, 712.89 (L8) to 778.56 mg AAE per 100 g (L3) among the lines and 703.39 (L8 × T4) to 820.36 mg AAE per 100 g (L3 × T2) among the crosses. The cross L5 × T2 recorded maximum positive and significant heterosis over better parent (5.83 %) and the cross L3 × T2 recorded high heterosis over best parent (5.37 %) and commercial check (11.08 %) significant heterosis. Among 40 crosses tested, 11 crosses over better parent, only three crosses over best parent and 18 crosses over commercial check recorded positive and significant heterosis for antioxidant content of fruits.

4.8.2.26 Total flavonoids (mg QE/100g) (Table 43 and 45)

The flavonoid content of the fruit ranged from 26.55 (T3) to 35.98 mg QE per 100 g (T2) among the testers, 24.75 (L8) to 36.12 mg QE per 100 g (L6) among the lines and from 27.89 (L8 × T4) to 45.32 mg QE per 100 g (L3 × T2) among the crosses. Maximum positive and significant heterosis over better parent was observed in the cross L10 × T3 (42.68 %) whereas, positive and significant heterosis over best parent (25.47 %) and commercial check (29.04 %) was observed in the cross L3 × T2. Out of 40 crosses tested, 28 crosses over better parent, 23 crosses over best parent and 24 crosses over commercial check exhibited positive and significant heterosis.

4.8.2.27 Crude fiber (%) (Table 43 and 46)

The amount of crude fiber content of the fruit varied significantly and it ranged from 6.56 (T3) to 7.02 % (T1) among testers, 6.12 (L6) to 7.34 % (L5 and L7) among lines and from 6.11 (L6 × T3) to 10.98 % (L5 × T1) among crosses. The magnitude of heterosis over better parent, best parent and the commercial check was significant in both the directions. The maximum positive heterosis over better parent (49.59 %), over best parent (49.59 %) and over the commercial check (46.01 %) was observed in the cross L5 × T1. Among the crosses, as many as 30 crosses each over better parent and best parent and 29 crosses over the commercial check exhibited positive and significant heterosis for crude fiber content of fruits.

Table 47. Heterosis (%) over better parent, best parent and standard check for total antioxidants and total flavonoids in sponge gourd

Sl. No.	Crosses	Total antioxidants (mg AAE/100 g)			Total flavonoids (mg QE/100 g)		
		BP	BTP	SC	BP	BTP	SC
1	L1 × T1	0.97	-1.50	3.84 **	18.41 **	12.35 **	15.55 **
2	L1 × T2	0.00	-4.39 **	0.79	-1.97	-2.35	0.43
3	L1 × T3	4.16 **	1.07	6.55 **	14.65 **	8.78 **	11.87 **
4	L1 × T4	4.98 **	1.78	7.30 **	18.49 **	15.50 **	18.79 **
5	L2 × T1	1.28	-1.19	4.16 **	18.75 **	10.27 **	13.41 **
6	L2 × T2	2.66 *	-0.40	5.00 **	7.59 **	7.17 **	10.22 **
7	L2 × T3	-4.21 **	-7.05 **	-2.01	9.03	-13.73 **	-11.28 **
8	L2 × T4	-0.53	-3.50 **	1.73	20.22 **	17.19 **	20.53 **
9	L3 × T1	-5.26 **	-5.26 **	-0.13	7.06 **	2.80	5.72 **
10	L3 × T2	5.37 **	5.37 **	11.08 **	25.96 **	25.47 **	29.04 **
11	L3 × T3	-3.79 **	-3.79 **	1.42	29.61 **	24.45 **	27.99 **
12	L3 × T4	2.89 *	2.89 *	8.47 **	24.00 **	20.87 **	24.32 **
13	L4 × T1	-0.92	-3.34 *	1.90	5.83 **	-0.03	2.82
14	L4 × T2	1.56	-2.89 *	2.37	3.31 *	2.91 *	5.84 **
15	L4 × T3	0.28	-2.69 *	2.58 *	3.25 *	-2.46	0.31
16	L4 × T4	-5.56 **	-8.44 **	-3.48 **	-11.28 **	-13.51 **	-11.05 **
17	L5 × T1	-2.70 *	-3.94 **	1.26	0.78	-6.42 **	-3.76 *
18	L5 × T2	5.83 **	4.48 **	10.14 **	23.21 **	22.73 **	26.22 **
19	L5 × T3	1.79	0.50	5.94 **	17.53 **	3.41 *	6.35 **
20	L5 × T4	-1.53	-2.78 *	2.49	0.20	-2.33	0.46
21	L6 × T1	2.39	-0.11	5.30 **	16.39 **	16.39 **	19.70 **
22	L6 × T2	3.20 *	-1.33	4.02 **	9.52 **	9.52 **	12.64 **
23	L6 × T3	-0.74	-3.68 **	1.54	19.85 **	19.85 **	23.26 **
24	L6 × T4	0.25	-2.80 *	2.46	18.30 **	18.30 **	21.67 **
25	L7 × T1	1.63	-0.85	4.52 **	15.38 **	7.14 **	10.19 **
26	L7 × T2	-3.47 **	-6.15 **	-1.07	-1.53	-1.91	0.88
27	L7 × T3	-4.30 **	-6.97 **	-1.93	-21.96 **	-32.31 **	-30.38 **
28	L7 × T4	-5.77 **	-8.39 **	-3.43 **	-30.25 **	-32.00 **	-30.07 **
29	L8 × T1	-7.35 **	-9.62 **	-4.72 **	-14.07 **	-20.21 **	-17.94 **
30	L8 × T2	-4.55 **	-8.74 **	-3.80 *	-13.76 **	-14.09 **	-11.65 **
31	L8 × T3	0.15	-2.82 *	2.45	-10.40 **	-34.14 **	-32.26 **
32	L8 × T4	-6.82 **	-9.66 **	-4.76 **	-20.79 **	-22.79 **	-20.59 **
33	L9 × T1	-1.19	-3.60 **	1.62	11.12 **	3.18 *	6.12 **
34	L9 × T2	2.88 *	-1.26	4.09 **	5.25 **	4.84 **	7.83 **
35	L9 × T3	3.27 *	0.21	5.64 **	15.72 **	-5.23 **	-2.53
36	L9 × T4	2.21	-0.90	4.47 **	-1.82	-4.29 **	-1.57
37	L10 × T1	-3.23 *	-5.59 **	-0.48	22.00 **	13.29 **	16.51 **
38	L10 × T2	-3.43 **	-7.28 **	-2.26	6.84 **	6.42 **	9.45 **
39	L10 × T3	5.37 **	2.25	7.79 **	42.68 **	17.91 **	21.27 **
40	L10 × T4	4.39 **	1.21	6.69 **	13.92 **	11.05 **	14.21 **
	S.Em±	0.91	0.91	0.91	1.03	1.03	1.03
	CD at 5%	2.58	2.58	2.58	2.91	2.91	2.91
	CD at 1%	3.43	3.43	3.43	3.88	3.88	3.88

* and ** indicate significance of values at p= 0.05 and p= 0.01, respectively. BP, BTP and SC: Heterosis over better parent, best parent and standard check (Kashi Rakshita), respectively.

Table 48. Heterosis (%) over better parent, best parent and standard check for crude fiber and ash content in sponge gourd

Sl. No.	Crosses	Crude fiber (%)			Ash (%)		
		BP	BTP	SC	BP	BTP	SC
1	L1 × T1	-7.35 **	-8.99 **	-11.17 **	-10.09 **	-10.09 **	-15.12 **
2	L1 × T2	14.42 **	12.40 **	9.71 **	-0.70	-4.85 **	-10.17 **
3	L1 × T3	3.33 **	1.50 **	-0.93	2.53 **	-1.75 **	-7.24 **
4	L1 × T4	22.47 **	20.30 **	17.42 **	25.80 **	21.40 **	14.61 **
5	L2 × T1	-6.13 **	-10.22 **	-12.37 **	11.71 **	11.71 **	5.46 **
6	L2 × T2	-11.13 **	-15.12 **	-17.15 **	12.82 **	6.59 **	0.64
7	L2 × T3	22.56 **	9.54 **	6.91 **	-0.57	-6.06 **	-11.31 **
8	L2 × T4	-2.01 **	-6.81 **	-9.04 **	-3.63 **	-7.00 **	-12.20 **
9	L3 × T1	-14.04 **	-16.62 **	-18.62 **	33.38 **	33.38 **	25.92 **
10	L3 × T2	32.72 **	28.75 **	25.66 **	25.00 **	20.46 **	13.72 **
11	L3 × T3	31.32 **	27.38 **	24.34 **	35.06 **	30.15 **	22.87 **
12	L3 × T4	32.02 **	28.07 **	25.00 **	-1.81 **	-5.25 **	-10.55 **
13	L4 × T1	24.07 **	18.66 **	15.82 **	-4.85 **	-4.85 **	-10.17 **
14	L4 × T2	19.40 **	14.03 **	11.30 **	15.79 **	9.56 **	3.43 **
15	L4 × T3	49.48 **	35.83 **	32.58 **	27.17 **	20.32 **	13.60 **
16	L4 × T4	22.64 **	16.62 **	13.83 **	-6.69 **	-9.96 **	-14.99 **
17	L5 × T1	49.59 **	49.59 **	46.01 **	3.77 **	3.77 **	-2.03
18	L5 × T2	42.37 **	42.37 **	38.96 **	13.75	6.86 **	0.89
19	L5 × T3	28.75 **	28.75 **	25.66 **	-0.29	-6.33 **	-11.56 **
20	L5 × T4	-4.09 **	-4.09 **	-6.38 **	6.83 **	3.10 **	-2.67 **
21	L6 × T1	-14.25 **	-17.98 **	-19.95 **	28.94 **	28.94 **	21.73 **
22	L6 × T2	11.41 **	6.40 **	3.86 **	8.71 **	-0.94 *	-6.48 **
23	L6 × T3	-6.86 **	-16.76 **	-18.75 **	15.45 **	-2.42 **	-7.88 **
24	L6 × T4	-10.74 **	-15.12 **	-17.15 **	35.15 **	30.42 **	23.13 **
25	L7 × T1	16.62 **	16.62 **	13.83 **	4.98 **	4.98 **	-0.89 *
26	L7 × T2	25.75 **	25.75 **	22.74 **	0.00	-7.54 **	-12.71 **
27	L7 × T3	39.37 **	39.37 **	36.04 **	10.33 **	2.02 **	-3.68 **
28	L7 × T4	48.50 **	48.50 **	44.95 **	20.50 **	16.29 **	9.78 **
29	L8 × T1	22.13 **	18.80 **	15.96 **	33.78 **	33.78 **	26.30 **
30	L8 × T2	35.57 **	31.88 **	28.72 **	25.03 **	24.36 **	17.41 **
31	L8 × T3	8.82 **	5.86 **	3.32 **	-3.11 **	-3.63 **	-9.02 **
32	L8 × T4	41.74 **	37.87 **	34.57 **	16.60 **	12.52 **	6.23 **
33	L9 × T1	34.62 **	28.75 **	25.66 **	20.86 **	20.86 **	14.10 **
34	L9 × T2	46.50 **	39.92 **	36.57 **	34.72 **	34.72 **	27.19 **
35	L9 × T3	43.51 **	32.56 **	29.39 **	24.23 **	24.23 **	17.28 **
36	L9 × T4	40.11 **	33.24 **	30.05 **	37.95 **	37.95 **	30.24 **
37	L10 × T1	0.28	-2.59 **	-4.92 **	4.04 **	4.04 **	-1.78 **
38	L10 × T2	10.80 **	7.63 **	5.05 **	37.08 **	24.90 **	17.92 **
39	L10 × T3	35.34 **	31.47 **	28.32 **	21.30 **	10.36 **	4.19 **
40	L10 × T4	38.01 **	34.06 **	30.85 **	33.33 **	28.67 **	21.47 **
	S.Em±	0.39	0.39	0.39	0.32	0.32	0.32
	CD at 5%	1.10	1.10	1.10	0.89	0.89	0.89
	CD at 1%	1.46	1.46	1.46	1.19	1.19	1.19

* and ** indicate significance of values at p= 0.05 and p= 0.01, respectively. BP, BTP and SC : Heterosis over better parent, best parent and standard check (Kashi Rakshita), respectively.

4.8.2.28 Ash content (%) (Table 45 and 48)

Sponge gourd genotypes differed significantly among themselves for ash content. It ranged between 6.28 (T3) to 7.43 % (T1) among testers, 6.06 (L6) to 7.43 % (L9) among lines and 6.68 (L1 $\times$ T1) to 10.25 % (L9 $\times$ T4) among crosses. Magnitude of heterosis over better parent, best parent and commercial check was highly significant in both the directions. Maximum positive and significant heterosis over best parent (37.95 %), better parent (37.95 %) and commercial check (30.24 %) was observed in the cross L9 $\times$ T4. Out of 40 crosses, as many as 30 crosses over better parent, 27 crosses over best parent and 20 crosses over commercial check exhibited positive and significant heterosis.

4.9 Combining ability effects and variances

The variance due to general combining ability (GCA), specific combining ability (SCA) and GCA to SCA ratio for various characters are presented in Table 49. Ratio GCA to SCA was high for node at first male flower (0.634). Ratio's of GCA to SCA were low for almost all traits viz., ascorbic acid content (0.586), crude fiber (0.565), total flavonoids (0.558), fruit diameter (0.546), total soluble solids (0.545), days to first harvest (0.495), fruit length (0.495), days to first male flower (0.459), days to first female flower (0.440), Vine length at 90 DAS (0.424), number of branches at 90 DAS (0.415), number of branches at 45 DAS (0.380), sponge yield (0.372), fruit yield per vine (0.361), fruit yield per plot (0.360), days to last harvest (0.357), vine length at 45 DAS (0.348), number of seeds per fruit (0.342), fruit yield per hectare (0.333), node at first female flower (0.281), potassium content (0.233), number of fruits per vine (0.223), average fruit weight (0.205), ash content (0.205), total anti-oxidants (0.160), fruit firmness (0.123), fruit color (a*) (0.120), fruit color (a*) (0.118), fruit color (b*) (0.083), phenol content (0.069) and protein content (0.059).

General combining ability effects and specific combining ability effects for various characters are presented here under.

Table 49. Variance due to general and specific combining ability for different characters in sponge gourd

Sl. No.	Character	GCA	SCA	GCA:SCA
1	Vine length at 45 DAS	0.020	0.059	0.348
2	Vine length at harvest time	0.113	0.266	0.424
3	Number of branches at 45 DAS	0.056	0.147	0.380
4	Number of branches at harvest time	0.250	0.601	0.415
5	Days to first male flower	3.043	6.623	0.459
6	Days to first female flower	3.275	7.440	0.440
7	Node at first male flower	0.240	0.378	0.634
8	Node at first female flower	0.777	2.770	0.281
9	Days to first harvest	4.393	8.841	0.497
10	Days to last harvest	4.691	13.157	0.357
11	Fruit length	2.328	4.701	0.495
12	Fruit diameter	3.807	6.976	0.546
13	Average fruit weight	48.764	238.160	0.205
14	Number of fruits per vine	3.341	15.008	0.223
15	Fruit yield per vine	0.159	0.439	0.361
16	Fruit yield per plot	15.625	43.393	0.360
17	Fruit yield per hectare	3.347	10.061	0.333
18	Number of seeds per fruit	462.473	1351.668	0.342
19	Sponge yield	1.596	4.286	0.372
20	Total soluble solids	0.059	0.108	0.545
21	Fruit firmness	2.741	22.326	0.123
22	Fruit color (L [*])	1.211	10.091	0.120
23	Fruit color (a [*])	0.025	0.213	0.118
24	Fruit color (b [*])	0.907	10.930	0.083
25	Protein	0.137	2.328	0.059
26	Ascorbic acid	0.226	0.385	0.586
27	Potassium content	0.014	0.060	0.233
28	Phenol content	33.496	488.616	0.069
29	Total antioxidants	119.081	745.544	0.160
30	Total flavonoids	7.512	13.469	0.558
31	Crude fiber	0.492	0.871	0.565
32	Ash content	0.176	0.858	0.205

GCA : Variance due to general combining ability

SCA : Variance due to specific combining ability

DAS : Days after sowing

4.9.1 Vine length (Table 50 and 51)

For vine length at 45 DAS, two lines exhibited positive and significant gca effects and four lines showed negative significant gca effects. Maximum positive and significant gca effects was observed in the line L2 (0.47) followed by L6 (0.31). The tester T1 (0.07) exhibited maximum significant positive gca effects. Among 40 crosses, eight crosses showed positive and significant sca effects, while, six crosses showed significantly negative sca effects. Maximum positive significant sca effect (0.38) was exhibited by the cross L10 $\times$ T1 followed by L6 $\times$ T1 (0.28) and L3 $\times$ T4 (0.23).

Among ten lines, only two lines exhibited positive and significant gca effects and four lines had negative and significant gca effects for vine length at 90 DAS. The maximum positive and significant gca effects was observed in the line L2 (1.08) followed by L6 (0.84). Maximum positive and significant gca effects was exhibited by tester T3 (0.16). Among 40 crosses, 10 crosses recorded positive and significant sca effects while, five crosses recorded significantly negative sca effects. The cross L2 $\times$ T1 showed maximum positive and significant sca effects (0.99) followed by L9 $\times$ T2 (0.81) and L7 $\times$ T4 (0.79) for this trait.

4.9.2 Number of branches per vine (Table 50 and 51)

For number of branches per at 45 DAS, two lines had shown significant positive gca effects and four lines had significantly negative gca effects. The highest positive gca effects was observed in the line L2 (0.72) followed by L6 (0.57). Among the testers only T1 recorded maximum significant positive gca effects (0.15). Among 40 crosses, five crosses showed positive significant sca effects and six crosses showed significantly negative sca effects. Highest positive sca effects was observed in the cross L10 $\times$ T1 (0.90) followed by L3 $\times$ T2 (0.74) and L7 $\times$ T4 (0.65) for number of branches per vine at 45 DAS.

The trait number of branches at 90 DAS, three lines each exhibited significant positive and negative gca effects. Maximum positive gca effects was observed in the line L2 (1.16) followed by L6 (1.04) and L7 (0.71). Among the testers, T1 (0.41) showed maximum significant positive gca effects. Out of 40 crosses, eight crosses

Table 50. General combining ability effects for growth parameters in sponge gourd

Sl. No.	Lines	Vine length (m)		Number of branches		Days to first male flower	Days to first female flower
		45 DAS	90 DAS	45 DAS	90 DAS		
1	L1	0.05	0.12	0.09	-0.41 *	-1.89 **	-1.08 *
2	L2	0.47 **	1.08 **	0.72 **	1.16 **	-5.42 **	-6.23 **
3	L3	0.02	-0.61 **	-0.26 *	-0.29	3.69 **	3.52 **
4	L4	-0.09 *	0.19	0.12	0.24	-0.57	-0.38
5	L5	-0.32 **	-0.60 **	-0.48 **	-0.76 **	2.04 **	1.97 **
6	L6	0.31 **	0.84 **	0.57 **	1.04 **	-4.39 **	-4.23 **
7	L7	0.03	-0.04	-0.26 *	0.71 **	3.19 **	2.82 **
8	L8	-0.16 **	-0.40 **	0.14	-0.29	2.64 **	2.52 **
9	L9	-0.05	0.08	-0.16	-0.16	2.31 **	2.52 **
10	L10	-0.26 **	-0.65 **	-0.48 **	-1.24 **	-1.59 *	-1.43 **
	S.Em±	0.04	0.10	0.10	0.16	0.66	0.46
	CD at 5%	0.09	0.21	0.20	0.32	1.33	0.93
	CD at 1%	0.12	0.28	0.27	0.42	1.78	1.25
	Testers						
1	T1	0.07 *	0.07	0.15 *	0.41 **	-0.57	-0.43
2	T2	0.03	-0.04	0.09	-0.36 **	-0.29	-0.21
3	T3	0.02	0.16 **	-0.11	-0.22 *	-0.01	-0.35
4	T4	-0.12 **	-0.19 **	-0.12	0.18	0.86 *	0.99 **
	S.Em±	0.03	0.07	0.06	0.10	0.42	0.29
	CD at 5%	0.06	0.13	0.13	0.20	0.84	0.59
	CD at 1%	0.08	0.18	0.17	0.27	1.13	0.79

* and ** indicate significance of values at p=0.05 and p=0.01, respectively.

DAS= Days after sowing

Table 51. Specific combining ability effects for growth parameter in sponge gourd

Sl. No.	Crosses	Vine length (m)		Number of branches		Days to first male flower	Days to first female flower
		45 DAS	90 DAS	45 DAS	90 DAS		
1	L1 × T1	0.00	-0.30	-0.47 *	-0.36	0.24	0.28
2	L1 × T2	0.02	0.06	0.29	1.31 **	1.06	2.06 *
3	L1 × T3	0.12	0.42 *	0.39	-0.93 **	0.98	0.40
4	L1 × T4	-0.14	-0.19	-0.20	-0.03	-2.28	-2.74 **
5	L2 × T1	0.15	0.99 **	0.10	1.35 **	-2.34	-2.17 *
6	L2 × T2	0.08	0.33	0.06	0.54	-0.62	-0.79
7	L2 × T3	-0.16	-0.69 **	-0.14	-0.40	1.81	0.55
8	L2 × T4	-0.07	-0.04	-0.03	-0.20	1.15	2.41 *
9	L3 × T1	0.19 *	-0.29	-0.12	-0.98 **	0.67	0.68
10	L3 × T2	-0.61 **	-0.21	0.74 **	-0.61	-0.62	-0.54
11	L3 × T3	0.19 *	0.77 **	-0.56 **	0.25	2.41	2.60 **
12	L3 × T4	0.23 *	-0.27	-0.05	0.07	-2.46	-2.74 **
13	L4 × T1	-0.31 **	0.03	0.30	-0.01	5.62 **	5.38 **
14	L4 × T2	0.15	-0.72 **	-0.04	0.66 *	-2.47	-2.64 **
15	L4 × T3	0.15	0.39	0.06	1.02 **	-0.55	-0.10
16	L4 × T4	0.01	-0.30	-0.33	-1.68 **	-2.61	-2.64 **
17	L5 × T1	-0.08	0.32	-0.30	1.29 **	2.62	2.43 *
18	L5 × T2	0.24 **	-0.36	0.56 **	-0.34	1.54	1.41
19	L5 × T3	0.12	0.39	-0.24	-0.88 **	-2.65	-2.05 *
20	L5 × T4	-0.28 **	-0.35	-0.03	-0.08	-1.51	-1.79
21	L6 × T1	0.28 **	0.57 **	0.15	0.09	-3.36 *	-3.17 **
22	L6 × T2	-0.16	0.45 *	-0.09	0.56	0.86	0.21
23	L6 × T3	-0.02	-0.47 *	0.21	0.12	1.48	1.35
24	L6 × T4	-0.10	-0.54 *	-0.28	-0.78 *	1.02	1.61
25	L7 × T1	-0.32 **	-0.30	-0.12	0.02	1.77	1.98 *
26	L7 × T2	0.07	-0.23	-0.66 **	-0.11	0.79	1.16
27	L7 × T3	0.15	-0.26	0.14	-0.15	-2.90 *	-3.70 **
28	L7 × T4	0.11	0.79 **	0.65 **	0.25	0.35	0.56
29	L8 × T1	-0.13	-0.59 **	-0.32	-0.38	1.32	1.08
30	L8 × T2	0.22 *	0.07	-0.46 *	-1.01 **	-0.27	-0.34
31	L8 × T3	-0.25 **	-0.05	0.54 **	0.75 *	-3.65 **	-3.20 **
32	L8 × T4	0.16	0.57 **	0.25	0.65 *	2.60	2.46 *
33	L9 × T1	-0.17	-0.28	-0.12	-0.11	-7.26 **	-6.92 **
34	L9 × T2	-0.03	0.81 **	0.04	-1.14 **	1.56	1.66
35	L9 × T3	0.22 *	-0.40	0.04	0.52	3.98 **	4.00 **
36	L9 × T4	-0.02	-0.13	0.05	0.72 *	1.72	1.26
37	L10 × T1	0.38 **	0.45 *	0.90 **	0.37	0.74	0.43
38	L10 × T2	0.03	-0.20	-0.44 *	0.14	-1.84	-2.19 *
39	L10 × T3	-0.52 **	-0.70 **	-0.44 *	-0.30	-0.92	0.15
40	L10 × T4	0.12	0.45 *	-0.03	-0.20	2.02	1.61
	S.Em±	0.09	0.21	0.20	0.31	1.32	0.92
	CD at 5%	0.18	0.42	0.40	0.63	2.66	1.86
	CD at 1%	0.24	0.56	0.53	0.84	3.57	2.50

* and ** indicate significance of values at p=0.05 and p=0.01, respectively.

DAS= Days after sowing

showed positive and significant sca effects and seven crosses showed negative and significant sca effects. Highest positive sca effects was observed in the cross $L3 \times T4$ (1.35) followed by the crosses $L5 \times T1$ (1.29) and $L1 \times T2$ (1.31).

4.9.3 Days to first male flower (Table 50 and 51)

Nine lines exhibited significant gca effects, of which four lines exhibited in negative direction, which is desirable and remaining five lines exhibited in positive direction. Maximum negative gca effects was observed in the line L2 (-5.42) followed by L6 (-4.39). Among the testers T4 (0.86) exhibited maximum significant positive gca effects and none of the testers exhibited significant negative gca effects. Among the crosses, only four crosses recorded negative significant sca effects and only two cross exhibited positive and significant gca effects. The maximum negative sca effects was observed in the cross $L9 \times T1$ (-7.26) followed by $L8 \times T3$ (-3.65) and $L6 \times T1$ (-3.36) for this trait.

4.9.4 Days to first female flower (Table 50 and 51)

Among the ten lines, five lines showed significant negative gca effects and four lines exhibited significant and positive gca effect for days to first female flowering. The highest negative gca effect was observed by the line L2 (-6.23) followed by L6 (-4.23). Among the testers, T4 (0.99) exhibited maximum positive and significant gca effects but none of the testers exhibited significant negative gca effects. Among total 40 crosses, 11 crosses exhibited significant and negative sca effects and eight crosses recorded positive and significant sca effects. Highest negative sca effects was observed in the cross $L9 \times T1$ (-6.92) followed by $L7 \times T3$ (-3.70) and $L8 \times T3$ (-3.20).

