"CHARACTERIZATION, YIELD COMPONENTS AND HETEROSIS IN BITTER GOURD (*Momordica charantia* L.)"

THESIS
SUBMITTED
TO BIDHAN CHANDRA KRISHI VISWAVIDYALAYA
IN PARTIAL FULFILMENT OF THE REQUIREMENTS FOR
THE AWARD OF THE DEGREE OF
DOCTOR OF PHILOSOPHY

In

HORTICULTURE (VEGETABLE SCIENCE)

By

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APPROVAL OF THE EXAMINERS FOR THE AWARD OF THE DEGREE OF DOCTOR OF PHILOSOPHY (HORTICULTURE) IN VEGETABLE SCIENCE

We, the undersigned, having been satisfied with the performance of Mr. **M. Lakshman Naik** in the viva-voce examination, conducted today, the ……, recommend that the thesis be accepted for the award of the Degree of **Doctor of Philosophy** in **Horticulture (Vegetable Science)** of Bidhan Chandra Krishi Viswavidyalaya.

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This is to certify that the work recorded in the thesis entitled **"Characterization, yield components and heterosis in bitter gourd (*Momordica charantia* L.)"** Submitted by Mr. **M. Lakshman Naik** for the award of the degree of **Doctor of Philosophy in Horticulture** (**Vegetable Science)** of Bidhan Chandra Krishi Viswavidyalaya, Mohanpur, Nadia, West Bengal is a faithful and bona fide research work carried out under my personal supervision and guidance. The result of the investigation reported in this thesis has not so far been submitted for any other Degree or Diploma. The assistance and helps received from various sources during the course of investigation have been duly acknowledged.

……

(S. B. Chattopadhyay)
Chairman Advisory Committee

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(M. Lakshman Naik)

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LIST OF ABBREVIATION

ANOVA	:	Analysis of variance
BCKV	:	Bidhan Chandra Krishi Viswavidyalaya
CD	:	Critical Difference
cm	:	Centimeter
CV	:	Coefficient of variation
et al.	:	and others
Fig	:	Figure
g	:	gram
kg	:	Kilogram
m	:	meter
ha	:	hectare
mg	:	milligram
SE (d)	:	Standard error difference
S.Em	:	Standard error mean
df	:	Degrees of freedom
RBD	:	Randomized Block Design
Vit-C	:	Ascorbic Acid
viz.,	:	Namely
vs.	:	Against
No.	:	Number
per se	:	As such with mean
L x T	:	Line x Tester
HD	:	Half diallel
FD	:	Full diallel
GCA	:	General combining ability
SCA	:	Specific combining ability
gca	:	General combining ability
sca	:	Specific combining ability
$\sigma^2 GCA$	:	Variance due to General combining
ability $\sigma^2 SCA$	:	Variance due to Specific combining
ability		
i.e.	:	That is
@	:	at the rate of
SS	:	Sum of Squares
MSS	:	Mean Sum of Squares
%	:	per cent
@	:	at the rate of
&	:	and
^0C	:	degree Celsius
W. B	:	West Bengal

Bidhan Chandra Krishi Viswavidyalaya
Faculty of Horticulture
Department of Vegetable Science

Title of the thesis	: "**Characterization, yield components and heterosis in bitter gourd (*Momordica charantia* L.)"**
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Abstract

The present study was carried out at Horticultural Research Station, Mandouri, Bidhan Chandra Krishi Viswavidyala under New Alluvial zone of West Bengal, India. The experimental material comprised of 33 genotypes of bitter gourd were collected from NBPGR, Thrissur and different parts of West Bengal were sown following RBD with three replications to study the genetic variability, to assess the genetic divergence for selecting parental materials for crossing, to estimate heterosis, combining ability and gene action for different quantitative characters with the following objectives.

Objectives:

(i) To characterize bitter gourd genotype on the basis of qualitative and quantitative traits as per minimal descriptors.

(ii) To determine the genetic variability parameters for important growth and fruit characters influencing yield, their interrelationships and their direct and indirect effects on fruit yield.

(iii) To analyses the genetic divergence of collected materials based on some important quantitative traits.

(iv) To assess the extent of heterosis in desired direction and to estimate the dominance reactions for yield and its components and quality parameters.

(v) To determine the nature of gene action for yield and other important attributes with a view to identify good combiners, as well as to frame the breeding strategy for the genetic improvement of such characters.

The summarized results and conclusions drawn out of this study are presented hereunder

- Thirty-three bitter gourd genotypes exhibited wide range of variations in twenty-one qualitative traits and twenty quantitative traits. Two genotypes Gangajali Karala and IC-541448 were found most promising in respect of fruit yield per plant and nutritional quality traits at the Gangetic plains of West Bengal. These two genotypes could be tested at the state and national levels before releasing as varieties.

- High, GCV coupled with broad sense heritability, and genetic advance was registered for number of primary branches, fruit yield per plant and beta carotene content, which might be under the control of additive gene action and could be improved upon by selection without progeny testing.

- Emphasis should be given on fruit weight and petiole length for selecting high yielding genotypes of bitter gourd.

- Based on superior mean performance for agronomic characters (fruit yield per plant, etc.), genetic distances, clustering pattern and consumer preference characters (color, fruit shape, etc.), six promising and diverse inbred lines or varieties of bitter gourd *viz*., IC-599428, K-85603, IC-65787, IC-541448, IC-596983 and Gangajali Karala were selected and these genotypes could be utilized as donor parents in hybridization programme to develop promising hybrids/improved lines.

- A 6 x 6 full diallel mating design was followed to study gene action of 20 quantitative characters. The relative magnitude and importance of additive and non-additive variances in the genetic control of various characters were revealed by σ^2gca/ σ^2sca. Preponderance of non-additive gene action was evident for vine length, number of primary branches, internode length, node number at female flower appearance, sex ratio, number of marketable fruit harvest, fruit weight, fruit length, 100 seed weight and number of seed per fruit ; additive gene action was noticed in petiole length, days to 50% flowering, peduncle length, number of fruits/plant and fruit diameter; both additive and non-additive gene action was important for days to last fruit harvest.

- On the basis of gca effects and *per se* performance, two parents IC-65787 and IC-541448 appeared as good general combiners in respect of fruit yield/plant and other important horticultural traits, and they could be utilized in future breeding.
- Two outstanding hybrids based on sca effects, heterobeltiosis and standard heterosis manifested in them, and *per se* values were 'IC-599428 × Gangajali Karala and IC- 599428 × K-85603', and they could be commercially exploited after critical evaluations in different agro-climatic situations of West Bengal. The significant difference between direct cross and reciprocal cross depicted that reciprocal effect existed for most traits under study. This investigation suggests bitter gourd breeders should include reciprocal crosses in their any mating design since it is imperative for high-yielding oriented breeding.
- Partial to over-dominance effects were found to be involved in the inheritance of fruit yield and most of the horticultural traits of bitter gourd under study.

Chapter 1

INTRODUCTION

CHAPTER-I

INTRODUCTION

Bitter gourd (*Momordica charantia* L.) is an economically important member of the Cucurbitaceae family. It is extensively cultivated in India, China, Malaysia, Africa, and South America (Raj *et al*., 1993; Singh, 1990). Its primary centre of origin is Tropical Asia particularly Eastern India (includes the states of Odisha, West Bengal, Assam, Jharkhand and Bihar) and Southern China *i.e.,* Indo Burma centre of origin (Zeven and Zhukovsky, 1975). The somatic chromosome number of bitter gourd is 2n = 2x = 22. It is known by different names such as Bitter cucumber or Balsam pear in English, Karela in Hindi, Gujarathi and Punjabi, Karala in Bengali and Marathi, Kakara kaya in Telugu, Beet Karela in Assam, Hagalakayi in Kannada and Pavakai in Malayalam and Tamil. The crop is highly cross pollinated due to monoecious nature. Other species belonging to this genus are *M. dioca, M. cochinchinensis, M. balsamina, M. tuberosa, M. subangulata, M. denudata and M. macrocarpa*.

Bitter gourd ranks first among the cucurbits in respect of iron and vitamin C contents (Singh *et al*. 2006; Aparna Upadhyay *et al*.2015; Hassan L.G. *et al.* 2006). Fruit of 100 g contains 83.20 g of moisture, 10.60 g of carbohydrates, 2.10 g of proteins, 1.70 g of fibre, 23 mg of calcium, 38 mg of phosphorus, 171 mg of potassium, 2.4 mg of sodium, 2 mg of iron, 0.19 mg of copper, 0.08 mg of manganese, 0.46 mg of zinc, 126 mg of beta- carotene and 96 mg of vitamin-C (Gopalan *et al.* 1993). India is the second largest producer of vegetables with a production of 184.39 million tonnes from the area of 10.25 million hectares and productivity of 17.98 tonnes per hectare in the world after China. Among the states of India, Uttar Pradesh is leading producer with a production of 28.31million tonnes from the area of 1.45 million hectares and a productivity of 19.43 tonnes per hectare and West Bengal ranks second with a production of 27.69 million tonnes from an area of 1.40million hectares and a productivity of 19.77 tonnes per hectare. Bitter gourd occupies an area of 97 thousand hectares with the annual production of 1.137 million tonnes in India (Anonymous, 2018).

Due to growing health awareness and information about anti-diabetic property and nutritive value of bitter gourd, the cultivation of bitter gourd has gained momentum in the recent years. Agricultural and processed food products exports development authority (APEDA) has identified bitter gourd has one of the potent vegetables for export

among cultivated cucurbitaceous vegetables (APEDA, 2017). Bitter gourd has numerous uses. The fruits are used as a vegetable in many ways and quite commonly consumed in cooked, fried and stuffed forms (L.G. Hassan, K.J. Umar. (2006), the fruits are also pickled, canned and dehydrated. Every part of the plant is used medicinally. The fruits have cooling, digestive, laxative, antipyretic, ant diabetic properties and its administration is useful in biliousness, blood diseases, rheumatism, and asthma (Leslie Taylor. 2002). The leaf is used internally as a laxative and as an ointment for sours, the juice of fresh leaves is prescribed for diabetes in ayurveda. It is claimed that the fruit powder is used for healing wounds, leprous and malignant ulcers (Prasad and V. Jain *et al.* 2006). It is reported for its usefulness in snakebites. The roots have abortifacient activity. It has been reported that protein of bitter gourd inhibited the growth of immune deficiency virus (HIV-1) in human beings (Singh A and Singh SP *et al.* 1990).

Although the general chemical composition of *M. charantia* in immature fruit is similar to other cucurbits, bitter gourd possesses comparatively high concentrations of ascorbic acid and iron (Behera, 2004). White-fruited Indian varieties are, in fact, relatively high in polypeptide-p, phenolics, polyphenolic compounds and natural oxidants and antioxidants (Horax *et al.* 2005; Khanna *et al*. 1981; Krawinkel and Keding *et al.* 2006). Bitter gourd has been used as a traditional medicine for diabetes in India, China, and Central America (Grover *et al*. 2002; Yeh *et al.* 2003) and other health-related ailments such as health promoting substances such as charantin (Yeh *et al.* 2003) and vicine (Dutta *et al.* 1981). The diverse morphological characters include sex expression, growth habit, maturity and fruit shape, size, colour, and surface texture (Robinson and Decker-Walters *et al*. 1997).

In India *M. charantia* provides for relatively broad phenotypic species variation. Genetic diversity assessments and linkage map construction can increase the effectiveness of breeding programs (Paterson *et al*., 1991; Fan *et al*., 2006).In spite of its high nutritive values, well acceptability among growers and consumers and wide range of available genetic variability, India is still lagging behind to attain the optimum productivity in bitter gourd owing to use of local unimproved cultivars and heavy infestations of insect-pest and diseases particularly viral disease. Therefore, much concentrated efforts are necessary to improve its yield and nutritional quality. Hence, evaluation of the potentialities of the indigenous germplasm is essential because promise for further improvement programme depends on the genetic diversity of the crop.

The magnitude of heritable and more particularly its genetic components, is clearly the most important aspect of the genetic constitution of the breeding material which has a close bearing on its response to selection. Again, selection of one trait invariably affects a number of associated traits which evokes the necessity in finding out the interrelationship of various yield components both among themselves and with yield. The proper choice of parents based on their combining ability is a prerequisite in any sound breeding programme. Parents are generally selected on the basis of their combining ability. Such studies not only provide necessary information regarding the choice of parents but also simultaneously illustrate the nature and magnitude of gene action involved in the expression of desirable traits. Estimates of combining ability parameters place heterosis breeding on a further scientific footing. Bitter gourd offers much scope of improvement through heterosis breeding which can further be utilized for the development of desirable recombinants (Tewari *et al.* 2001; Sundaram et al. 2008a; Jhadav *et al.*2009). Diallel (Griffing, 1956) is one such analysis which is a useful tool for preliminary evaluation of genetic stock for use in hybridization programme with a view to identify good general- as well as specific-combiners.

Keeping this information in view, and the lack of research done in the Gangetic plains of West Bengal, the present investigation has been undertaken with the following objectives:

(i) To characterize bitter gourd genotype on the basis of qualitative and quantitative traits as per minimal descriptors.

(ii) To determine the genetic variability parameters for important growth and fruit characters influencing yield, their interrelationships and their direct and indirect effects on fruit yield.

(iii) To analyses the genetic divergence of collected materials based on some important quantitative traits.

(iv) To assess the extent of heterosis in desired direction and to estimate the dominance reactions for yield and its components and quality parameters.

(v) To determine the nature of gene action for yield and other important attributes with a view to identify good combiners, as well as to frame the breeding strategy for the genetic improvement of such characters.

Chapter 2

REVIEW OF LITERATURE

CHAPTER-II

REVIEW OF LITERATURE

Keeping in view of the objectives of present investigation "Characterization, yield components and heterosis in bitter gourd (*Momordica charantia* L.)" the available literature has been reviewed and presented under the following headings.

2.1 Genetic variability, heritability and genetic advance

2.2 Correlation analysis

2.3 Path coefficient analysis

2.4 Genetic diversity

2.5 Heterosis

2.6 Combining ability and gene action

2.1 Genetic variability, heritability and genetic advance

Genetic variability for yield and its components is essential in the base population for successful crop improvement (Allard, 1960). Yield and its components for quantitative characters are polygenically inherited which are greatly influenced by environment. The phenotype of a character is the resultant of interaction between genotype and environment. Partitioning of observed variability into heritable and non-heritable components is essential to get a true indication of the genetic variation of the trait. Genetic parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2) and genetic advance (GA) are commonly used in describing the variability and genetics of a character.

Heritability as described by Smith (1936) is the ratio expressed as percentage of variance component due to additive (fixable) gene effects (σ^2A) to the sum of additive (σ^2A), dominance (σ^2D) and epistatic (σ^2E) gene effects. Heritability in broad sense may be defined as the ratio of genetic variance to phenotypic variance (Lush, 1949). Characters with high estimates of heritability are of great importance to the plant breeder as it enables the plant breeder to formulate criteria based on phenotypic performance. If heritability of a character is very high, selection for the character is fairly easy. This is because there would be a close correspondence between genotype and phenotype due to a relatively smaller contribution of environment to the phenotype. But for character with

low heritability, selection may be considerably difficult due to masking effect of environment on the genotype effects. Genetic advance is the expected genetic gain or improvement in the next generation by selecting the superior individuals under a certain amount of selection pressure. Chhonkar *et al.* (1979) reported that heritability estimates and genetic advance were more valid for selection than heritability estimates alone. It was observed that a greater amount of genetic advance may be expected if the heritability is chiefly due to additive gene action. It was further stated that high heritability does not necessarily increase genetic advance. If heritability is coupled with high genetic advance, it indicates that the character is chiefly governed by additive genes and will be most effective for selection and further utilization in breeding programmes.

Table-2.1: Different components of genetic variability, heritability and genetic advance for different characters of bitter gourd

Characters	Components of variability	References
Vine length (cms)	High heritability coupled with high genetic advance	Maneesh *et al.* (2014)
	High heritability along with low genetic advance (GAM)	Rani *et al*. (2015)
	High heritability along with Moderate GCV and PCV values	Vivek *et al*. (2017)
	High heritability along with low PCV and GCV values	Rani *et al*. (2015)
Number of primary branches per vine	High heritability coupled with high PCV and GCV values	Maneesh *et al*. (2014)
	High PCV and GCV values	Khan *et al*. (2015)
	High heritability coupled with low PCV and GCV values	Rani *et al.* (2015)
	High heritability along with high gam	Vivek e*t al*. (2017)
	Moderate PCV and GCV values along with high GAM	Devendra *et al*. (2018)
Node number at female flower appearance	High heritability couple with high PCV and low GCV values	Mudassar *et al*. (2015)
	High heritability coupled with low gam	Rani *et al.* (2015)
	High heritability along with low PCV and GCV values	Vivek *et al*. (2017)
	High heritability coupled with high GAM	Tyagi *et al.* (2017)

Characters	Components of variability	References
Days to first female flower appearance	High heritability coupled with low PCV and GCV values	Maneesh *et al*. (2014)
	Low PCV and GCV values	Rani *et al.* (2015)
	High heritably along with low GAM	Vivek *et al*. (2017)
	Moderate heritability along with low PCV and GCV values	Devendra *et al*. (2018)
Days to 50% flowering	Moderate heritably along with low PCV and GCV values	Yadagiri *et al*. (2017)
	Moderate heritability coupled with low gam	Debendra *et al. (*2015)
Days to first fruit harvest	High heritability along with low PCV and GCV values	Maneesh *et al.* (2014)
	Moderate heritability along with low PCV and GCV values	Yadagiri *et al*. (2017)
	High heritably coupled with high gam	Vivek *et al.* (2017)
	Low PCV and GCV values	Tiwari *et al*. (2018)
Fruit length (cm)	High heritability along high gam	Maneesh *et al*. (2014)
	High heritability coupled with low PCV and GCV values	Rani *et al*. (2015)
	High PCV and GCV values	Khan *et al*. (2015)
	High heritability along with high PCV and GCV values	Yadagiri *et al*. (2017)
	Low heritability along with low PCV and GCV values	Tiwari *et al.* (2018)
Fruit dimeter (cm)	High heritability along with high PCV and GCV values	Maneesh *et al*. (2014)
	High heritability coupled with low gam	Rani *et al*. (2015)
	Moderate heritability along with low PCV and GCV values	Yadagiri *et al*. (2017)
	High heritability along with high PCV and GCV values	Devendra *et al*. (2018)
	Low PCV and GCV values	Tyagi *et al.* (2017)

Characters	Components of variability	References
Average fruit weight	High heritability along with high PCV and GCV values	Maneesh *et al.* (2014)
	High heritably along with low GAM	Rani *et al.* (2015)
	High PCV and GCV values	Khan *et al*. (2015)
	Low PCV and GCV values	Tiwari *et al*. (2018)
Number of fruits per plant	High heritability along with high PCV and GCV values	Maneesh *et al.* (2014)
	High PCV and GCV values	Khan *et al.* (2015)
	High heritably along with low PCV and GCV values	Rani *et al*. (2015)
	High heritably along with high PCV and low GCV values	Yadagiri *et al*. (2017)
	High heritably along with high GAM	Vivek *et al*. (2017)
Fruit yield per plant	High heritably along with high PCV and GCV values	Maneesh *et al.* (2014)
	High heritability along high GAM	Rani *et al.* (2015)
	High PCV and GCV values	Yadagiri *et al*. (2017)
	High heritability along with high PCV and low GCV values	Tyagi *et al.* (2017)
Number of seeds per fruit	High heritably along with high PCV and GCV values	Maneesh *et al*. (2014)
	Low heritability couple with low PCV and GCV values	Rani *et al*. (2015)
	High heritably along with high PCV and GCV values	Yadagiri *et al*. (2017)
Ascorbic acid content	Low PCV and GCV values	Dey *et al.* (2006)
	High heritably along with high PCV and GCV values	Mudassar *et al*. (2015)
	High heritably along with low PCV and GCV values	Vivek *et al*. (2017)

2.2 Correlation analysis

Correlation studies are of considerable importance to a plant breeder especially for selection and for breeding of high yielding varieties of crop plants. Hence, knowledge of both phenotypic and genotypic correlations among important characters is of more importance in planning efficient breeding programmes. The characters which are positively correlated with yield are of considerable importance to a plant breeder for selection purposes. Phenotypic correlations are subjected to changes in environment. The genotypic correlations measure the association of breeding values and phenotypic correlations measure the environmental deviations together with non-additive gene action (Falconer, 1982).

Association of characters determined by correlation coefficients may not provide a clear picture of the relative importance of direct and indirect influence of each of the yield components towards yield. As more variables are included in the correlation study, the indirect associations become more complex.

Table- 2.2: Correlation of different characters with yield and direct their effects on yield

Character	Correlation and effect	References
Vine length (cm)	Significantly Positive association	Ramachandran and Gopalakrishnan (1979) Mangal *et al.* (1981) Geetashri *et al.* (1995) Bhave *et al*. (2003b) Sundaram (2010) NE- Islam *et al*. (2009)
Internode length (cm)	Positive association	Bhave *et al*. (2003b)
Number of primary branches per vine	Positive association	Srivastava and Srivastava (1976) Geetashri *et al.* (1995) Bhave *et al.* (2003a) Bhave *et al*. (2003b) NE- Mangal *et al.* (1981)
Days to first female flower appearance	Significant and positive association	Ramachandran and Gopalakrishnan (1979) Geetashri *et al*. (1995) Ram *et al.* (2006) Islam *et al*. (2009)

Character	Correlation and effect	References
	Significant and negative association	Sundaram (2010) Srivastava and Srivastava (1976) Mangal *et al*. (1981) Bhave *et al.* (2003b) Dey *et al.* (2005)
Node of first female flower appearance	Significant and positive association Significant and negative association	Ramachandran and Gopalakrishnan (1979) Sundaram (2010) Geetashri *et al*. (1995) Dey *et al*. (2005)
Days to first fruit harvest	Positive association Negative association	Geetashri *et al.* (1995) Bhave *et al*. (2003b) Dey *et al.* (2005)
Fruit length (cm)	Significantly positive association	Mangal *et al.* (1981) Geetashri *et al*. (1995) Bhave *et al*. (2003a) Bhave *et al*. (2003b) Dey *et al*. (2005) Islam *et al*. (2009) Sundaram (2010)
Fruit diameter (cm)	Significantly positive association	Geetashri *et al*. (1995) Bhave *et al.* (2003b) Dey *et al.* (2005) Islam *et al*. (2009) Sundaram (2010)
Average fruit weight (g)	Positive association	Srivastava and Srivastava (1976) Mangal *et al*. (1981) Geetashri *e*t al. (1995) Bhave *et al*. (2003a) Bhave *et al*. (2003b) Dey *et al.* (2005) Ram *et al*. (2006) Islam *et al.* (2009) Sundaram (2010)

Character	Correlation and effect	References
Number of fruits per vine	Significantly positive association	Srivastava and Srivastava (1976) Mangal *et al*. (1981) Geetashri *et al.* (1995) Bhave *et al*. (2003a) Bhave *et al.* (2003b) Dey *et al*. (2005) Ram *et al.* (2006) Islam *et al.* (2009) Sundaram (2010)
No. of seed per fruit	Significantly positive association	Mangal *et al*. (1981) Geetashri *et al.* (1995) Bhave *et al*. (2003a)

2.3 Path co-efficient analysis

Knowledge of inter-character relationships is very important in plant breeding for indirect selection of characters that are not easily measured and for those that exhibit low heritability. Correlation studies between characters have also been of great value. In the determination of the most effective breeding procedures as the number of independent characters affecting a dependent character increases, there is bound to be some amount of interdependence. Under such a complex situation, correlation alone becomes insufficient to explain relationships among the characters. Path coefficient analysis permits identification of direct and indirect causes of association and measures the relative importance of each character.

The literature on the direct effects of various quantitative traits on fruit yield of bitter gourd is reviewed and presented in Table 2.3.

Table 2.3: Review of literature on genotypic direct effects of various characters on fruit yield in bitter gourd

Character	Direction	Direct effect and Degree				
		Negligible (0.00 -0.09)	**Low (0.10-0.19)**	**Moderate (0.20-0.29)**	**High (0.30-0.99)**	**Very high (>1.00)**
Vine length (cm)						
	+Ve	Bhave *et al*. (2003a) Bhave *et al*. (2003b)	Sundaram (2010)	-	Geetashree *et al*. (1995)	Islam *et al*. (2009)
Internodal length (cm)						
	-	-	-	-	-	-
Number of primary branches per vine						
	+Ve	Geetashree *et al*. (1995) Bhave *et al*. (2003a)	-	-	Srivastava and Srivastava (1976)	-
Days to first female flower appearance						
	+Ve	-	-	Dey *et al*. (2005) Sundaram (2010)	-	Geetashree *et al*. (1995)
	-Ve	Bhave *et al*. (2003b)	Srivastava and Srivastava (1976)	-	-	-
Node no at first female flower appearance						
	-Ve	-	-	-	Geetashree *et al*. (1995) Dey *et al*. (2005) Sundaram (2010)	-
Days to first fruit harvest						
	-Ve	-	-	-	Geetashree *et al*. (1995) Dey *et al*. (2005)	-
Fruit length (cm)						
	+Ve	Geetashree *et al*. (1995) Bhave *et al*. (2003a) Bhave *et al*. (2003b), Dey (2005)	-	Sundaram (2010)	Dey *et al*. (2005) Islam *et al*. (2009)	-

Character	Direction	Direct effect and Degree				
		Negligible (0.00 -0.09)	**Low (0.10-0.19)**	**Moderate (0.20-0.29)**	**High (0.30-0.99)**	**Very high (>1.00)**
Fruit diameter (cm)						
	+Ve	-	Dey *et al*. (2005)	-	Sundaram (2010), Singh (2014)	Geetashree *et al*. (1995)
Average fruit weight (g)						
	+Ve	Sundaram (2010),	-	-	Srivastava and Srivastava (1976) Bhave *et al*. (2003b) Dey *et al*. (2005),	-
	-Ve	Bhave *et al*. (2003a)	-	-	Geetashree *et al*. (1995)	-
Number of fruits per plant						
	+Ve	Geetashree *et al*. (1995) Bhave *et al*. (2003a),	-	-	Srivastava and Srivastava (1976) Bhave *et al*. (2003b) Dey *et al*. (2005), Dey (2005), Behera (2013), Sundaram (2010),	Islam *et al*. (2009) Sundaram (2010)
Number of seeds per fruit						
	+Ve	-	-	-	Geetashree *et al*. (1995) Bhave *et al*. (2003a)	-

2.4 Genetic diversity

Genetic diversity has been considered as an essential pre-requisite for obtaining high yielding progenies through hybridization. D^2 statistics measures the degree of diversification of parents and determines the relative contribution of each component character to the total divergence. In any breeding programme inclusion of such genetically diverse parents for crossing will produce desirable recombinants in their progenies for further selection. The importance of genetic diversity has long been appreciated by breeders and it has been proved in many crops that diversity between the parents used in hybridization programme is the key to success in most cases. It is commonly found that the level of heterosis exhibited by a hybrid is a function of the genetic divergence between the parents. Multivariate analysis (Mahalanobis generalized distance) has been found to be a potential biometrical tool in qualifying the degree of divergence in germplasm collection of various crop plants (Rao, 1952).

The latest (since 2005) available literature on bitter gourd is reviewed here under.

Kutty and Dharmatti (2005) observed that the bitter gourd genotypes falling in cluster II had the maximum divergence, followed by the cluster IV and I. The maximum inter-cluster distance was between cluster VI and IX followed by cluster VII and IX. The characters like number of leaves at 50% flowering and productive length of vine contributed maximum to divergence.

Dey *et al.* (2007) found that the maximum inter-cluster distance was obtained between cluster II and IV while minimum distance was between II and VI. Cluster IV followed by cluster III showed superiority for yield and other desirable traits in bitter gourd.

Sundaram (2010) showed the presence of wide range of genetic diversity in bitter gourd and the clustering pattern of genotypes revealed that the genetic diversity was independent of the geographical diversity. He also found that individual fruit weight constituted a maximum of 26.83 per cent to the divergence, followed by fruit yield of fruits per vine and length of fruit. Ranking of genotypes based on intra cluster mean performance for those characters which are major contributors of genetic diversity revealed its usefulness in selecting parents for heterosis breeding.

Laxuman *et al.* (2012) assessed the magnitude of heterosis and its relation to parental divergence in the diallel cross material involving eight parents and 28 hybrids

during summer season, 2005. Parents were classified into 4 clusters through distance analysis. Parental divergence was classified into four divergence classes. DC1 (298.173) was highly diverse class and DC4 (209.090-278.047) was lower diverse class while DC2 and DC3 were optimum divergence classes. Genetic diversity analysis indicated the high frequency of hybrids in classes DC2 and DC3 indicating moderate genetic diversity is most desirable to produce highly heterotic hybrids.

Kundu *et al.* (2012) studied that genetic divergence among 36 genotypes of bitter gourd using multivariate analysis based on 22 characters, 36 genotypes were grouped into 6 distant clusters. Days to 1st male flower opening, primary branches per vine, fruit yield per vine, days to green fruit maturity, seed weight per fruit and mature seed width had the highest contribution towards the divergence. From cluster diagram, it can be concluded that the genotypes in the cluster III were diverse from the genotypes of cluster IV but the genotypes belonging to the cluster II and VI were distantly related.

Singh *et al.* (2013) grouped the genotypes of bitter gourd into 6 clusters based on Mahalanobis D^2 statistics using Tocher's method and found that the genetic diversity was independent of the geographical diversity. They were also observed that individual fruit weight constituted a maximum of 64.14% contribution to the divergence followed by days to first female flower appearance. Ranking of genotypes based on intra-cluster mean performance for these characters which are major contributors of genetic diversity revealed its usefulness in selecting parents for heterosis breeding.

Singh *et al.* (2015) carried out an experiment to analyse multivariate analysis based on cluster and principal component (PC) for yield and its 11 contributing traits in 32 bitter gourd genotypes including 2 checks, i.e. Pusa Do Mausami and Kalyanpur Sona during summer. The cluster analysis categorized all 32 bitter gourd genotypes into 6 major clusters. Extreme genetic divergence was estimated among clusters. Average inter-cluster distance was found maximum (717.86) between cluster V (NDBT-12) and cluster VI (NDBT-76). The contribution of fruit weight and fruit length towards genetic divergence was noted as 74 and 13%, respectively. Highest cluster mean values for fruits per plant, fruit weight (g) and fruit yield per plant (kg) was found in cluster V followed by cluster II.

Gowda (2017) revealed among the different quantitative characters, average fruit weight (37.27%), primary branches per vine (15.1%) and fruit yield per vine (7.76%)

were found to be major contributors towards genetic divergence. Tushi x Pusa Do Mousumi and Tushi were much more divergent from rest of the genotypes used in the experiment. Similarly, the genotypes of cluster VII and genotypes of II, III, V and VI were found to be genetically more divergent from each other. The results of canonical analysis as a supplement to classification based on the Tocher's method were similar to the results of D^2 analysis with some discrepancies.

2.5 Heterosis

The term heterosis is now widely used, which refers to the phenomenon in which the F_1 hybrid obtained by crossing the two genetically dissimilar homozygous gametes or individuals, shows increased or decreased vigour over the parental values. Shull (1948) referred to this phenomenon as the stimulus of heterozygosis. The expression of heterosis may be due to factors such as heterozygosity, allelic interaction such as dominance or over dominance, nonallelic interaction or epistasis and maternal interactions. The degree of heterosis depends upon the number of heterozygous alleles. The higher the number of heterozygous loci, more the heterosis expected (East and Hayes, 1912). The term heterobeltiosis has been coined by Fonesca and Patterson (1968), which refers to the increased or decreased vigour of F_1 over its better parent. Hybrids have offered advantages for improvement in productivity, earliness, uniformity, quality, wider adoptability and for rapid deployment of dominant genes for resistance to diseases and pests (Riggs, 1988). A considerable degree of heterosis has been documented in bitter gourd for various characters. The heterosis for some of the traits as reported by various workers is reviewed in Table 2.5.