4.9.5 Node to first male flower (Table 52 and 53)

The trait node number for first male flowering, five lines recorded negative and significant gca effects and four line had positive and significant gca effects. Maximum negative gca effects was observed in the line L3 (-0.98) followed by L2 (-0.68). In the four testers, T1 (-0.44) had shown maximum negative and significant GCA effects. Among the crosses, only two crosses exhibited significant negative sca effects and three

Table 52. General combining ability effects for earliness and yield parameters in sponge gourd

Sl. No.	Lines	Node at first male flower	Node at first female flower	Days to first harvest	Days to last harvest	Fruit length (cm)	Fruit diameter (mm)
1	L1	-0.58 **	0.76	-1.22 *	-1.99 **	-0.37	-0.07
2	L2	-0.68 **	-2.15 **	-6.92 **	-5.96 **	4.50 **	5.42 **
3	L3	-0.98 **	-1.30 **	2.30 **	3.19 **	-1.23 **	-1.03 **
4	L4	-0.46 **	1.23 **	-0.25	-0.96	0.31	-3.04 **
5	L5	1.04 **	0.63	3.28 **	2.24 **	-1.14 **	-0.62
6	L6	-0.68 **	-1.60 **	-4.17 **	-3.46 **	3.99 **	5.02 **
7	L7	0.77 **	0.73	2.43 **	1.24 *	-2.58 **	-1.30 **
8	L8	0.77 **	-1.40 **	3.38 **	5.04 **	-1.74 **	-1.90 **
9	L9	1.07 **	2.46 **	3.58 **	4.64 **	-0.15	0.59
10	L10	-0.26	0.63	-2.40 **	-3.96 **	-1.59 **	-3.08 **
	S.Em±	0.17	0.40	0.45	0.59	0.38	0.34
	CD at 5%	0.35	0.81	0.92	1.19	0.78	0.69
	CD at 1%	0.46	1.08	1.23	1.59	1.04	0.92
	Testers						
1	T1	-0.44 **	-0.76 **	-1.17 **	-0.32	-0.55 **	1.26 **
2	T2	0.16 *	0.16	0.09	-0.79 *	1.32 **	1.08 **
3	T3	0.01	0.01	-0.21	-0.34	-1.08 **	-1.37 **
4	T4	0.26 *	0.59 *	1.30 **	1.46 **	0.31	-0.97 **
	S.Em±	0.11	0.25	0.29	0.37	0.24	0.22
	CD at 5%	0.22	0.51	0.58	0.75	0.49	0.44
	CD at 1%	0.29	0.68	0.78	1.01	0.66	0.58

* and ** indicate significance of values at p=0.05 and p=0.01, respectively.

Table 53. Specific combining ability effects for earliness and yield parameters in sponge gourd

Sl. No.	Crosses	Node at first male flower	Node at first female flower	Days to first harvest	Days to last harvest	Fruit length (cm)	Fruit diameter (mm)
1	L1 × T1	0.06	2.29 **	1.07	1.55	-2.16 **	-2.10 **
2	L1 × T2	0.56	-2.44 **	0.81	-0.68	2.23 **	0.33
3	L1 × T3	-0.29	-0.79	-0.49	-1.03	-0.94	-1.50 *
4	L1 × T4	-0.34	0.94	-1.40	0.17	0.86	3.27 **
5	L2 × T1	-0.14	-1.37	-2.03 *	0.92	2.41 **	3.92 **
6	L2 × T2	-0.74 *	-1.99 *	-1.59	-0.01	-0.55	2.23 **
7	L2 × T3	-0.29	1.27	2.61 **	-1.06	0.77	-2.27 **
8	L2 × T4	1.16 **	2.09 *	1.00	0.14	-2.63 **	-3.88 **
9	L3 × T1	0.36	0.24	-5.15 **	0.17	1.72 *	-0.58
10	L3 × T2	-0.24	-0.09	1.49	1.24	0.34	-0.08
11	L3 × T3	0.21	-0.44	4.19 **	1.99	0.81	3.16 **
12	L3 × T4	-0.34	0.29	-0.52	-3.41 **	-2.87 **	-2.50 **
13	L4 × T1	0.24	0.61	6.70 **	4.92 **	1.92 *	-0.05
14	L4 × T2	-0.66	1.39	-3.16 **	-2.61 *	-0.17	0.19
15	L4 × T3	0.99 **	0.54	-1.16	-1.06	1.55 *	0.69
16	L4 × T4	-0.56	-2.54 **	-2.37 *	-1.26	-3.30 **	-0.83
17	L5 × T1	0.64	-0.99	2.97 **	1.72	-2.59 **	-0.46
18	L5 × T2	-0.26	1.59	1.31	2.59 *	0.37	0.90
19	L5 × T3	-0.41	-1.56	-2.39 *	-2.66 *	-1.78 *	-2.63 **
20	L5 × T4	0.04	0.96	-1.90 *	-1.66	4.01 **	2.19 **
21	L6 × T1	-0.34	-0.42	-3.58 **	-2.18	2.50 **	3.65 **
22	L6 × T2	-0.34	-0.04	1.76	2.09	-2.13 **	-2.05 **
23	L6 × T3	0.31	0.62	0.06	-1.56	-1.64 *	-1.13
24	L6 × T4	0.36	-0.17	1.75	1.64	1.27	-0.47
25	L7 × T1	-0.19	-0.79	2.42 *	2.12	-0.37	-3.31 **
26	L7 × T2	0.01	0.29	0.56	1.19	-0.15	0.36
27	L7 × T3	-0.14	1.44	-3.34 **	-3.26 **	0.37	4.34 **
28	L7 × T4	0.31	-0.94	0.35	-0.06	0.14	-1.40 *
29	L8 × T1	-0.09	3.24 **	1.67	-1.48	2.39 **	2.98 **
30	L8 × T2	2.01 **	-1.19	-0.79	-3.01 *	-2.11 **	-1.73 *
31	L8 × T3	-1.24 **	-1.64 *	-3.29 **	-2.06	-0.47	-1.17
32	L8 × T4	-0.69 *	-0.42	2.40 *	6.54 **	0.19	-0.08
33	L9 × T1	-0.29	-4.22 **	-5.73 **	-9.08 **	-4.47 **	-5.46 **
34	L9 × T2	0.11	1.27	0.21	-1.21	1.25	0.78
35	L9 × T3	0.66	2.32 **	4.51 **	11.74 **	2.72 **	2.13 **
36	L9 × T4	-0.49	0.64	1.00	-1.46	0.50	2.55 **
37	L10 × T1	-0.26	1.41	1.65	1.32	-1.35	1.41 *
38	L10 × T2	-0.46	1.19	-0.61	0.39	0.91	-0.93
39	L10 × T3	0.19	-1.76 *	-0.71	-1.06	-1.39	-1.63 *
40	L10 × T4	0.54	-0.84	-0.32	-0.66	1.83 *	1.15
	S.Em±	0.34	0.80	0.91	1.18	0.77	0.68
	CD at 5%	0.69	1.61	1.84	2.38	1.55	1.38
	CD at 1%	0.92	2.16	2.46	3.19	2.08	1.85

* and ** indicate significance of values at p=0.05 and p=0.01, respectively.

cross exhibited significant and positive sca effects. Maximum negative sca effects was observed in the cross $L8 \times T3$ (-1.24) followed by $L2 \times T2$ (-0.74) and $L8 \times T4$ (-0.29).

4.9.6 Node to first female flower (Table 52 and 53)

For number of nodes to first female flower appearance, four lines exhibited negative and significant gca effects. Maximum negative gca effects was observed in the line $L2$ (-2.15) followed by $L6$ (-1.60). Among the testers one tester each had exhibited negative significant and positive significant GCA effects. Tester $T1$ (-0.76) had recorded maximum negative significant GCA effects. Among the crosses, four crosses exhibited significant and negative sca effects and six crosses exhibited significant and positive sca effects. Highest negative sca effects was observed in the cross $L9 \times T1$ (-4.22) followed by $L4 \times T4$ (-2.54) and $L1 \times T2$ (-2.44) for this trait.

4.9.7 Days to first harvest (Table 52 and 53)

Among the ten lines, four lines recorded significant and negative gca effects while, five lines exhibited significant and positive gca effects. Maximum negative gca effects was observed in the line $L2$ (-6.92) followed by $L6$ (-4.17). Among the testers, $T1$ (-1.17) exhibited highest significantly negative gca effects. Among the crosses, seven crosses exhibited significant negative sca effects and ten crosses exhibited significant positive sca effects. The maximum negative sca effects was observed in the cross $L9 \times T1$ (-5.73) followed by $L3 \times T1$ (-5.15) and $L6 \times T1$ (-3.58).

4.9.8 Days to last harvest (Table 52 and 53)

For days to last harvest, five lines showed significant positive gca effects and four lines showed negative and significant gca effects. Maximum and positive gca effects was observed in the line $L8$ (5.04) followed by $L9$ (4.64). Among testers, only one tester each had exhibited significantly positive and significantly negative gca effects. In the testers, $T4$ (1.46) had registered maximum significant positive gca effects. Among the 40 crosses, only four crosses exhibited significant positive sca effects. In the crosses, highest significant and positive sca effects was observed in the cross $L9 \times T3$ (11.74) followed by $L8 \times T4$ (6.54) and $L4 \times T1$ (4.92) for days to last harvest.

4.9.9 Fruit length (Table 52 and 53)

For fruit length, two lines had positive and significant gca effects and five lines had significantly negative gca effects. The highest and significantly positive gca effects was observed in the line L2 (4.50) followed by L6 (3.99). Among testers, only one tester T2 (1.32) exhibited maximum significant positive gca effects and two other testers had exhibited negative significant gca effects. Among crosses, 10 crosses each showed significantly positive and negative sca effects. The highest positive and significant sca effects was exhibited by the cross L5 $\times$ T4 (4.01) followed by L9 $\times$ T3 (2.72) and L6 $\times$ T1 (2.50) for fruit length.

4.9.10 Fruit diameter (Table 52 and 53)

Out of ten lines, two lines exhibited significant positive gca effects and five lines exhibited significant negative gca effects. The highest positive significant gca effects was exhibited by the line L2 (5.42) followed by L5 (5.02). Among the testers, T1 (1.26) followed by T2 (1.08) had exhibited maximum positive and significant gca effects. Among the crosses, 11 crosses each exhibited positive and negative significant sca effects. Maximum and significant sca effects was observed in the cross L7 $\times$ T3 (4.34) followed by L2 $\times$ T1 (3.92) and L6 $\times$ T1 (3.65).

4.9.11 Average fruit weight (Table 54 and 55)

For average fruit weight, three lines each had positive and negative significant gca effects. The highest positive and significant gca effects was observed in the line L2 (17.07) followed by L6 (15.88). Among the testers one tester exhibited positive and significant gca effects and two testers had significantly negative gca effects. The highest and significantly positive gca effects was observed in the tester T1 (4.61). Among crosses, 19 crosses showed significantly positive sca effects and 18 crosses showed significantly negative sca effects. The highest positive and significant sca effects was exhibited by the cross L7 $\times$ T3 (30.74) followed by L4 $\times$ T2 (18.91) and L6 $\times$ T1 (17.33) for this trait.

Table 54. General combining ability effects for yield and yield parameters in sponge gourd

Sl. No.	Lines	Average fruit weight (g)	Number of fruits/ vine	Fruit yield/ vine (kg)	Fruit yield/ plot (kg)	Fruit yield/ hectare (t)	No. of seeds/ fruit
1	L1	-0.57	0.75 **	0.11	1.57 **	0.87 **	-15.53 **
2	L2	17.07 **	4.60 **	1.22 **	11.99 **	5.68 **	36.82 **
3	L3	-1.05 *	2.20 **	0.31 ***	2.95 **	1.19 **	37.47 **
4	L4	-14.95 **	1.70 **	-0.10	-1.31 **	-0.76 **	-41.13 **
5	L5	9.70 **	-2.46 **	-0.10	-0.64	-0.37	-32.51 **
6	L6	15.88 **	3.20 **	0.77 **	7.52 **	3.89 **	-2.73
7	L7	-6.60 **	-2.61 **	-0.54 **	-5.54 **	-2.94 **	-9.23 **
8	L8	0.23	-0.26	-0.09	-0.95 *	-0.38	60.77 **
9	L9	0.44	-2.41 **	-0.44 **	-4.59 **	-1.99 **	11.52 **
10	L10	-20.16 **	-4.71 **	-1.12 **	-11.01 **	-5.17 **	-45.43 **
	S.Em±	0.52	0.26	0.07	0.40	0.23	1.73
	CD at 5%	1.05	0.52	0.14	0.81	0.47	3.50
	CD at 1%	1.41	0.70	0.19	1.08	0.63	4.68
	Testers						
1	T1	4.61 **	0.32	0.15 **	1.50 **	0.52 **	-3.57 **
2	T2	-0.52	1.24 **	0.21 **	2.11 **	0.92 **	-1.70
3	T3	-2.59 **	-1.35 **	-0.28 **	-2.54 **	-0.92 **	-8.52 **
4	T4	-1.50 **	-0.21	-0.08	-1.07 **	-0.52 **	13.80 **
	S.Em±	0.33	0.16	0.04	0.25	0.15	1.09
	CD at 5%	0.67	0.33	0.09	0.51	0.30	2.21
	CD at 1%	0.89	0.44	0.12	0.68	0.40	2.96

* and ** indicate significance of values at p=0.05 and p=0.01, respectively.

Table 55. Specific combining ability effects for yield and yield parameters in sponge gourd

Sl. No.	Crosses	Average fruit weight (g)	Number of fruits/ vine	Fruit yield/ vine (kg)	Fruit yield/ plot (kg)	Fruit yield/ hectare (t)	No. of seeds/ fruit
1	L1 × T1	5.33 **	-3.07 **	-0.32 *	-2.77 **	-1.11 *	-35.93 **
2	L1 × T2	-2.83 **	-1.59 **	-0.25	-2.54 **	-0.81	-32.60 **
3	L1 × T3	6.40 **	-0.01	0.15	1.55	-0.01	68.82 **
4	L1 × T4	-8.90 **	4.66 **	0.42 **	3.76 **	1.93 **	-0.30
5	L2 × T1	11.39 **	3.29 **	0.87 **	8.20 **	3.87 **	32.52 **
6	L2 × T2	14.92 **	1.57 **	0.66 **	6.52 **	2.79 **	20.05 **
7	L2 × T3	-15.91 **	-0.66	-0.49 **	-4.99 **	-2.57 **	-47.33 **
8	L2 × T4	-10.39 **	-4.20 **	-1.03 **	-9.73 **	-4.08 **	-5.25
9	L3 × T1	-8.38 **	-5.52 **	-1.02 **	-9.79 **	-4.74 **	22.87 **
10	L3 × T2	9.53 **	0.17	0.28	3.36 **	1.67 **	13.30 **
11	L3 × T3	-10.06 **	3.55 **	0.17	0.62	1.24 *	-11.58 **
12	L3 × T4	8.92 **	1.81 **	0.56 **	5.80 **	1.83 **	-24.60 **
13	L4 × T1	-19.99 **	0.79	-0.50 **	-4.79 **	-2.37 **	-25.43 **
14	L4 × T2	18.91 **	-0.14	0.43 **	4.51 **	2.19 **	-7.80 *
15	L4 × T3	-6.21 **	-4.16 **	-0.64 **	-6.57 **	-3.19 **	24.32 **
16	L4 × T4	7.29 **	3.51 **	0.72 **	6.85 **	3.37 **	8.90 *
17	L5 × T1	-16.34 **	-0.07	-0.49 **	-4.62 **	-2.71 **	12.65 **
18	L5 × T2	-3.70 **	2.82 **	0.44 **	4.17 **	2.62 **	8.58 *
19	L5 × T3	14.58 **	-1.61 **	0.10	1.33	0.52	-48.00 **
20	L5 × T4	5.46 **	-1.15 *	-0.04	-0.88	-0.43	26.78 **
21	L6 × T1	17.33 **	4.09 **	1.27 **	12.47 **	6.08 **	69.87 **
22	L6 × T2	-28.11 **	-1.44 **	-1.09 **	-10.94 **	-5.28 **	-6.50
23	L6 × T3	2.88 **	-0.66	-0.04	0.22	-0.01	-29.98 **
24	L6 × T4	7.90 **	-1.99 **	-0.15	-1.75 *	-0.79	-33.40 **
25	L7 × T1	-14.92 **	1.69 **	-0.05	-0.49	0.29	6.77
26	L7 × T2	-10.38 **	-3.24 **	-0.67 **	-6.88 **	-3.91 **	-31.50 **
27	L7 × T3	30.74 **	-3.86 **	0.01	-0.04	0.10	-25.08 **
28	L7 × T4	-5.44 **	5.41 **	0.71 **	7.42 **	3.52 **	49.80 **
29	L8 × T1	13.76 **	-0.47	0.24	2.30 **	1.03 *	4.17
30	L8 × T2	15.78 **	-1.59 **	0.10	0.95	0.66	6.10
31	L8 × T3	-11.94 **	5.80 **	0.51 **	5.08 **	2.26 **	9.92 **
32	L8 × T4	-17.60 **	-3.75 **	-0.85 **	-8.32 **	-3.95 **	-20.20 **
33	L9 × T1	13.57 **	-5.92 **	-0.63 **	-6.15 **	-3.25 **	-66.58 **
34	L9 × T2	-12.86 **	5.57 **	0.43 **	4.29 **	2.11 **	37.55 **
35	L9 × T3	-8.73 **	3.75 **	0.48 **	4.55 **	2.17 **	22.37 **
36	L9 × T4	8.02 **	-3.40 **	-0.28	-2.69 **	-1.03 *	6.65
37	L10 × T1	-1.74	5.19 **	0.63 **	5.63 **	2.91 **	-20.93 **
38	L10 × T2	-1.27	-2.14 **	-0.34 *	-3.43 **	-2.03 **	-7.20 *
39	L10 × T3	-1.75	-2.16 **	-0.24	-1.75 *	-0.51	36.52 **
40	L10 × T4	4.76 **	-0.90	-0.05	-0.45	-0.37	-8.40 *
	SEm±	1.04	0.51	0.14	0.80	0.47	3.46
	CD at 5%	2.11	1.04	0.29	1.61	0.94	6.99
	CD at 1%	2.82	1.39	0.38	2.16	1.27	9.36

* and ** indicate significance of values at p=0.05 and p=0.01, respectively.

4.9.12 Number of fruits per vine (Table 54 and 55)

Among the ten lines tested, five lines showed positive and significant gca effects and four lines exhibited negative and significant gca effects. The highest positive and significant gca effect was observed in the line L2 (4.60) followed by the L6 (3.20). Among the testers, one tester each had positive T2 (1.24) and negative significant gca effects. In the 40 crosses, 14 crosses exhibited positive and significant sca effects and 17 crosses recorded significant negative sca effects. Maximum and significant sca effects was observed in the cross L8 $\times$ T3 (5.80) followed by the crosses L9 $\times$ T2 (5.57) and L7 $\times$ T4 (5.41).

4.9.13 Fruit yield per vine (Table 54 and 55)

The trait fruit yield per vine, three lines recorded significant and positive gca effects, the highest was observed in the line L2 (1.22) followed by L6 (0.77) and three lines showed significant negative gca effects. Among the four testers studied, two testers exhibited significantly and positive gca effects and one tester exhibited significant negative gca effects. Maximum positive and significant effect of gca was observed by tester T2 (0.21) followed by T1 (0.15). Among crosses, 13 crosses exhibited positively significant and 12 crosses exhibited negatively significant sca effects. Maximum and positive significant sca effects was observed in the cross L6 $\times$ T1 (1.27) followed by the cross L2 $\times$ T1 (0.87) and L7 $\times$ T4 (0.71) for fruit yield per vine.

4.9.14 Fruit yield per plot (Table 54 and 55)

Among ten lines tested, four lines recorded positive and significant gca effects while, five lines exhibited negative and significant gca effects. The highest positive and significant gca effects was observed in the line L2 (11.99) followed by L6 (7.52). Among the testers, two testers each had exhibited positive and negative significant gca effects. Tester T2 (2.11) followed by T1 (1.50) exhibited maximum significant and positive gca effects. Among the crosses, 16 crosses each had exhibited positive and negative significant sca effects. The maximum positive and significant sca effects was observed in the cross L6 $\times$ T1 (12.47) followed by L2 $\times$ T1 (8.20) and L7 $\times$ T4 (7.42) for this trait.

4.9.15 Fruit yield per hectare (Table 54 and 55)

The four lines each had shown positive and negative significant gca effects respectively for fruit yield per hectare. The highest positive and significant gca effects was observed in the line L2 (5.68) followed by L6 (3.89). Among the testers, two testers each had exhibited positive and negative significant gca effects. The tester T2 (0.92) had exhibited maximum significant positive gca effects followed by T1 (0.52). Among the crosses studied, 16 and 13 crosses recorded positive and negative significant sca effects respectively. The highest and significant sca effects was observed in the cross L6 $\times$ T1 (6.08) followed by L2 $\times$ T1 (3.87) and L7 $\times$ T4 (3.52).

4.9.16 Number of seeds per fruit (Table 54 and 55)

Among ten lines tested, four lines showed positive and significant gca effects while, five lines exhibited negative and significant gca effects. The highest positive and significant gca effects was observed in L8 (60.77) followed by L3 (37.47). Among the testers one tester exhibited significant positive gca effects while, two other testers exhibited significant negative gca effects. Maximum positive gca effects was observed in the tester T4 (13.80). Among the crosses, 16 crosses exhibited positive and significant sca effects and 17 crosses exhibited negative and significant sca effects. Maximum and significant sca effects was observed in the cross L6 $\times$ T1 (69.87) followed by L1 $\times$ T3 (68.82) and L7 $\times$ T4 (49.80) for number of seeds per fruit.

4.9.17 Sponge yield (Table 56 and 57)

The trait sponge yield, three lines recorded positive and significant gca effects and four lines registered negative and significant gca effects. The highest positive and significant gca effects was observed in the line L2 (3.98) followed by L6 (2.85). Among the testers, only one tester exhibited significant and positive gca effects and two testers exhibited significant negative gca effects. Maximum positive and significant gca effects was observed in the tester T2 (0.80). Among the crosses, eight crosses each had exhibited positive and negative significant sca effects. Highest significant sca effects was observed in the cross L3 $\times$ T4 (3.83) followed by L10 $\times$ T1 (3.49) and L1 $\times$ T2 (2.44).

Table 56. General combining ability effects for sponge yield and quality parameters in sponge gourd

Sl. No.	Lines	Sponge yield (g)	TSS (^o Brix)	Fruit firmness (N)	Fruit color (L [*])	Fruit color (a [*])	Fruit color (b [*])	Protein (%)
1	L1	0.24	-0.52 **	0.59	1.40 **	-0.03	-0.19	-0.35
2	L2	3.98 **	-0.08	-1.62 **	-1.96 **	0.03	-0.55 *	-0.60 *
3	L3	-0.09	-0.21 **	1.28 **	-0.69 *	-0.10	-1.06 **	0.93 **
4	L4	-2.33 **	-0.06	0.85	-0.96 **	0.03	1.82 **	0.96 **
5	L5	1.25 **	-0.27 **	-1.62 **	-3.06 **	-0.20	0.02	1.01 **
6	L6	2.85 **	-0.11	-4.55 **	0.81 **	-0.17	-0.98 **	0.14
7	L7	-2.22 **	0.72 **	3.28 **	1.12 **	0.06	-0.04	-0.08
8	L8	-0.65 *	-0.30 **	1.48 **	1.54 **	-0.55 **	2.21 **	-0.48 *
9	L9	-2.77 **	0.35 **	1.54 **	-0.36	0.56 **	-2.01 **	-0.89 **
10	L10	-0.24	0.47 **	-1.22 *	2.16 **	0.38 *	0.78 **	-0.64 **
	S.Em±	0.28	0.08	0.46	0.27	0.17	0.25	0.23
	CD at 5%	0.56	0.15	0.92	0.54	0.34	0.51	0.46
	CD at 1%	0.75	0.21	1.23	0.72	0.45	0.68	0.62
Testers								
1	T1	0.06	0.04	-0.85 **	-0.72 **	-0.15	-0.85 **	-0.05
2	T2	0.80 **	-0.05	-1.53 **	-0.49 **	0.18	0.19	-0.01
3	T3	-0.37 *	0.20 **	0.99 **	0.17	0.03	-0.36 *	0.21
4	T4	-0.49 **	-0.19 **	1.38 **	1.03 **	-0.06	1.02 **	-0.15
	S.Em±	0.18	0.05	0.29	0.17	0.11	0.16	0.15
	CD at 5%	0.35	0.10	0.58	0.34	0.21	0.32	0.29
	CD at 1%	0.47	0.13	0.78	0.46	0.29	0.43	0.39

* and ** indicate significance of values at p=0.05 and p=0.01, respectively.

Table 57. Specific combining ability effects for sponge yield and quality parameters in sponge gourd

Sl. No.	Crosses	Sponge yield (g)	TSS (^o Brix)	Fruit firmness (N)	Fruit color (L [*])	Fruit color (a [*])	Fruit color (b [*])	Protein (%)
1	L1 × T1	-2.23 **	0.53 **	2.89 **	4.46 **	-0.44	3.22 **	0.80
2	L1 × T2	2.44 **	-0.27	-0.51	-4.31 **	-0.64	-3.48 **	0.56
3	L1 × T3	0.44	-0.20	-1.86 *	-0.62	0.80 *	-0.85	-1.91 **
4	L1 × T4	-0.66	-0.06	-0.53	0.47	0.27	1.10 *	0.54
5	L2 × T1	1.61 **	0.22	-3.88 **	-1.38 *	0.21	-2.25 **	-1.27 **
6	L2 × T2	-0.69	0.34 *	-0.99	0.89	0.32	-1.03 *	-0.89
7	L2 × T3	0.05	-0.16	7.22 **	-1.00	-0.71 *	3.34 **	0.99 *
8	L2 × T4	-0.96	-0.39 *	-2.35 *	1.48 **	0.19	-0.07	1.16 *
9	L3 × T1	-4.13 **	-0.14	3.81 **	-0.50	0.03	0.67	0.29
10	L3 × T2	-0.58	0.03	4.12 **	2.70 **	-0.01	2.19 **	-0.01
11	L3 × T3	0.88	-0.20	-4.32 **	-2.44 **	-0.02	-3.30 **	-0.88
12	L3 × T4	3.83 **	0.31 *	-3.61 **	0.25	0.00	0.45	0.60
13	L4 × T1	0.35	-0.10	-1.93 *	-0.38	0.16	3.42 **	-2.40 **
14	L4 × T2	-0.21	0.01	3.90 **	0.29	0.03	-1.72 **	1.00 *
15	L4 × T3	1.02	0.15	3.66 **	-0.51	-0.16	-4.25 **	0.89
16	L4 × T4	-1.16 *	-0.05	-5.62 **	0.59	-0.03	2.55 **	0.52
17	L5 × T1	0.83	0.05	6.31 **	-0.65	-0.03	-2.57 **	0.63
18	L5 × T2	-3.63 **	0.12	-3.32 **	-0.31	-0.12	-5.85 **	1.43 **
19	L5 × T3	2.31 **	-0.53 **	-4.45 **	-0.25	-0.17	6.66 **	-2.21 **
20	L5 × T4	0.50	0.37 *	1.47	1.20 *	0.31	1.77 **	0.16
21	L6 × T1	1.96 **	0.39 *	-5.71 **	-0.22	-0.23	2.93 **	-0.96 *
22	L6 × T2	0.48	0.19	-1.14	0.84	-0.16	1.63 **	0.25
23	L6 × T3	-1.77 **	-0.26	2.26 *	1.33 *	0.61	-2.40 **	-0.02
24	L6 × T4	-0.66	-0.32 *	4.59 **	-1.96 **	-0.22	-2.16 **	0.73
25	L7 × T1	0.44	-0.31 *	0.23	1.46 **	0.85 *	-2.41 **	1.29 **
26	L7 × T2	0.02	-0.16	4.70 **	-2.52 **	-0.39	1.42 **	-1.58 **
27	L7 × T3	-0.37	0.56 **	-6.99 **	0.61	-0.46	-1.26 *	1.77 **
28	L7 × T4	-0.10	-0.09	2.07 *	0.46	-0.01	2.24 **	-1.47 **
29	L8 × T1	-0.01	-0.13	3.09 **	5.18 **	-1.57 **	0.83	0.84
30	L8 × T2	0.14	-0.22	-6.45 **	-2.80 **	0.76 *	2.69 **	-2.58 **
31	L8 × T3	-0.90	0.20	5.52 **	-3.53 **	0.51	-0.31	1.47 **
32	L8 × T4	0.76	0.14	-2.16 *	1.16 *	0.31	-3.21 **	0.26
33	L9 × T1	-2.32 **	0.17	2.43 *	-9.35 **	0.81 *	-5.48 **	2.03 **
34	L9 × T2	1.41 *	-0.09	-4.28 **	5.56 **	-0.01	2.79 **	2.16 **
35	L9 × T3	2.39 **	-0.32 *	0.31	5.00 **	-0.62	1.46 **	-1.38 **
36	L9 × T4	-1.48 *	0.24	1.55	-1.22 *	-0.18	1.23 *	-2.81 **
37	L10 × T1	3.49 **	-0.67 **	-7.23 **	1.38 *	0.21	1.63 **	-1.25 **
38	L10 × T2	0.62	0.06	3.98 **	-0.35	0.22	1.37 **	-0.35
39	L10 × T3	-4.05 **	0.77 **	-1.35	1.41 *	0.21	0.91	1.28 **
40	L10 × T4	-0.06	-0.16	4.60 **	-2.44 **	-0.64	-3.92 **	0.32
	S.Em±	0.55	0.15	0.91	0.53	0.34	0.50	0.46
	CD at 5%	1.12	0.31	1.84	1.08	0.68	1.02	0.93
	CD at 1%	1.50	0.41	2.47	1.44	0.91	1.37	1.24

* and ** indicate significance of values at p=0.05 and p=0.01, respectively.

4.9.18 Total soluble solids (Table 56 and 57)

Out of the ten lines, three lines recorded significant and positive gca effects and four lines exhibited significant negative gca effects for this character. Highest positive gca effects was observed in the line L7 (0.72) followed by L10 (0.47). Among the tester only one tester each had exhibited significant positive and significant negative gca effects. Tester T3 (0.20) had shown highest significant positive gca effects. Among 40 crosses, seven crosses registered significant positive sca effects while, six crosses exhibited negative and significant sca effects. Maximum and significant positive sca effects was noticed in the cross L10 $\times$ T3 (0.77) followed by L7 $\times$ T3 (0.56) and L1 $\times$ T1 (0.53) for total soluble solids.

4.9.19 Fruit firmness (Table 56 and 57)

Among the lines tested, four lines each had exhibited positive and negative and significant gca effects. The highest positive gca effects was observed in the line L7 (3.28) followed by L9 (1.54). Among the four testers, two testers each had exhibited negative significant and positive significant gca effects. T4 (1.38) and T3 (0.99) exhibited maximum positive and significant gca effects. Among the 40 crosses, 16 crosses each had recorded positive and negative significant sca effects respectively. The highest and positive significant sca effects were observed in the cross L2 $\times$ T4 (7.22) followed by L5 $\times$ T1 (6.31) and L10 $\times$ T4 (4.60) for this trait.

4.9.20 Fruit color (Table 56 and 57)

For fruit color value (L^*) five lines had noticed positive and significant gca effects while, four lines exhibited negative and significant gca effects. Highest positive significant gca effects was observed in the line L10 (2.16) followed by L8 (1.54). Among the testers, one tester registered positive significant gca effects while two testers exhibited negative significant gca effects. The maximum positive significant gca effects was observed by the line T4 (1.03). Out of 40 crosses, 12 crosses exhibited significant and positive sca effects and 10 crosses registered negative and significant sca effects. Highest and significant positive sca effects was observed in the cross L9 $\times$ T2 (5.56) followed by L8 $\times$ T1 (5.18) and L9 $\times$ T3 (5.00).

Only two line had noticed positive and significant gca effects and one lines exhibited negative and significant gca effects for fruit color value (a^*). Highest positive

significant gca effects was observed in the line L9 (0.56 followed by L10 (0.38). None of the testers exhibited significant gca effects. Out of 40 crosses, only two crosses exhibited significant and negative sca effects whereas, four crosses indicated positive and significant sca effects. Highest and significant positive sca effects was observed in the cross $L7 \times T1$ (0.85) followed by $L9 \times T1$ (0.81) for fruit color value (a*).

Among the lines for fruit color value (b*) three lines had shown positive and significant gca effects and four lines exhibited negative significant gca effects. Highest positive significant gca effects was observed in the line L8 (2.21) followed by L4 (1.82). Among the testers, one tester each had exhibited positive and negative significant gca effects. The maximum positive significant gca effects was observed by tester T4 (1.02). Out of 40 crosses, eighteen crosses exhibited significant and positive sca effects and fifteen crosses exhibited negative and significant sca effects. Highest and significantly positive sca effects was observed in the cross $L5 \times T3$ (6.66) followed by $L4 \times T1$ (3.42) and $L2 \times T3$ (3.34) for this trait.

4.9.21 Protein content (Table 56 and 57)

Three lines had noticed positive and significant gca effects for protein content of fruits and highest was observed in the line L5 (1.01) followed by L4 (0.96) and four lines exhibited negative significant gca effects. None of the testers exhibited significant gca effects. Out of 40 crosses, 10 crosses exhibited significant and positive sca effects and 11 crosses exhibited negative significant sca effects. Highest and significantly positive sca effects was observed by the cross $L9 \times T2$ (2.16) followed by $L9 \times T1$ (2.03) and $L7 \times T3$ (1.77).

4.9.22 Ascorbic acid content (Table 58 and 59)

For ascorbic acid content, three lines exhibited positive and significant gca effects and highest was observed in the line L10 (1.82) followed by L9 (0.80) whereas, five lines exhibited negative significant gca effects. Among the testers two testers each had exhibited positive and negative significant gca effects. The highest positive significant gca effects was observed by the tester T3 (0.18) followed by T4 (0.12). In the total 40 crosses, nine crosses exhibited significant and positive sca effects while, 11 crosses exhibited negative and significant sca effects. Highest and significantly positive sca effects was observed in the cross $L4 \times T1$ (1.68) followed by $L8 \times T4$ (0.90) and $L6 \times T4$ (0.72) for ascorbic acid content of fruits.

4.9.23 Potassium content of fruit (Table 58 and 59)

Among the ten lines, three lines each had exhibited positive and negative significant gca effects for potassium content of fruits. The highest positive and significant gca effects was observed in the line L10 (0.26) followed by L4 (0.24). Among the testers, only one tester T3 (0.07) exhibited maximum significant positive gca effects while, two testers exhibited negative significant gca effects. Among the 40 crosses, five crosses exhibited significant and positive sca effects and eight crosses exhibited negative and significant sca effects. Highest and significant positive sca effects was observed in the cross L7 $\times$ T1 and L10 $\times$ T3 (0.42) followed by L8 $\times$ T1 (0.39) and L3 $\times$ T2 (0.37).

4.9.24 Fruit phenol content (Table 58 and 59)

The trait phenol content of fruits, five lines exhibited positive and significant gca effects and four lines exhibited negative significant gca effects. The highest positive and significant gca effects was observed in L9 (10.47) followed by L1 (7.76). Among the testers two testers each had exhibited positive and negative significant gca effects. Maximum significant positive gca effects was observed by T3 (3.59) and T4 (2.67). Among 40 crosses, 13 crosses exhibited significant and positive sca effects while, 21 crosses exhibited negative and significant sca effects. Highest and significantly positive sca effects was observed in the cross L6 $\times$ T3 (50.06) followed by L9 $\times$ T4 (33.89) and L2 $\times$ T4 (31.76) for this trait.

4.9.25 Total antioxidants (Table 58 and 59)

Six lines exhibited positive and significant gca effects and four lines exhibited negative significant gca effects. The highest positive and significant gca effects was observed in L3 (20.09) followed by L5 (18.25). Among the testers two testers each exhibited significant positive and significant negative gca effects. Maximum significant positive gca effects was observed by T4 (4.04) followed by T3 (3.76). Among the 40 crosses, 18 crosses exhibited significant and positive sca effects and 19 crosses exhibited negative and significant sca effects. Highest and significantly positive sca effects was observed in the cross L7 $\times$ T1 (42.51) followed by L8 $\times$ T3 (34.32) and L5 $\times$ T2 (34.25).

Table 58. General combining ability effects for quality parameters in sponge gourd

Sl. No.	Lines	Ascorbic acid (mg/100g)	Potassium (%)	Phenol (mg GAE/100g)	Anti-oxidants (mg AAE/100g)	Flavonoids (mg QE/100g)	Crude fiber (%)	Ash (%)
1	L1	-0.59 **	-0.30 **	7.76 **	15.74 **	2.30 **	-0.72 **	-0.73 **
2	L2	-0.14	-0.27 **	7.23 **	-1.98 **	1.09	-1.60 **	-0.71 **
3	L3	-0.97 **	-0.20 **	-2.58 **	20.09 **	5.85 **	0.06	0.65 **
4	L4	0.68 **	0.24 **	-6.22 **	-12.17 **	-1.98 **	0.38	-0.53 **
5	L5	-0.60 **	0.14 *	5.70 **	18.25 **	0.77	1.28 **	-0.67 **
6	L6	-0.07	0.05	-21.01 **	6.21 **	4.99 **	-1.98 **	0.23
7	L7	-0.62 **	0.06	2.06 **	-21.89 **	-6.14 **	1.21 **	-0.52 **
8	L8	-0.31 **	-0.05	-3.71 **	-38.37 **	-9.54 **	0.55 *	0.43 *
9	L9	0.80 **	0.06	10.47 **	10.83 **	-0.93	0.70 **	1.40 **
10	L10	1.82 **	0.26 **	0.30	3.30 **	3.60 **	0.11	0.45 *
	S.Em±	0.10	0.06	0.60	0.49	0.57	0.21	0.18
	CD at 5%	0.19	0.11	1.22	1.00	1.16	0.43	0.36
	CD at 1%	0.26	0.15	1.63	1.34	1.56	0.57	0.48
Testers								
1	T1	-0.14 *	-0.07 *	-3.75 **	-5.62 **	0.40	-0.73 **	-0.32 **
2	T2	-0.16 **	-0.07 *	-2.51 **	-2.18 **	1.40 **	0.24	0.05
3	T3	0.18 **	0.07 *	3.59 **	3.76 **	-1.29 **	0.25	0.26 *
4	T4	0.12 *	0.06	2.67 **	4.04 **	-0.51	0.23	0.02
	S.Em±	0.06	0.04	0.38	0.31	0.36	0.13	0.11
	CD at 5%	0.12	0.07	0.77	0.63	0.73	0.27	0.23
	CD at 1%	0.16	0.10	1.03	0.85	0.98	0.36	0.30

* and ** indicate significance of values at p=0.05 and p=0.01, respectively.

Table 59. Specific combining ability effects for quality parameters in sponge gourd

Sl. No.	Crosses	Ascorbic acid (mg/100 g)	Potassium (%)	Phenol (mg GAE/100 g)	Anti-oxidants (mg AAE/100g)	Flavonoids (mg QE/100g)	Fiber (%)	Ash (%)
1	L1 × T1	-0.61 **	-0.13	11.56 **	-0.13	0.96	-0.40	-1.09 **
2	L1 × T2	0.42 *	-0.14	-9.29 **	-32.32 **	-5.34 **	0.21	-0.50
3	L1 × T3	-0.33	0.05	1.84	10.50 **	1.36	-0.61	0.10
4	L1 × T4	0.52 **	0.22	-4.10 **	21.95 **	3.01 *	0.80	1.49 **
5	L2 × T1	-0.48 *	-0.06	-6.69 **	19.98 **	1.42	0.39	0.52
6	L2 × T2	0.37	0.05	-18.81 **	16.46 **	-0.69	-0.93 *	0.35
7	L2 × T3	0.10	0.27 *	-6.26 **	-34.99 **	-5.56 **	0.86 *	-0.23
8	L2 × T4	0.01	-0.26 *	31.76 **	-1.44	4.83 **	-0.32	-0.64
9	L3 × T1	0.30	-0.10	-18.19 **	-33.82 **	-6.04 **	-1.73 **	0.76 *
10	L3 × T2	-0.09	0.37 **	15.01 **	39.31 **	1.16	0.63	0.01
11	L3 × T3	-0.11	-0.10	12.18 **	-31.73 **	3.47 **	0.52	1.10 **
12	L3 × T4	-0.11	-0.17	-9.00 **	26.23 **	1.41	0.59	-1.87 **
13	L4 × T1	1.68 **	0.07	-12.33 **	13.44 **	0.77	0.53	-0.90 *
14	L4 × T2	-0.07	-0.07	1.21	7.23 **	0.84	-0.78	0.38
15	L4 × T3	-1.09 **	-0.13	-8.18 **	9.07 **	1.58	0.82	1.54 **
16	L4 × T4	-0.52 **	0.13	19.31 **	-29.74 **	-3.19 **	-0.57	-1.03 **
17	L5 × T1	0.33	-0.38 **	0.48	-21.68 **	-4.29 **	1.48 **	-0.11
18	L5 × T2	-0.12	0.02	-5.37 **	34.25 **	5.25 **	0.98 *	0.33
19	L5 × T3	0.27	0.19	-7.90 **	3.52 **	0.95	-0.03	-0.30
20	L5 × T4	-0.48 *	0.17	12.79 **	-16.08 **	-1.90	-2.42 **	0.08
21	L6 × T1	-0.20	0.05	-6.73 **	20.17 **	-0.26	0.20	0.85 *
22	L6 × T2	-0.13	-0.12	-7.62 **	1.03	-3.74 **	1.03 *	-1.16 **
23	L6 × T3	-0.39 *	0.07	50.06 **	-16.97 **	2.67 *	-0.69	-0.90 *
24	L6 × T4	0.72 **	0.00	-35.70 **	-4.22 **	1.34	-0.54	1.20 **
25	L7 × T1	0.59 **	0.42 **	-2.86 *	42.51 **	7.51 **	-0.45	-0.18
26	L7 × T2	-0.29	0.14	14.87 **	-8.43 **	3.25 **	-0.74	-0.90 *
27	L7 × T3	0.09	-0.26 *	-17.82 **	-14.47 **	-5.05 **	0.25	0.17
28	L7 × T4	-0.39 *	-0.30 *	5.81 **	-19.619 **	-5.71 **	0.94 *	0.91 *
29	L8 × T1	-0.90 **	0.39 **	16.71 **	-9.24 **	-0.96	0.38	1.01 **
30	L8 × T2	-0.60 **	-0.38 **	27.08 **	-12.09 **	2.25	0.37	0.52
31	L8 × T3	0.60 **	-0.21	1.50	34.32 **	-2.31	-1.56 **	-1.20 **
32	L8 × T4	0.90 **	0.20	-45.29 **	-12.98 **	1.02	0.82	-0.33
33	L9 × T1	-0.55 **	0.19	0.12	-11.64 **	0.89	0.37	0.35
34	L9 × T2	-0.08	0.15	-8.02 **	-3.02 **	0.49	0.22	0.42
35	L9 × T3	0.57 **	-0.29 *	-25.98 **	8.68 **	-0.47	-0.33	-0.10
36	L9 × T4	0.06	-0.04	33.89 **	5.98 **	-0.91	-0.26	-0.68
37	L10 × T1	-0.17	-0.45 **	17.95 **	-19.59 **	0.00	-0.76	-1.22 **
38	L10 × T2	0.58 **	-0.01	-9.05 **	-42.41 **	-3.47 **	-0.98 *	0.54
39	L10 × T3	0.29	0.42 **	0.57	32.08 **	3.36 **	0.76	-0.18
40	L10 × T4	-0.71 **	0.05	-9.46 **	29.92 **	0.11	0.98 *	0.86 *
	S.Em±	0.19	0.11	1.20	0.99	1.15	0.42	0.35
	CD at 5%	0.39	0.23	2.43	2.00	2.32	0.85	0.72
	CD at 1%	0.52	0.31	3.25	2.68	3.11	1.14	0.96

* and ** indicate significance of values at p=0.05 and p=0.01, respectively.

4.9.26 Total flavonoids (Table 58 and 59)

Among the lines, four lines exhibited positive and significant gca effects and three lines exhibited negative significant gca effects. The highest positive and significant gca effects was observed in L3 (5.85) followed by L6 (4.99). Among the testers one tester each had exhibited positive and negative significant gca effects. Maximum significant positive gca effects was observed by tester T2 (1.40). Among 40 crosses, eight crosses exhibited significant and positive sca effects while, nine crosses exhibited negative and significant sca effects. Whereas, highest and significantly positive sca effects was observed in the cross $L7 \times T1$ (7.51) followed by $L5 \times T2$ (5.25) and $L2 \times T4$ (4.83) for total flavonoids.

4.9.27 Crude fiber (Table 58 and 59)

Four lines had registered positive and significant gca effects and three lines exhibited negative significant gca effects for crude fiber content of fruits. The highest positive and significant gca effects was observed by the line L5 (1.28) followed by L7 (1.21). None of the testers exhibited significant positive gca effects and only one line had exhibited significant negative gca effects. The maximum significant positive gca effects was observed by T2 (1.40). Among the 40 crosses, six crosses exhibited significant and positive sca effects and five crosses exhibited negative and significant sca effects. Highest and significant positive sca effects was observed in the cross $L5 \times T1$ (1.48) followed by $L6 \times T2$ (1.03) and $L10 \times T4$ (0.98) for this trait.

4.9.28 Ash content (Table 58 and 59)

Out of ten lines tested, four lines exhibited positive and significant gca effects and five lines exhibited negative significant gca effects for ash content of fruits. The highest positive and significant gca effects was observed in L9 (1.40) followed by L3 (0.65). Among the testers, one tester each had exhibited positive and negative significant gca effects. The maximum significant positive gca effects was observed by the tester T3 (0.26). Among 40 crosses, nine crosses each had exhibited positive and negative significant sca effects. Highest and significantly positive sca effects was observed in the cross $L4 \times T4$ (1.54) followed by $L1 \times T4$ (1.49) and $L6 \times T4$ (1.20) for ash content of fruit.

5. DISCUSSION

Sponge gourd (*Luffa cylindrica* L. Roem.) is an annual vegetable crop grown throughout India. Due to its high adaptability, it can be cultivated under a wide range of environmental conditions. Further, it is also a crop of significant nutritional as well as medicinal value. In spite of the availability of wide range of genetic variability in plant and fruit characters and also produce large number of hybrid seeds at reasonable cost, very little attention was given to exploit the hybrid vigour in this crop. Therefore, heterosis breeding is one of the method to achieve a quantum jump in yield and quality.

Further, success in genetic improvement of hybrids depends on the understanding of the nature of inheritance of yield and its component traits as well as identification of parents showing genetic prepotency for yield. This emphasized the importance of testing the parents for their combining ability because many times the high-yielding parents may not combine well to give good segregation. Combining ability analysis is frequently being used for testing the performance of various hybrids and also for characterizing the nature and magnitude of gene action involved in controlling various quantitative attributes. Besides, GCA also helps in the selection of superior parents and SCA for superior hybrids. Thus, heterosis and combining ability are basic requirements for a thorough knowledge of the genetic architecture of yield and its components. Keeping the above facts in consideration, the current investigation was carried with the objectives of characterization of sponge gourd genotypes for morphological and molecular variability, heritability and development of superior F₁ hybrids to increase the yield and the results obtained are discussed under the following sub headings.

- 5.1 Analysis of variance
- 5.2 Genetic variability studies
- 5.3 Genetic diversity studies
- 5.4 Molecular characterization
- 5.5 Correlation co-efficient analysis

- 5.6 Path co-efficient analysis
- 5.7 Magnitude of heterosis
- 5.8 Combining ability effects and variances

5.1 Analysis of variance

In the current study, the results of the analysis of variance indicated, highly significant differences among the 40 genotypes for all the traits viz., vine length at 45 and 90 DAS, number of branches per vine at 45 and 90 DAS, days to first male flower, days to first female flower, node at first male flower, node at first female flower, days to first harvest, days to last harvest, fruit length, fruit diameter, average fruit weight, number of fruits per vine, fruit yield per vine, fruit yield per plot, fruit yield per hectare, number of seeds per fruit, sponge yield, TSS, fruit firmness, fruit color, protein, ascorbic acid, potassium, phenol, total antioxidants, total flavonoids, crude fiber and ash content. All the genotypes exhibited considerable amount of differences in their mean performance with respect to all the characters studied. Therefore, the germplasm under present study was genetically diverse. The similar results were also noticed by Sharma *et al.* (2017), Singh *et al.* (2017b), Abhijeet *et al.* (2018b), Parveen *et al.* (2019), Singh *et al.* (2019c), Kumar *et al.* (2020b), Yadav (2020), Som *et al.* (2020a) and Purushottama (2022) in their studies with sponge gourd.

5.2 Genetic variability studies

The presence of genetic variability is the prerequisite in any crop improvement programme. One of the ways to assess the variability of these characters is through a simple approach of examining the range of variation. Genetic variation for growth, yield and quality traits in sponge gourd genotypes were represented in Fig. 3 and 4. The observed phenotypic variability is not very reliable since, it includes genotypic, environmental and genotype $\times$ environmental interaction components. Therefore, it becomes essential to split the observed variability into the phenotypic and genotypic coefficient of variation (PCV and GCV) which ultimately indicate the extent of variability existing for various traits.