Table 2.5: Review of literature on Heterosis in bitter gourd

Sl. No	Character	Number of hybrids studied	Heterosis	Heterobeltiosis	Standard heterosis	References
1	Vine length (m)	10	0.23 to 18.20	-	-7.27 to 24.99	Celine and Sirohi (1996)
		24		- 29.29 to 41.23	-	Ram *et al.* (1997)
		03	-22.93 to 92.98	-	-22.98 to 33.07	Tewari and ram 1999
		28	-	-	-28.6 to 36.4	Chaubey and Ram (2004)
		25	-11.05** to 24.04**	-11.44** to 23.60**	-17.22** to 15.53**	Mohan *et al*. 2005
		28	-21.74 to 5.37	-17.50 to 10.81		Jadav *et al.* 2009
		28	-	-140.50** to 107.00**	-22.70** to 14.64**	Laxuman *et al*. 2012b
		19	-2.65 to 6.97	-20.25 to 29.52	-14.35 to 56.35	Shridhar (2012)
		40	-2.67 to 68.75	-	-1.30 to 65.48	Danareddy (2013)
2	Number of primary branches per vine	28	3.30 to 25.85	-	-	Singh *et al.* (1997)
		03	-8.52 to 29.26	-	14.73 to 10.27	Tewari and Ram (1999)
		28	-	-	-24.4 to 18.5	Chaubey and Ram (2004)
		25	-23.19** to 78.44**	-37.65** to 76.75**	-44.83** to 23.62**	Mohan (2005)
		28	-23.58** to 28.9**	-28.79** to 26.67**	-13.46 **to 30.77**	Laxuman (2005)
		28	-21.59 to 8.93	-18.70 to 23.76		Jadav *et al.* (2009)
		19	15.65 to 36.73	-	-19.35 to 63.41	Shridhar (2012)
		36	-6.33 to 11.99	-	-	Mahaboob (2014)
3	Days to first female flower appearance	10	-3.15to .11	1.23 to 7.67	-7.63 to 33.44	Celine and srirohi 1996

Sl. No	Character	Number of hybrids studied	Heterosis	Heterobeltiosis	Standard heterosis	References
		24	-	15.72to 7.48	-	Ram *et al* 1997
		03	-4.40 to 10.00	-	-18.50 to -8.33	Tewari and ram 1999
		21	-	-6.08 to -18.37	0.00 to -5.74	Singh *et al* 2000
		28	-	-	-2.6 to 50.00	Chaubey and ram2004
		25	-21.11**t0 6.50**	-20.65** to 10.65**	-8.04** to 18.97**	Mohan 2005
		19	-15.65 to 6.97	-20.25 to 36.73	-19.35 to 63.41	Shridhar (2012)
		36	-11.97to -68.92	-11.97 to 18.54	-10.63 to 150.50	Mahaboob (2014)
4	Node of first pistillate flower appearance	21	-	-14.71 to -27.80	-14.44 to -34.45	Singh *et al.* 2000
		28	-	-	-19.2 to 84.6	Chaubey and Ram 2004
5	Days to first fruit harvest	10	-1.98	-7.72 to -4.47	-	Celine and Sirohi (1996)
		28	-0.42 to 15.06	-	-	Sing *et al.* (1997)
		21	-	-6.19 to -22.20	0.00 to -6.20	Singh *et al.* (2000)
		25	-8.97** to 7.83** -	-5.45** to 10.08**	-6.03** to 11.38**	Mohan (2005)
		28	18.94** to 14.66**	-18.83** to 14.85**	-2.17** to 1.37**	Laxuman (2005)
		28	-12.67 to 12.02	16.39 to 11.49	-	Jadav *et al.* (2009)
		12	-19.40** to 3.60	-	-	Dey *et al.* (2010)
		90	-	-	-9.70** to 10.26**	Thangamani *et al*. (2011b)
6	Fruit length (cm)	10	0.25 to 12.90	-	-	Celine and Sirohi (1996)
		24	-	-73.07 to 0.00	-	Ram *et al*. (1997)
		28	0.90 to 17.75	-	-	Singh *et al.* (1997)

Sl. No	Character	Number of hybrids studied	Heterosis	Heterobeltiosis	Standard heterosis	References
		03	3.54 to -12.22	-	-26.24 to 37.08	Tewari and Ram (1999)
		28	-	-	38.70 to 103.70	Chaubey and Ram (2004)
		25	-12.37** to 56.00**	-30.44** to 28.18**	-37.14** to 11.87**	Mohan (2005)
		56	-	-	-68.38** to 16.31**	Sundaram (2008a)
		28	-35.87 to 24.71	-	-32.14 to 38.10	Laxuman *et al*. (2012a)
		19	-15.65 to 6.97	-20.25 to 36.73	-19.35 to 63.41	Shridhar (2012)
		40	-20.67 to 68.75	-	-28.30 to 6.48	Danareddy (2013)
		28	-0.64 to 30.03	-	-	Singh *et al.* (2013)
		90	-	-	-1.04 to 4.25	Thangamani and Pugalendhi (2013)
		36	-36.19 to 6.28	-36.19 to 13.17	-33.03 to 23.54	Mahaboob (2014)
7	Fruit diameter(cm)	10	7.67 to 9.11	19.84 to 32.44	-	Celine and Sirohi (1996)
		24	-	-51.84 to 0.00	-	Ram *et al.* (1997)
		28	0.29 to 8.98	-	-	Singh *et al.* (1997)
		03	-1.72 to 14.33	-	-22.98 to -8.95	Tewari and Ram (1999)
		28	-	-	-22.80 to 8.4	Chaubey and Ram (2004)
		25	-11.48** to 14.56**	-19.78** to 6.82**	-18.33** to 9.05**	Mohan (2005)
		56	-	-18.33** to 9.05**	-	Sundaram (2008a)
		28	-	-	-5.59 to 78.09**	Jadav *et al*. (2009)
		12	-20.68 to 6.05	-15.65 to 11.08	-	Dey *et al*. (2010)
		90	2.30 to 10.50**	-	-	Thangamani *et al*. (2011b)
		28	-	-	-13.43** to 26.32**	Laxuman *et al*. (2012a)

Sl. No	Character	Number of hybrids studied	Heterosis	Heterobeltiosis	Standard heterosis	References
		28	-34.14** to 29.27**	-	-32.14** to 38.1**	Laxuman *et al*. (2012b)
		90	-	-	-2.43 to 36.28	Thangamani and Pugalendhi (2013)
		36	-25.18 to 8.25	0.29to 8.96	35.64 to 77.19	Mahaboob (2014)
8	Average fruit weight(g)	28	-	-	19.2 to 81.1	Chaubey and Ram (2004)
		25	-9.09** to 38.54**	-12.67** to 37.18**	-21.92** to 8.09**	Mohan (2005)
		56	-	-	-70.31** to 99.16**	Sundaram (2008a)
		28	-32.72 to 10.22	-32.72 to 16.46	-	Jadav *et al*. (2009)
		12	5.00 to 14.50**	-	-	Dey *et al*. (2010)
		90	-	-	-19.96** to 35.96**	Thangamani *et al*. (2011b)
9	Number of fruits per plant	10	2.18 to 44.85	2.18 to 44.85	6.47 to 51.65	Celine and Sirohi (1996)
		24	-	-66.67 to 30.61	-	Ram *et al.* (1997)
		28	2.38 to 75.59	-	-	Singh *et al.* (1997)
		03	-21.64 to 59.1	-	2.15 to 59.14	Tewari and Ram (1999)
		21	-	13.15 to 130.06	25.39 to 86.20	Singh *et al.* (2000)
		28	-	-	-32.3 to 45.3	Chaubey and Ram (2004)
		25	-28.37** to 47.75**	-34.34** to 38.38**	-42.76* to 15.86**	Mohan (2005)
		56	-	-	-29.82** to 506.93**	Sundaram (2008a)
		28	-23.10 to 29.54	-23.10 to 43.72	-	Jadav *et al.* (2009)
		12	74.12** to100.23**	-	-	Dey *et al*. (2010)
		90	-	-	-16.30** to 140.15**	Thangamani *et al*. (2011b)

Sl. No	Character	Number of hybrids studied	Heterosis	Heterobeltiosis	Standard heterosis	References
10	Fruit yield per plant (kg)	10	0.47 to 54.00	0.47 to 54.00	1.63 to 55.80	Celine and Sirohi (1996)
		24	-	-71.88 to 98.17	-	Ram *et al.* (1997)
		28	4.35 to 64.28	-	-	Singh *et al*. (1997)
		03	-10.31 to 50.02	-	2.15 to 50.14	Tewari and Ram (1999)
		21	-	25.85 to 200.00	38.13 to 100.00	Tewari *et al.* (2001)
		16	-	-24.03** to 112.79**	0.91 to 144.00**	Chaubey and Ram (2004)
		28	-	-	-11.2 to 85.9	Mohan (2005)
		25	-27.78** to 92.88**	-31.11** to 84.88**	-50.42** to 25.43**	Sundaram (2008a)
		56	-	-	9.59* to 151.49**	Jadav *et al.* (2009)
		28	-38.91 to 41.48	-38.91 to 63.14	-	Dey *et al.* (2010)
		12	38.22** to 97.49**	-	-	Thangamani *et al.* (2011b)
		90	-	-	-10.61** to 72.73**	Laxuman *et al.* (2012a)
		28	-51.24** to 99.68	-	-56.83** to 23.16**	Laxuman *et al.* (2012b)
		28	-8.45 to 74.55	-	-	Singh *et al.* (2013)
		36	-15.65 to 6.97	-20.25 to 36.73	-19.35 to 63.41	Mahaboob *et al.* (2014)
11	Ascorbic acid content	24	0.00 to 52.20	-	-	Yadav *et al.* (2009)
		90	-	-	-7.11 to 8.01	Thangamani *et al.* (2011)
		19	-15.65 to 6.97	-20.25 to 36.73	-19.35 to 63.41	Shridhar (2012)
		90	-	-	-0.89 to 48.90	Thangamani and Pugalendhi (2013)
		36	-1.30 to 2.70	-13.60 to 65.48	-35.00 to 18.00	Mahaboob (2014)

2.6 Combining abilities and gene action

Selection of parents based on per se performance does not always lead to the identification of desirable genotypes (Allard, 1960). A comparison on the performances of different inbred lines for hybridization work can be made on the basis of the concept of general and specific combining abilities (Narain, 1999). The terms general combining ability (GCA) and specific combining ability (SCA) were first defined by Sprague and Tatum (1942). A combining ability test is employed to specify the ability of an individual parent or in some cases two specific parents, to produce a high yielding progeny (Stoskopf *et al.* 1999). The term GCA is used to designate the average performance of a line in a hybrid combination, while SCA is used to designate those cases in which certain combinations do relatively better or worse than would be expected on the basis of average performance of the lines involved.

The GCA is specific for the set of lines and testing environment and hence it becomes meaningless, unless its value is considered in relation to at least one other line and the tester population as well as the environment. In simpler terms, the GCA effect refers to the average performance of strain or genotype in series of hybrid combinations and SCA effect in simpler term refers to the performance of a parent in a specific cross combination (Sharma, 1994). The concept of combining ability, besides aiding in the choice of parents for hybridization, also helps to deduce the gene action. The GCA component is primarily a function of additive variance, but if epistasis is present gca will also involve additive x additive type of non-allelic interaction, while SCA is mainly a function of dominance variance, but if epistasis is present, the dominance variance would also include all the three types of epistatic interaction components (additive x additive (i), additive x dominance (j) and dominance x dominance (l)). The concept of combining ability is becoming increasingly important in plant breeding to compare the performances of lines in hybrid combination. A diallel crossing system is one in which a set of "n" inbred lines are crossed to give rise to a maximum of n^2 combinations. The n^2 combinations comprise of the parental lines themselves, one set of F1's and a set of reciprocal F_1's (Griffing, 1956). By using a set of inbred lines in a diallel crossing system, a genetic interpretation in terms of quantitative inheritance is made possible by the fact that the analysis is really a "gamete" combining ability analysis.

Table 2.6: Review of literature on combining ability and gene action

Sl. No.	Character	Material and methods	Combining ability variance		Gene Action		References
			GCA	SCA	Additive	Non-additive	
1	Vine length (cm)	10 X 10 HD	Highly significant	Highly significant	+	+	Munshi and Sirohi (1994)
		10 X 3 L X T	Highly significant	Highly significant	+	+	Khattra *et al*. (2000)
		8 X 8 HD	Highly significant	-	+	-	Singh *et al*. (2004)
		9 X 9 HD	Highly significant	Highly significant	-	+	Gupta *et al.* (2006)
		6 X 4 L x T	Highly significant	Highly significant	-	+	Kumara *et al.* (2011)
2	Number of primary branches per vine	8 X 8 HD	Highly significant	Highly significant	+	+	Khattra *et al.* (1994)
		6 X 6 HD	Significant	-	+	-	Bhave *et al.* (2004)
		6 X 6 HD	Highly significant	Highly significant	+	+	Kushwaha and Karnwal (2011)
		6 X 4 L x T	Highly significant	Highly significant	-	+	Kumara *et al.* (2011)
3	Internodal length (cm)	8 X 8 HD	Highly significant	Highly significant	-	+	Laxuman (2005)
4	Days to first female flower appearance	8 X 8 HD	Highly significant	Highly significant	+	+	Khattra *et al*. (1994)
		10 X 3 L X T	-	Highly significant	-	+	Khattra *et al.* (2000)
		8 X 8 HD	Significant	Significant	+	+	Singh *et al.* (2004)
		6 X 6 HD	-	Significant	-	+	Bhave *et al.* (2004)
		9 X 9 HD	Highly significant	Highly significant	+	-	Gupta *et al*. (2006)
		10 X 10 D	Highly Significant	Highly Significant	+	+	Thangamani *et al.* (2011a)
		6 X 6 HD	Highly significant	Highly significant	+	+	Kushwaha and Karnwal (2011)
		6 X 4 L X T	Highly significant	Highly significant	-	+	Kumara *et al.* (2011)
5	Node of first female flower appearance	8 X 8 HD	Significant	Significant	+	+	Singh *et al.* (2004)
		9 X 9 HD	Highly significant	Highly significant	+	-	Gupta *et al.* (2006)

Sl. No.	Character	Material and methods	Combining ability variance		Gene Action		References
			GCA	SCA	Additive	Non-additive	
		9 x 9 HD	Significant	Significant	+	+	Dey *et al*. (2010)
		10 X 10 FD	Highly Significant	Highly Significant	+	+	Thangamani *et al.* (2011a)
		6 X 4 L X T	Highly significant	Highly significant	-	+	Kumara *et al.* (2011)
6	Days to first fruit harvest	8 X 8 HD	Highly significant	Highly significant	+	+	Khattra *et al*. (1994)
		10 X 10 HD	Highly significant	Highly significant	+	+	Munshi and Sirohi (1994)
		10 X 3 L X T	Highly significant	Highly significant	-	+	Khattra *et al*. (2000)
		6 X 6 HD	-	Highly significant	-	+	Bhave *et al*. (2004)
		9 X 9 HD	Highly significant	Highly significant	+	-	Gupta *et al*. (2006)
		9 x 9 HD	Significant	Highly significant	+	-	Dey *et al*. (2010)
		10 X 10 D	Highly Significant	-	+	+	Thangamani *et al.* (2011a)
		6 X 6 HD	Highly significant	Significant	+	+	Kushwaha and Karnwal (2011)
		6 X 4 L X T	Highly significant	Highly significant	-	+	Kumara *et al.* (2011)
7	Fruit length(cm)	8 X 8 HD	Highly significant	Highly significant	+	+	Khattra *et al.* (1994)
		9 X 9 HD	Highly significant	Highly significant	+	+	Mishra *et al*. (1994)
		10 X 10 HD	Highly significant	Highly significant	+	+	Munshi and Sirohi (1994)
		10 X 3 L X T	Highly significant	Highly significant	+	+	Khattra *et al.* (2000)
		8 X 8 HD	Significant	Significant	+	+	Singh *et al*. (2004)
		6 X 6 HD	Highly significant	Highly significant	-	+	Bhave *et al.* (2004)
		9 X 9 HD	Highly significant	Highly significant	-	+	Gupta *et al*. (2006)
		9 x 9 HD	Significant	-	+	-	Dey *et al*. (2010)
		10 X 10 D	Highly Significant	Highly Significant	+	+	Thangamani *et al.* (2011a)
8	Fruit diameter (cm)	8 X 8 HD	Highly significant	Highly significant	+	+	Munshi and Sirohi (1994)
		9 X 9 HD	Highly significant	Highly significant	+	+	Matoria and Khandelwal (1999)