Genetic parameters

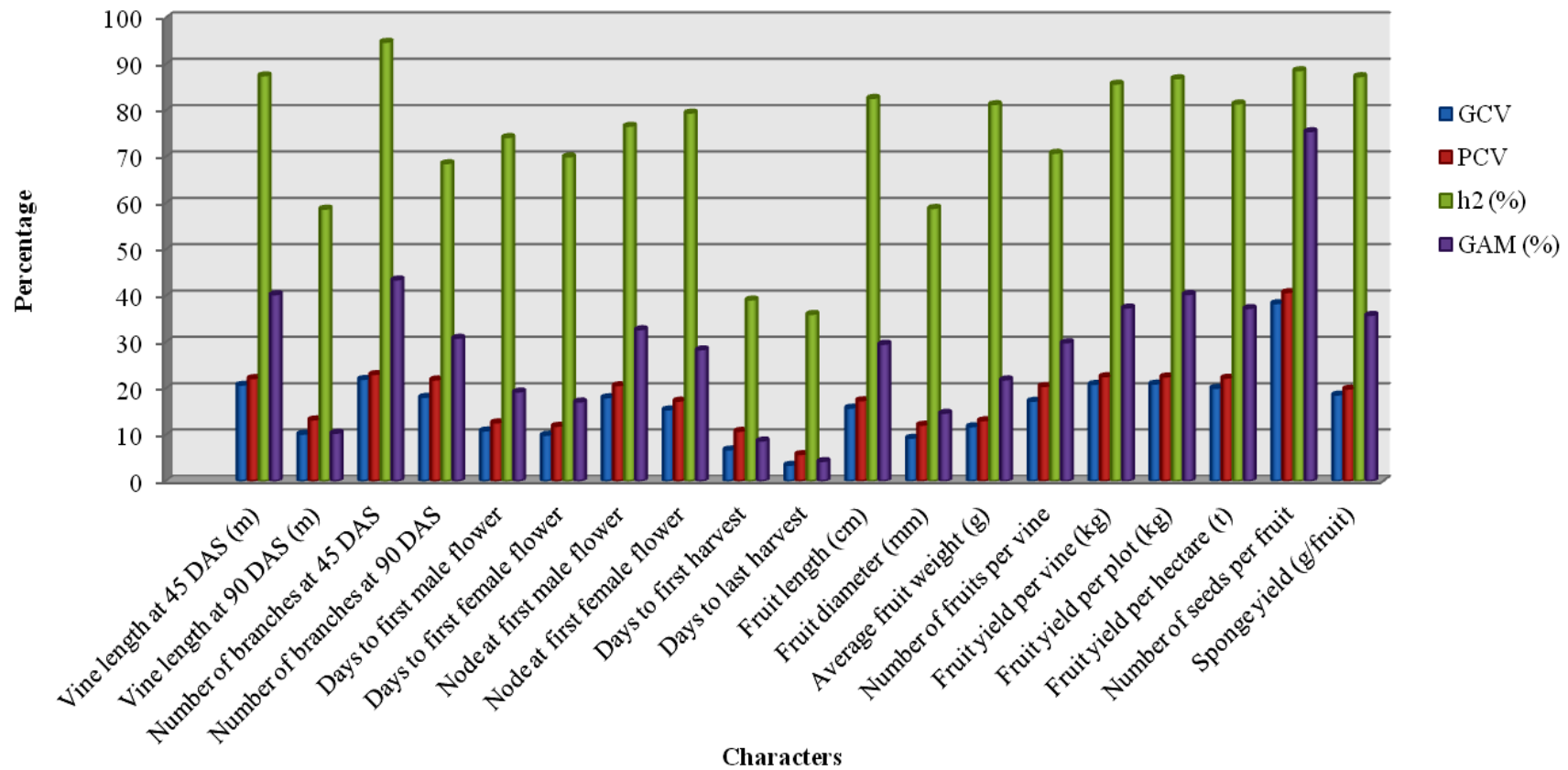


Fig. 3. Genetic variation for growth and yield in sponge gourd genotypes

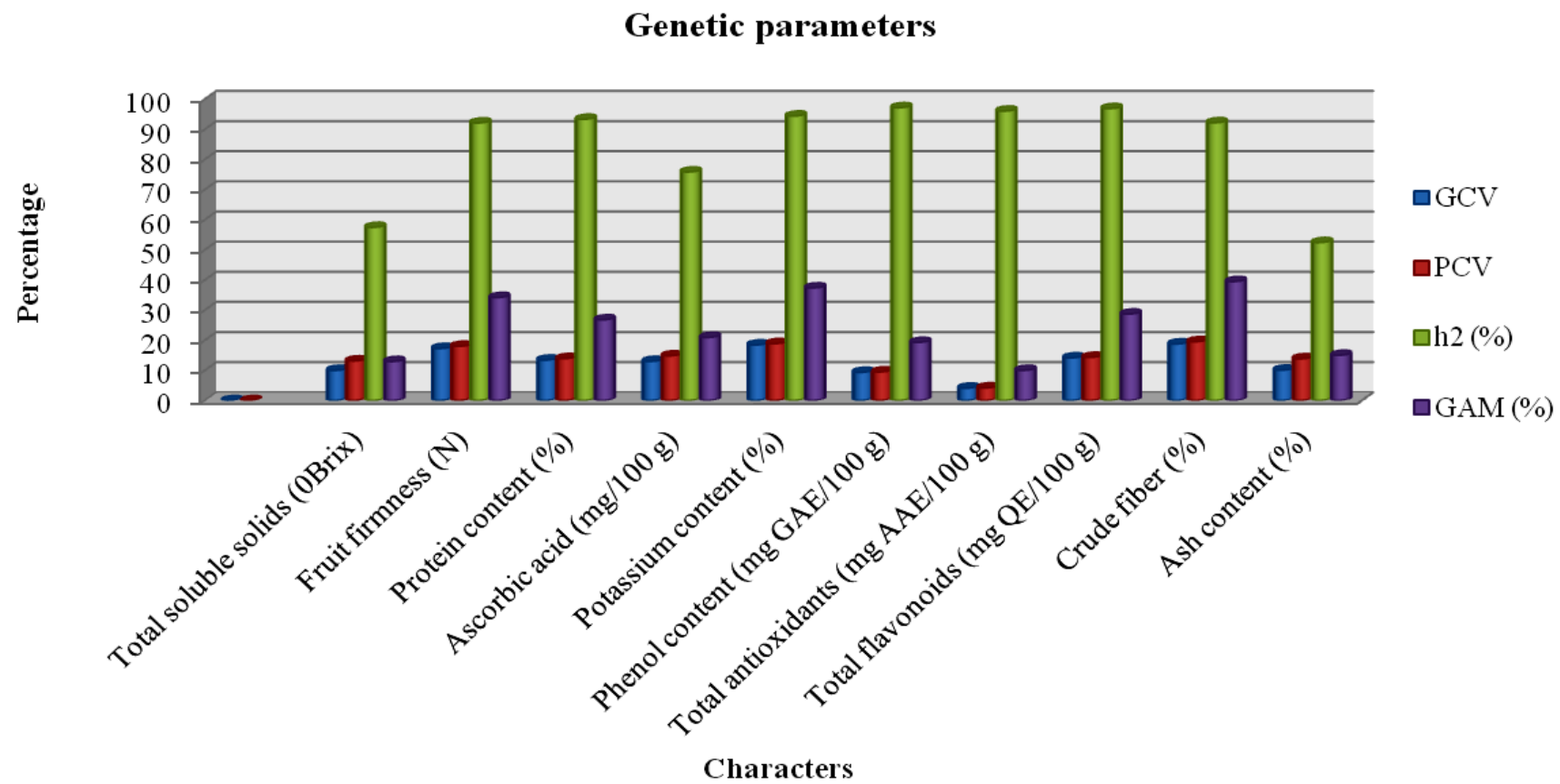


Fig. 4. Genetic variation for different quality traits in sponge gourd genotypes

Estimation of GCV alone does not reveal the extent of variation that is heritable. Therefore, in order to assess the proportion of total genetic variation, heritability in a broad sense must be estimated, which includes both additive and non-additive gene effects. Higher heritability of character suggests that, it is more stable in varied environments, providing a better opportunity for selecting a favourable genotype (Randhawa *et al.*, 1975). In general, heritability is determined by the amount of genetic variations present in a population as well as the conditions under which the genotypes are assessed.

According to Panse (1957), only additive gene action can result in high genetic advance. Therefore, heritability combined with genetic gain would be more useful than the heritability alone in selecting effective genotypes. Hence, it is essential to consider the predicted genetic advance along with heritability estimate as a tool in the selection programme for better efficiency.

In the present study, for all the characters studied, genotypic coefficient of variability was lower in magnitude than the phenotypic coefficient of variability. High values of these characters indicate wider variability and vice versa. Accordingly, a narrow difference between the phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) implies the lesser effect of environment on the expression of these traits. The results of the variability observed in 40 sponge gourd genotypes with respect to growth, yield and quality parameters are briefly discussed below.

The high values of genotypic and phenotypic co-efficients of variation (> 20 %) were recorded for vine length at 45 DAS, number of branches at 45 DAS, fruit yield per vine, fruit yield per plot, fruit yield per hectare, number of seeds per fruit and fruit color (b*). This indicates existence of wider genetic variation in the genotypes for these characters. These results are in accordance with the findings of Singh *et al.* (2017b), Kumar *et al.* (2019) and Singh *et al.* (2019c) for fruit yield per vine; Kumar *et al.* (2013) and Purushottama (2022) for vine length, number of branches per vine, number of seeds per fruit and fruit color in sponge gourd; Saklesh (2016) in ridge gourd for fruit yield per plot; Divyaraj *et al.* (2019), Karthik *et al.* (2017), Akhila and Singh (2020) and Krishnamoorthy (2020a) for fruit yield per hectare in ridge gourd.

High PCV (> 20 %) and moderate GCV (10-20 %) were observed for number of branches at 90 DAS, node at first male flower and number of fruits per vine indicating the role of environment on the expression of these characters. Similar findings were also reported in sponge gourd by Sharma *et al.* (2017), Abhijeet *et al.* (2018b), Singh *et al.* (2019c), Kumar *et al.* (2020b) and Yadav (2020) for node at first male flower; Annigeri (2020) and Som *et al.* (2020a) for number of fruits per vine; Choudhary and Kumar (2011) and Panda *et al.* (2022) in ridge gourd for number of branches per vine.

The estimates of GCV and PCV (10-20 %) were moderate for vine length at 90 DAS, days to first male flower, node at first female flower, fruit length, average fruit weight, sponge yield, total soluble solids, fruit firmness, fruit color (L*), fruit color (a*), protein content, ascorbic acid, potassium content, total flavonoids, crude fiber and ash content which indicates presence of moderate amount of variability for these traits. This is in conformity with the findings of Yadav *et al.* (2016) for total flavonoids; Sharma *et al.* (2017) and Kumar *et al.* (2019) for vine length, days to first male flower, female flower, fruit length and average fruit weight; Krishnamoorthy (2020a) and Yadav (2020) for TSS; Ogunyemi *et al.* (2020) for potassium content; Purushottama (2022) for fruit firmness and fruit color in sponge gourd; Swetha and Muthukumar (2016) and Harshitha *et al.* (2019a) in ridge gourd for protein and ash content; Madhuri (2018) in ridge gourd for ascorbic acid content; Sushmitha *et al.* (2019) and Sravani *et al.* (2021) in ridge gourd for crude fiber content.

Moderate PCV (10-20%) and low GCV (<10 %) were observed for days to first female flower, days to first harvest and fruit diameter which indicated that need to create variability for these traits. These results are in line with results of earlier works of Pandey *et al.* (2012b) and Singh *et al.* (2017b) for days to first harvest; Kumar *et al.* (2013), Singh *et al.* (2017b), Abhijeet *et al.* (2018b), Som *et al.* (2020a) and Yadav (2020) for days to first female flower and fruit diameter in sponge gourd.

The low values of GCV and PCV (<10 %) were also registered for days to last harvest, phenol content and total anti-oxidants indicated lack of variability in the tested breeding material. This indicated need for generation of variability, either through introduction or mutation or exploration or hybridization and further identification of best plants in segregating population. Similar results were earlier reported by Yadav *et*

al. (2016) in sponge gourd for phenol and total anti-oxidant content and Divyaraj *et al.* (2019) and Akhila and Singh (2020) in ridge gourd for days to last harvest.

Estimates of high heritability (> 60 %) coupled with high genetic advance as per cent of mean (> 20 %) were recorded for vine length at 45 DAS, number of branches at 45 DAS, number of branches at 90 DAS, node at first male and female flower, fruit length, average fruit weight, number of fruits per vine, yield per vine, fruit yield per plot, fruit yield per hectare, number of seeds per fruit, sponge yield, fruit firmness, fruit color (L^* , a^* , b^*), protein, ascorbic acid, potassium content, total flavonoids and crude fiber content. High heritability along with high GAM indicates the predominance of additive gene effects, implying that the genotypic constitution plays a significant role in the expression of characters. Therefore, simple selection could be sufficient to improve these characters. These results are in line with results of Yadav *et al.* (2016) for flavonoids; Annigeri (2020) and Som *et al.* (2020a) for number of fruits per vine and number of seeds per fruit; Ogunyemi *et al.* (2020) for potassium content; Singh *et al.* (2017), Abhijeet *et al.* (2018b), Singh *et al.* (2019c), Kumar *et al.* (2020b) and Purushottama (2022) for vine length and number of branches per vine, node at first male and female flower, fruit length, average fruit weight, yield per vine, fruit firmness and fruit color (L^* , a^* , b^*) in sponge gourd. Similar findings were also reported in ridge gourd by Saklesh (2016) for yield per plot; Harshitha *et al.* (2019a) and Swetha and Muthukumar (2016) for protein content; Karthik *et al.* (2017), Divyaraj *et al.* (2019) and Krishnamoorthy (2020a) for yield per hectare; Madhuri (2018) for ascorbic acid content and Sravani *et al.* (2021) for crude fiber content.

The high estimates of heritability (>60 %) coupled with moderate genetic advance as per cent of mean (10-20 %) was recorded for days to first male flower, days to first female flower, phenol content and total antioxidants. It is also due to additive gene action conditioning their expression. The simple phenotypic selection for their amenability can be brought about. The findings are in close proximity with the reports of Yadav *et al.* (2016) for phenol and total antioxidant content; Sharma *et al.* (2017), Singh *et al.* (2017b), Abhijeet *et al.* (2018b), Singh *et al.* (2019c), Kumar *et al.* (2020b), Som *et al.* (2020a) and Yadav (2020) for node at first male flower; Pandey *et al.* (2012b), Kumar *et al.* (2019) and Purushottama (2022) for node at first female flower in sponge gourd.

The moderate heritability (30-60 %) with moderate genetic advance as per cent of mean (10-20 %) were recorded for vine length at 90 DAS, fruit diameter, total soluble solids and ash content indicating that these characters are less influenced by environmental factors and are under the control of additive gene effects. Similar findings were also reported in ridge gourd by Swetha and Muthukumar (2016) for ash content; Varalakshmi *et al.* (2015), Kannan and Rajamanickam (2019) and Methela *et al.* (2019) for fruit diameter; Karthik *et al.* (2017) and Vijayakumar *et al.* (2020) for vine length and Krishnamoorthy (2020a) for TSS.

The character days to first harvest and days to last harvest recorded moderate heritability (30-60 %) with low genetic advance as per cent of mean (<10 %) which revealed the influence of non-additive gene action and considerable influence of environment on the expression of these traits. These results are in agreement with the reports of Pandey *et al.* (2012b) and Singh *et al.* (2017b) in sponge gourd for days to first harvest; Koppad *et al.* (2015) and Harshitha *et al.* (2019a) in ridge gourd for days to last harvest.

Prevalence of high degree of additive components like high estimates of heritability coupled with high GAM and presence of high GCV and PCV for the traits like vine length and number of branches at 45 DAS, fruit yield per vine, fruit yield per plot, fruit yield per hectare and number of seeds per fruit, indicated additive gene action hence, higher degree of genetic improvement for these traits can be achieved through selection using the existing germplasm stock.

5.3 Genetic diversity study

Information on genetic divergence among the available germplasm is of vital importance to a plant breeder for an efficient choice of parents for hybridization. It was also observed that more diverse the parents, greater are the chances of obtaining high heterotic F_1 s. Hence, there is a need to quantify the degree of divergence among available germplasm. Multivariate analysis serves as a useful tool to quantify the degree of divergence between the biological populations at genotypic level and to assess the relative contribution of different components to the total divergence both at inter and intra cluster levels. The D^2 technique of Mahalanobis based on multivariate analysis

serves to be a good index for estimating genetic diversity Mahalanobis (1936). Therefore, genetic divergence among 40 genotypes of sponge gourd was assessed by adopting Mahalanobis D^2 statistic based on 17 quantitative and qualitative characters.

5.3.1 Relative contribution of different characters towards divergence

The relative contribution of different quantitative characters towards expression of genetic divergence was calculated. Among all the characters studied, average fruit weight contributed maximum to the genetic diversity followed by fruit yield per vine, number of seeds per fruit, phenol content, sponge yield, potassium content, days to first harvest, fruit diameter, total soluble solids, number of branches per vine, ascorbic acid, days to first female flower, number of fruits per vine, node at first female flower, vine length 90 DAS, fruit length and crude fiber. Similar results were reported by Kumar *et al.* (2019), Singh *et al.* (2019b), Kumar *et al.* (2020c), (Yadav, 2020), Ray (2021) and Purushottama (2022) in sponge gourd.

5.3.2 Classification of sponge gourd genotypes

The material for present study includes 40 genotypes grouped into seven clusters using Tocher's method. Of the seven clusters studied, the cluster I had maximum number of nineteen genotypes followed by cluster II with ten genotypes, cluster III with seven genotypes while, cluster IV, cluster V, cluster VI and cluster VII were with single genotype each. These clusters were grouped irrespective of geographic divergence indicating no parallelism between geographic distribution and genetic diversity. Similar results were found by Gaffar *et al.* (2015), Abhijeet *et al.* (2018a), Kumar *et al.* (2020c) and Ray (2021) in sponge gourd. Dendrogram showing clustering pattern of sponge gourd genotypes were presented in Figure 4.

5.3.3 Intra and inter-cluster distance

The intra-cluster D^2 values ranged from 0 to 667.55. Among the clusters, cluster III had the maximum intra-cluster distance ($D^2=667.55$) followed by cluster II ($D^2=665.10$) and cluster I ($D^2=466.27$). The clusters like IV, V, VI and VII had no inter cluster distance (zero) as they were represented by single genotypes. Maximum intra-cluster distance was observed in cluster I indicating existence of wide genetic

divergence among the constituent genotypes within a cluster. High degree of divergence among the genotypes within a cluster would produce more segregating breeding material and selection within such cluster might be executed based on maximum mean value for the desirable characters. These results are in agreement with the findings of Abhijeet *et al.* (2018a), Kumar *et al.* (2019), Kumar *et al.* (2020c) and Ray (2021) in sponge gourd.

The inter cluster D^2 values ranged from 629.38 to 10081.40. Maximum inter cluster D^2 value was found between cluster IV and VI ($D^2=10081.40$) followed by cluster IV and VII ($D^2=8163.44$), cluster III and IV ($D^2=5374.53$), cluster II and cluster VI ($D^2=4944.16$), cluster II and cluster VII ($D^2=4498.17$) and cluster I and IV ($D^2=3771.80$). The minimum inter-cluster D^2 values were observed between cluster VI and VII ($D^2=629.38$) followed by cluster V and VII ($D^2=897.04$). Maximum inter-cluster D^2 values was observed between the clusters IV and VI indicating that the genotypes in these clusters can be used as a parents in hybridization programme to get higher heterotic hybrids and to create good variability in segregating population. The cluster VI had least inter-cluster distance with cluster VII indicating that close relationship and less divergence between the genotypes included in these clusters. Similar results were reported by Abhijeet *et al.* (2018a), Kumar *et al.* (2019) and (Yadav, 2020) in sponge gourd.

5.3.4 Cluster mean analysis

Highest cluster mean for vine length was observed in cluster IV (7.07 m) followed by cluster VII (6.86 m) and cluster V (6.41 m). The inter-cluster distance between cluster IV and VII ($D^2=8163.44$), cluster IV and V ($D^2=4643.08$) were high. Therefore, crosses between the genotypes belonging to these respective clusters may be tried to isolate tall viny type genotypes, which ultimately help in increasing the branches, flowers, fruit set and finally the yield as revealed by correlation studies.

The mean for number of branches per vine was highest in cluster IV (6.20) followed by cluster VII (6.10) and cluster V (5.90). The inter-cluster distance between cluster IV and VII ($D^2=10081.40$), cluster IV and V ($D^2=4643.08$) were high. Therefore, crosses can be made between the genotypes belonging to the respective clusters to

isolate genotypes with more number of branches, which ultimately helps in increasing flowers and fruit set which ultimately contributed to the total yield.

The cluster IV (42.80 days) showed lowest cluster mean for days to first female flower opening followed by cluster V (43.30 days) and cluster VII (43.50 days). The inter-cluster distance between cluster IV and V ($D^2=4643.08$), cluster IV and VII ($D^2=8163.44$) were comparatively high. Hence, hybridization between genotypes of respective clusters is advisable to improve the earliness.

The cluster IV and cluster VII (9.30) exhibited lowest cluster mean for node at first female flowering followed by cluster V (10.80) and cluster VI (11.40). The inter-cluster distance between cluster IV and VII ($D^2=8163.44$), cluster IV and V ($D^2=4643.08$), VII and V ($D^2=897.04$) were comparatively high. Hence, hybridization between genotypes of respective clusters may yield desirable results.

The lowest cluster mean for days to first fruit picking was observed in the cluster IV (51.80 days) followed by cluster VII (52.50 days) and cluster V (54.30 days). The inter-cluster distance between cluster IV and VII ($D^2=8163.44$), cluster IV and V ($D^2=4643.08$), were comparatively high. Hence, hybridization between genotypes of these respective clusters could be attempted to get early fruit yield.

The fruit length recorded highest cluster means in cluster IV (27.12 cm) followed by cluster VII (26.06 cm) and cluster V (24.65 cm). The inter-cluster distance between cluster IV and VII ($D^2=8163.44$), cluster IV and V ($D^2=4643.08$) were comparatively high. Hence, hybridization between genotypes of respective clusters can be attempted to improve fruit length that ultimately contributes towards yield.

The highest cluster mean for fruit diameter was observed in cluster IV (37.43 mm) followed by cluster VII (36.17 mm) and cluster V (35.11 mm). The inter-cluster distance between cluster IV and VII ($D^2=8163.44$), cluster IV and V ($D^2=4643.08$) were comparatively high. Therefore it would be logical to attempt crossing among the genotypes belonging to these cluster so as to evolve desirable high fruit diameter.

The character average fruit weight had highest cluster mean in cluster IV (170.25 g) followed by cluster VII (165.50 g) and cluster V (161.42 g). The inter-cluster

distance between cluster IV and VII ($D^2=8163.44$), cluster IV and V ($D^2=4643.08$) were comparatively high. Hence, crosses can be made between the genotypes of these respective clusters for improvement of average fruit weight that contributes for yield.

Cluster IV recorded highest mean (24.80) for number of fruits per vine followed by cluster VII (23.80) and cluster V (23.40). The inter-cluster distance between cluster IV and VII ($D^2=8163.44$), cluster IV and V ($D^2=4643.08$) were comparatively high. Hence, hybridization between genotypes of these respective clusters could be attempted to get more number of fruits per vine.

The cluster IV (3.85 kg) showed highest cluster mean for fruit yield per vine followed by cluster VII (3.69 kg) and cluster V (3.68 kg). The inter-cluster distance between cluster IV and VII ($D^2=8163.44$), cluster IV and V ($D^2=4643.08$) were comparatively high. Hence, crosses can be made between the genotypes of these respective clusters for improvement of total fruit yield per vine.

Number of seeds per fruit showed highest cluster means in cluster IV (338.00) followed by cluster VII (322.20) and cluster V (276.40). The inter-cluster distance between cluster IV and VII ($D^2=8163.44$), cluster IV and V ($D^2=4643.08$) were comparatively high. Hence hybridization between genotypes of respective clusters to improve number of seeds per fruit is suggested.

The highest cluster mean for sponge yield was observed in cluster IV (18.09 g) followed by cluster VII (15.91 g) and cluster V (17.84 g). The inter-cluster distance between cluster IV and VII ($D^2=8163.44$), cluster IV and V ($D^2=4643.08$) were comparatively high. Hence crosses between the genotypes of these respective clusters may be tried for the improvement of sponge yield.

The cluster I (4.95 °Brix) showed highest cluster mean for total soluble solids followed by cluster III (4.71 °Brix) and cluster II (4.66 °Brix). The inter cluster distances between I and III ($D^2=1151.48$) and I and II ($D^2=1317.70$) were comparatively high. Hence, crosses between the genotypes of these respective clusters may be tried for improvement of TSS.

The highest cluster mean for ascorbic acid content was observed in cluster II (7.46 mg) followed by cluster III (7.08 mg) and cluster I (7.07 mg). The inter cluster distances between II and III ($D^2=1732.32$) and I and II ($D^2=1317.70$) were comparatively high. Hence, crosses between the genotypes of these respective clusters may be tried for improvement of the ascorbic acid content of fruits.

Cluster I recorded highest mean (2.33 %) for potassium content followed by cluster II (2.30 %) and cluster III (2.15 %). The inter cluster distances between I and II ($D^2=1317.70$) and I and III ($D^2=1151.48$) were comparatively high. Hence, hybridization between genotypes of respective clusters can be attempted to improve potassium content of fruits.

Highest cluster mean for phenol content was noted in the cluster I (293.81 mg GAE) followed by cluster III (292.96 mg GAE) and cluster II (286.41 mg GAE). The inter cluster distances between I and III ($D^2=1151.48$) and I and II ($D^2=1317.70$) were comparatively high. Hence, crosses between the genotypes of these respective clusters may be tried for improvement of the phenol content of fruits.

The cluster I observed highest cluster mean (10.16 %) for crude fiber content, followed by cluster III (9.17 %) and cluster II (8.95 %). The inter cluster distances between I and III ($D^2=1151.48$) and I and II ($D^2=1317.70$) were comparatively high. Hence, crosses between the genotypes of these respective clusters may be tried for improvement of the crude fiber content of fruits.

The top three characters contributing most towards the genetic divergence were average fruit weight, fruit yield per vine and number of seeds per fruit. These characters may be used in selecting genetically diverse parents for hybridization programme to exploit either maximum heterosis or to execute efficient selection in the segregating generation.

Larger the divergence between the genotypes, higher will be the heterosis (Falconer, 1981). Hence, crossing between the genotypes of more divergent clusters would be helpful in getting novel recombinants with high heterosis. The genotypes G2, G22, G28, G38 (cluster I), G34, G39, G21 (cluster II), G31, G33, G36 (cluster III), G9

(cluster IV), G16 (cluster V), G37 (cluster VI), G24 (cluster VII) showed high genetic diversity giving room to improvement through hybridization between these genotypes.

5.4 Molecular characterization

Diversity studies are very important. Present work was thus, carried out to study the genetic diversity in 40 sponge gourd genotypes, so that they can be utilized effectively by breeders in selection of diverse parents for future crossing programs. SSR markers were utilized in the study considering their high polymorphism, specificity, reproducibility and high variability (Brown *et al.*, 1996). Polymorphism of simple sequence repeats (SSR) is a marker system extensively used in the assessment of genetic diversity in many plant species (Kalia *et al.*, 2011).

The number of alleles per locus (N_a) ranged from 2 to 6 with an average of 3.65. The number of effective alleles per locus (N_e) ranged from 1.34 to 3.36 with an average of 2.17. The major allele frequency ranged from 0.12 to 0.50 with a mean of 0.30. Shanon's information index (I) ranged from 0.51 to 1.31 with an average of 0.89. Fixation index ranged from -0.15 to 1.00 with a mean value of 0.62.

Markers with high PIC value are highly informative for genetic studies and are extremely useful in determining the polymorphism rate of a marker at a specific locus (DeWoody *et al.*, 1995). Current study showed PIC value ranged from 0.24 to 0.65 a mean value of 0.44. The highest PIC value found was 0.65 for SG_La_28 marker followed by the marker SG_La_11, SG_La_15 (0.61), SG_La_27 (0.59), SG_La_13 (0.56), SG_La_25 (0.51) and SG_La_8 (0.50) indicating it's most informative and suitable marker among them. The observed heterozygosity (H_o) in the total sample was 0.19, which deviated from the expected heterozygosity (H_e) (0.49). The results were permissible with the results of Saxena *et al.* (2014) in bitter melon and Bhutia *et al.* (2017) in *Luffa* species.

Unrooted neighbor joining tree was constructed using DARwin 6.0 and broadly divided 40 genotypes into three main clusters, cluster II had maximum number of twenty one genotypes followed by cluster III with fourteen genotypes, cluster I with five genotypes. It may provide the basic information to the breeders or researchers to select parent in the breeding programme or other programme as per their objective. These

results are in agreement with the findings of Kumar *et al.* (2020a) and Alhariri *et al.* (2021) in bitter gourd.

From the morphological diversity analysis it was indicated that the genotypes G2 and G22 located in cluster I, the genotypes G34, and G21 in cluster II, the genotypes G31, G33 and G36 in cluster III whereas, the genotype G9 in cluster IV, the genotype G16 in cluster V and genotype G24 VII in cluster VII. From molecular characterization it was noticed that the cluster I containing G34 and G36 genotypes, the cluster II containing G2, G22, G33, G21, G16 and G24 genotypes whereas, the genotype G31 and G9 located in cluster III. From both the study it was revealed that these ten genotypes are located in different clusters which indicated that they are genetically diverse and these genotypes are further selected for hybridization programme to exploit either maximum heterosis or to execute efficient selection in the segregating generation.

5.5 Correlation co-efficient analysis

The yield is a complex character, which is influenced by many other quantitative traits. Variability studies provide information on the extent of improvement possible in different characters, but they do not throw light on the extent and nature of relationship existing between yield and various yield contributory characters. Hence, the knowledge regarding the association of various characters among themselves and with economic characters (correlation studies) is necessary for making direct and indirect selection for improvement of economic characters. In general, genotypic correlation was higher than phenotypic correlations for most of the characters studied. This indicates that, the phenotypic expression of correlation is reduced due to the influence of environment.