Sl. No.	Character	Material and methods	Combining ability variance		Gene Action		References
			GCA	SCA	Additive	Non-additive	
		6 X 6 HD	Highly significant	Highly significant	+	-	Bhave *et al.* (2004)
		9 X 9 HD	Highly significant	Highly significant	+	-	Gupta *et al.* (2006)
		10 X 10 D	Highly Significant	Highly Significant	+	+	Thangamani *et al.* (2011a)
9	Average Fruit weight (g)	9 x 9 HD	Highly significant	Highly significant	-	+	Gupta *et al.* (2006)
		9 x 9 HD	Significant	Significant	+	+	Dey *et al.* (2010)
		10 X 10 D	Significant	Highly significant	+	+	Thangamani *et al.* (2011a)
		6 X 6 HD	Highly significant	Highly significant	+	+	Kushwaha and Karnwal (2011)
		6 X 4 L X T	Highly significant	Highly significant	-	+	Kumara *et al.* (2011)
10	Fruit diameter (cm)	8 X 8 HD	Highly significant	Highly significant	+	+	Munshi and Sirohi (1994)
		9 X 9 HD	Highly significant	Highly significant	+	+	Matoria and Khandelwal (1999)
		6 X 6 HD	Highly significant	Highly significant	+	-	Bhave *et al*. (2004)
		9 X 9 HD	Highly significant	Highly significant	+	-	Gupta *et al.* (2006)
		10 X 10 D	Highly Significant	Highly Significant	+	+	Thangamani *et al*. (2011a)
11	Average Fruit weight (g)	9 x 9 HD	Highly significant	Highly significant	-	+	Gupta *et al.* (2006)
		9 x 9 HD	Significant	Significant	+	+	Dey *et al*. (2010)
		10 X 10 D	Significant	Highly significant	+	+	Thangamani et al. (2011a)
		6 X 6 HD	Highly significant	Highly significant	+	+	Kushwaha and Karnwal (2011)
		6 X 4 L X T	Highly significant	Highly significant	-	+	Kumara *et al.* (2011)
12	Number of fruits per vine	8 X 8 HD	Highly significant	Highly significant	+	+	Khattra *et al.* *(*1994)
		9 X 9 HD	Highly significant	Highly significant	+	+	Mishra *et al*. (1994)
		10 X 10 HD	Highly significant	Highly significant	+	+	Matoria and Khandelwal (1999)
		10 X 3 L X T	Highly significant	Highly significant	+	+	Khattra *et al.* (2000)

Sl. No.	Character	Material and methods	Combining ability variance		Gene Action		References
			GCA	SCA	Additive	Non-additive	
		8 X 8 HD	Significant	Significant	+	+	Singh *et al.* (2004)
		6 X 6 HD	Highly significant	Highly significant	+	-	Bhave *et al.* (2004)
		9 X 9 HD	Highly significant	Highly significant	-	+	Gupta *et al*. (2004)
		10 X 10 FD	Highly Significant	Highly Significant	+	+	Thangamani *et al*. (2011a)
		6 X 6 HD	Highly significant	Highly significant	+	+	Kushwaha and Karnwal (2011)
		6 X 4 L X T	Highly significant	Highly significant	-	+	Kumara *et al.* (2011)
13	Fruit yield per vine (kg)	8 X 8 HD	Highly significant	Highly significant	+	+	Khattra *et al*. (1994)
		10 X 10 HD	Highly significant	Highly significant	+	+	Munshi and Sirohi (1994)
		9 X 9 HD	Highly significant	Highly significant	+	+	Mishra *et al.* (1994)
		10 X 10 HD	Highly significant	Highly significant	+	+	Matoria and Khandelwal (1999)
		10 X 3 L X T	Highly significant	Highly significant	+	+	Khattra *et al.* (2000)
		8 X 8 HD	Highly significant	-	+	-	Singh *et al.* (2004)
		9 x 9 HD	Highly significant	Highly significant	-	+	Gupta *et al.* (2006)
		9 x 9 HD	Significant	Significant	+	+	Dey *et al*. (2010)
14	Number of seeds per fruit	10 x 3 L x T	Highly significant	Highly significant	+	+	Khattra *et al.* (2000)
		6 X 6 HD	Highly significant	Significant	+	-	Bhave *et al.* (2004)
		6 X 4 L x T	Highly significant	Highly significant	-	+	Kumara *et al.* (2011)
15	Number of seeds per fruit	10 x 3 L x T	Highly significant	Highly significant	+	+	Khattra *et al*. (2000)
		6 X 6 HD	Highly significant	Significant	+	-	Bhave *et al.* (2004)
		6 X 4 L x T	Highly significant	Highly significant	-	+	Kumara *et al.* (2011)

Chapter 3

MATERIALS AND METHODS

CHAPTER-III

MATERIALS AND METHODS

The present investigation on "**C**haracterization, yield components and heterosis in bitter gourd (*Momordica charantia* L.)" was carried out for three consecutive years during spring-summer seasons (planting in mid of February) of 2015, 2016 and 2017 in New Alluvial Zone of West Bengal, at Horticultural Research Station, Mondouri, Bidhan Chandra Krishi Vishwavidyalaya. The details of the materials and methods adopted during investigation are furnished in this chapter.

3.1 Experimental Site

3.1.1 Location of experimental site

The present investigation was conducted at Horticultural Research Station, Mondouri, Faculty of Horticulture, Bidhan Chandra Krishi Vishwavidyalaya, Nadia, West Bengal. The research station is located approximately at 23.5°N latitude, 89°E longitude having an average altitude of 9.75m from the sea level.

3.2 Agro-climatic condition

The experimental site comes under sub-tropical humid climate as it is situated just south of tropic of cancer. The average temperature ranges from 25º- 36.5ºC during summer months and between 12ºC and 25ºC during winter months. The average rainfall is about 1500 mm. Meteorological data during the crop growth period (*rabi* seasons of 2012 and 2013) was collected from the Department of Agricultural Meteorology and Physics, Bidhan Chandra Krishi Vishwavidyalaya, Faculty of Agriculture, Mohanpur, Nadia, West Bengal.

Table 3.1: Month wise meteorological data at the experimental site during the experimental periods in the field

Month, Year	Temperature (^{0}C)		Rainfall (mm)	Relative humidity (%)	
	Max.	Min.		Max.	Min.
February, 2015	29.1	14.3	7.2	96	48
March, 2015	33.1	17.9	21.2	87	48
April, 2015	34.2	21.6	87.9	91	64
May, 2015	29.6	15.4	0.0	97	45
June, 2015	24.9	11.1	0.0	98	57
February, 2016	25.8	11.9	0.1	93	53
March, 2016	37.6	23.0	1.1	92	54
April, 2016	34.3	21.8	1.2	91	47
May, 2016	34.2	21.6	87.9	91	64
June, 2016	35.9	23.1	638.9	89	65
February, 2017	29.4	12.61	0.0	92.2	42.6
March, 2017	32.23	17.25	0.2	92.1	48.8
April, 2017	34.9	22.6	0.4	91.0	57.4
May, 2017	32.4	21.9	0.0	93	66
June, 2017	30.4	16.9	12.9	98	58

(Source: Department of Agril. Meteorology & Physics, B.C.K.V, Nadia, W.B.)

3.3 Materials

The present investigation was carried out employing 33 genetic materials of bitter gourd collected from different sources as represented in Table 3.2.

Table 3.2: Sources of different Bitter gourd genotypes used as experimental materials

S.no	Accession	Source of collection
1.	IC-68250	NBPGR, Thrissur
2.	IC-599426	NBPGR, Thrissur
3.	IC-599428	NBPGR, Thrissur
4.	IC-599429	NBPGR, Thrissur
5.	IC-68343	NBPGR, Thrissur
6.	K-85603 (TCR-76)	NBPGR, Thrissur
7.	K-68237	NBPGR, Thrissur
8.	K-85608	NBPGR, Thrissur
9.	IC-470557	NBPGR, Thrissur
10.	IC-65787	NBPGR, Thrissur
11.	IC-44438	NBPGR, Thrissur
12.	IC-45350	NBPGR, Thrissur
13.	IC-599420	NBPGR, Thrissur
14.	IC-599434	NBPGR, Thrissur
15.	IC-470565	NBPGR, Thrissur
16.	IC-68236	NBPGR, Thrissur
17.	IC-541448	NBPGR, Thrissur
18.	IC-536670	NBPGR, Thrissur
19.	IC-599421	NBPGR, Thrissur
20.	IC-596981	NBPGR, Thrissur
21.	IC -264699	NBPGR, Thrissur
22.	IC 596983	NBPGR, Thrissur
23.	IC-599423	NBPGR, Thrissur
24.	IC-467680	NBPGR, Thrissur
25.	IC-418486	NBPGR, Thrissur
26.	IC-398610	NBPGR, Thrissur
27.	IC-427694	NBPGR, Thrissur
28.	IC-599424	NBPGR, Thrissur
29.	IC-45358	NBPGR, Thrissur
30.	IC-32817	NBPGR, Thrissur
31.	DON NO-1	Local collection of W.B.
32.	Dhaka Karala	Local collection of W.B.
33.	Gangajali Karala	Local collection of W.B.

3.4 Details of the experiment

First year

"Evaluation of the genotypes for determination of genetic variability parameters"

Thirty-three genotypes of bitter gourd will be evaluated during *Pre-kharif*, 2015 following Randomized Block Design with three replications. Seeds of the genotypes were sown at 100 cm x 60 cm spacing in a plot size of 3.0 m x 1.20 m accommodating ten plants per plot in each replication. Standard cultural practices for raising of good crops were followed (Chattopadhyay *et al*., 2007). Both qualitative and quantitative traits were taken from five randomly selected plants from each replication.

3.5 Crop Husbandry

3.5.1 Land preparation

The selected land of the experimental site was thoroughly prepared by repeated ploughing with power tiller followed by harrowing. The soil was then pulverized to make it loose and in friable condition. All the weeds and stubbles were removed. The field was properly leveled and divided by the irrigation channels into several plots as per layout.

3.5.2 Manures and Fertilizers

After the land was prepared about 25 tonnes of FYM was applied. The recommended dosage of N, P and K (100: 50: 50 kg per ha) was applied in the form of urea, single super phosphate and murate of potash, respectively. Nitrogen was applied in two split doses, the first dose as basal application and the other split dose at 30 days after planting. The entire dose of phosphorus and potash were applied at the time of sowing as basal dose.

3.5.3 Sowing

After the layout, the genotypes were assigned to different plots in each replication by using random numbers. The seeds of each genotype were soaked in water for overnight before sowing for getting uniform germination. The presoaked seeds were then sown by dibbling two to four seeds per hill. The gap filling was done by re-sowing within a week after germination.

3.5.4 Thinning of excess seedlings

The weak seedlings were thinned out leaving only one vigorous seedling per hill after 25 days of sowing.

3.5.5 Irrigation

The first irrigation was given before sowing and subsequent irrigations as and when required.

3.5.6 Weed control

Hand weeding was followed to control the weeds as and when required.

3.5.7 Plant protection

A plant protection measure particularly against red pumpkin beetles and fruit flies was taken by spraying Chlorpyriphos 20% EC and Acephate 75% SP when required.

3.5.8 Harvesting

Harvesting of the fruit was done manually when fruits attained proper tender stage.

3.6 Observations Recorded

3.6.1 Qualitative traits

The parents were evaluated for 21 qualitative characters and the following observations were recorded on single plant basis on five randomly selected plants in each treatment and in each replication. early plant vigor, plant growth habit, stem pubescence, stem shape, twining tendency, tendril branching, leaf margin, leaf shape, leaf size, leaf pubescence, sex type, flower color, peduncle separation from fruit, fruit shape, fruit surface, nature of tubercles, blossom-end fruit shape, fruit skin color, fruit skin luster, fruit bitterness, seediness and seed luster.

3.6.2 Quantitative traits:

The parents and their hybrids were evaluated for 20 morphological characters and the following observations were recorded on single plant basis on five randomly selected plants in each treatment and in each replication.

3.6.2.1 Vine length (cm)

The length of the main stem was measured with a meter scale at 90 days after planting from base of the plant to the tip of the main shoot and expressed in meters (cm).

3.6.2.2 Number of primary branches on main stem

The branches arising on main axis were counted at the time of 90 days after transplanting/end of the flowering stage.

3.6.2.3 Internodal length (cm)

The node length at the middle of vine was recorded as internodal length.

3.6.2.4 Petiole length

Mean length of petiole was measured using scale and expressed in centimeters.

3.6.2.5 Node number at which first female flower appeared

The node number from the cotyledonary leaves at which the first female flower appeared was recorded.

3.6.2.6 Days to 50% flowering.

Days to 50% flowering was calculated by recording the number of days following transplanting (DAT) until 50% of plants in a plot had at least one open flower.

3.6.2.7 Sex ratio (M/F)

The fully opened male and female flowers were counted daily and sex ratio was expressed as a ratio of total male to total female flowers.

It was calculated as follows:

$$\text{Sex ratio} = \frac{\text{Total no of male flowers}}{\text{Total no of female flowers}}$$

3.6.2.8 Peduncle length.

Mean length of peduncle was measured using scale and expressed in centimeters.

3.6.2.9 Days to first fruit harvest

Number of days taken from sowing to the harvest of first marketable fruit was recorded. Stage of marketable maturity was judged by experience on the basis of attaining full size and before change in color of the fruits.

3.6.2.10 Days to last fruit harvest

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

3.6.2.11 Number of marketable fruit harvest.

The fruits were bulky harvested in a gunny bag separately as per the treatments and graded the fruits based on size and shape for market and data was recorded.

3.6.2.12 Number of fruits per plant

The number of fruits per vine over all the harvests were counted and recorded.

3.6.2.13 Average fruit weight (g)

The weight of five individual fruits harvested at the edible stage was recorded and the average weight of the fruit was calculated.

3.6.2.14 Fruit length (cm)

Length of five fruits harvested at edible maturity was recorded from base to the apex of fruit and average length of fruit was calculated.

3.6.2.15 Fruit diameter (cm)

Girth of the same five fruits selected for recording the length, was measured in centimeters at maximum thickness.

3.6.2.16 Seed index/100 seed weight.

The seeds extracted from five fruits per treatment per replication were dried separately and 100 dried seeds from each fruit were randomly selected, weighed and their mean was expressed in grams.

3.6.2.17 Number of Seeds per fruit.

The fruits were cut open and the total number of seeds per fruit was counted and recorded.

3.6.2.18. Ascorbic acid content of the pulp

Composite pulp of five randomly sampled fruits per replication was used to estimate ascorbic acid content in the fresh fruits following standard biochemical methods (AOAC, 1990).

Materials required:

1. Metaphosphoric acid 3%
2. Dye solution: 42 mg Sodium bicarbonate was taken into a small volume of distilled water and 52 mg of 2, 6-dichlorophenol indophenol was dissolved in it. Volume was made up to 200 ml with distilled water.

3. Stock standard solution: 100 mg ascorbic acid was dissolved in 100 ml of 3% metaphosphoric acid solution in a standard flask (1mg/ml)
4. Working Standard: 10 ml of the stock solution was diluted to 100 ml with 3% metaphosphoric acid.

Procedure:

1. 5 ml of the working standard solution was pipetted out into a 100 ml conical flask.
2. 10 ml metaphosphoric acid was added in it and titrated against the dye solution (V1ml). End point was the appearance of pink color which persists for a few minutes. The amount of the dye consumed was equivalent to the amount of ascorbic acid.
3. 5g of pulp sample was crushed and extracted in 3% metaphosphoric acid. Volume was made up to 100ml and centrifuged for 20 minutes
4. 5 ml of this supernatant was pipetted out and added into the 10 ml of 3% metaphosphoric acid.
5. It was titrated against the dye (V2 ml).