In the present study, fruit yield per vine had significant and positive correlation ($p=0.05$) with number of fruits per vine, vine length, number of branches per vine, fruit length, sponge yield and average fruit weight at both genotypic and phenotypic levels. These could be used as traits of interest for indirect selection to improve fruit yield per vine in sponge gourd. Significant and positive association with fruit yield per vine with these parameters were also noticed by Patidar (2014), Kumar *et al.* (2019), Parveen *et al.* (2019), Som *et al.* (2020b) and Ray (2021) in their studies with sponge gourd.

The vine length had highly significant and positive association with number of fruits per vine, sponge yield, fruit length apart from fruit yield per vine at both phenotypic and genotypic level. The increase in vine length was facilitated in production of more number of branches and fruits per vine, which leads to increase in both fruit and sponge yield. This indicates that vine length is an important trait while selecting high yielding genotypes in sponge gourd. Similar results were also reported by Patidar (2014), Kumar *et al.* (2019) and Parveen *et al.* (2019), Som *et al.* (2020b) and Purushottama (2022) in sponge gourd.

The number of branches per vine showed significant and positive association with number of fruits per vine, fruit length and sponge yield apart from trait yield per vine at both phenotypic and genotypic level. As the increase in number of branches, there will be increased flower and fruit production and there by it increases the fruit yield per vine and sponge yield also. Similar associations between characters were revealed by Dubey *et al.* (2013), Kumar *et al.* (2013), Kumar *et al.* (2019), Yadav (2020) and Purushottama (2022) in sponge gourd.

Days to first female flower appearance had showed positive and significant correlation with average fruit weight and days to first harvest. It had a negative and highly significant correlation with number of fruits per vine and sponge yield at both genotypic and phenotypic level. This is one of the desirable trait to explore, because it denotes that early maturing plants will give higher yield because this trait is negatively correlated with number of fruits per vine which ultimately increases the fruit yield per plant. So, by selecting these plants we can improve the yield as well as earliness. These results are in accordance with the findings of Dubey *et al.* (2013) and Singh and Tiwari (2018) and Singh *et al.* (2019c) in sponge gourd.

Node at first female flower had exhibited negative and significant association with fruit yield per vine while it had positive and significant association with number of fruits per vine, potassium content and sponge yield at genotypic level only. Which indicates that the plants which produce fruits in earliest nodes will also going to give more number of fruits per vine which ultimately increases the fruit yield per plant and sponge yield. These results are in agreement with the findings of Hanumegowda *et al.* (2012) and Madhuri (2018) in ridge gourd.

Days to first fruit harvest had exhibited significant and negative association with sponge yield and number of fruits per vine at both phenotypic and genotypic level. This is one of the desirable trait to explore which indicates earliness. These results are in conformity with the results of Singh *et al.*, (2011) and Dubey *et al.* (2013) in sponge gourd; Akhila and Singh (2020) and Vinitha *et al.* (2021) in ridge gourd.

Fruit length had recorded positive and significant correlation with fruit yield per vine, number of fruits per vine and sponge yield at both phenotypic and genotypic level. The increase in fruit length leads more average fruit weight which ultimately increases the yield of fruit and sponge. These traits can be considered for simultaneously improvement of yield along with these traits. These results are in agreement with the reports of Dubey *et al.* (2013), Parveen *et al.* (2019), Som *et al.* (2020b) and Purushottama (2022) in sponge gourd. Similarly, the average fruit weight was recorded significant and positive association with fruit yield per vine at both phenotypic and genotypic level. The individual fruit weight is increases automatically yield is also increases. Sharma *et al.* (2017), Singh and Tiwari (2018), Kumar *et al.* (2019), Parveen *et al.* (2019) and Ray (2021) also observed similar results with sponge gourd.

Number of fruits per vine had exhibited positive and highly significant correlation with fruit yield per vine and sponge yield at both phenotypic and genotypic level. More number of fruits per vine leads to more yield per plant and more sponge yield which indicating that these traits were most important associates for fruit yield. These results are similar with earlier reports of Yadav *et al.* (2017), Singh and Tiwari (2018), Parveen *et al.* (2019), Annigeri (2020) and Purushottama (2022) in sponge gourd.

5.6 Path co-efficient analysis

Analysis of correlation indicates the association pattern of component traits with yield. It simply represents the general association of a particular trait with yield rather than providing cause and effect relationship. The technique of path coefficient analysis developed by Wright (1921) and demonstrated by Dewey and Lu (1959) facilitates partitioning the correlation coefficients into direct and indirect involvement of various component characters on yield. Positive direct effect of this trait on fruit yield per plant

is main cause for positive correlation of this trait with yield per plant. Hence, this trait proves to be a reliable character for improvement through selection.

Path coefficient analysis revealed that the traits like number of fruits per vine, average fruit weight, fruit length, number of branches per vine and vine length had positive direct effect on fruit yield per vine. Thus the higher magnitude of positive direct effect of these traits explains the higher value of association between these traits on yield per vine. Therefore, direct selection for these traits would reward for yield improvement in sponge gourd. Similar impact of these traits on fruit yield per plant was observed by Patidar (2014), Sharma *et al.* (2017), Kumar *et al.* (2019), Parveen *et al.* (2019), Annigeri (2020) and Purushottama (2022) in sponge gourd. Whereas, node at first female flower, days to first harvest and days to first female flower had negative direct effect (desirable) at both genotypic and phenotypic levels. Similar negative impact of these parameters was found on fruit yield per vine by Patidar (2014), Kumar *et al.* (2019) and Annigeri (2020) in sponge gourd.

The character number of fruits per vine exhibited high positive direct effect on fruit yield per vine. It also exhibited positive and indirect effects through vine length, sponge yield, number of branches per vine, fruit length, node at first female flower, TSS, potassium content, number of seeds per fruit and crude fiber content. These results are in compliance with the reports of Annigeri (2020) and Purushottama (2022) in sponge gourd.

Average fruit weight had positive direct effect on fruit yield per vine through its indirect effects of days to first harvest, days to first female flower, fruit length, node at first female flower, vine length, number of branches per vine, phenol content and crude fiber content. Similar results were reported by Annigeri (2020) and Purushottama (2022) in sponge gourd.

Fruit length showed positive direct effect on fruit yield per vine via indirect effect of vine length, number of branches per vine, number of fruits per vine, average fruit weight, node at first female flower and phenol content. These results are in accordance with the reports of Annigeri (2020) and Purushottama (2022) in sponge gourd.

The trait, number of branches per vine showed positive direct effect on fruit yield per vine via days to first harvest, days to first female flower, fruit diameter, ascorbic acid, phenol content, crude fiber content and TSS at genotypic level. The findings of Singh and Tiwari (2018) and Som *et al.* (2020b) in sponge gourd are in conformity with present findings.

The vine length had positive and direct effect on fruit yield per vine but it had indirect positive effect through days to first harvest, days to first female flower, phenol content, node at first female flower, fruit diameter, ascorbic acid and crude fiber content at genotypic level. Similar results were also reported by Singh and Tiwari (2018), Som *et al.* (2020b) and Purushottama (2022) in sponge gourd.

Days to appearance of first female flower indicated negative direct effect on fruit yield per vine through indirect effect of average fruit weight, fruit diameter and phenol content. Node at first female flower appear exhibits negative direct effect on fruit yield per vine but it also had negative and indirect effect (which is desirable) via days to first female flower and number of seeds per fruit. The character days to first fruit harvest reported to have negative direct effect on yield per vine through indirect effects of sponge yield, number of fruits per vine, number of branches per vine, vine length, TSS, number of seeds per fruit, potassium content and crude fiber content. These results are in agreement with the findings of (Patidar, 2014) and Som *et al.* (2020b).

From the performance study, the genotypes G9 (3.85 kg/vine), G24 (3.69 kg), G33 (3.67 kg) and G21 (3.65 kg) were identified as best high yielding genotypes over commercial check variety Kashi Divya (2.72 kg/vine) and is shown in the Plate 14.

5.7 Magnitude of heterosis

Heterosis is manifested by superiority of F_1 hybrids over its parents and F_1 hybrids derived from crossing of pure lines are uniform in growth and development possess better adaptability to changing and adverse environmental conditions and give early as well as higher total yield (Riggs, 1988). In practical plant breeding, superiority of the F_1 over mid parent is of little value, since, it does not offer any advantage to exploit it commercially. The commercial usefulness of the hybrid would depend on its

performance in comparison to the best existing commercial variety or hybrid. However, heterosis over better parent, the best parent and the commercial check were worked out in the present study for identification of superior hybrid but more emphasis is given only to best parent and commercial check.

The success of any breeding programme procedure is determined by useful gene combinations organised in the form of higher combining inbred and heterosis in the crosses. The line $\times$ Tester analysis is one of the techniques where, a large number of genotypes could be tested for their combining ability. It is also necessary to assess the genetic potentialities of the parents in hybrid combination through systematic studies in relation to general and specific combining abilities which are due to additive and non additive gene effects, respectively (Griffing, 1956). The line $\times$ Tester method developed by Kempthorne (1957) has been used in the present study for estimating combining ability and other genetic parameters.

There was highly significant difference among genotypes for all the growth, earliness, yield and quality parameters under study. Genetic diversity among parents can ensure higher magnitude of heterosis and mean sum of squares of genotypes were found to be highly significant for all studied traits, this provides evidence for presence of considerable amount of genetic variation among the genotypes. These results are in same line with those obtained by Naliyadhara *et al.* (2010), Sonavane *et al.* (2013b) and Kumar and Pandit (2019) in sponge gourd.

Heterosis for growth parameters is an indication of heterosis for yield as the growth and yield parameters are strongly associated which was also reported previously by Singh *et al.* (2011). Significant and high magnitude of heterosis over better parent, the best parent and the commercial check were observed in the desirable direction for vine length at 45 and 90 DAS, and number of branches at 45 and 90 DAS. Heterosis over better parent and the commercial check was also reported by Chauhan *et al.* (2018) and Kumar and Pandit (2019) in sponge gourd for vine length and number of branches.

Farmers prefer to grow early and high yielding hybrids in order to catch early market to get higher prices and to avoid market glut therefore earliness is an important trait in vegetables like sponge gourd. Days to first male and female flowering, node to first male and female flowering and days to first harvest are indicators of earliness. The

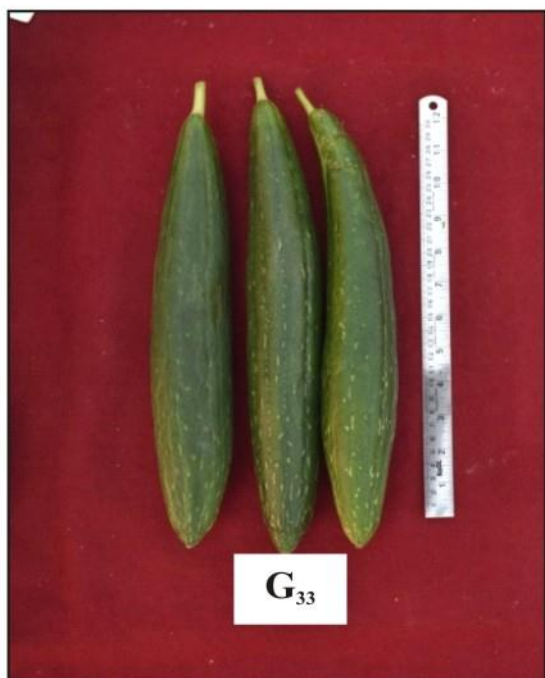


Plate 14. Top four high yielding genotypes of sponge gourd

negative heterosis for these traits are desirable. For all these traits, significant variability was observed among the genotypes and significant negative heterosis was also observed.

Among 40 crosses, 22 crosses over the better parent and 11 crosses over best parent and 15 crosses over commercial check exhibited negative and significant heterosis for days to first male flowering. Similar frequency of heterobeltosis and standard heterosis for days to first male flowering were reported by Sonavane *et al.* (2013b), Singh and Singh (2018) and Kumar and Pandit (2019) in sponge gourd.

For days to first female flowering, 22 crosses over better parent, 13 crosses over best parent and 17 crosses over commercial check exhibited negative and significant heterosis. The maximum and significant negative heterosis over better parent (-20.75 %), best parent (-20.75 %) and the commercial check (-21.13 %) was observed in the cross L2 × T1. This hybrid (L2 × T1) took least number of days (33.60) for days to first female flower appearance among all the crosses. Heterosis with reference to days to female flower appearance was also reported by Kumar and Pandit (2019) in sponge gourd, Bairwa *et al.* (2017) and Varalakshmi *et al.* (2019) in ridge gourd.

For node at first male flower, 18 crosses over better parent, seven crosses over best parent and as many as 28 crosses over commercial check exhibited significant heterosis in desirable direction. The maximum and significant negative heterosis over better parent and commercial check were observed in the cross L2 × T1 and L6 × T1 (-21.05 %). Similar results were observed by Chauhan *et al.* (2018) in sponge gourd; Narasannavar *et al.* (2014a) and Muthaiah *et al.* (2017a) in ridge gourd. Position of node which has first male flower is considered as index of earliness.

For node at first female flower, 12 crosses over better parent, nine crosses over best parent and as many as 21 crosses over commercial check exhibited negative (desirable) and significant heterosis. The maximum and significant negative heterosis over the better parent was observed in the cross L5 × T1 (-20.00 %). However, the cross L2 × T1 exhibited the significant and negative heterosis over the best parent (-7.61 %) and commercial check (-26.72 %). Similar results were also reported by Chauhan *et al.* (2018), Kumar and Pandit (2019) and Lakhnotra *et al.* (2019) in sponge gourd.

For days to first harvest, among 40 crosses, 23 crosses over better parent, 21 crosses over best parent and 11 crosses over commercial check exhibited significant negative heterosis in the desirable (negative) direction, which was observed in the cross $L2 \times T1$ over (-21.71 %), best parent (-21.71 %) and commercial check (-18.88 %). Significant and negative heterosis was also reported by Sonavane *et al.* (2013b), Singh and Singh (2018) in sponge gourd and Bhalerao *et al.* (2022) in ridge gourd. For days to last harvest, two crosses each over better parent and best parent and 14 crosses over commercial check exhibited significant positive heterosis and significant positive heterosis was observed in the crosses $L8 \times T3$ and $L9 \times T3$ over better parent (7.41 %) and maximum positive heterosis over best parent (7.41 %) and over commercial check (15.79 %) was observed in the cross $L9 \times T3$. These results are in agreement with the findings of Naliyadhara *et al.* (2007) and Reddy *et al.* (2019b) in sponge gourd.

Ultimate goal of the plant breeder is to develop high yielding varieties or hybrids. The yield components greatly influence yield and higher magnitude of heterosis was observed for the yield components in the present investigation. Number of fruiting branches per vine, number of fruits per vine and average fruit weight can greatly contribute for heterosis observed for total fruit yield per vine are very closely related to productivity parameters. For all these traits positive heterosis is desirable. For fruit length, 10 crosses over better parent, five crosses over best parent and 26 crosses over commercial check recorded positive and significant heterosis. The cross $L6 \times T1$ showed maximum and positive significant heterosis over better parent (13.56 %), whereas, the cross $L2 \times T1$ showed maximum positive significant heterosis over best parent (10.83 %) and over commercial check (40.62 %) and is same as reported by Kumar and Pandit (2019), Singh and Singh (2018) and Bhardwaj and Kumar (2021) in sponge gourd in their studies.

For fruit diameter, eight crosses over better parent, only three crosses over the best parent and 26 crosses over the commercial check exhibited positive and significant heterosis. The cross $L6 \times T1$ showed maximum heterosis of 18.99 % over better parent and cross $L2 \times T1$ exhibited maximum and positive heterosis over best parent (17.59 %) and commercial check (42.83 %). Lodam *et al.* (2014), Narasannavar *et al.* (2014a) and Jadav and Sapovadiya (2018) in ridge gourd reported the same results.

Among 40 crosses, nine crosses over better parent, four crosses over best parent and twelve crosses over commercial check manifested positive and significant heterosis for average fruit weight. The cross L5 $\times$ T3 exhibited maximum heterosis of 13.57 % over better parent and L2 $\times$ T1 showed maximum and significant heterosis over best parent (12.02 %) and commercial check (20.11 %) and is same as reported by Chauhan *et al.* (2018), Singh and Singh (2018) and Lakhotra *et al.* (2019) in sponge gourd.

For number of fruits per vine, 24 crosses over better parent, 19 crosses over best parent and 26 crosses over the commercial check exhibited positive and significant heterosis. The maximum and positively significant heterosis (34.75 %) was observed in the crosses L6 $\times$ T1 over better parent. The cross L2 $\times$ T1 exhibited positive and significant heterosis over the best parent (31.71 %) and commercial check (43.36 %). Earlier findings, significant and positive heterosis was observed by Rajneesh and Singh (2018), Kumar and Pandit (2019) and Reddy *et al.* (2019a) in sponge gourd. The variation is because of the different genetic stocks being used in the present study.

For fruit yield per vine out of 40 crosses, 24 crosses over better parent, 18 crosses over the best parent and 23 crosses over commercial check showed positive and significant heterosis. The maximum and positively significant heterosis over better parent exhibited by L6 $\times$ T1 (60.99 %) followed by the crosses L2 $\times$ T1 (57.18 %) and L2 $\times$ T3 (53.19 %). The cross L2 $\times$ T1 (57.18 %) followed by L6 $\times$ T1 (55.85 %) and L2 $\times$ T2 (53.19 %) crosses exhibited positive and significant heterosis over the best parent and the crosses L2 $\times$ T1 (67.90 %) followed by L6 $\times$ T1 (66.48 %) and L2 $\times$ T2 (63.64 %) also showed significant positive heterosis over the commercial check. These results were in agreement with the findings of Lodam *et al.* (2014) Poshia *et al.* (2015), Wakale *et al.* (2018) and Srikanth *et al.* (2020a) in ridge gourd.

Out of 40 crosses, 21 crosses over better parent, 13 crosses over the best parent and 22 crosses over the commercial check manifested positive and significant heterosis for the character fruit yield per plot. Maximum and significantly positive heterosis over the best parent was showed in the cross L2 $\times$ T1 (54.77 %) followed by L6 $\times$ T1 (54.19 %) and L2 $\times$ T2 (51.87 %), whereas maximum positive and significant heterosis over the commercial check was exhibited by the cross L2 $\times$ T1 (65.24 %) followed by

L6 $\times$ T1 (64.63 %) and L2 $\times$ T2 (62.15 %). These studies were similar with findings of Narasannavar *et al.* (2014a) and Prakash *et al.* (2015) in ridge gourd.

For fruit yield per hectare, 22 crosses over better parent, 12 crosses over the best parent and 20 crosses over the commercial check showed positive and significant heterosis. The maximum and positively significant heterosis over better parent was recorded in the cross L2 $\times$ T1 (49.50 %) followed by L6 $\times$ T1 (48.13 %) and L2 $\times$ T2 (42.01 %) and Maximum and significantly positive heterosis over the best parent was showed in the cross L2 $\times$ T1 (49.50 %) followed by L6 $\times$ T1 (48.13 %) and L2 $\times$ T2 (42.01 %), whereas for heterosis over the commercial check, the cross L2 $\times$ T1 (66.18 %) followed by L6 $\times$ T1 (64.64 %) and L2 $\times$ T2 (57.84 %) and is comparable with that reports by Wakale *et al.* (2018) and Varalakshmi *et al.* (2019) in ridge gourd.

Thirteen crosses exhibited significant standard heterosis in desirable direction and maximum was observed in the cross L8 $\times$ T2 (40.58 %) for number of seeds per fruit. Magnitude of heterosis is comparable with the findings of Kumar and Pandit (2019) and Lakhotra *et al.* (2019) in sponge gourd. Out of 40 crosses for sponge yield, six crosses over better parent, only two crosses over best parent and 19 crosses over commercial check showed positive and significant heterosis. Maximum and positively significant heterosis was observed in the cross L1 $\times$ T1 over better parent (16.13 %) whereas, the cross L2 $\times$ T1 exhibited maximum heterosis over best parent (10.20 %) and commercial check (43.44 %).

For total soluble solids, 13 crosses over better parent, four crosses over best parent and 19 crosses over commercial check had exhibited positive and significant heterosis. Maximum positive and significant heterosis over better parent was observed in the cross L10 $\times$ T3 (53.95 %). Whereas, the cross L7 $\times$ T3 exhibited maximum and positive significant heterosis over best parent (22.58 %) and commercial check (38.35 %). These results are in same line with those obtained by Srikanth *et al.* (2020a) in ridge gourd. For fruit firmness only seven crosses over better parent, six crosses over best parent and as many as 18 crosses over the commercial check manifested significant positive heterosis. The cross L6 $\times$ T1 recorded maximum positive and significant heterosis over the better parent (21.18 %), best parent (19.47 %) and commercial check (47.23 %). These results are in line with findings of Khot (2017) in bottle gourd.

For protein content, 32 crosses over better parent, 28 crosses over the best parent and 28 crosses over the commercial check has exhibited positive and significant heterosis. The maximum positive heterosis over better parent (54.80 %) was observed in the cross L8 $\times$ T3. Whereas, the cross L5 $\times$ T1 exhibited maximum positive heterosis over best parent (25.86 %) and over the commercial check (27.83 %). These values are low as compared with the reports of Parmar and Mamatapathak (2018) in ash gourd gourd.

For ascorbic acid content, 27 crosses over better parent, 26 crosses over best parent and 19 crosses over commercial check exhibited positive and significant heterosis. Maximum positive and significant heterosis over better parent was observed in the cross L8 $\times$ T3 (54.80 %). However, maximum positive and significant heterosis over best parent (44.41 %) and commercial check (35.45 %) was observed in the cross L9 $\times$ T4. These values are high as compared with the reports of Srikanth *et al.* (2020) in ridge gourd.

For, potassium content of fruits, 36 crosses over better parent, 33 crosses over best parent and 29 crosses over commercial check exhibited positive and significant heterosis. Maximum positive and significant heterosis over better parent (65.56 %), best parent (45.35 %) and commercial check (37.36 %) was observed in the cross L10 $\times$ T3. This is high as compared to reports of Singh *et al.* (2017a) in ridge gourd. For phenol content of fruits, 14 crosses over better parent, three crosses over best parent and six crosses over commercial check had reported maximum and positive significant heterosis. The cross L7 $\times$ T2 over better parent (10.66 %) and the cross L1 $\times$ T4 over best parent (7.93 %) and commercial check (11.72 %) showed maximum and positive significant heterosis. These results are in agreement with the findings of Yadav *et al.* (2016) in sponge gourd.

For antioxidant content of fruits, 11 crosses over better parent, three crosses over best parent and 18 crosses over commercial check recorded positive and significant heterosis. The cross L5 $\times$ T2 showed maximum and positive significant heterosis over better parent (5.83 %) and the cross L3 $\times$ T2 over best parent (5.37 %) and over commercial check (11.08 %) exhibited maximum positive significant heterosis. Similar results were noticed by Hosen *et al.* (2022) in pumpkin for antioxidants. Whereas, for

flavonoid content of fruits, maximum positive and significant heterosis over better parent was observed in the cross L10 $\times$ T3 (42.68 %). While, maximum positive and significant heterosis over best parent (25.47 %) and commercial check (29.04 %) was observed in the cross L3 $\times$ T2. Out of 40 crosses, 28 crosses over better parent, 23 crosses over best parent and 24 crosses over commercial check exhibited positive and significant heterosis for flavonoids. Similar results were obtained by Yadav *et al.* (2016) in sponge gourd.

Among the crosses, 30 crosses over better parent, 30 crosses over the best parent and 29 crosses over the commercial check was exhibited the positive and significant heterosis for crude fiber content of fruits. The maximum positive heterosis over better parent (49.59 %), over best parent (49.59 %) and over the commercial check (46.01 %) was observed in the cross L5 $\times$ T1. Which is high as compared to reports of Srikanth *et al.* (2020a) in ridge gourd. For ash content of fruits, 30 crosses over better parent, 27 crosses over best parent and 20 crosses over commercial check had shown positive and significant heterosis. Maximum positive and significant heterosis over best parent (37.95 %), better parent (37.95 %) and commercial check (30.24 %) was observed in the cross L9 $\times$ T4. Similar results were also made by Parmar and Mamatapathak (2018) in ash gourd.

5.8 Combining ability effects and variances

Exploitation of the heterosis needs, the information on gca effects should be supplemented with sca effects and hybrid performance. Heterosis in F_1 's indicates operation of non-additive gene effects, but it cannot give any idea about the relative magnitude of non-additive (dominance + epistasis) and additive gene action. Hence, analysis of combining ability is one of the important tools for identifying prospective parents to develop commercial F_1 hybrids (Griffing, 1956). General combining ability and specific combining effects and variances obtained from a set of F_1 's would enable a breeder to select desirable parents and crosses for each of quantitative and qualitative components. General combining ability effects of parents and sca effects of crosses were highly significant for the characters studied.

Among the ten lines, L2 exhibited significant and maximum gca effects for vine length at 45 and 90 DAS, number of branches at 45 and 90 DAS, fruit length, fruit diameter, average fruit weight, number of fruits per vine, fruit yield per vine, fruit yield per plot, fruit yield per hectare and sponge yield. Similar results were also made by Naliyadhara *et al.* (2010), Kumar *et al.* (2018), Chauhan *et al.* (2019), Kumar and Pandit (2020) for vine length at 45 and 90 DAS, number of branches at 45 and 90 DAS, fruit length, fruit diameter, average fruit weight, number of fruits per vine and fruit yield per vine in sponge gourd. Narasannavar *et al.* (2014b) and Malve *et al.* (2020) in ridge gourd for fruit yield per plot and fruit yield per hectare. The L2 exhibited maximum and significant gca effects for days to first male flower, days to first female flower, node at first female flower and days to first harvest in desirable (negative) direction. Significant gca effects was also reported by Kumar *et al.* (2018) and Rajneesh and Singh (2018b) in sponge gourd.

Among the lines tested, L3 reported maximum and significant gca effects for antioxidants and flavonoids and node at first male flower appearance in desirable direction. Significant gca effects were also reported by Yadav *et al.* (2016) for flavonoids in sponge gourd; Kumar *et al.* (2018), Rajneesh and Singh (2018b) and Chauhan *et al.* (2019) for node at first male flower appearance in sponge gourd and Hosen *et al.* (2022) for anti-oxidants in pumpkin. The line L5 showed maximum and significant gca effects for protein content and crude fiber content. Significant gca effects was also reported by Parmar and Mamatapathak (2018) for protein content in ash gourd gourd, Chandan *et al.* (2019) and Srikanth *et al.* (2020b) for crude fiber content of fruits in ridge gourd.