Calculation:

$$\text{Ascorbic acid (mg / 100 g)} = \frac{\text{Titre value} \times \text{Dye factor} \times \text{Vol. made up}}{\text{Vol. taken} \times \text{weight of the pulp}} \times 100$$

3.6.2.19- β Carotene content of fruit (mg/100 g).

500 mg of fresh product was taken in a clear mortar, 200 ml of 80% acetone was added and ground for 5 minutes. The liquid was transferred to a Buchner funnel containing a layer of Whatman no-1filter paper. The extract was filtered using solution. Final volume of filter was adjusted to 50 ml by adding enough 80% acetone. Then it was measured at 440, 645, 663nm.

$$\text{B- Carotene (mg/100 g)} = 4.69.\ A_{440} - 0.286(20.2A_{645} + 8.02A_{603}).$$

3.6.2.20 Fruit yield per plant (kg)

All the marketable fruits harvested and weighed during each picking were collected and recorded as total yield per plant which was expressed in grams (kg).

Second year

1. Evaluation of the genotypes for determination of genetic variability parameters (Repetition)

On the basis of the evaluation and characterization study in the first year, 6 widely divergent genotypes were selected as parental lines.

Table 3.2: Parents involved in the diallel programme

Sl. No.	Symbol of parent	Parent
1	P1	IC -599428
2	P2	K-85603 (TCR-76)
3	P3	IC -65787
4	P4	IC -541448
5	P5	IC-596983
6	P6	Gangajali Karala

2. Raising of F_1 seeds

A 6 × 6 full diallel mating design was performed during the spring-summer seasons (planting in mid of February) of 2017 followed Randomized Block Design with three replications. Seeds of the genotypes were sown at 100 cm x 60 cm spacing in a plot size of 3.0 m x 1.00 m accommodating ten plants per plot in each replication.

Crossing technique

A day before anthesis, fully matured male flower buds of male parent and female flower buds of seed parent were wrapped using cotton wrap. On the next day, between 6 and 8 am the pollen grains from the male flowers of male parent were collected and dusted on to the stigmatic surface of the female flowers of the female parent. The pollinated flowers were labelled and covered with cotton wrap again. After three days of pollination the cotton wrap was removed. The ripened fruits were collected, properly dried and stored for next season evaluation.

Third year

Raising of F_1s and parents for evaluation of different characters

Thirty F_1s along with six parents were evaluated following Randomized Block Design with three replications during *Pre-kharif*, 2017. Seeds of thirty F_1s and six parents will be sown at 100 cm x 60 cm spacing in a plot size of 3.0 m x 1.00 m accommodating ten plants per plot in each replication. The following quantitative data were recorded from five randomly selected plants from each replication. The observations which were recorded in first season were followed during this experiment is vine length (cm), number of primary branches, internode length (cm), petiole length (cm), node number at which first female flower appearance, days to 50% flowering, sex ratio, peduncle length (cm), days to first fruit harvest, days to last fruit harvest, number of marketable fruit harvest, number of fruits per plant, fruit weight (g), fruit length (cm), fruit diameter (cm), number of seeds per fruit, 100 seed weight (g), ascorbic acid content (mg/100g), ß-carotene content of fruit ((mg/100g) and fruit yield per plant (kg).

3.7 Statistical Analysis

Statistical analysis was carried out using sample mean values. All the analysis was done in computer using appropriate programs.

3.7.1 Analysis of variance

Analysis of variance was carried out as per the procedure given by Panse and Sukhatme (1985). Partitioning the total variance into that due to replications and treatments represents the expectations of the variance and the appropriate degrees of freedom in each case. Differences between genotypes for different characters were tested for significance using analysis of variance. Analysis of variance was do ne by using the following model.

$$Yij = \mu + gi + rj + eij$$

Where,

Yij = yield corresponding to i^{th}genotype in j^{th} replication.

μ = Grand mean

gi = effect of i^{th}replication

rj = effect of j^{th} replication effect

eij= Random error effect associated with i^{th}genotype in j^{th} replication.

Source of variation	Degrees of freedom	Sum of squares	Expected MSS
Replication	r-1	M1	$\sigma_e^2 + t\,\sigma_r^2$
Genotypes	t-1	M2	$\sigma^2 e + r\,\sigma^2 g$
Error	(t-1) (r-1)	M3	$\sigma^2 e$
Total	tr-1	(M1 + M2 + M3)	

Where,

r = Number of replications

t = Number of genotypes (treatments)

$\sigma^2 e$ = Error variance

$\sigma^2 g$ = Genotypic variance

Statistical significance of variation due to genotypes was tested by comparing calculated values to F-table values at one per cent and five per cent level of probability, respectively.

3.7.2 Critical Difference

To compare the means of various entries, we have to calculate the critical difference (C.D.) by the following formula: -

C.D. = S. E. (mean) x t error d.f.

Where,

S.E. (mean) = Standard error of difference of the treatment mean to be compared to is equal to SE (mean) = $\sqrt{\frac{2EMS}{r}}$ with EMS as error mean sum of square and „r" as the number of replication and „t" as the tabulated value at 5% level of significance for the error degrees of freedom.

Thus, CD= $\sqrt{\frac{2EMS}{r}}$ x t 0.05, error d.f.

3.7.3 Coefficient of Variation (CV)

The coefficient of variation (CV) being a unit less measurement, is a good basis for comparing the extent of variation between different characters with different scales.

$$C.V. = \frac{S.D}{\overline{X}} \times 100$$

Where, S.D. = Standard deviation = $\sqrt{\text{variance}}$

$$S.D. = \sqrt{E.MS.}$$

$\overline{X}$ = Grand mean

3.7.4 Components of Variance

Considering that all this genotype tested here, were genetical uniform, the expected mean sum of square for error (EMS), i.e. $\sigma^2 e$ will be purely a random environmental variance. The mean squares between genotypes will consist of two variances i.e.,

i) Attributing to varietals difference (i.e. genotypic difference) and

ii) Due to environmental variation among individuals of each genotypes

Thus, the expected mean sum of squares is as follows: -

$$GMS = \sigma^2 e + r\,\sigma^2 g$$

$$EMS = \sigma^2 e$$

Therefore,

$$\sigma^2 g = \frac{GMS - EMS}{r}$$

Thus, the genotypic variance being $\sigma^2 g$ and environmental variance as $\sigma^2 e$ thus phenotypic variances i.e. $\sigma^2 p$ will be equal to $\sigma^2 g + \sigma^2 e$

Therefore, $\sigma^2 p = \sigma^2 g + \sigma^2 e$

Genotypic Coefficient of Variation (GCV):

$$GCV = \frac{\sqrt{\sigma^2 g}}{\overline{X}} \times 100 = \frac{\text{Genotypic standard deviation}}{\text{Grand mean}} \times 100$$

Phenotypic Coefficient of Variation (PCV):

$$PCV = \frac{\sqrt{\sigma^2 p}}{\overline{X}} \times 100 = \frac{\text{Phenotypic standard deviation}}{\text{Grand mean}} \times 100$$

3.7.5 Heritability

Heritability in broad sense refers to the proportion of genetic variation to the total observed variance in the population. It has been estimated as per the formula given by Allard (1960). Heritability in broad sense is the ratio of genotypic variance to the phenotypic variance and is expressed in percentage.

$$h^2 = \frac{\sigma^2 g \text{ Genotypic variance}}{\sigma^2 p \text{ Phenotypic variance}} \times 100$$

3.7.6 Genetic advance (GA)

Genetic advance is the expected genetic gain of superior individual under certain amount of selection pressure. Genetic advance for each character was worked out by adopting the formula given by Johnson *et al*. (1955).

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

Where,

GA = Genetic advance.

h^2 = Heritability in broad sense.

K = Selection differential which is equal to 2.06 at 5 % intensity of selection

σ_p = Phenotypic standard deviation

Further, the genetic advance as per cent of mean was computed by using the following formula:

$$\text{GA as per cent of mean} = \frac{GA}{\text{Grand mean}} \times 100$$

3.7.7 Correlation coefficient analysis

Correlation coefficient analysis reveals the association of characters *i.e.,* a change in one character brought about by a change in the other character Phenotypic and genotypic correlation coefficients between different variables were calculated by using covariance technique (Al-Jibourib *et al*., 1958). To determine the degree of association of characters with yield and also among the yield components, the correlation coefficients were calculated.

The phenotypic and genotypic correlations among yield and other characters were computed as:

$$r_g(xy) = \frac{Cov_g(xy)}{\sqrt{\sigma_g^2(x) \,.\, \sigma_g^2(y)}} \qquad r_p(xy) = \frac{Cov_p(xy)}{\sqrt{\sigma_p^2(x) \,.\, \sigma_p^2(y)}}$$

Where,

r_g (x y), r_p (x y) are the genotypic and phenotypic correlation coefficients respectively.

Cov_g, $Cov_p$are the genotypic and phenotypic covariance of x and y respectively.

σ^2_g and σ^2_p are the genotypic and phenotypic variance of x and y, respectively.

Significance of correlation coefficients was tested by comparing phenotypic correlation coefficients with the table values (Fisher and Yates, 1967) at (n-2) degrees of freedom at 5 % and 1 % level where 'n' denotes the total number of pairs of observations used in the calculation.

3.7.8 Path coefficient analysis

The direct and indirect contribution of various characters to yield were calculated through path coefficient analysis as suggested by Wright (1921) and elaborated by Dewey and Lu (1959). The following simultaneous equations were formed and solved for estimating various direct and indirect effects.

Path coefficients were obtained by solving the following simultaneous equations.

$$r_{ly} = P_{ly} + r_{12}P_{2y} + r_{13}P_{3y} + \ldots\ldots\ldots + r_{lk}P_{ky}$$

Where,

r_{ly} = Simple correlation coefficient between x_1 and y, the dependent character

P_{ly} = Direct effect of x_1 on y, the dependent character

$r_{12}P_{2y}$ = Indirect effect of x_1 on y through x_2.

r_{12} = Correlation coefficient between x_1 and x_2.

$r_{lk}P_{ky}$ = Indirect effect of x_1 only through k^{th} variable.

In the same way, equations for r_{2y}, r_{3y}, r_{4y}, $uptor_{ky}$ were obtained. The direct and indirect effects were calculated by solving the simultaneous equations. Besides the direct and indirect effects, the residual effect was computed by using the formula.

Residual effect (Pr_y) = $1-R^2$

Where, $R^2 = P_{ly}r_{ly} + P_{2y}r_{2y} + P_{3y}r_{3y} + \ldots\ldots\ldots\ldots P_{iy}r_{iy}$

Pr_y = Residual effect

P_{ly} = Direct effect of x_1 on y.

r_{1y} = Correlation coefficient of x1 and y

P_{2y} = Direct effect of x_2 on y

r_{2y} = Correlation coefficient of x_2 and y.

P_{3y} = Direct effect of x_3 on y

r_{3y} = Correlation coefficient of x_3 and y

P_{iy}= Direct effect of x_i on y

r_{jy} = Correlation coefficient of x_i and y

Pry = $\sqrt{1 - P_{1y}\, r_{1y} + P_{2y}\, r_{2y} + \ldots\ldots P_{ky}\, r_{ky}}$

Where P_{ry} = residual effect

P_{ly} = direct effect of x_1 only

r_{ly} = correlation coefficient of x_1 only

Scales for path coefficients

Values of direct (or) indirect effects	Rate (or) scale
0.00 to 0.09	Negligible
0.10 to 0.19	Low
0.20 to 0.29	Moderate
0.30 to 0.99	High
> 1.00	Very high

3.7.9 Genetic divergence analysis

The genetic divergence between genotypes was estimated using Mahalanobis D^2 statistics (1936).

3.7.9.1 Mahalanobis D^2 statistics

The data collected on different characters were analyzed using Mahalanobis D^2 analysis (1936) to determine the genetic divergence among the genotypes.

D^2 value between ijthgenotypes for 'p' characters was calculated as

$$D^2_{ij} = \sum_{t=1}^{p} (Y_i^t - Y_j^t)^2$$

Where,

$Y_{it}$is uncorrelated mean value of ith genotype for `t' characters

$Y_{jt}$is uncorrelated mean value of ith genotype for `t' characters

D^2_{ij} is D^2 between ith and jth genotypes.

3.7.9.1.1 Test of significance

Variances were calculated for all the characters and test of significance was done. Analysis of covariance for the character pairs was estimated on the basis of mean values (Panse and Sukhatme, 1985). After testing the difference between genotypes for each of the character, a simultaneous test of significance for differences in the mean values of a number of correlated variables with regard to the pooled effect of characters was carried out using 'V' statistic, which in turn utilizes Wilk's criterion. The sum of squares and sum of products of error and error + variety, variance - covariance matrix was used for this purpose. The estimation of Wilk's criterion was done using the following relationship.

$$\wedge = \frac{(E)}{(E+V)}$$

Where,

$\wedge$ = Wilk' s criterion

(E) = Determinant of error matrix and

(E + V) = Determinant of error + variety matrix

$$V\,(Stat) = -m \log_e \wedge = - \left[n - \frac{P+Q+1}{2} \right] \log_e \text{`}\wedge\text{'}$$

Where, m = n-(P + Q + 1) / 2

n = Degrees of freedom for error + varieties

log e '^'= 2.3026 log 10 `^'

P = Number of variables or characters. (19)

Q = Number of genotypes – 1 (or d.f. for genotypes) 47

V (stat) is distributed as x^2 with PQ (912= 19 x47) degrees of freedom.

χ^2 table value at 5 per cent level of significance is 106.50 (approx) distributed with 893 degrees of freedom.

3.7.9.1.2 Transformation of correlated variables

In the present model, computation of D^2 values was reduced to simple summation of the differences in mean values of various characters of the two genotypes *i.e.* Σd^2_i. Therefore, transformation of correlated variables into uncorrelated ones was done before working out the D^2 values. Transformation was done using pivotal condensation method.

3.7.9.1.3 Computation of D^2 values

For the given combination of i^{th} and j^{th} genotype, the mean deviation *i.e* .$Y_i^t - Y_j^t$ for t = 1, 2 ... p variables are computed and the D^2 values were calculated as

$$D^2_{ij} = \sum_{t=1}^{p} (Y_i^t - Y_j^t)^2$$

3.7.9.1.4 Testing the significance of D^2 values

The D^2 value obtained for a pair of population was taken as calculated value of χ^2 and was tested against the tabulated value of $\chi^2$for P (19) degrees of freedom where P (19) is the number of characters considered.

3.7.9.1.5 Grouping of genotypes into various clusters

The grouping of genotypes into different clusters was done using the Tocher's method as described by Rao (1952). The criterion was that the two genotypes belonging to the same cluster should at least on an average show a smaller D^2 value than those belonging to different clusters. For this purpose, D^2 values of all combinations of each genotype were arranged in ascending order of magnitude in a tabular form as described by Singh and Chaudhary (1977). To start with, two populations having the closest distance from each other were considered, to which the third population having the smallest D^2 value from the first two populations was added. Similarly, the next nearest

fourth population was considered and this procedure was continued. At certain stage, when it was felt that after adding a particular population there was an abrupt increase in the average D^2, that population was not considered for including in that cluster. The genotypes of the first cluster were then eliminated and the rest were treated in a similar way. This procedure was continued until all the genotypes were included into one or other cluster.

3.7.9.1.6 Intra cluster distance

The average intra cluster distances were calculated by the formula given by Singh and Chaudhary (1977).

$$\text{Square of intra cluster distance} = \Sigma Di^2 / n$$

Where,

ΣDi^2 = sum of distance between all possible combinations.

n = Number of all possible combinations

3.7.9.1.7 Inter cluster distance

The average inter cluster distances were calculated by the formula described by Singh and Chaudhary (1977).

$$\text{Square of inter cluster distance} = \Sigma Di^2 / n_i n_j$$

Where,

ΣDi^2 = sum of distances between all possible combinations ($n_i n_j$) of the entries included in the cluster study.

n_i = Number of entries in cluster i

n_j = Number of entries in cluster j

3.7.9.1.8 Contribution of individual characters towards genetic divergence

The character contribution towards genetic divergence was computed using the method given by Singh and Chaudhary (1977). In all the combinations, each character was ranked on the basis of $di = y_i^j - y_i^k$ values.