The line L7 reported maximum and significant gca effects for TSS and fruit firmness. Significant gca effects for TSS was also reported by Reddy *et al.* (2018) in sponge gourd and for fruit firmness by Khot (2017) in bottle gourd. The line L8 showed maximum and significant gca effects for days to last harvest, number of seeds per fruit and fruit color (a*). Naliyadhara *et al.* (2010) for days to last harvest and Kumar and Pandit (2020) for number of seeds per vine were also noticed significant gca effects in sponge gourd.

The maximum and significant gca effects for fruit color (a^*), phenol and ash content of fruits was recorded in L9 line. Whereas, the line L10 had maximum and significant gca effects for fruit color (L^*), ascorbic acid content and potassium content. Similar results were also reported by Chittora *et al.* (2018a), Chandan *et al.* (2019) and Srikanth *et al.* (2020b) in ridge gourd for ascorbic acid content.

Among the testers, T1 exhibited maximum and significant gca effects for for vine length 45 DAS, number of branches at 45 and 90 DAS, fruit diameter, average fruit weight. Similar results were also made by Kumar *et al.* (2018), Chauhan *et al.* (2019) and Kumar and Pandit (2020) in sponge gourd. The tester T1 also exhibited maximum and significant gca effects for node at first male and female flower appearance and days to first harvest in desirable direction. Rajneesh and Singh (2018b) were also noticed such results in sponge gourd.

Whereas, tester T2 exhibited significant gca effects for fruit length, number of fruits per vine, fruit yield per vine, fruit yield plot, fruit yield per hectare, sponge yield and flavonoid content of fruits. Significant gca effects for these characters were also reported by Sonavane *et al.* (2013a), Rajneesh and Singh (2018b) and Chauhan *et al.* (2019) in sponge gourd for fruit length, number of fruits per vine, fruit yield per vine, Malve *et al.* (2020) in ridge gourd for fruit yield per plot and fruit yield per hectare.

The tester, T3 exhibited positive significant gca effects for vine length at 90 DAS, TSS, fruit firmness, ascorbic acid, potassium, phenol, crude fiber and ash content of fruits. Similar results were reported by Parmar and Mamatapathak (2018) in ash gourd gourd for protein and ash content, Reddy *et al.* (2018) in sponge gourd for TSS, Chauhan *et al.* (2019) for vine length, ascorbic acid and crude fiber content. T4 exhibited positive significant gca effects for days to last harvest, number of seeds per fruit, fruit firmness, fruit color (L^* and b^*) and total antioxidants. Significant gca effects was also noticed by Naliyadhara *et al.* (2010) for days to last harvest and Kumar and Pandit (2020) for number of seeds per fruit in sponge gourd, Hosen *et al.* (2022) in pumpkin for antioxidants.

The exploitation of heterosis needs the information of gca with sca and hybrid performance. Estimation of sca effects for 40 crosses has resulted in identification of good specific combiners for various traits. Among crosses, the cross L10 $\times$ T1 showed

maximum and significant sca effects for vine length and number of branches at 45 DAS. Whereas, the cross L2 $\times$ T1 exhibited significant sca effects for vine length and number of branches at 90 DAS. Similar observations were also noticed by Naliyadhara *et al.* (2010), Sonavane *et al.* (2013a), Kumar *et al.* (2018), Singh *et al.* (2018a) and Chauhan *et al.* (2019) in sponge gourd.

The cross L9 $\times$ T1 exhibited significant sca effects for days to first male and female flower, node at first female flower and days to first harvest. Rajneesh and Singh (2018b), Singh *et al.* (2018a) and Chauhan *et al.* (2020) also reported significant sca effects for those parameters in sponge gourd. While the cross L8 $\times$ T3 showed significant sca effects for node at first male flower and number of fruits per vine. Similar results were also found by Singh *et al.* (2018b) for node at first male flower and Chauhan *et al.* (2020) for number of fruits per vine in sponge gourd.

Among the total 40 crosses, L9 $\times$ T3 exhibited significant sca effects for days to last harvest and fruit length. Similar significant results were also noticed by Naliyadhara *et al.* (2010) for days to last harvest, Sonavane *et al.* (2013a), Kumar *et al.* (2018), Rajneesh and Singh (2018b) and Chauhan *et al.* (2020) for fruit length in their studies. The cross L7 $\times$ T3 exhibited significant sca effects for fruit diameter, average fruit weight, which is in line with findings of Rajneesh and Singh (2018b) and Chauhan *et al.* (2019) in sponge gourd.

The cross L6 $\times$ T1 exhibited significant sca effects for fruit yield per vine, fruit yield per plot, fruit yield per hectare and number of seeds per fruit. Similar results were obtained by Sonavane *et al.* (2013a) and Chauhan *et al.* (2019) for fruit yield per vine and Kumar and Pandit (2020) for number of seeds per vine in sponge gourd. Similarly, Malve *et al.* (2020) for fruit yield per plot and fruit yield per hectare in ridge gourd.

In the present experiment, the significant sca effects for sponge yield was observed in the cross L3 $\times$ T4. While, the cross L2 $\times$ T3 for fruit firmness, L9 $\times$ T2 fruit color (L*), L5 $\times$ T3 fruit color (b*) and the cross L10 $\times$ T3 exhibited significant sca effects for TSS. Similar results were reported by Reddy *et al.* (2018) for TSS in sponge gourd. Similarly, the cross, L9 $\times$ T2 exhibited significant sca effects for protein content, L4 $\times$ T1 for ascorbic acid content, L7 $\times$ T1 for fruit color (a*), total antioxidants and flavonoid content and the cross L6 $\times$ T3 for phenol content. Such significant sca effects

were also reported by Parmar and Mamatapathak (2018) in ash gourd for protein content, Chandan *et al.* (2019) and Srikanth *et al.* (2020b) in ridge gourd for ascorbic acid content and Hosen *et al.* (2022) in pumpkin for antioxidants in their studies.

The crosses, L7 $\times$ T1 and L10 $\times$ T3 were exhibited significant sca effects for potassium content while, the cross L5 $\times$ T1 for crude fiber content. Similar observations were also noticed by Nandhini *et al.* (2018b), Chandan *et al.* (2019) and Srikanth *et al.* (2020b) in ridge gourd for crude fiber content of fruits. Similarly, the cross L4 $\times$ T3 exhibited significant sca effects for ash content in this study. These results are in accordance with the results of Parmar and Mamatapathak (2018) in ash gourd.

An assessment was carried out by selection of best parents and hybrids by considering all the combining ability characters related to yield and other economic traits. For every character, a parent was scored '0' for non-significant gca effects and the value '1' for significant gca effects in the desirable direction and '-1' for significant gca effects in undesirable direction. Similarly, for every character, a hybrid was scored '0' for non-significant standard heterosis '1' for significant standard heterosis in desirable direction and '-1' for standard heterosis in undesirable direction. All the parents and crosses were scored for each character and final score was computed by adding scores obtained in 32 characters. Finally, the parents or hybrids were classified as low, average and high based on the mean value of the total scores obtained over all the 32 characters and details are presented in the Table 58 for parents and Table 59 for F₁ hybrids.

The comprehensive assessment of parents by considering gca effects of 32 characters studied in this experiment resulted into identification of lines, viz., L1, L2 and L6 as good combiners for over all characters. Whereas, the remaining lines (L3, L4, L5, L7, L8, L9 and L10) were identified as poor combiners for all the characters. Among the testers, T1 and T2 were identified as good general combiner. Whereas, T3 and T4 testers were identified as poor combiner for all the characters.

The heterosis values of 32 characters in 40 crosses revealed, 18 crosses were highly heterotic, two crosses were average heterotic and remaining 20 crosses were low heterotic. Out of 18 heterotic crosses, nine crosses involved high $\times$ high parental

combinations, two crosses involved high X low parental combinations and seven crosses involved low X low parental combinations for over all gca status. These results indicated that high frequency of highly heterotic hybrids could be obtained from parental combinations with high x low or low x high general combining ability which clearly indicates that, the parental contribution to the heterosis is mainly through non additive gene effects. Hence, exploitation of heterosis appears to be an appropriate strategy for improvement in sponge gourd using this gene pool. These crosses can also be improved through recurrent selection.

Ratio of general combining ability variances (GCA) to specific combining ability variances (SCA) is an indication of predominance of additive or non additive genetic variance. Ratio GCA to SCA was high for node at first male flower (0.634). Ratio of GCA to SCA was low for ascorbic acid content (0.586), crude fiber (0.565), total flavonoids (0.558), fruit diameter (0.546), total soluble solids (0.545), days to first harvest (0.495), fruit length (0.495), days to first male flower (0.459), days to first female flower (0.440), vine length at 90 DAS (0.424), number of branches at 90 DAS (0.415), number of branches at 45 DAS (0.380), sponge yield (0.372), fruit yield per vine (0.361), fruit yield per plot (0.360), days to last harvest (0.357), vine length at 45 DAS (0.348), number of seeds per fruit (0.342), fruit yield per hectare (0.333), node at first female flower (0.281), potassium content (0.233), number of fruits per vine (0.223), average fruit weight (0.205), ash content (0.205), total antioxidants (0.160), fruit firmness (0.123), fruit color (L*) (0.120) and fruit color (a*) (0.118), fruit color (b*) (0.083), phenol content (0.069) and protein content (0.059). It indicates that there is greater involvement of non additive gene action in the inheritance of all the studied parameters in this study. Hence, these traits can be improved through recurrent selection or heterosis breeding.

From ongoing discussion it was concluded that the cross L2 × T1 (Plate 15a) was the best hybrid selected for fruit yield per hectare (27.12 t/ha) with 66.18 per cent standard heterosis. High magnitude of heterosis observed in this hybrid for fruit yield per hectare is attributed by significant heterosis observed over the commercial check in desirable direction for vine length at 45 and 90 DAS, number of branches at 45 and 90 DAS, days to first male and female flower appearance, node at first male and female

flower appearance, days to first harvest, fruit length, fruit diameter, average fruit weight, number of fruits per vine, fruit yield per vine, fruit yield per plot and sponge yield. This hybrid also showed specific combiner for vine length at 45 and 90 DAS, days to first female flower appearance, fruit length, fruit diameter and sponge yield. The line L2 which was involved in the development of this hybrid was identified as good general combiner for vine length at 45 and 90 DAS, number of branches at 45 and 90 DAS, days to first male and female flower appearance, node at first male and female flower appearance, days to first harvest, fruit length, fruit diameter, average fruit weight, number of fruits per vine, fruit yield per vine, fruit yield per plot, fruit yield per hectare and sponge yield. In other hand another parent T1 was a good combiner for vine length at 45 DAS, number of branches at 45 and 90 DAS, number of branches at 45 and 90 DAS, node at first male and female flower, days to first harvest, fruit diameter, average fruit weight, fruit yield per vine, fruit yield per plot and fruit yield per hectare. The cross $L2 \times T1$ was found to be moderately resistant to fruit fly attack, moderate leaf mining intensity, showed moderately resistant to downy mildew and powdery mildew incidence.

The second best hybrid $L6 \times T1$ (Plate 15b) was selected based on fruit yield per hectare which had total yield of 26.87 t/ha with 64.64 per cent standard heterosis. Hybrid performance is attributed by significant standard heterosis observed in the desirable direction for vine length at 45 and 90 DAS, number of branches at 45 and 90 DAS, days to first male and female flower, node at first male and female flower, days to first harvest, fruit length, fruit diameter, average fruit weight, number of fruits per vine, fruit yield per vine, fruit yield per plot, sponge yield, fruit firmness, number of seeds, TSS, fruit color (a^* and b^*), protein, ascorbic acid, potassium content, total antioxidants, flavonoids and ash content. This hybrid $L6 \times T1$ also exhibited desirable significant sca effects for vine length at 45 and 90 DAS, days to first male and female flower appearance, days to first harvest, fruit length, fruit diameter, average fruit weight, number of fruits per vine, fruit yield per vine, fruit yield per plot, fruit yield per hectare, number of seeds per fruit, sponge yield, TSS, total antioxidants and ash content. Among two parents involved in the development of this hybrid, the parent L6 was good combiner for vine length at 45 and 90 DAS, number of branches at 45 and 90 DAS, days to first male and female flower appearance, node at first male and female flower

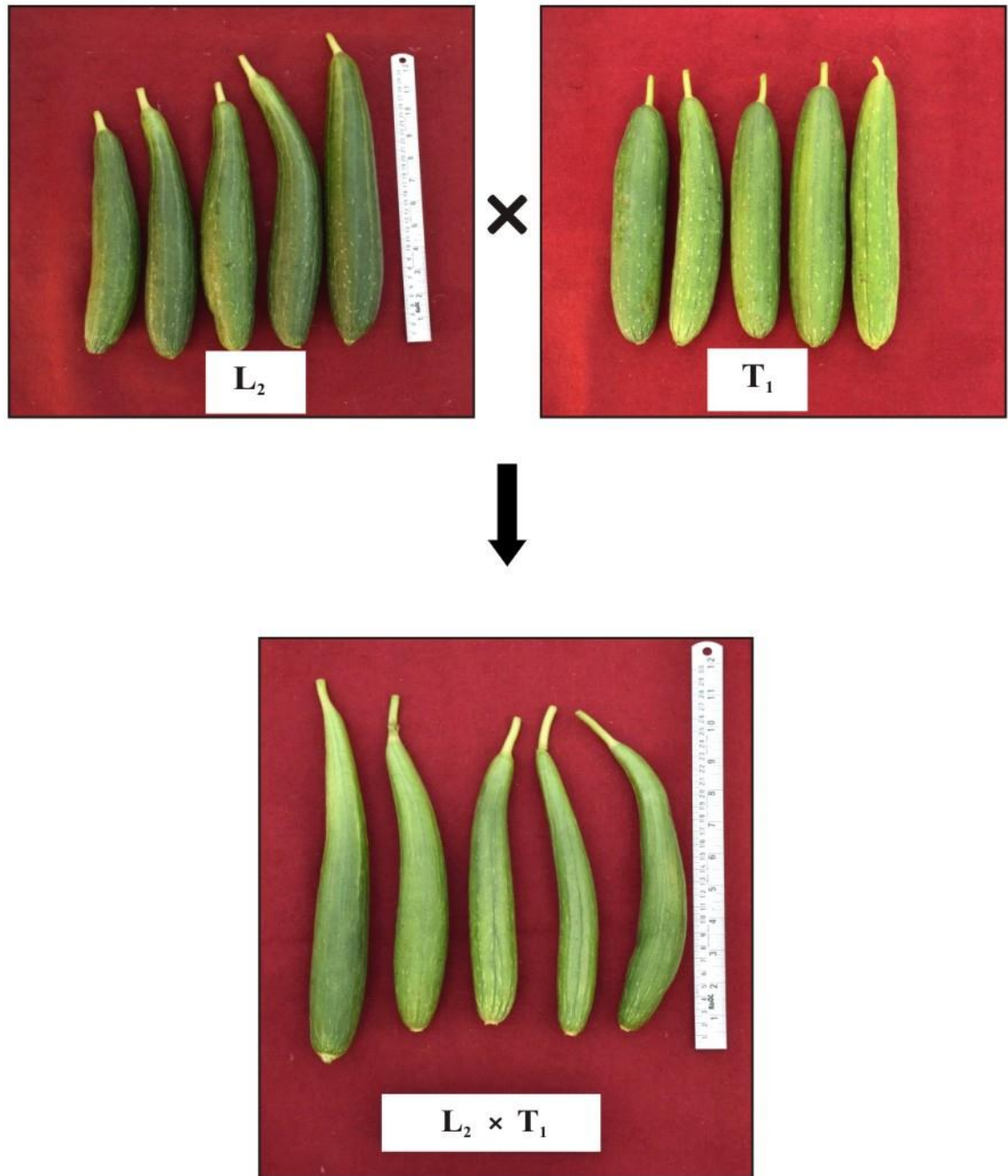


Plate 15a. Fruits of top hybrid ($L_2 \times T_1$) identified for yield

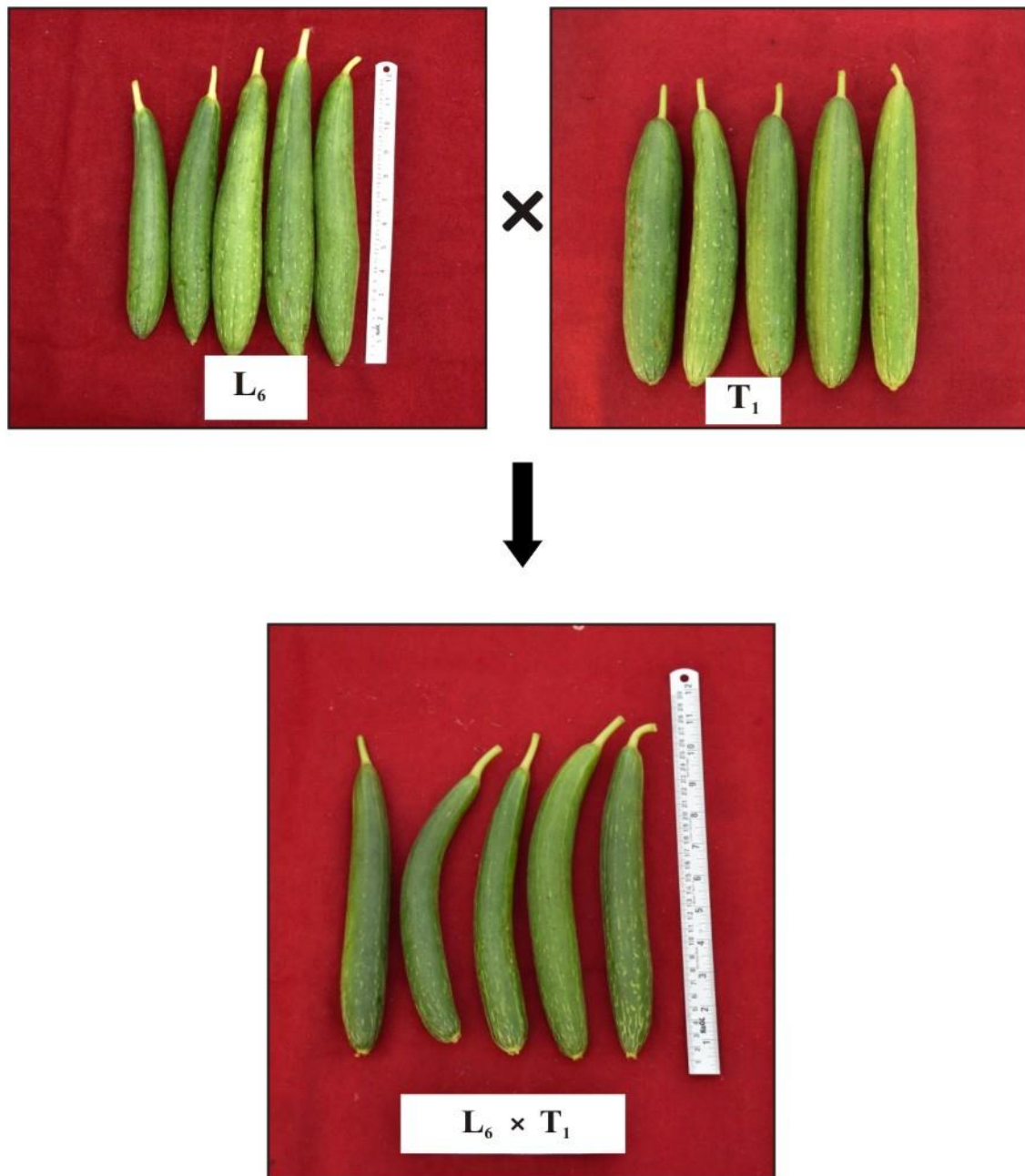


Plate 15b. Fruits of top hybrid ($L_6 \times T_1$) identified for yield

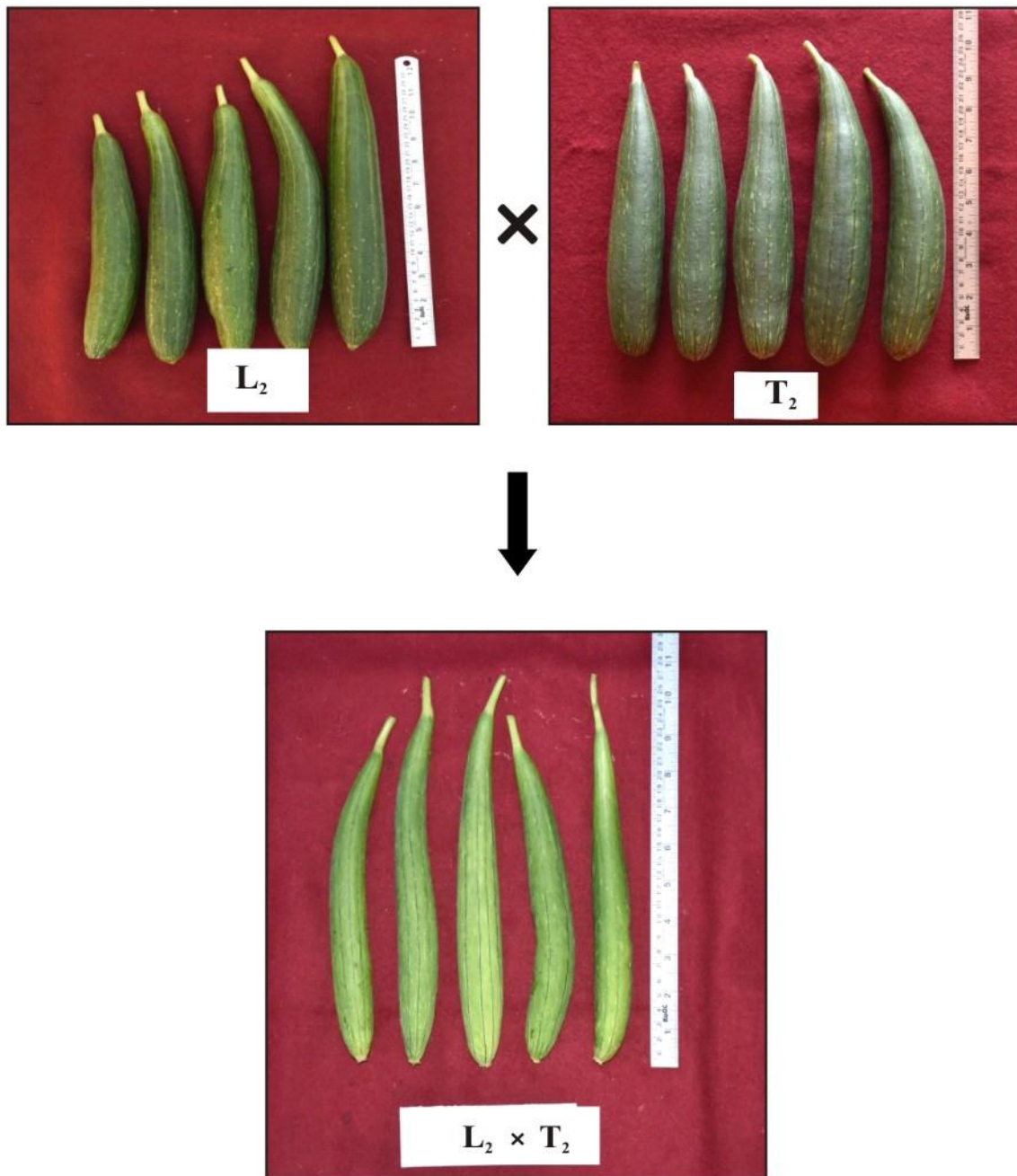


Plate 15c. Fruits of top hybrid ($L_2 \times T_2$) identified for yield

appearance, days to first harvest, fruit length, fruit diameter, average fruit weight, number of fruits per vine, fruit yield per vine, fruit yield per plot, fruit yield per hectare, sponge yield, fruit color (L^*), protein content, total antioxidants and total flavonoids. Another parent T1 was good general combiner for vine length at 45 DAS, number of branches at 45 and 90 DAS, number of branches at 45 and 90 DAS, node at first male and female flower, days to first harvest, fruit diameter, average fruit weight, fruit yield per vine, fruit yield per plot and fruit yield per hectare. The cross $L6 \times T1$ was found to be moderately resistant to fruit fly attack, leaf mining intensity, downy mildew and powdery mildew incidence.

The next best hybrid selected was $L2 \times T2$ (Plate 15c) and it exhibited 57.84 per cent standard heterosis for fruit yield per hectare which also had yielding ability of 25.76 t/ha. Good performance of this hybrid with respect to total yield is attributed by significant standard heterosis was observed in the desirable directions for vine length at 45 and 90 DAS, number of branches at 45 and 90 DAS, days to first male and female flower appearance, node at first male and female flower appearance, days to first harvest, fruit length, fruit diameter, average fruit weight, number of fruits per vine, fruit yield per vine, fruit yield per plot, number of seeds per fruit, sponge yield, TSS, fruit firmness, ascorbic acid content, potassium content, total antioxidants and total flavonoids. This hybrid $L2 \times T2$ also exhibited significant sca effects for node at first male and female flower, fruit diameter, average fruit weight, number of fruits per vine, fruit yield per vine, fruit yield per plot, number of seeds per fruit, TSS and total antioxidants. Whereas, the line L2 which was involved in the development of this hybrid was identified as good general combiner for vine length at 45 and 90 DAS, number of branches at 45 and 90 DAS, days to first male and female flower, node at first male and female flower, days to first harvest, fruit length, fruit diameter, average fruit weight, number of fruits per vine, fruit yield per vine, fruit yield per plot, fruit yield per hectare and sponge yield. The second parent (T2) involved in the development of this hybrid was good general combiner for fruit length, fruit diameter, number of fruits per vine, fruit yield per vine, fruit yield per plot, fruit yield per hectare, sponge yield and total flavonoids. The cross $L2 \times T2$ was found to be moderately resistant to fruit fly attack, leaf mining intensity, downy mildew and powdery mildew incidence.

Future line of work

1. From the performance study, the genotypes G9, G24, G33 and G21 were identified as best high yielding genotypes over commercial check variety Kashi Divya and these lines stability can be further assessed to develop as a variety.
2. The developed microsatellite markers in this study can be further utilized in cultivar identification, mapping and marker assisted selection programme.
3. The most of the characters under this study was predominantly governed by non-additive gene action (based on heritability + GAM estimates). Hence, heterosis breeding or recurrent selection can be employed for further improvement of these characters.
4. The parents L2, L3 and L6 are the good general combiners for fruit yield per vine, fruit yield per plot and fruit yield per hectare. These can be used for identifying superior heterotic combinations. However, the parents L1, L2, L6, T1 and T2 also shows good general combining ability for many characters and these can also be subjected to recurrent selection for improvement of genetic stock.
5. The crosses $L2 \times T1$, $L6 \times T1$ and $L2 \times T2$ were identified as superior hybrids based on yield, significant heterosis over commercial check (Kashi Rakshita) and also significant positive sca effects for fruit yield and other characters. Therefore, these crosses can be further assessed for their yield stability and may be exploited on commercial scale.