Where,

di = mean deviation

y_i^j = mean value of the j^{th}genotype for the i^{th} character and

y_i^k = mean value of the k^{th} genotype for the i^{th} character.

Rank 'I' is given to the highest mean difference and rank 'P' is given to the lowest mean difference

Where,

P is the total number of characters.

Finally, the number of times that each character appeared in the first rank is computed and per cent contribution of characters towards divergence was estimated using the formula

$$\text{Percentage contribution of character} \quad x = \frac{N \times 100}{M}$$

N = Number of genotype combinations where the character was ranked first.

M = All possible combinations of number of genotypes considered.

3.7.10. Estimation of heterosis

The magnitude of heterosis was studied using information on various quantitative characters. Heterosis expressed as per cent increase or decrease in the mean values of F_1's (hybrid) over better-parent (Heterobeltiosis) and standard variety as Pusa Naveen (standard heterosis) was calculated according to method suggested by Hayes *et al.* (1955). The formulas used for estimation of heterosis are as follows:

3.7.10.1 Relative heterosis (Heterosis over mid parent)

Relative heterosis (average heterosis) was expressed as per cent increase or decrease observed in the F_1 over the mid-parent as per the following formula.

$$\text{Relative heterosis } (h_1) = \frac{\overline{F}_1 - \overline{MP}}{\overline{MP}} x100$$

Where,

$\overline{F_1}$ = Mean of F_1

MP = $\overline{\text{Mean of parents}}$

3.7.10.2 Heterobeltiosis (Heterosis over better parent)

Heterobeltiosis was expressed as per cent increase or decrease observed in F_1 over the better parent.

$$\text{Heterobeltiosis } (h_2) = \frac{\overline{F}_1 - \overline{BP}}{\overline{BP}} x100$$

Where,

F_1 = Mean of F_1

BP = Mean of better parent (for the characters like days to 50% flowering, earliness is desirable, so the early parents are taken as better parents).

3.7.10.3 Test of significance of heterosis

The significance of heterosis was tested by using t-test as suggested by Wynne *et al*. (1970).

$$\text{Standard error for relative heterosis } (d_i) = \sqrt{\frac{3}{2r} EMS}$$

$$\text{Standard error for heterobeltiosis } (d_{ii}) = \sqrt{\frac{2}{r} EMS}$$

$$t \text{ value for relative heterosis} = \frac{\overline{F}_1 - \overline{MP}}{d_i}$$

$$t \text{ value for heterobeltiosis} = \frac{\overline{F}_1 - \overline{BP}}{d_{ii}}$$

Where,

EMS = Error mean square, which is taken from analysis of variance table of RBD

r = Number of replications

The calculated t-value was compared with table t-value at error degrees of freedom.

3.7.11. Combining ability analysis

The combining ability analysis for different characters was carried out following the method 2 model 1 of Griffing (1956 b), where parents and F_1's were included but not

the reciprocals. Thus, the experimental material for this method comprises of n (n+1)/2 genotypes.

The mathematical model for the combining ability analysis is assumed to be:

$$Y_{ij} = \mu + g_i + g_j + s_{ij} + \frac{1}{bc}\sum_{k}\sum_{l} e_{ijkl}$$

Where,

i,j. = 1, 2,----------, p (p = number of parents involved in diallel)

k = 1, 2, ----------, r (r = number of replications)

l = 1, 2, ----------, c (c = number of observations taken in each plot)

μ = the population mean

g_i, g_j = gca effect of i^{th} and j^{th} parents, respectively

Sij = the interaction, *i.e.* the specific combining ability (sca) for the cross between i^{th} and j^{th} parents such that Sij = Sji.

e_{ijkl} = environmental effect associated with $ijkl^{th}$ observation

The restriction imposed on this mathematical model are:

(i) $\sum_{i} g_i = 0$

(ii) $\sum_{j} s_{ij} = 0$

The orthogonal partitioning of the variety sum of squares in the ANOVA is as follows:

3.7.11.1 Analysis of variance table for method 2, model 1, with expectations of mean squares

Sources	d.f.	Sum of square	Mean square	Expectations of mean squares
g.c.a.	p-1	S_g	M_g	$\sigma_e^2 + (p+2)\left[\frac{1}{p-1}\right]\sum_{x=l}^{p} g_i^2$
s.c.a.	p(p-1)/2	S_s	M_s	$\sigma_e^2 + \frac{2}{p(p-1)}\sum_{i=l}^{p}\sum_{j=l}^{p} s_{ij}^2$
Error	(r-1) (t-1)	S_e	M_e	σ_e^2

Where,

P = number of parents

$$S_g = \frac{1}{P+2}\left[\sum_{i=l}(Yi+Yii)^2 - \frac{4}{p}Y_{..}^2\right]$$

$$S_s = \sum_i \leq \sum_j Y_{ij}^2 - \frac{1}{P+2}\sum_{i=l}(Yi+Yii)^2 + \frac{2}{(P+1)(P+2)}Y_{..}^2$$

Y_i = total of the array involving of i^{th} parent

Y_{ii} = mean value of the i^{th} parent of the array

Y_{ij} = mean value of i x j^{th} cross

Y.. = total of all the elements in the diallel table without

$$\text{reciprocals}\left[\frac{P\,(P-1)}{2}\text{ progenies and P parental lines}\right]$$

Me = error mean square

Mg, Ms and Me were obtained by dividing each sum of squares by the corresponding degree of freedom. The following 'F' ratios were used for testing the significance of g.c.a. and s.c.a. effects.

(i) To test significance of differences among g.c.a. variance of character.

$$F = \frac{M_g}{M_e}$$

The calculated F-value is tested against table F-value at (P-1) vs. error degree of freedom.

(ii) To test the significance of differences among sca variance of a character,

$$F = \frac{M_s}{M_e}$$

The calculated F-value is tested against table F-value at [P- (P-1)/2] vs, error degree of freedom.

3.8.11.2. Estimation of variance components

Variance components are calculated as,

$$\sigma_g^2 = \frac{(M_g - M_e)}{(P+2)}$$

$$\sigma_g^2 = M_S - M_e$$

$$\hat{\sigma}_g^2 = M_e^{'}$$

Hence,

VA (additive variance) $= 2\sigma_g^2$

VD (Dominance variance) $= \sigma_s^2$ ˆ

3.8.11.3. Estimation of combining ability effects

When MS_g and MS_s both are significant, they justify the adequacy of calculating general combining ability or gca (g_i) and specific combining ability or sca (S_{ij}) effects for each parent and cross, respectively. These were obtained by using the following formulae:

(a) Estimation of gca effects

$$g_i = \frac{1}{P+2}\left[\sum (Y_i + Y_{ii}) - \frac{2}{P} Y..\right]$$

(b) Estimation of sca effects

$$s_{ij} = Y_{ij} \frac{1}{(P+2)} (Y_i + Y_{ii} + Y_j + Y_{ij}) + \frac{2}{(P+1)(P+2)} Y..$$

Where,

Y_j = total of the array involving j^{th} parent

3.8.11.4. Standard errors

The standard errors, which are necessary in connection with testing the significance of gca and sca effects and differences between various gca effects as well as effects were calculated as:

(i) Standard error of combining ability effects

$$SE(g_i) = \left[\frac{P-1}{P(P+2)} \sigma_e^2\right]^{\frac{1}{2}}$$

$$SE(s_{ij}) = \left[\frac{P(P-1)}{(P+1)(P+2)} \sigma_e^2 \right]^{\frac{1}{2}}$$

To test the significance of each g_i and S_{ij}, 't' value are calculated as follows:

a) For gca effect

$$t(g_i) = \frac{g_i}{SE(g_i)}$$

b) For sca effect

$$t(S_{ij}) = \frac{s_{ij}}{SE(s_{ij})}$$

The calculated 't'-value for each g_i and S_{ij} is tested against the table 't'-value at (P-1) and P (P-1)/2degree of freedom, respectively.

(ii) Standard error of the difference of combining ability effects

(a) Differences between gca effects of parents

$$SE_d(g_i - g_j) = \left[\frac{2}{P+2} \sigma_e^2 \right]^{\frac{1}{2}}$$

(b) Difference between sca effects of two crosses, which include one common parent

$$SE_d(s_{ij} - s_{ik}) = \left[\frac{2(P+1)}{P+2} \sigma_e^2 \right]^{\frac{1}{2}}$$

(c) Differences between sca effects of two crosses, having no parent in common

$$SE_d(s_{ij} - s_{kl}) = \left[\frac{2P}{P+2} \sigma_e^2 \right]^{\frac{1}{2}}$$

The critical difference of each pair of g_i's and that of g_{ij}'s was calculated as a product of the standard error and 't' value for error degree of freedom at 5 and 1 per cent level of significance.

CD $(g_i - g_j) = SE_d(g_i - g_j) \times t_{5\%}$ or $t_{1\%}$ at (P-1) d.f.

CD $(s_i - s_{ik}) = SE_d(s_{ij} - g_{ik}) \times t_{5\%}$ or $t_{1\%}$ at [P(P-1)/2] d.f.

CD $(s_{ij} - s_{kl}) = SE_d(s_{ij} - s_{kl}) \times t_{5\%}$ or $t_{1\%}$ at [P(P-1)/2] d.f.

3.8.11.4. Estimation of components of genetic variance

The following genetic components of variation were calculated for the analysis of numerical approach followed the method given by ass and Hayman (1953), Hayman (1954a) and Askel and Johnson (1962).

$\hat{D}$ = components of variation due to additive effects of gene

$\hat{H}_1$ = components of variation due to dominance effects of gene

$\hat{H}_2$ = dominance, indicating asymmetry of positive and negative effects of genes,

$= \hat{H}_1 [1-(\mu-v)^2]$

μ = proportion of the positive genes in the parents

v = proportion of the negative genes in the parents and where $\mu + v = 1$

$\hat{F}$ = the mean of F_r over the arrays

Where,

F_r = the covariance of additive and dominance effects in single array

$\hat{h}^2$ = dominance effects (as the algebraic sum over all the loci in heterozygous phase in all the crosses)

The estimates of these components of genetic variation were determined based on the following formula suggested by Hayman (1954a).

$\hat{D} = V_0L_0-\hat{E}$

$\hat{F} = 2\ V_0L_0-4W_0L_{01} - \frac{2(n-2)}{n}\ \hat{E}$

$\hat{H}_1 = 4\ V_1L_1+V_0L_0 - 4\ W_0\ L_{01}-\frac{3n-2}{n}\ \hat{E}$

$\hat{H}_2 = 4\ V_1L_1- 4\ V_0\ L_1-2\hat{E}$

$\hat{h}^2 = 4\ (ML_1- ML_0)^2 - \frac{4(n-1)}{n^2}\ \hat{E}$

$Fr = 2\ (V_0L_0 - W_0L_{01} + V_1L_1 - Wr-Vr)- \frac{2(n-2)}{n}\ \hat{E}$

The estimates of the above formulae may be explained as follows:

N = number of parents

V_0L_0 = variance of the parents

Vr = variance of all the progenies in each parent of array

V_0L_1 = the variance of means of arrays

V_1L_1 = mean variance of the arrays (mean of all the Vr values)

Wr = the covariance between the parents and their offspring in r^{th} array

W_0L_{01} = the mean covariance between the parents and the arrays (mean of all Wr values)

ML_1 = mean of all F_1's

ML_0 = mean of parents

$\hat{E}$ = the expected environmental component of variation

In order to estimate the accuracy of the above components (D, $\hat{H}_1$, $\hat{H}_2$, $\hat{E}$, F, $\hat{h}^2$) variance, the terms of main diagonal of the matrix given by Hayman (1954a) with common multipliers S^2 was used where,

$$S^2 = \frac{1}{2} \text{ [var. (Wr-Vr)]}$$

Consequently, the standard error of

$$S.E._D = \left[\frac{n^5 + n^4}{n^5} S^2\right]^{\frac{1}{2}}$$

$$S.E._{H_1} = \left[\frac{n^5 + 41n^4 - 12n^3 + 4n^2}{n^5} S^2\right]^{\frac{1}{2}}$$

$$S.E._{H_2} = \left[\frac{36n^4}{n^5} S^2\right]^{\frac{1}{2}}$$

$$S.E._{h^2} = \left[\frac{16n^4 + 16n^2 - 32n + 16}{n^5} S^2\right]^{\frac{1}{2}}$$

$$S.E._F = \left[\frac{4n^5 + 20n^4 - 16n^3 + 16n^2}{n^5} S^2\right]^{\frac{1}{2}}$$

and $$S.E._E = \left[\frac{n^4}{n^5} S^2\right]^{\frac{1}{2}}$$

Where n is the number of inbred lines.

The significance of each components of variation was tested by means of 't' test at n-2 degree of freedom using the respective standard errors.

$$t = \frac{\text{Parameter}}{\text{SE of parameter}}$$

The above genetic components were used in computation of following genetic ratios:

(i) $(\hat{H}_1/\hat{D})^{\frac{1}{2}}$ = mean degree of dominance over all loci

If the ratio obtained is equal to 1, this indicated presence of complete dominance; if more than 1, it indicates presence of over dominance and if less than 1, it reveals presence of partial dominance; if equal to 0, it indicates no dominance.

(ii) $\hat{H}_2/4\ \hat{H}_1$ = the proportion of dominant genes with positive or negative effects among the parents.

The maximum theoretical value of this ratio is 0.25, which arises when p = q = 0.5 at all loci. A deviation from 0.25 would seem when $p \neq q$. Thus, $\hat{H}_2/4\ \hat{H}_1 \approx 0.25$ would means symmetrical distribution of positive and negative dominant genes in parents; and when $\hat{H}_2/4\ \hat{H}_1 \neq 0.25$ it means asymmetrical distribution.

Where,

p = proportion of dominant alleles and

q = proportion of recessive alleles

(iii) $(4\ D\hat{H}_1)^{1/2} + F\ /(4D\hat{H}_1)^{1/2} - F$ = the proportion of dominant and recessive genes among the parents when this ratio is equal to 1 it indicates nearly equal proportion of dominant and recessive alleles in parents (p=q=0.5). If the ratio is greater than 1, it refers to preponderance of dominant alleles (p>q) and when this ratio is less than 1, it means minority of dominant alleles and excess of recessive alleles (p<q)

(iv) $\hat{h}^2/\ \hat{H}_2$ = the number of groups of genes which control the characters and exhibit dominance

The coefficient of correlation (r) between parental order of dominance (Wr-Vr) and parental measurements (Yr) was calculated to get an idea about the dominance of genes with positive and negative effects.

(V) Estimation of heritability: Heritability in narrow sense is defined as the ratio of additive/ or additive x additive genetic variance to the total phenotypic variance.

$$\text{Heritability} = \frac{\frac{1}{2}D + \frac{1}{2}H_1 - \frac{1}{2}H_2 - \frac{1}{2}F}{\frac{1}{2}D + \frac{1}{2}H_1 - \frac{1}{2}H_2 - \frac{1}{2}F + E}$$

Testing of hydrometers

(1) t^2 test

$$t^2 = \frac{n-2}{4}\left[\frac{(\text{Var Vr} - \text{Var} - \text{Wr})^2}{(\text{Var} \times \text{Var Wr}) - \text{Cov}^2(\text{Vr}, \text{Wr})}\right]$$

This is tested against table value of F with 4 and (n-2) degree of freedom. Significant values indicates failure of hypothesis

(2) Regression coefficient (b):

$$b = \frac{\text{Cov (Wr, Vr)}}{\text{Var (Vr)}}$$

Where,

Cov (Wr, Vr)= [Σ VrWr – ΣVrΣWr] / (n-1)

And

$$\text{Var (Vr)} = \left[\sum \text{vr}^2 - \frac{(\sum \text{vr})^2}{n}\right] / n - 1$$

Standard error (b)= [(Vrwr- b Covwrvr)/ var Vr $(n-2)^{1/2}$]

Significance of b from zero and unity can be tested as follows

H_0: b =0

= (b-0)

And

Ho: b = 1

= (1-b)/ SE (b)

These values are tested against table value of 't' for n-2 degree of freedom.

The significant values indicate failure of hypothesis.

3.12.3 Estimation of dominance effect

The dominance estimates (D.E.) also referred to as "potence ratio" was computed using the following formula as suggested by Smith (1952).

D.E. = F_1-MP/ 0.5 × P_2-P_1,

Where, F_1 = mean value of the hybrid population; MP= Mid-parent; P_2= Mean of the highest parent; P_1= Mean of the lowest parent

Complete dominance was realized when D.E. = +1; while partial dominance is indicated when D.E. is between −1 and +1; D.E. = zero indicates absence of dominance. Over dominance was considered when D.E. exceeds ±1. The '+' and '–' signs indicate the direction of dominance of either parent.

Chapter 4

RESULTS AND DISCUSSION

CHAPTER-IV

RESULTS AND DISCUSSION

The study was initiated to examine variations in 20 characters of 33 bitter gourd genotypes on genetic diversity subjected to biometrical analysis and the results were presented. Six bitter gourd lines selected based on genetic diversity were crossed in a full- diallel fashion and the resulting thirty hybrids along with their parents and a commercial check Gangajali Karala were evaluated. Results were presented on the following heads:

4.1 Analysis of variance (ANOVA) of twenty characters in bitter gourd.

4.2 Analysis of components of fruit yield

4.3 Genetic diversity of genotypes through multivariate analysis

4.4 Genetic control of characters

4.5 Identification of good general and specific combiners

4.6 Variation among the parents and hybrids

4.7 Manifestation of heterosis with per se performance for different characters

4. 8 Dominance estimates of characters

4.1 Analysis of variance (ANOVA) of twenty characters in bitter gourd.

Analysis of variance revealed that mean squares due to genotypes were highly significant for most traits under study except node no at first female flower appearance, days to 50% flowering and days to first fruit harvest (Table-1). The co-efficient of variation (CV) was less than 10 % for characters vine length (cm), number of primary branches, internode length (cm), petiole length (cm), days to 50% flowering, sex ratio, peduncle length (cm), days to first fruit harvest, days to last fruit harvest, number of fruits/plants, fruit weight(g), fruit length (cm), fruit diameter (cm), 100 seed weight (g), number of seed/fruits, ascorbic acid (mg/100g) confirming the reliability of the experiment and also suggesting less G × E interactions. However, CV values varied from 10.75% to 20.44% for rest of the characters suggesting moderate G × E interactions.

Table-1: Analysis of variance (ANOVA) of twenty characters in bitter gourd

Sl. No	Character	Mean sum of squares			General mean	S. E.	C.D (5%)	C.D (1%)
		Replications (2)	Genotypes (32)	Error (64)				
1	Vine length (cm)	163.7677	2451.6445**	25.3718	214.02	2.9081	8.2161	10.9188
2	Number of primary branches	0.0909	24.5265**	1.2367	13.09	0.6421	1.8140	2.4107
3	Internode length (cm)	0.1003	3.9029**	0.0445	6.11	0.1219	0.3444	0.4577
4	Petiole length (cm)	0.0110	3.1372**	0.0485	5.85	0.1272	0.3593	0.4774
5	Node no at first female flower appearance	9.2525	3.8472	2.5650	14.88	0.9247	2.6124	3.4717
6	Days to 50% flowering	1.7676	5.8737	4.1218	41.68	1.1722	3.3116	4.4009
7	Sex ratio	0.1039	0.5543**	0.2755	8.10	0.3030	0.8562	1.1378
8	Peduncle length (cm)	0.0758	2.1993**	0.0867	5.45	0.1701	0.4806	0.6386
9	Days to first fruit harvest	32.4949	7.2553	4.6464	68.14	1.5551	4.3936	5.8389
10	Days to last fruit harvest	2.9494	34.2525**	5.6161	111.61	1.13682	3.8655	5.1371
11	Number of marketable fruit harvest	2.7373	6.0441*	3.5082	9.16	1.0814	3.0552	4.0601
12	Number of fruits/ plants	26.6767	12.8055**	5.2288	15.11	1.3202	3.7299	4.9568
13	Fruit weight (g)	0.9546	115.7987**	8.4426	64.07	1.6776	4.7395	6.2985
14	Fruit length (cm)	0.1725	13.3096**	0.2041	15.10	0.2609	0.7370	0.9794
15	Fruit diameter (cm)	0.0825	5.1929**	0.0404	11.52	0.1161	0.3280	0.4539
16	100 seed weight (g)	1.5139	8.4034**	0.6549	18.02	0.4673	1.3201	1.7543
17	Number of seed/fruits	2.1919	6.1616**	2.9523	18.07	0.9920	2.8027	3.7246
18	Ascorbic acid (mg/100g)	18.1982	174.3062**	5.7200	72.68	1.3808	3.9011	5.1844
19	β carotene content (mg/100g)	0.0424	0.1038**	0.0124	0.89	0.0644	0.1820	0.2243
20	Fruit yield/plant (kg)	0.0113	0.5765**	0.0189	1.26	0.0794	0.2243	0.2981

*Significant at 5 per cent level; ** Significant at 1 per cent level Values in parenthesis indicating degrees of freedom.

Table-2: Mean performance of 33 genotypes for twenty characters in bitter gourd

Sl. No.	Genotypes	VL (cm)	NPB	IL (cm)	PTL (cm)	NNFF	DA50%F	SR	PDL (cm)	DTFFH	DTLFH
		1	2	3	4	5	6	7	8	9	10
1.	IC-68250	218.00	10.66	5.96	5.83	13.33	44.00	8.26	5.33	67.33	110.33
2.	IC -599426	183.33	11.66	4.73	4.43	15.33	40.00	7.63	4.33	67.33	108.00
3.	IC -599428	260.00	17.00	7.93	7.60	14.00	40.33	7.73	6.36	68.00	113.00
4.	IC -599429	165.33	15.66	5.66	6.03	16.00	41.33	8.36	4.33	67.33	105.66
5.	IC -68343	173.33	14.66	6.13	4.60	14.00	40.00	8.40	5.16	67.33	108.66
6.	K-85603 (TCR-76)	260.66	16.33	7.63	7.50	14.66	40.00	7.73	6.70	70.33	114.00
7.	K-68237	236.00	11.00	6.13	5.66	15.66	41.66	7.73	4.76	67.66	107.00
8.	K-85608	197.66	16.00	4.60	6.53	13.00	44.00	8.26	6.23	67.66	107.00
9.	IC -470557	216.33	9.33	7.30	4.40	16.33	42.33	7.83	4.66	67.00	110.66
10.	IC -65787	248.33	17.00	7.50	7.26	12.66	40.00	7.60	7.13	69.33	114.33
11.	IC -44438	191.00	10.33	4.63	4.30	15.66	41.66	8.23	4.76	69.33	109.33
12.	IC -45350	204.00	11.33	6.20	5.56	14.33	42.33	7.63	4.33	67.66	112.00
13	IC -599420	225.00	16.00	7.53	6.16	15.66	41.66	8.16	6.20	67.66	118.33
14	IC -599434	227.33	16.00	6.23	5.30	15.33	42.66	7.50	4.53	69.00	107.66
15	IC -470565	192.33	10.33	4.56	5.06	16.00	42.33	8.73	5.33	68.00	112.66
16	IC- 68236	247.00	17.00	7.33	7.00	13.66	39.00	7.30	5.83	68.33	109.66
17	IC -541448	211.66	14.33	6.73	6.83	15.66	44.66	8.86	6.10	69.33	111.66
18	IC -536670	221.33	12.33	6.13	6.33	16.66	41.33	8.73	6.30	68.00	108.33
19	IC -599421	248.00	16.66	7.06	6.50	15.00	42.00	8.73	5.63	70.00	112.66
20	IC -596981	196.33	10.00	5.76	4.56	15.00	41.66	8.43	4.23	70.00	112.66
21	IC -264699	164.33	9.66	4.70	5.70	16.00	40.00	7.96	5.33	67.66	109.33

Sl. No.	Genotypes	VL (cm)	NPB	IL (cm)	PTL (cm)	NNFF	DA50%F	SR	PDL (cm)	DTFFH	DTLFH
		1	2	3	4	5	6	7	8	9	10
22	IC 596983	263.33	16.66	7.36	6.76	13.66	40.66	7.70	6.13	67.33	116.33
23	IC -599423	187.33	9.33	4.56	4.63	15.33	41.66	7.76	4.23	68.33	113.33
24	IC -467680	186.00	11.00	4.53	6.26	13.66	41.66	7.56	6.33	69.66	118.66
25	IC -418486	227.66	14.00	6.20	5.36	14.00	43.66	8.50	4.73	67.66	112.33
26	IC -398610	223.33	11.00	6.33	4.26	14.00	41.33	8.43	5.16	65.66	110.66
27	IC -427694	191.33	9.33	4.76	7.13	14.33	39.66	8.43	6.60	67.33	112.66
28	IC 599424	184.00	10.00	4.63	4.56	15.33	42.33	7.96	4.56	69.00	108.66
29	IC -45358	251.33	16.00	7.63	7.40	13.00	40.33	7.60	6.43	66.00	115.00
30	IC -32817	203.66	12.33	5.26	5.76	15.66	43.00	8.63	4.53	69.33	109.33
31	Don No-1	246.33	10.66	6.56	6.23	15.33	43.33	8.20	5.66	68.00	110.33
32	Dhaka Karala	196.66	11.66	5.73	6.23	16.33	42.33	8.33	5.76	65.66	118.33
33	Gangajali Karala	214.33	16.66	7.80	5.50	16.66	42.66	8.30	6.23	70.33	114.66
	Mean	214.02	13.09	6.11	5.85	14.88	41.68	8.10	5.45	68.14	111.61
	C.V	2.35	8.49	3.45	3.75	10.75	4.87	6.48	5.40	3.95	2.12
	S.E.	2.90	0.64	0.12	0.12	0.92	1.17	0.30	0.17	1.55	1.36
	C.D. 5%	8.21	1.81	0.34	0.35	2.61	3.31	0.85	0.48	4.39	3.86
	C.D. 1%	10.91	2.41	0.45	0.47	3.47	4.40	1.13	0.63	5.83	5.13

1.VL (cm)- Vine length (cm) ;2. NPB- Number of primary branches; 3. IL (cm)- Internode length (cm);4. PTL (cm)- Petiole length (cm);5. NNFF-Node no at first female flower appearance; 6. DA50%F- Days to 50% flowering ;7. SR- Sex ratio; 8. PDL (cm)- Peduncle length (cm); 9. DTFFH- Days to first fruit harvest; 10. DTLFH- Days to last fruit harvest

Table 2 conti…

Sl. No.	Genotypes	NMFH	NFPP	FW(g)	FL (cm)	FD (cm)	100 SW (g)	NSPF	AA mg/100g	BC mg/100g	FYPP
		11	12	13	14	15	16	17	18	19	20
1.	IC-68250	8.66	14.66	66.66	13.00	10.50	20.10	18.33	85.56	0.60	1.43
2.	IC -599426	8.66	16.66	48.33	11.46	10.20	17.60	18.33	67.06	0.58	0.60
3.	IC -599428	10.66	18.33	66.66	17.63	12.76	17.16	20.33	72.23	1.11	1.83
4.	IC -599429	8.33	13.66	70.00	17.36	13.36	15.10	16.66	61.93	1.00	1.43
5.	IC -68343	7.66	12.00	57.00	12.03	9.63	17.96	15.66	63.60	0.79	0.73
6.	K-85603 (TCR-76)	11.00	18.33	68.33	18.06	12.83	20.83	15.66	64.90	0.74	1.56
7.	K-68237	9.00	16.66	60.00	16.76	10.33	14.96	19.00	76.33	0.68	1.26
8.	K-85608	10.00	16.00	68.33	15.50	12.50	17.00	18.00	80.26	0.73	1.46
9.	IC -470557	8.33	13.00	53.66	11.40	9.56	17.50	18.33	73.36	0.92	0.63
10.	IC -65787	13.66	18.00	70.33	17.50	12.93	19.23	20.66	77.90	0.99	1.66
11.	IC -44438	8.66	12.66	53.66	12.13	9.56	18.10	18.00	74.80	1.24	0.80
12.	IC -45350	9.00	14.66	63.33	14.66	10.33	18.06	18.66	85.56	0.98	1.26
13	IC -599420	8.33	14.00	65.00	15.66	11.53	17.80	18.66	66.20	0.75	1.50
14	IC -599434	10.00	17.33	63.66	15.80	10.63	15.76	18.33	68.80	0.62	0.76
15	IC -470565	8.66	14.00	64.00	15.86	11.50	20.46	17.00	85.56	0.57	0.70
16	IC- 68236	11.00	18.33	71.83	17.66	12.66	16.13	16.66	74.13	1.22	1.73
17	IC -541448	9.00	15.00	68.83	16.36	12.90	19.96	17.33	68.66	0.77	1.90
18	IC -536670	9.66	16.00	70.83	15.93	12.80	18.56	17.66	63.53	0.79	1.83
19	IC -599421	8.33	14.00	68.66	16.20	13.30	17.00	16.33	63.60	0.92	1.20
20	IC -596981	7.33	12.00	58.00	12.27	12.63	18.83	19.00	64.90	0.77	0.76
21	IC -264699	8.33	14.00	63.33	16.50	9.93	16.03	17.33	69.10	0.83	0.86
22	IC 596983	12.00	18.66	71.66	17.73	13.03	17.46	15.33	69.46	1.06	1.80

Sl. No.	Genotypes	NMFH	NFPP	FW(g)	FL (cm)	FD (cm)	100 SW (g)	NSPF	AA mg/100g	BC mg/100g	FYPP
		11	12	13	14	15	16	17	18	19	20
23	IC -599423	8.33	13.66	56.66	12.60	9.70	18.13	17.66	70.70	1.08	0.80
24	IC -467680	8.66	14.00	69.36	15.45	12.90	18.76	18.00	72.36	0.88	1.20
25	IC -418486	8.33	14.33	67.50	16.43	12.36	16.40	19.66	72.36	0.72	1.46
26	IC -398610	8.00	14.66	53.33	12.33	9.56	18.80	21.00	73.26	1.02	0.83
27	IC -427694	8.33	14.00	71.66	14.50	12.63	20.93	19.33	73.36	0.89	1.63
28	IC 599424	10.00	15.33	61.00	12.73	10.80	15.00	16.33	79.76	0.89	0.86
29	IC -45358	11.33	19.66	69.33	16.90	11.63	19.63	18.00	83.13	1.21	1.26
30	IC -32817	7.33	13.33	59.66	12.83	10.76	20.10	19.33	87.33	1.08	0.83
31	Don No-1	9.66	13.66	63.33	15.36	11.43	19.00	18.66	82.13	0.95	1.20
32	Dhaka Karala	8.00	13.00	63.33	14.63	12.53	17.30	20.00	63.10	0.98	1.93
33	Gangajali Karala	8.00	15.00	67.00	17.20	10.53	19.16	17.00	63.60	1.00	1.96
	Mean	9.16	15.11	64.07	15.10	11.52	18.02	18.07	72.68	0.89	1.26
	C.V	20.44	15.13	4.53	2.99	1.74	4.48	9.50	3.29	12.48	10.86
	S.E.	1.08	1.3202	1.67	0.26	0.11	0.46	0.99	1.38	0.06	0.07
	C.D. 5%	3.05	3.7299	4.73	0.73	0.32	1.32	2.80	3.90	0.18	0.22
	C.D. 1%	4.06	4.9568	6.29	0.97	0.43	1.75	3.72	5.18	0.24	0.29

11. NMFH-Number of marketable fruit harvest; 12. NFPP-Number of fruits/ plants;13. FW(g)- Fruit weight (g);14. FL(cm)- Fruit length (cm);15. FD (cm)- Fruit diameter (cm); 16. 100 SW (g)- 100 seed weight (g); 17. NSPF- Number of seed/fruits ;18. AA mg/100g - Ascorbic acid (mg/100g); 19. BC mg/100g- β carotene content (mg/100g) ; 20. FYPP-Fruit yield/plant (kg).

Mean performance pertaining to 20 quantitative characters of 33 bitter gourd genotypes are presented in Table- 2.

4.1.1 Vine length (cm)

Vine length ranged from 164.33 cm to 263.33 cm with a mean of 214.02 cm. Among the 33 genotypes IC -264699 had significantly minimum vine length (164.33), while IC 596983 recorded maximum vine length (263.33) followed by IC-599428 (260 cm) and IC-45358 (251.33 cm).