Table 60. Over all analysis of general combining ability status of parents in sponge gourd

Sl. No.	Parents	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	Total		gca status
																																	+	-		
	Lines																																			
1	L1	0	0	0	-1	+1	+1	+1	0	+1	-1	0	0	0	+1	0	+1	+1	-1	0	-1	0	+1	0	0	0	-1	-1	+1	+1	+1	-1	-1	11	08	H
2	L2	+1	+1	+1	+1	+1	+1	+1	+1	+1	-1	+1	+1	+1	+1	+1	+1	+1	+1	+1	0	-1	-1	0	-1	-1	0	-1	+1	-1	0	-1	-1	19	09	H
3	L3	0	-1	-1	0	-1	-1	+1	+1	-1	+1	-1	-1	-1	+1	+1	+1	+1	+1	0	-1	+1	-1	0	-1	+1	-1	-1	-1	+1	+1	0	+1	13	14	L
4	L4	-1	0	0	0	0	0	+1	-1	0	0	0	-1	-1	+1	0	-1	-1	-1	-1	0	0	-1	0	+1	+1	+1	+1	-1	-1	-1	0	-1	06	13	L
5	L5	-1	-1	-1	-1	-1	-1	-1	0	-1	+1	-1	0	+1	-1	0	0	0	-1	+1	-1	-1	-1	0	0	0	-1	+1	+1	+1	0	+1	-1	07	16	L
6	L6	+1	+1	+1	+1	+1	+1	+1	+1	+1	-1	+1	+1	+1	+1	+1	+1	+1	0	+1	0	-1	+1	0	-1	+1	0	0	-1	+1	+1	-1	0	21	05	H
7	L7	0	0	-1	+1	-1	-1	-1	0	-1	+1	-1	-1	-1	-1	-1	-1	-1	-1	-1	+1	+1	+1	0	0	0	-1	0	+1	-1	-1	+1	-1	07	18	L
8	L8	-1	-1	0	0	-1	-1	-1	+1	-1	+1	-1	-1	0	0	0	-1	0	+1	-1	-1	+1	+1	-1	+1	-1	-1	0	-1	-1	-1	+1	+1	09	16	L
9	L9	0	0	0	0	-1	-1	-1	-1	-1	+1	0	0	0	-1	-1	-1	-1	+1	-1	+1	+1	0	+1	-1	-1	+1	0	+1	+1	0	+1	+1	09	13	L
10	L10	-1	-1	-1	-1	+1	+1	0	0	+1	-1	-1	-1	-1	-1	-1	-1	-1	-1	0	+1	-1	+1	+1	+1	-1	+1	+1	0	+1	+1	0	+1	11	16	L
	Testers																																			
1	T1	+1	0	+1	+1	0	0	+1	+1	+1	0	-1	+1	+1	0	+1	+1	+1	-1	0	0	+1	-1	0	-1	0	-1	-1	-1	-1	0	-1	-1	12	10	H
2	T2	0	0	0	-1	0	0	-1	0	0	-1	+1	+1	0	+1	+1	+1	+1	0	+1	0	+1	-1	0	0	0	-1	-1	-1	-1	+1	0	0	09	08	H
3	T3	0	+1	0	-1	0	0	0	0	0	0	-1	-1	-1	-1	-1	-1	-1	-1	-1	+1	-1	0	0	-1	0	+1	+1	+1	+1	-1	0	+1	07	13	L
4	T4	-1	-1	0	0	-1	-1	-1	-1	-1	+1	0	-1	-1	0	0	-1	-1	+1	-1	-1	-1	+1	0	+1	0	+1	0	+1	+1	0	0	0	07	14	L

1= Vine length at 45 DAS

6= Days to first female flower

11= Fruit length

16= Fruit yield per plot

21= Fruit firmness

26= Ascorbic acid

31= Crude fiber

2= Vine length at 90 DAS

7= Node at first male flower

12= Fruit diameter

17= Fruit yield per hectare

22= Fruit color (L*)

27= Potassium content

32= Ash content

3= Number of branches at 45 DAS

8= Node at first female flower

13= Average fruit weight

18= No. of seeds per fruit

23= Fruit color (a*)

28= Phenol content

4= Number of branches at 90 DAS

9= Days to first harvest

14= Number of fruits per vine

19= Sponge yield

24= Fruit color (b*)

29= Total antioxidants

5= Days to first male flower

10= Days to last harvest

15= fruit yield per vine

20= TSS

25= Protein content

30= Total flavonoids

Table 61. Overall analysis of heterosis status of hybrids/ crosses in sponge gourd

Sl. No.	Parents	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	Total		Status of	
																																		+	-	CH	PG
1	L1 × T1	0	0	-1	0	0	0	0	-1	0	0	-1	-1	+1	-1	-1	-1	-1	-1	-1	+1	+1	+1	0	+1	0	-1	0	+1	0	0	0	-1	06	12	L	H × H
2	L1 × T2	0	0	0	+1	0	-1	0	+1	0	0	+1	0	-1	-1	0	-1	0	-1	+1	0	0	-1	0	-1	0	+1	0	-1	-1	-1	0	0	05	10	L	H × H
3	L1 × T3	0	+1	0	-1	0	0	0	0	0	0	0	-1	+1	0	0	0	0	+1	0	0	-1	0	+1	0	-1	0	0	0	+1	0	0	0	05	04	H	H × L
4	L1 × T4	0	0	0	0	0	+1	0	0	0	0	0	+1	-1	+1	+1	+1	+1	0	0	0	0	0	0	+1	0	+1	0	-1	+1	+1	0	+1	11	02	H	H × L
5	L2 × T1	0	+1	0	+1	0	+1	0	0	+1	0	+1	+1	+1	+1	+1	+1	+1	+1	+1	0	-1	-1	0	-1	-1	-1	0	-1	+1	0	0	0	14	06	H	H × H
6	L2 × T2	0	0	0	0	0	0	+1	+1	0	0	0	+1	+1	+1	+1	+1	+1	+1	0	+1	0	0	0	-1	0	0	0	-1	+1	0	-1	0	11	03	H	H × H
7	L2 × T3	0	-1	0	0	0	0	0	0	-1	0	0	-1	-1	0	-1	-1	-1	-1	0	0	+1	0	-1	+1	+1	0	+1	-1	-1	-1	+1	0	05	12	L	H × L
8	L2 × T4	0	0	0	0	0	-1	-1	-1	0	0	-1	-1	-1	-1	-1	-1	-1	0	0	-1	-1	+1	0	0	+1	0	-1	+1	0	+1	0	0	04	13	L	H × L
9	L3 × T1	+1	0	0	-1	0	0	0	0	+1	0	+1	0	-1	-1	-1	-1	-1	+1	-1	0	+1	0	0	0	0	0	0	-1	-1	-1	-1	+1	06	11	L	H × H
10	L3 × T2	-1	0	+1	0	0	0	0	0	0	0	0	0	+1	0	0	+1	+1	+1	0	0	+1	+1	0	+1	0	0	+1	+1	+1	0	0	0	11	01	H	H × H
11	L3 × T3	+1	+1	-1	0	0	-1	0	0	-1	0	0	+1	-1	+1	0	0	+1	-1	0	0	-1	-1	0	-1	0	0	0	+1	-1	+1	0	+1	08	09	L	L × L
12	L3 × T4	+1	0	0	0	0	+1	0	0	0	-1	-1	-1	+1	+1	+1	+1	+1	-1	+1	+1	-1	0	0	0	0	0	0	-1	+1	0	0	-1	10	07	H	L × L
13	L4 × T1	-1	0	0	0	-1	-1	0	0	-1	+1	+1	0	-1	0	-1	-1	-1	-1	0	0	-1	0	0	+1	-1	+1	0	-1	+1	0	0	-1	05	13	L	H × H
14	L4 × T2	0	-1	0	+1	0	+1	0	0	+1	-1	0	0	+1	0	+1	+1	+1	-1	0	0	+1	0	0	-1	+1	0	0	0	+1	0	0	0	10	06	H	H × H
15	L4 × T3	0	0	0	+1	0	0	-1	0	0	0	+1	0	-1	-1	-1	-1	-1	+1	0	0	+1	0	0	-1	0	-1	0	-1	+1	0	0	+1	06	09	L	L × L
16	L4 × T4	0	0	0	-1	0	+1	0	+1	+1	0	-1	0	+1	+1	+1	+1	+1	+1	-1	0	-1	0	0	+1	0	-1	0	+1	-1	-1	0	-1	11	06	H	L × L
17	L5 × T1	0	0	0	+1	0	-1	0	0	-1	0	-1	0	-1	0	-1	-1	-1	+1	0	0	+1	0	0	-1	0	0	-1	0	-1	-1	+1	0	04	11	L	H × H
18	L5 × T2	+1	0	+1	0	0	0	0	0	0	+1	0	0	-1	+1	+1	+1	+1	+1	-1	0	-1	0	0	-1	+1	0	0	-1	+1	+1	+1	0	12	05	H	H × H
19	L5 × T3	0	0	0	-1	0	+1	0	0	+1	-1	-1	-1	+1	-1	0	0	0	-1	+1	-1	-1	0	0	+1	-1	0	0	-1	+1	0	0	0	06	10	L	L × L
20	L5 × T4	-1	0	0	0	0	0	0	0	+1	0	+1	+1	+1	-1	0	0	0	+1	0	+1	0	+1	0	+1	0	-1	0	+1	-1	0	-1	0	09	05	H	L × L
21	L6 × T1	+1	+1	0	0	+1	+1	0	0	+1	0	+1	+1	+1	+1	+1	+1	+1	+1	+1	+1	-1	0	0	+1	-1	0	0	-1	+1	0	0	+1	18	03	H	H × H
22	L6 × T2	0	+1	0	0	0	0	0	0	0	0	-1	-1	-1	-1	-1	-1	-1	0	0	0	0	0	0	+1	0	0	0	-1	0	-1	+1	-1	03	10	L	H × H
23	L6 × T3	0	-1	0	0	0	0	0	0	0	0	-1	0	+1	0	0	0	0	-1	-1	0	+1	+1	0	-1	0	-1	0	+1	-1	+1	0	-1	05	08	L	H × L
24	L6 × T4	0	-1	0	-1	0	0	0	0	0	0	0	0	+1	-1	0	-1	0	-1	0	-1	+1	-1	0	-1	0	+1	0	-1	-1	0	0	+1	04	10	L	H × L
25	L7 × T1	-1	0	0	0	0	-1	0	0	-1	0	0	-1	-1	+1	0	0	0	0	0	-1	0	+1	+1	-1	+1	+1	+1	-1	+1	+1	0	0	08	08	A	H × H
26	L7 × T2	0	0	-1	0	0	0	0	0	0	0	0	0	-1	-1	-1	-1	-1	-1	0	0	+1	-1	0	+1	-1	0	0	+1	-1	+1	0	-1	04	11	L	H × H

Table 61. *Contd...*

Sl. No.	Parents	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	Total		Status of	
																																	+	-	CH	PG	
27	L7 × T3	0	0	0	0	+1	+1	0	0	+1	-1	0	+1	+1	-1	0	0	0	-1	0	+1	-1	0	0	-1	+1	0	-1	-1	-1	-1	0	0	07	09	L	L × L
28	L7 × T4	0	+1	+1	0	0	0	0	0	0	0	0	-1	-1	+1	+1	+1	+1	0	0	+1	0	0	+1	-1	-1	-1	+1	-1	-1	+1	+1	12	09	H	L × L	
29	L8 × T1	0	-1	0	0	0	0	0	-1	0	0	+1	+1	+1	0	0	+1	+1	0	0	0	+1	+1	-1	0	0	-1	+1	+1	-1	0	0	+1	10	05	H	H × H
30	L8 × T2	+1	0	-1	-1	0	0	0	0	0	-1	-1	-1	+1	-1	0	0	0	0	0	0	-1	-1	+1	+1	-1	-1	-1	+1	-1	0	0	0	05	12	L	H × H
31	L8 × T3	-1	0	+1	+1	+1	+1	-1	+1	+1	0	0	0	-1	+1	+1	+1	+1	+1	0	0	+1	-1	0	0	+1	+1	0	0	+1	0	-1	-1	15	06	H	L × L
32	L8 × T4	0	+1	0	+1	0	-1	+1	0	-1	+1	0	0	-1	-1	-1	-1	-1	0	0	-1	+1	0	-1	0	+1	0	-1	-1	0	0	0	06	10	L	L × L	
33	L9 × T1	0	0	0	0	+1	+1	+1	+1	+1	-1	-1	-1	+1	-1	-1	-1	-1	-1	0	+1	-1	+1	-1	+1	-1	0	0	-1	0	0	0	09	13	L	H × H	
34	L9 × T2	0	+1	0	-1	0	0	0	0	0	0	0	0	-1	+1	+1	+1	+1	+1	0	-1	+1	0	+1	+1	0	0	-1	-1	0	0	0	10	05	H	H × H	
35	L9 × T3	+1	0	0	0	-1	-1	0	-1	-1	+1	+1	+1	-1	+1	+1	+1	+1	+1	-1	0	+1	0	+1	-1	+1	-1	-1	+1	0	0	0	14	09	H	L × L	
36	L9 × T4	0	0	0	+1	0	0	0	0	0	0	0	+1	+1	-1	0	-1	-1	0	-1	0	0	-1	0	+1	-1	0	0	+1	+1	0	0	0	06	06	A	L × L
37	L10 × T1	+1	+1	+1	0	0	0	0	0	0	0	0	+1	0	+1	+1	+1	+1	-1	+1	-1	+1	0	+1	-1	0	-1	+1	-1	0	0	-1	12	07	H	H × H	
38	L10 × T2	0	0	-1	0	0	+1	0	0	0	0	0	0	0	-1	-1	-1	-1	-1	0	0	+1	0	0	+1	0	+1	0	-1	-1	-1	-1	0	04	10	L	H × H
39	L10 × T3	-1	-1	-1	0	0	0	0	+1	0	0	0	-1	0	-1	0	-1	0	+1	-1	+1	0	+1	0	0	+1	0	+1	0	+1	+1	0	0	08	07	H	L × L
40	L10 × T4	0	+1	0	0	0	0	0	0	0	0	+1	0	+1	0	0	0	0	-1	0	0	+1	-1	0	-1	0	-1	0	-1	+1	0	+1	+1	07	05	H	L × L

1= Vine length at 45 DAS

2=Vine length at 90 DAS

3=Number of branches at 45 DAS

4= Number of branches at 90 DAS

5= Days to first male flower

6= Days to first female flower

7=Node at first male flower

8= Node at first female flower

9=Days to first harvest

10=Days to last harvest

11= Fruit length

12= Fruit diameter

13= Average fruit weight

14= Number of fruits per vine

15= fruit yield per vine

16=Fruit yield per plot

17=Fruit yield per hectare

18=No. of seeds per fruit

19= Sponge yield

20= TSS

21=Fruit firmness

22=Fruit color (L*)

23=Fruit color (a*)

24=Fruit color (b*)

25=Protein content

26=Ascorbic acid

27=Potassium content

28= Phenol content

29=Total antioxidants

30=Total flavonoids

31=Crude fiber

32=Ash content

6. SUMMARY AND CONCLUSION

The present investigation on “Molecular diversity assessment and manifestation of heterosis for growth and yield in sponge gourd (*Luffa cylindrica* (L.) Roem.)” was undertaken at the experimental plot, Department of Vegetable Science, College of Horticulture, Bagalkot (Karnataka) during 2020-2022. Considering the importance of the crop, the present investigation was undertaken with the objectives viz., characterization of sponge gourd genotypes for morphological and molecular variability, diversity, character association and development of F₁ hybrids to increase the yield. Forty sponge gourd genotypes were evaluated in a Randomized Complete Block Design (RCBD) with two replications and the results obtained from the study are summarized in this chapter.

Analysis of variance revealed highly significant differences among 40 genotypes for all the parameters studied. Means of genotypes also varied greatly for several characters indicating the presence of higher magnitude of variability in the germplasm.

From the performance study, the genotypes G9 (3.85 kg/vine), G24 (3.69 kg), G33 (3.67 kg) and G21 (3.65 kg) were identified as best high yielding genotypes over commercial check variety Kashi Divya (2.72 kg/vine).

The phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the traits. High (> 20%) genotypic coefficient of variation (GCV) and phenotypic coefficient variation (PCV) were observed for vine length and number of branches at 45 DAS, fruit yield per vine, fruit yield per plot, fruit yield per hectare, number of seeds per fruit and fruit color (b*) indicated existence of broad genetic base for these characters, which would be amenable for further crop improvement.

Moderate (10-20 %) GCV and PCV were observed for vine length at 90 DAS, days to first male flower, node at first female flower, fruit length, average fruit weight, sponge yield, total soluble solids, fruit firmness, fruit color (L*), fruit color (a*), protein content, ascorbic acid, potassium content, total flavonoids, crude fiber and ash content which indicates presence of moderate amount of variability for these traits. Whereas, low (<10 %) GCV and PCV were registered for days to last harvest, phenol content and total anti-oxidants indicating the narrow genetic base, therefore selection for these traits

may not give desirable results. The creation of genetic variability is needed for these characters for further improvement.

High estimates of heritability ($> 60\%$) coupled with high genetic advance as per cent of mean ($> 20\%$) were recorded for vine length at 45 DAS, number of branches at 45 and 90 DAS, node at first male and female flower, fruit length, average fruit weight, number of fruits per vine, fruit yield per vine, fruit yield per plot, fruit yield per hectare, number of seeds per fruit, sponge yield, fruit firmness, fruit color (L^* , a^* , b^*), protein, ascorbic acid, potassium content, total flavonoids and crude fiber content. This indicates predominance of additive component for these traits and hence, direct selection would be more effective in improving these traits.

The high estimates of heritability ($>60\%$) coupled with moderate genetic advance as per cent of mean ($10-20\%$) were recorded for days to first male flower, days to first female flower, phenol content and total antioxidants. This indicates that prevalence of non additive components and there can be little response to selection and these characters can be exploited through heterosis breeding.

The moderate heritability ($30-60\%$) with low to moderate genetic advance as per cent of mean ($<10-20\%$) were recorded for vine length at 90 DAS, days to first harvest, days to last harvest, fruit diameter, total soluble solids and ash content. This indicates prevalence of non additive components and higher influence of environment on these characters and hence, selection would be ineffective. Therefore, these traits can be improved either through heterosis breeding or recurrent selection.

The estimates of high GCV, PCV along with high broad sense heritability and genetic advance as per cent of mean were observed for vine length at 45 DAS, number of branches at 45 DAS, fruit yield per vine, fruit yield per plot, fruit yield per hectare, number of seeds per fruit indicated presence of more variability along with prevalence of additive gene action in their inheritance. Therefore, these traits can be improved by simple selection.

Fruit yield per vine was significantly and positively correlated with vine length, number of branches per vine, fruit length, average fruit weight and number of fruits per vine and sponge yield at both genotypic and phenotypic levels. Hence, more success can

be achieved to improve fruit yield per vine by applying selection pressure on these characters.

Path coefficient analysis revealed that the traits like number of fruits per vine, average fruit weight, fruit length, number of branches per vine, and vine length had positive direct effect on fruit yield per vine. Whereas, node at first female flower, days to first harvest and days to first female flower had negative direct effect (desirable) at both genotypic and phenotypic levels. It indicates direct selection for these traits would reward the improvement of yield.

A genetic diversity study was also carried out in 40 genotypes using Mahalanobis D^2 statistics with Trocher's method and these 40 genotypes were grouped into seven clusters. Among which cluster I is the largest cluster with 19 genotypes followed by cluster II with ten genotypes, cluster III with seven genotypes and remaining cluster IV, cluster V, cluster VI and cluster VII having only one genotype each.

The maximum intra-cluster distance was recorded in cluster III ($D^2=667.55$) followed by cluster II ($D^2=665.10$) and cluster I ($D^2=466.27$), it indicates that the genotypes included in these clusters were very diverse. Whereas, the clusters IV, V, VI and VII had no inter cluster distance ($D^2=0.000$) as they possessed single genotype in each. It indicates that the genotypes included in these clusters were less diverse from each other.

The maximum inter-cluster distance was observed between cluster IV and VI ($D^2=10081.40$) followed by IV and VII ($D^2=8163.44$), cluster III and IV ($D^2=5374.53$), cluster II and cluster VI ($D^2=4944.16$), cluster II and cluster VII ($D^2=4498.17$). In heterosis breeding, genotypes of diverse clusters are known to play an important role as potential parents and they are likely to produce high heterotic combinations. The least inter cluster distance was observed between cluster VI and VII ($D^2=629.38$) followed by cluster V and VII ($D^2=897.04$). It indicates that genotypes included in these clusters were less diverse for each other.

Among the 17 characters studied for D^2 analysis, average fruit weight (14.54 %) contributed maximum to the total divergence among the genotypes followed by fruit

yield per vine (13.25 %), number of seeds per fruit (11.20 %), phenol content (8.59 %), sponge yield (8.54 %), potassium content (7.69 %), days to first harvest (6.25 %) fruit diameter (5.22 %), total soluble solids (4.65 %) and number of branches per vine (4.00 %).

In the molecular diversity studies, total 30 SSR markers were used to screen the fourty genotypes. Among them, only twenty markers showed polymorphism. The high polymorphism information content (PIC) value was recorded by the marker SG_La_28 marker followed by the marker SG_La_28 (0.65) followed by the marker SG_La_11, SG_La_15 (0.61), SG_La_27 (0.59), SG_La_13 (0.56), SG_La_25 (0.51) and SG_La_8 (0.50). These markers performed significant diversity analysis in 40 genotypes. The PIC value helps in predicting the usefulness of DNA markers for identification of diverse genotypes and germplasm evaluation.

Unrooted neighbor joining tree was constructed using DARwin 6.0 and broadly divided 40 genotypes into three main clusters, cluster II had maximum number of twenty one genotypes followed by cluster III with fourteen genotypes, cluster I with five genotypes. It may provide the basic information to the breeders or researchers to select parent in the breeding programme or other programme as per their objective.

Based on morphology and molecular diversity analysis, the ten divesre parents were selected and crossed with four testers in a Line $\times$ Tester fashion to develop 40 F₁ hybrids. All these crosses were evaluated along with the parents and check hybrid (Kashi Rakshita) in randomized block design with two replications for earliness, growth, yield and quality parameters. The data was subjected to estimate magnitude of heterosis and combining ability. The results obtained are summarized as below.

The magnitude of heterosis over the commercial check (Kashi Rakshita) was high in the desirable direction and it is ranged from -24.62 to 31.15 % for vine length at 45 DAS, -8.47 % to 37.63 % for vine length at 90 DAS, -29.17 to 54.17 % for number of branches at 45 DAS, -13.46 to 51.92 % for number of branches at 90 DAS, -20.41 to 16.84 % for days to first male flower, -21.13 to 14.08 % for days to first female flower, -42.31 to 17.31 % for node at first male flower, -26.72 to 13.79 % for node at first female flower, -18.88 to 17.27 % for days to first harvest, -5.44 to 15.79 % for days to last harvest, -13.46 to 40.62 % for fruit length, -11.71 to 42.83 % for fruit diameter, -

19.84 to 20.11 % for average fruit weight, -28.32 to 43.36 % for number of fruits per vine, -42.33 to 67.90 % for fruit yield per vine, -42.67 to 65.24 % for fruit yield per plot, -40.07 to 62.07 % for fruit yield per hectare, -44.54 to 40.58 % for number of seeds per fruit, -35.25 to 43.44 % for sponge yield, -18.20 to 38.35 % for total soluble solids, -28.94 to 47.23 % for fruit firmness, -26.35 to 15.82 % for fruit color (L*), -26.60 to 17.90 % for fruit color (a*), -34.56 to 37.46 % for fruit color (b*), -27.56 to 27.83 % for protein content, and -18.32 to 35.45 % for ascorbic acid, -14.84 to 37.36 % for potassium content -22.05 to 11.72 % for phenol content -4.76 to 11.08 % for total antioxidants, -32.26 to 29.04 % for total flavonoids, -19.95 to 46.01 % for crude fiber and -15.12 to 30.24 % for ash content.

Among 40 crosses, 22 crosses over better parent, 12 crosses over the best parent and 20 crosses over commercial check exhibited positive and significant heterosis for fruit yield per hectare. The crosses L2 × T1 (66.18 %) followed by L6 × T1 (64.64 %) and L2 × T2 (57.84 %) showed significant heterosis over the commercial check in order of merit.

The lines L1, L2, L3 and L6 were identified as good general combiners for fruit yield per hectare in order of merit. Similarly, the lines L2 and L6 for vine length at 45 and 90 DAS, number of branches at 45 DAS, L2, L6 and L7 for number of branches at 90 DAS, L1, L2, L6 and L10 for days to first male and female flower, L1, L2, L3, L4, L6 for node at first male flower, L2, L3, L6 and L8 for node at first female flower, L1, L2, L6 and L10 for days to first harvest, L3, L5, L7, L8 and L9 for days to last harvest, L2, L6 for fruit length and fruit diameter, L2, L5 and L6 for average fruit weight, L2, L3, L4 and L6 for number of fruits per vine, L2, L3 and L6 for fruit yield per vine, L1, L2, L3 and L6 for fruit yield per plot, L2, L3, L8 and L9 for number of seeds per fruit, L2, L5 and L6 for sponge yield, L7, L9 and L10 for total soluble solids, L2, L5, L6 and L10 for fruit firmness, L1, L6, L7, L8 and L10 for fruit color (L*), L8 for fruit color (a*), L4, L8 and L10 for fruit color (b*), L3, L4 and L6 for protein content, L4, L9 and L10 for ascorbic acid, L4, L5 and L10 for potassium content, L1, L2, L5, L7 and L9 for phenol content, L1, L3, L5, L6, L9 and L10 for total antioxidants, L1, L3, L6 and L10 for total flavonoids, L5, L7, L8 and L9 for crude fiber and L3, L8, L9 and L10 for ash content were observed as good general combiners.

The crosses L6 × T1, L2 × T1, L7 × T4, L4 × T4, L2 × T2 and L5 × T2 were identified as good specific combiners for fruit yield per hectare in order of merit. The crosses L10 × T1, L6 × T1 and L3 × T4 for vine length at 45 DAS, L2 × T1, L9 × T2 and L7 × T4 for vine length at 90 DAS, L10 × T1, L3 × T2 and L7 × T4 for number of branches at 45 DAS, L3 × T4, L5 × T1 and L1 × T2 for number of branches at 90 DAS, L9 × T1, L8 × T3 and L6 × T1 for days to first male flower, L9 × T1, L7 × T3 and L8 × T3 for days to first female flower, L8 × T3, L2 × T2 and L8 × T4 for node at first male flower, L9 × T1, L4 × T4 and L1 × T2 for node at first female flower, L9 × T1, L3 × T1 and L6 × T1 for days to first harvest, L9 × T3, L8 × T4 and L4 × T1 for days to last harvest, L5 × T4, L9 × T3 and L6 × T1 for fruit length, L7 × T3, L2 × T1 and L6 × T1 for fruit diameter, L7 × T3, L4 × T2 and L6 × T1 for average fruit weight, L8 × T3, L9 × T2 and L7 × T4 for number of fruits per vine, L6 × T1, L2 × T1 and L7 × T4 for fruit yield per vine, L6 × T1, L2 × T1 and L7 × T4 for fruit yield per plot, L6 × T1, L1 × T3 and L7 × T4 for number of seeds per fruit, L3 × T4, L10 × T1 and L1 × T2 for sponge yield, L10 × T3, L7 × T3 and L1 × T1 for total soluble solids, L10 × T1, L7 × T3 and L8 × T2 for fruit firmness, L9 × T2, L8 × T1 and L9 × T3 for fruit color (L*), L8 × T1, L2 × T3 for fruit color (a*), L5 × T3, L4 × T1 and L2 × T3 for fruit color (b*), L9 × T2, L9 × T1 and L7 × T3 for protein content, L4 × T1, L8 × T4 and L6 × T4 for ascorbic acid, L7 × T1, L10 × T3, L8 × T1 and L3 × T2 for potassium content, L6 × T3, L9 × T4 and L2 × T4 for phenol content, L7 × T1, L8 × T3 and L5 × T2 for total antioxidants, L7 × T1, L5 × T2 and L2 × T4 for total flavonoids, L5 × T1, L6 × T2 and L10 × T4 for crude fiber and L4 × T4, L1 × T4 and L6 × T4 for ash content were identified as good specific combiners in order of merit.

Comprehensive assessment of parents by considering gca effects of all the 32 characters studied has resulted into identification of lines viz, L1, L2, L6, T1 and T2 as good combiners for most the characters which can be used in future breeding programme. Assessment of crosses by considering standard heterosis values of 32 characters revealed that, out of 40 crosses, 18 crosses were highly heterotic, two crosses were average heterotic and remaining 20 crosses were low heterotic. Out of 18 heterotic crosses, six crosses involved high X high parental combinations, five crosses involved high X low parental combinations and seven crosses involved low X low parental combinations for overall gca status. These results indicated that high frequency of

highly heterotic hybrids could be obtained from parental combinations with high x low or low x high general combining ability which clearly indicates that, the parental contribution to the heterosis is mainly through non additive gene effects.

Studies on combining ability variance revealed that predominance of non additive genetic variance for node at first male flower, ascorbic acid content, crude fiber, total flavonoids, fruit diameter, total soluble solids, days to first harvest, fruit length, days to first male flower, days to first female flower, vine length at 90 DAS, number of branches at 90 DAS, number of branches at 45 DAS, sponge yield, fruit yield per vine, fruit yield per plot, days to last harvest, vine length at 45 DAS, number of seeds per fruit, fruit yield per hectare, node at first female flower, potassium content, number of fruits per vine, average fruit weight, ash content, total antioxidants, fruit firmness, fruit color (L^*), fruit color (a^*), fruit color (b^*), phenol content and protein content.

The results of heterosis study indicated that the hybrid $L2 \times T1$ said to be the best hybrid recording 66.18 % of commercial heterosis with fruit yield of 27.12 t/ha. This hybrid also exhibited significant and high standard heterosis in the desirable direction for vine length at 45 and 90 DAS, number of branches at 45 and 90 DAS, days to first male and female flower, node at first male and female flower, days to first harvest, fruit length, fruit diameter, average fruit weight, number of fruits per vine, fruit yield per vine, fruit yield per plot and sponge yield. It also showed specific combiner for vine length at 45 and 90 DAS, days to first female flower, fruit length, fruit diameter and sponge yield.

The second best hybrid $L6 \times T1$ was selected based on fruit yield per hectare which had total yield of 26.87 t/ha with 64.64 per cent standard heterosis. This hybrid exhibited significant and standard heterosis in the desirable direction for all most all the traits studied except for days to last harvest, fruit color (L^*), phenol and crude fiber content. This hybrid also exhibited desirable significant sca effects for vine length at 45 and 90 DAS, days to first male and female flower, days to first harvest, fruit length, fruit diameter, average fruit weight, number of fruits per vine, fruit yield per vine, fruit yield per plot, fruit yield per hectare, number of seeds, sponge yield, TSS, total antioxidants and ash content.

The next best hybrid was L2 × T2 exhibited 57.84 per cent standard heterosis for fruit yield per vine which had yielding ability of 25.76 t/ha. This hybrid exhibited significant and standard heterosis in the desirable direction for all most all the traits studied except for days to last harvest, TSS, fruit color (L^* , a^* and b^*), protein, phenol, ash content and crude fiber content. This hybrid L2 × T2 also recorded significant sca effects for node at first male and female flower, fruit diameter, average fruit weight, number of fruits per vine, fruit yield per vine, fruit yield per plot, number of seeds per fruit, TSS and total antioxidants.

From the present investigation, elaborative information has been generated with respect to detailed phenotypic characterization including growth, earliness, yield and biochemical parameters. Molecular marker profiling using most useful co-dominant microsatellite markers are also been utilized in the present study. The detailed statistical analysis like variability, heritability components, morphological and molecular characterization provided the beneficial variance occurring in these genotypes whereas, association and path analysis would help in the selection of characters to be considered for improvement in economic terms. Hence this investigation showed that there is significant variation among the studied sponge gourd genotypes for various morphological traits. This genetic diversity study can also be used to select contrasting parents for formation of mapping population.

The genotypes identified with higher yield per vine from the present study were further crossed with four testers to get high yielding hybrids. From the heterosis and combining ability studies it was concluded that, lines evaluated in the present investigation possessed wide range of variation for various traits. The combining ability analysis revealed the occurrence of non-additive gene actions for growth, yield and quality parameters. This suggested that heterosis breeding or recurrent selection is best for the improvement of sponge gourd crop. However, superior hybrids were need to be evaluated for stability and then later recommended for commercial cultivation.

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*- Originals not seen

Appendix-I: Meteorological data during the experimental period recorded at the meteorological observatory of MHREC, UHS, Bagalkot

Months	Year	Rainfall (mm)	Temp °C		Relative humidity	
			Maximum	Minimum	Morning	Afternoon
Dec	2020	0.0	29.50	16.59	95.48	33.00
Jan	2021	2.00	33.90	14.20	90.00	37.00
Feb	2021	2.00	34.80	12.90	76.25	23.87
Mar	2021	5.00	39.40	14.70	66.00	16.00
Apr	2021	21.00	38.60	22.96	80.30	21.20
Sep	2021	139.00	28.48	21.80	78.73	53.20
Oct	2021	93.00	29.66	20.98	76.55	60.12
Nov	2021	29.00	29.55	16.97	65.77	43.23
Dec	2021	7.00	28.78	14.52	62.37	55.23
Jan	2022	2.00	29.07	21.85	97.80	69.26
Feb	2022	2.00	33.70	16.60	79.40	23.40
Mar	2022	4.50	37.01	20.70	66.00	20.20
Apr	2022	5.80	37.90	23.50	74.30	24.20
May	2022	133.10	35.51	23.94	88.80	42.10
June	2022	69.00	32.24	23.00	92.83	57.20

Appendix-II: Reaction of sponge gourd F₁ hybrids and their parents to fruit fly, leaf miner, downy mildew and powdery mildew incidence

Sl. No.	Genotypes	Per cent fruit fly incidence	Per cent leaf miner incidence	Per cent downy mildew incidence	Per cent powdery mildew incidence
	Crosses				
1	L1 × T1	36.25	26.33	41.31	35.45
2	L1 × T2	34.80	39.12	36.65	33.12
3	L1 × T3	31.35	27.88	31.65	37.50
4	L1 × T4	25.11	28.96	36.58	34.26
5	L2 × T1	24.63	25.44	33.69	33.26
6	L2 × T2	25.36	21.68	34.72	36.65
7	L2 × T3	25.10	23.45	35.00	37.98
8	L2 × T4	35.15	31.25	36.45	31.89
9	L3 × T1	24.27	25.66	33.64	32.45
10	L3 × T2	26.36	32.65	31.59	31.98
11	L3 × T3	39.88	28.96	45.78	29.00
12	L3 × T4	24.96	26.45	32.55	37.00
13	L4 × T1	25.00	35.44	30.85	33.65
14	L4 × T2	30.33	31.45	38.55	35.00
15	L4 × T3	33.68	33.54	42.45	33.45
16	L4 × T4	24.55	29.66	52.12	30.25
17	L5 × T1	24.98	31.45	61.00	38.54
18	L5 × T2	30.55	40.12	37.10	37.45
19	L5 × T3	42.55	27.88	39.85	36.88
20	L5 × T4	25.32	26.45	51.00	32.55
21	L6 × T1	25.70	23.65	51.85	30.00
22	L6 × T2	37.60	29.68	43.25	30.87
23	L6 × T3	35.95	25.00	38.65	29.85
24	L6 × T4	44.00	26.45	53.00	31.11
25	L7 × T1	37.05	29.77	51.00	39.14
26	L7 × T2	35.50	29.88	62.00	39.75
27	L7 × T3	36.20	35.45	44.75	37.15
28	L7 × T4	25.13	23.65	42.62	36.25
29	L8 × T1	35.37	34.69	44.05	37.00
30	L8 × T2	25.00	33.89	39.20	35.12
31	L8 × T3	26.55	31.57	35.00	33.12
32	L8 × T4	27.98	29.88	36.20	33.45
33	L9 × T1	29.66	28.44	41.00	30.47
34	L9 × T2	31.92	34.65	43.75	38.15

Contd...

Sl. No.	Genotypes	Per cent fruit fly incidence	Per cent leaf miner incidence	Per cent downy mildew incidence	Per cent powdery mildew incidence
	Crosses				
35	L9 × T3	29.87	29.88	35.35	36.15
36	L9 × T4	33.45	31.24	40.75	33.55
37	L10 × T1	28.92	33.65	41.75	39.35
38	L10 × T2	26.46	35.45	36.78	37.36
39	L10 × T3	27.99	26.82	33.22	35.12
40	L10 × T4	25.11	23.98	31.45	36.85
Lines					
41	L1	30.23	26.98	36.12	37.33
42	L2	32.38	28.97	33.89	34.50
43	L3	31.00	27.63	34.90	36.47
44	L4	25.40	23.65	37.85	26.00
45	L5	30.30	22.65	31.75	30.45
46	L6	24.88	27.15	32.85	34.46
47	L7	25.12	26.00	37.75	29.88
48	L8	33.58	31.25	37.35	30.35
49	L9	37.98	33.65	41.35	35.16
50	L10	33.56	24.65	36.11	38.28
Testers					
51	T1	31.75	31.65	31.35	28.85
52	T2	33.25	29.98	34.83	31.00
53	T3	36.36	22.45	35.87	35.12
54	T4	27.65	24.65	37.88	34.00
55	SC	28.34	29.31	36.89	29.89
	SEm±	4.89	4.89	5.20	4.90
	CD at 5%	9.98	9.15	10.45	9.89
	CD at 1%	13.35	12.89	13.89	12.96

SC : Standard check (Kashi Rakshita)

Appendix-III: Fruit characteristics of crosses, parents and commercial check

Sl. No.	Crosses	Fruit shape	Fruit color	Fruit surface
1	L1 × T1	Elliptical	Light green	Rough
2	L1 × T2	Elliptical	Dark green	Rough
3	L1 × T3	Oblong blocky	Green	Smooth
4	L1 × T4	Elliptical	Light green	Smooth
5	L2 × T1	Elongate slim	Green	Smooth
6	L2 × T2	Elongate slim	Green	Smooth
7	L2 × T3	Elongate elliptical	Green	Smooth
8	L2 × T4	Elongate elliptical	Dark green	Smooth
9	L3 × T1	Elongate slim	Dark green	Smooth
10	L3 × T2	Elongate slim	Light green	Rough
11	L3 × T3	Elliptical	Green	Rough
12	L3 × T4	Elongate slim	Dark green	Smooth
13	L4 × T1	Elongate elliptical	Dark green	Smooth
14	L4 × T2	Elongate slim	Dark green	Smooth
15	L4 × T3	Elongate slim	Dark green	Rough
16	L4 × T4	Elongate slim	Green	Smooth
17	L5 × T1	Elongate slim	Dark green	Rough
18	L5 × T2	Elongate slim	Dark green	Smooth
19	L5 × T3	Elongate elliptical	Green	Rough
20	L5 × T4	Elongate slim	Green	Smooth
21	L6 × T1	Elongate slim	Dark green	Rough
22	L6 × T2	Elongate elliptical	Green	Smooth
23	L6 × T3	Elliptical	Dark green	Rough
24	L6 × T4	Elongate slim	Dark green	Smooth
25	L7 × T1	Elongate slim	Green	Smooth
26	L7 × T2	Elongate elliptical	Green	Smooth
27	L7 × T3	Elliptical	Green	Smooth
28	L7 × T4	Elongate slim	Light green	Smooth
29	L8 × T1	Elliptical	Light green	Rough
30	L8 × T2	Elongate slim	Light green	Smooth
31	L8 × T3	Elliptical	Green	Smooth
32	L8 × T4	Elliptical	Green	Rough
33	L9 × T1	Elliptical	Whitish	Smooth
34	L9 × T2	Elongate slim	Green	Smooth

Contd...

Sl. No.	Crosses	Fruit shape	Fruit color	Fruit surface
35	L9 × T3	Elongate elliptical	Green	Smooth
36	L9 × T4	Elongate elliptical	Light green	Rough
37	L10 × T1	Elongate slim	Light green	Rough
38	L10 × T2	Elongate slim	Green	Rough
39	L10 × T3	Elongate slim	Green	Rough
40	L10 × T4	Elliptical	Green	Smooth
Lines				
41	L1	Elongate slim	Dark green	Rough
42	L2	Elongate elliptical	Dark green	Smooth
43	L3	Elongate elliptical	Green	Rough
44	L4	Elongate elliptical	Green	Smooth
45	L5	Elongate slim	Green	Smooth
46	L6	Elongate slim	Green	Smooth
47	L7	Elongate slim	Whitish	Smooth
48	L8	Elongate elliptical	Dark green	Rough
49	L9	Elongate elliptical	Dark green	Smooth
50	L10	Elliptical	Whitish	Smooth
Testers				
51	T1	Elliptical	Light green	Smooth
52	T2	Elongate elliptical	Dark green	Smooth
53	T3	Elongate slim	Dark green	Rough
54	T4	Elongate slim	Dark green	Smooth
55	SC	Elongate elliptical	Green	Smooth

SC : Standard check (Kashi Rakshita)

**MOLECULAR DIVERSITY ASSESSMENT AND MANIFESTATION OF
HETEROSIS FOR GROWTH AND YIELD IN SPONGE GOURD
(*Luffa cylindrica* (L.) Roem.)**

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2023

Dr. SHASHIKANTH EVOOR

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ABSTRACT

An experiment entitled “Molecular diversity assessment and manifestation of heterosis for growth and yield in sponge gourd (*Luffa cylindrica* (L.) Roem.)” was carried out at College of Horticulture, UHS, Bagalkot during 2020-22. The experiment consists of 40 genotypes of sponge gourd which were evaluated in a randomized complete block design with two replications. Analysis of variance revealed highly significant differences among the genotypes for all the 32 characters under study. Among the genotypes studied, the genotypes G9 (18.17 t/ha), G24 (17.29 t/ha), G33 (16.34 t/ha) and G21 (16.12 t/ha) were identified as best high yielding genotypes over commercial check variety Kashi Divya (13.24 t/ha).

The estimates of high GCV, PCV, broad sense heritability and genetic advance as per cent of mean were observed for vine length, number of branches at 45 DAS, fruit yield per vine, plot and hectare and number of seeds per fruit indicated the presence of more variability along with prevalence of additive gene action in their inheritance. Divergence studies revealed that, highest inter cluster distance was observed between cluster IV and VI ($D_2=10081.40$). From the molecular diversity assessment it was found that, out of the 30 SSR primers designed, 20 markers exhibited polymorphism with PIC value ranged from 0.24 to 0.65 with a mean of 0.44.

The character association and path analysis studies indicated that the traits like, number of fruits per vine, average fruit weight, fruit length, number of branches per vine and vine length had positive direct effect on fruit yield per vine. Hence, more success can be achieved to improve fruit yield per vine by applying selection pressure on these characters.

The combining ability studies in this genetic stock indicated that the genotypes L1, L2, L6, T1 and T2 were found to be good general combiners. Whereas, the crosses $L2 \times T1$, $L6 \times T1$, $L8 \times T3$ and $L9 \times T3$ were identified as best specific combiners. In the heterosis studies, the crosses $L2 \times T1$ (66.18 %) followed by $L6 \times T1$ (64.64 %) and $L2 \times T2$ (57.84 %) were showed significant heterosis over the commercial check for fruit yield per hectare in order of merit. This suggested that heterosis breeding or recurrent selection is best to improve the yield and other characters in this genetic stock of sponge gourd.

ಅಣ್ವಿಕ ವೈವಿಧ್ಯತೆಯ ಮೌಲ್ಯಮಾಪನ ಮತ್ತು ತುಪ್ಪದ ಹೀರೆಕಾಯಿಯಲ್ಲಿ ಬೆಳವಣಿಗೆ ಮತ್ತು ಇಳುವರಿಗಾಗಿ ಸಂಕರಣ ತಳಿಗಳ ಅಭಿವೃದ್ಧಿ ಮತ್ತು ಅಧ್ಯಯನ (ಲೂಫಾ ಸಿಲಿಂಡ್ರಿಕಾ (ಎಲ್.) ರೋಮ್)

ಚಿತ್ರ ಕೆ

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ಡಾ. ಶಶಿಕಾಂತ್ ಏವೂರ್

ಪ್ರಧಾನ ಸಲಹೆಗಾರರು

ಸಾರಾಂಶ

ತುಪ್ಪದ ಹೀರೆಕಾಯಿಯಲ್ಲಿ “ಅಣ್ವಿಕ ವೈವಿಧ್ಯತೆಯ ಮೌಲ್ಯಮಾಪನ ಮತ್ತು ತುಪ್ಪದ ಹೀರೆಕಾಯಿಯಲ್ಲಿ ಬೆಳವಣಿಗೆ ಮತ್ತು ಇಳುವರಿಗಾಗಿ ಸಂಕರಣ ತಳಿಗಳ ಅಭಿವೃದ್ಧಿ ಮತ್ತು ಅಧ್ಯಯನ (ಲೂಫಾ ಸಿಲಿಂಡ್ರಿಕಾ (ಎಲ್.) ರೋಮ್)” ಬಗ್ಗೆ ತಿಳಿಯಲು ಪ್ರಸ್ತುತ ಅಧ್ಯಯನವನ್ನು ೨೦೨೦-೨೦೨೨ರ ಸಾಲಿನಲ್ಲಿ ಕೈಗೊಳ್ಳಲಾಯಿತು. ಈ ಅಧ್ಯಯನಕ್ಕಾಗಿ ತುಪ್ಪದ ಹೀರೆಕಾಯಿಯ ನಲವತ್ತು ವಿವಿಧ ಬಗೆಯ ಸಾಲುಗಳನ್ನು ಎರಡು ಪ್ರತಿಕೃತಿಗಳ ಖಾಸಾ ವಿನ್ಯಾಸದಲ್ಲಿ ನಡೆಸಲಾಯಿತು. ವ್ಯತ್ಯಾಸದ ವಿಶ್ಲೇಷಣೆಯ ಪ್ರಕಾರ ಅಧ್ಯಯನ ಮಾಡಿದ 32 ಗುಣಗಳಲ್ಲಿಯೂ ಗಮನಾರ್ಹ ವ್ಯತ್ಯಾಸ ಕಂಡುಬಂದಿದೆ.

ಅಧ್ಯಯನ ಮಾಡಿದ 40 ಜಿನೋಟೈಪ್‌ಗಳಲ್ಲಿ, ಜಿ-9 (18.17 t/ha), ಜಿ-24 (17.29 t/ha), ಜಿ-33 (16.34 t/ha) ಮತ್ತು ಜಿ-21 (16.12 t/ha) ತಳಿಗಳು ವಾಣಿಜ್ಯ ತಳಿ ಕಾಶಿ ದಿವ್ಯ (13.24 t/ha) ಗಿಂತ ಉತ್ತಮ ಇಳುವರಿ ನೀಡಿರುವ ಸಾಲುಗಳೆಂದು ಗುರುತಿಸಲಾಗಿದೆ. ಅನುವಂಶೀಯ ಅಧ್ಯಯನದಲ್ಲಿ ಹೆಚ್ಚಿನ ಅನುವಂಶೀಯ ಸಾಮರ್ಥ್ಯ ಮತ್ತು ಸರಾಸರಿ ಅನುವಂಶೀಯ ಮುಂದುವರಿಕೆಯು ೪೫ ದಿನಗಳಲ್ಲಿ ಬಳ್ಳಿಯ ಉದ್ದ, ಪ್ರತಿ ಬಳ್ಳಿಯಲ್ಲಿ ಕವಲುಗಳ ಸಂಖ್ಯೆ, ಕಾಯಿಯ ಇಳುವರಿ ಪ್ರತಿ ಬಳ್ಳಿಗೆ, ಪ್ರತಿ ತಾಕಿಗೆ ಮತ್ತು ಪ್ರತಿ ಹೆಕ್ಟೇರಿಗೆ ಮತ್ತು ಪ್ರತಿ ಕಾಯಿಯ ಬೀಜಗಳ ಸಂಖ್ಯೆಯು ಹೆಚ್ಚಿನ ವೈವಿಧ್ಯತೆ ಮತ್ತು ಅಧಿಕ ಜೀನ್ ಆಕ್ಸ್‌ನ್ ಅನ್ನು ಒಳಗೊಂಡಿರುತ್ತವೆ. ವೈವಿಧ್ಯತೆಯನ್ನು ಗಮನಿಸಿದಾಗ ಗುಂಪು IV ಮತ್ತು VII ಗುಂಪಿನ ನಡುವೆ ಹೆಚ್ಚಿನ ವೈವಿಧ್ಯತೆಯನ್ನು ಹೊಂದಿವೆ ($D^2 = 10081.40$). ಅಣ್ವಿಕ ಗುಣಲಕ್ಷಣಕ್ಕಾಗಿ 30 SSR ಮಾರ್ಕರ್‌ಗಳನ್ನು ಬಳಸಲಾಗಿದ್ದು, ಅದರಲ್ಲಿ 20 ಮಾರ್ಕರ್‌ಗಳು ಬಹುರೂಪಿಯಾಗಿ ಕಂಡುಬಂದಿದೆ. SSR ಮಾರ್ಕರ್‌ಗಳ (PIC) ಮೌಲ್ಯವು 0.24 ರಿಂದ 0.65 ರವರೆಗೆ ಇದ್ದು ಸರಾಸರಿ 0.44 ಮೌಲ್ಯವನ್ನು ಹೊಂದಿವೆ.

ಪರಸ್ಪರ ಸಂಬಂಧ ಮತ್ತು ಮಾರ್ಗ ವಿಶ್ಲೇಷಣೆಯ ಪ್ರಕಾರ, ಬಳ್ಳಿಯ ಉದ್ದ, ಪ್ರತಿ ಬಳ್ಳಿಗೆ ಕವಲುಗಳ ಸಂಖ್ಯೆ, ಹಣ್ಣಿನ ಉದ್ದ, ಸರಾಸರಿ ಹಣ್ಣಿನ ತೂಕ ಮತ್ತು ಪ್ರತಿ ಬಳ್ಳಿಗೆ ಹಣ್ಣುಗಳ ಸಂಖ್ಯೆ, ಈ ಎಲ್ಲಾ ಗುಣಗಳು ಪ್ರತಿ ಬಳ್ಳಿಗೆ ಹಣ್ಣಿನ ಇಳುವರಿಯ ಮೇಲೆ ಸಕಾರಾತ್ಮಕ ಮತ್ತು ನೇರ ಪರಿಣಾಮವನ್ನು ಬೀರಿರುವುದನ್ನು ಗಮನದಲ್ಲಿಟ್ಟುಕೊಂಡು ತುಪ್ಪದ ಹೀರೆಕಾಯಿಯಲ್ಲಿ ಕಾಯಿಯ ಇಳುವರಿಯನ್ನು ವೃದ್ಧಿಸಲು ಈ ಗುಣಗಳ ಮೇಲೆ ಹೆಚ್ಚಿನ ಗಮನಕೊಡಬೇಕು.

ಸಾಲುಗಳ ಸಂಯೋಜಿತ ಸಾಮರ್ಥ್ಯದ ಅಧ್ಯಯನದ ಪ್ರಕಾರ L_1 , L_2 , L_6 ಸಾಲುಗಳು, T_1 ಮತ್ತು T_2 ತಳಿಗಳು ಉತ್ತಮ ಸಾಮರ್ಥ್ಯ ಸಂಯೋಜಿಕಗಳಾಗಿ ಕಂಡುಬಂದಿವೆ. ಸಂಕರಣ ತಳಿಗಳಾದ $L_2 \times T_1$, $L_6 \times T_1$, $L_8 \times T_3$ ಮತ್ತು $L_9 \times T_3$ ಗಳು ಉತ್ತಮ ನಿರ್ದಿಷ್ಟ ಸಂಯೋಜಿಕಗಳೆಂದು ಗುರುತಿಸಲಾಗಿದೆ. ಈ ಸಂಕರಣ ತಳಿಗಳು ಪ್ರಚಲಿತ ತಳಿಗಳಿಗಿಂತ ಅತಿ ಹೆಚ್ಚು ಸಂಕರಣತೆಯನ್ನು ತೋರಿವೆ. ತುಪ್ಪದ ಹೀರೆಕಾಯಿಯಲ್ಲಿ ಇಳುವರಿ ಮತ್ತು ಇತರ ಗುಣಲಕ್ಷಣಗಳನ್ನು ಅಭಿವೃದ್ಧಿ ಪಡಿಸಲು ಸಂಕರಣ ತಳಿಗಳ ಅಭಿವೃದ್ಧಿ ಅಥವಾ ಮರುಕಳಿಸುವ ಆಯ್ಕೆಯ ವಿಧಾನ ಉತ್ತಮವಾಗಿದೆ ಎಂದು ಪ್ರಸ್ತುತ ಅಧ್ಯಯನದಲ್ಲಿ ಕಂಡುಬಂದಿದೆ.