4.1.2 Number of primary branches

Number of primary branches ranged from 9.33 to 17.00 with a mean of 13.09. Among the 33 genotypes IC-599423 had significantly lower number of primary branches (9.33), while IC-599428, IC-65787 and IC-68236 recorded maximum number of primary branches (17.00) followed by IC-599421, IC-596983 and Gangajali Karala (16.66).

4.1.3 Internode length (cm)

Internode length ranged from 4.53 cm to 7.93 cm with a mean of 6.11 cm. Among the 33 genotypes IC-467680 had significantly minimum internode length (4.53cm), while IC-599428 recorded maximum internode length (7.93cm) followed by Gangajali Karala (7.80cm), K-85603 (TCR-76) (7.63Cm) and IC-599420 (7.53cm).

4.1.4 Petiole length (cm)

Petiole length ranged from 4.26 cm to 7.60 cm with a mean of 5.85 cm. Among the 33 genotypes IC-398610 had minimum petiole length (4.26 cm), while IC-599428 recorded maximum petiole length (7.60 cm) followed by K-85603 (TCR-76) (7.50 cm) and IC-45358 (7.40 cm).

4.1.5 Node no at first female flower appearance

Node no at first female flower appearance ranged from 12.66 to 16.66 with a mean of 14.88. IC-65787 (12.66) recorded minimum node no at first female flower appearance, while IC-536670 (16.66) and Gangajali Karala recorded maximum node no at first female flower followed by Dhaka karala, ic-470557 (16.33) and IC-599429, IC-264699 and IC-470565 (16.00).

4.1.6 Days to 50% flowering

Number of days taken to 50 % flowering ranged from 39.00 to 44.66 with mean of 41.68 days. Among all the genotypes, IC-68236 (39.00 days) was the earliest followed by IC-427694 (39.66 days) and IC-599426, IC-68343, K-85603 (tcr-76) and IC-264699 (40.00 days), while IC-541488 flowered in 44.66 days.

4.1.7 Sex ratio

Among all the 33 genotypes studied, sex ratio ranged from 7.30:1 to 8.86:1, with a mean of 8.10:1. IC-470565, IC-536670 and IC-599421 had wider sex ratio (8.73:1), followed by IC-32817(8.63:1), while IC-68236 (7.30:1) had narrow sex ratio followed by IC-599434 (7.50:1) and IC-467680 (7.56:1).

4.1.8 Peduncle length (cm)

Peduncle length ranged from 4.23 cm to 7.13 cm with a mean of 5.45 cm. Among the 33 genotypes IC-596981 had minimum peduncle length (4.23 cm), while IC-65787 (7.13 cm) recorded maximum peduncle length followed by K-85603(TCR-76) (6.70 cm), IC-427694 (6.60cm) and IC-45358 (6.43 cm).

4.1.9 Days to first fruit harvest

Days to first fruit harvest ranged from 65.66 days to 70.33 days with a mean 68.14 days. Among the 33 genotypes IC-398610 and Dhaka karala had recorded earliest fruit harvest (65.66 days) followed by IC-45358 (66.00 days) and IC-470557 (67.00 days), while Gangajali Karala and K-85603(TCR-76) (70.33 days) had recorded the highest days for first fruit harvest followed by IC-599421 and IC-596981 (70.00 days).

4.1.10 Days to last fruit harvest

Days to last fruit harvest ranged from 105.66 days to 118.66 days with a mean 111.61 days. Among the 33 genotypes IC-467680 (118.66 days) recorded highest days for last fruit harvest followed by IC-Dhaka karala (118.33 days) and IC-596983 (116.33 days), while IC-599429 (105.66 days) recorded the lowest days for first fruit harvest followed by K-68237, K-85608 (107.00 days) and IC-599434 (107.66 days)

4.1.11 Number of marketable fruit harvest

Number of marketable fruit harvest ranged from 7.33 to 13.66 with a mean 9.16. Among the 33 genotypes IC-65787 (13.66) recorded highest number of marketable fruit harvest followed by IC-596983 (12.00) and IC-45358(11.33), while IC-596981 (7.33) had recorded for lowest marketable fruit harvest followed by IC-68343 (7.66) and IC-398610 (8.00).

4.1.12 Number of fruits/ plants

Higher number of fruits per plant leads to more fruit yield per plant. Number of fruits varied widely among genotypes, ranging from 12.00 to 1966 with an average value of 15.11. The maximum number of fruits was produced by genotype IC-45358(19.66) followed by IC-596983 (18.66) and the lowest was recorded in IC-68343 and IC-596981 (12.00).

4.1.13 Fruit weight (g)

Wide variation in fruit weight was observed among bitter gourd genotypes ranging from 48.33g to 71.83g with an average fruit weight 64.07g. The heaviest fruit was recorded in IC- 68236 (71.83g) and the lightest was found in IC-599426 (48.33g).

4.1.14 Fruit length (cm)

Fruit length ranged from 11.40cm to 18.06cm with mean of 15.10cm. The genotype IC-K-85603 (TCR -76) produced longest fruit among the genotypes followed by IC-596983 (17.73cm) and IC-68236 (17.66 cm), while IC-470557 (11.40) produced lowest fruit length among the genotypes.

4.1.15 Fruit diameter (cm)

Fruit dimeter ranged from 9.56 cm to 13.36 cm with mean of 11.52 cm. The genotype IC- 599429 (13.36cm) produced fruits with maximum fruit diameter followed by IC- 599421 (13.30cm) and IC-596983 (13.03cm), while IC-470557 and IC-44438 (9.56 cm) recorded the lowest fruit diameter among the genotypes followed by IC-68343 (9.63 cm) and IC-599423 (9.70 cm)

4.1.16 Seed index / 100 seed weight (g)

Among the genotypes studied, seed index ranged from 14.96g to 20.93g with mean of 18.02g. Genotype IC-427694 (20.93 g) recorded maximum fruit weight, followed by K-85603 (TCR-76) (20.83g) and IC-470565 (20.46g), while K-68237 (14.96 g) were recorded minimum seed index.

4.1.17 Number of seed/fruits

Among all the genotypes studied the numbers of seeds per fruit were ranged from 15.33 to 21.00 with a mean 18.07. The maximum number of seeds per fruit were recorded in IC- 398610 (21.00 seeds), followed by IC-65787 (20.66 seeds) and IC-499428 (20.33 seeds), Whereas IC- 596983 recorded minimum number of seeds per fruit (15.33 seeds).

4.1.18 Ascorbic acid (mg/100 g)

Ascorbic acid, also known as vitamin C, is water soluble, and the body does not store it. To maintain adequate levels of vitamin C, humans need a daily intake of food that contains it. It is a potent reducing agent and possesses a strong capacity to scavenge free radicals (Niki, 1991), particularly during oxidative stress. Vitamin C is involved in synthesis of collagen tissue, metal ion metabolism, antihistamine reactions, and enhancement of immune system (Combs, 1992).

The range of this vitamin-c content in the present study varied between 61.93 and 87.33 mg/100 g with an average value of 72.68 mg/100 g (Table-2). The maximum content was recorded in IC-32817 (87.33 mg/100 g) followed by IC-68250, IC-45350 and IC-470565 (85.56 mg/100 g), while IC- 599429 (61.93 mg/100 g) recorded lowest vitamin-c among the genotypes.

4.1.19 β carotene content (mg/100 g)

Access and consumption of vegetables have been increasing in urban and peri-urban areas, but meeting requirements for macro-and micro-nutrients and vitamins, particularly β-carotene and ascorbic acid, for most population groups in south Asian countries seems far off due to low consumption of vegetables (Akhtar *et al*., 2012). Consumption of vitamin A-rich food is a preventive solution to this crisis (de Pee and West, 1996).

This essential compound varied between 0.58 and 1.24 mg/100 g among the present plant materials (Table-2). The maximum content was found in IC-44438 (1.24 mg/100g) followed by IC-68236, while IC-599426 recorded lowest β-carotene content among the genotypes.

4.1.20 Fruit yield/plant (kg)

High fruit yield per plant in bitter gourd is always preferred by the growers. In spite of its high nutritive values, well acceptability among growers and consumers and wide range of available genetic variability, India is still lagging behind to attain the optimum productivity in bitter gourd owing to use of local unimproved cultivars and heavy infestations of insect-pest and diseases particularly viral disease. Therefore, much concentrated efforts are necessary to judge its potentiality.

Fruit yield per plant among genotypes varied from 0.60 to 1.96 kg with a mean value of 1.26 kg per plant (Table-2). The maximum fruit yield per plant was recorded in Gangajali Karala (1.96 kg) closely followed by Dhaka karala 1.93 kg and IC-541448 (1.90 kg), while IC-599426 (0.60 kg) recorded lowest yield. Ten out of 33 genotypes produced more than 1.15 kg fruit yield per plant.

From the mean data it was observed that the genotypes 'Gangajali Karala' and 'IC-541448' were found most promising with respect to fruit yield per plant and nutritional quality traits at the Gangetic plains of West Bengal. These two genotypes could be utilized in future breeding programme in bitter gourd.

4.2 Analysis of components of fruit yield

The development of suitable plant type is of great importance for all crops through planned designing programme. Attempts have, therefore, been made by several scientists to analyse different morphological characters to provide meaningful information about the significance of characters in relation to fruit yield in bitter gourd. An ideal plant ideotype would only be defined if the different components of bitter gourd fruit are analysed and their relative importance can be assessed. In the present study, genetic diversity of bitter gourd genotypes collected from different sources were examined and yield component analyses were carried out to identify important fruit yield components.

4.2.1 Analysis of genetic variability and heritability

The nature and extent of genetic variability is one of the most important criteria in formulating an efficient breeding programme and the knowledge of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) is much helpful in predicting the amount of variation present in a given assemblage of genotypes. The genotypic coefficient of variation (GCV) helps to measure the range of genetic variability in the character and provides a measure to compare the genetic variability present in various characters. In genetic studies, characters with high genotypic coefficient of variation indicate the potential for an effective selection (Sadiq *et al.*, 1986). However, with the help of genotypic coefficient of variations alone, the heritable variation cannot be measured (Singh *et al*., 1974). Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) are categorized as low (0-10 %), moderate (10-20 %) and high (>20 %) as indicated by Sivasubramanian and Madhavamenon (1973) although, this classification is not a rigid one.

Phenotypic co-efficient of variation (PCV) agreed closely with genotypic co-efficient of variation (GCV) but the magnitude of PCV was higher than GCV for all characters under study which indicated that the apparent variation was not only due to genotypes but also due to the influence of environment in the expression of traits (Table-3). PCV values varied between 3.48% to 35.75 % and GCV values varied from 1.36 % to 34.06 %. The characters number of primary branches, number of marketable fruit harvest, fruit yield per plant, β-carotene content mg/100g were recorded high PCV values (more than 20.00 %). For vine length, internode length, petiole length, node no at first female flower appearance, peduncle length, number of fruits per plant, fruit length, fruit girth, number of seeds per fruit, ascorbic acid were recorded moderate PCV values (11-20 %) and for rest of the characters days to 50% flowering, sex ratio, days to first fruit harvest, days to last fruit harvest 100 seed weight recorded the low PCV value (less than 10%).

Likewise, high GCV values (more than 20.00 %) were recorded for number of primary branches and fruit yields per plant; The moderate values (11-20 %) were noticed for vine length, internode length, petiole length, peduncle length, number of marketable fruit harvest, number of fruits per plant, fruit length, fruit girth, ascorbic acid content,

beta carotene content; and in rest of the characters were noticed low GCV values (less than 10%). High to moderate magnitude of GCV and PCV generally indicated ample scope for improvement through selection. The present findings clearly suggested the worth of vine length, number of primary branches, internode length, petiole length, peduncle length, number of marketable fruit harvest, number of fruits per plant, fruit length, fruit girth, beta carotene content and fruit yield per plant for the study of genetic variability in bitter gourd. The proportion of genotypic variation to phenotypic variation was very high (more than 90 %) for all characters except days to 50% flowering and days to last fruit harvest indicating that the traits are under genetic, rather than environmental control. Their use as important discriminatory variables for bitter gourd classification seems relatively reliable.

Genotypic coefficients of variation do not estimate the variations that are heritable hence, estimation of heritability becomes necessary (Falconer, 1960). Heritability is of interest to the plant breeder primarily as a measure of the value of selection for particular character in various types of progenies and as an index of transmissibility (Hayes *et al*., 1955). So, the concept of heritability is important to evaluate the relative magnitude of the effect of genes and environments on total phenotypic variability. The heritability value becomes a measure of genetic relationship between parent and progeny. The concept of heritability has originally been proposed by Lush (1940). According to Lush (1949), genotypic coefficient of variation represents the total genetic variation whereas heritability measures the proportion to which the variability of a character is transmitted to offspring. Lush (1943) proposed heritability as the ratio of the variance due to hereditary difference (genotypic variance) to the total observed variance (phenotypic variance). He also defined heritability in broad sense and narrow sense and emphasized that characters are subjected to different amount of non-heritable variation. Robinson *et al.* (1949) considered that additive genetic variance, which indicate the degree to which the progeny is likely to resemble the parents and defined heritability as the additive genetic variance in percent of the total variance.

Heritability is classified as low (below 30%), medium (30-60 %) and high (above 60 %) as suggested by Johnson *et al*. (1955). Considering this delineation, very high to moderate broad sense heritability were observed for all characters under study except

days to 50% flowering (12.00%) , days to first fruit harvest (13.00%), node no at first female flower appearance (14.00%), number of marketable fruit harvest (19.00%) and number of seeds per fruit (26.00%) (Table-3). High heritability indicates less environmental influence in the observed variation (Songsri *et al*., 2008) which suggested that selection based on phenotypic expression could be relied upon as there was major role of genetic constitution in the expression of these characters. However, this broad sense heritability values were likely to be overestimated as in this calculation it was not possible to exclude variation due to different genetic components and their interrelations. At the same time, heritability value alone cannot provide information on amount of genetic progress that would result from selection of best individuals.

Genetic advance is the improvement in performance of selected lines over the original population. Johnson *et al.* (1955) suggested that heritability estimate in combination with substantial amount of genetic advance would be more reliable than heritability alone for predicting the effect of selection in segregating generation. Genetic advance or genetic gain depends on (i) the amount of genetic variability i.e. magnitude of the differences among different individuals (or families) in the base population (ii) the magnitude of masking effect of the genetic diversity (iii) the intensity of selection (Comstock and Robinson, 1952; Johnson *et al*., 1955).

According to Hanson (1961), heritability and genetic gain are complementary aspects, thus values of heritability can also be used for computing the expected genetic progress possible through selection. Lush (1949) reported that heritability (broad sense), specifies the proportion of the total variability that is due to genetic causes, or the ratio of the genetic variance to the total variance. Johnson *et al*. (1955) had suggested that heritability estimates along with genetic gain is usually more helpful than the heritability alone in predicting the resultant effect from selecting the best individuals.

Table-3: Mean, range and estimates of genetic parameters of 33 genotypes of bitter gourd

Character	Range		Mean	PCV (%)	GCV (%)	h^2 (%)	GA as per cent of mean
	Min	Max					
Vine length (cm)	164.33	263.33	214.02	13.49	13.28	97.00	26.95
Number of primary branches	9.33	17.00	13.09	22.91	21.28	86.00	40.72
Internode length (cm)	4.53	7.93	6.11	18.85	18.53	96.00	37.53
Petiole length (cm)	4.26	7.60	5.85	17.72	17.32	95.00	34.86
Node no at first female flower appearance	12.66	16.66	14.88	11.61	4.39	14.00	3.41
Days to 50% flowering	39.00	44.66	41.68	5.20	1.83	12.00	1.33
Sex ratio	7.30	8.86	8.10	7.49	3.76	25.00	3.89
Peduncle length (cm)	4.23	7.13	5.45	16.30	15.38	89.00	29.89
Days to first fruit harvest	65.66	70.33	68.14	3.70	1.36	13.00	1.04
Days to last fruit harvest	105.66	118.66	111.61	3.48	2.76	63.00	4.52
Number of marketable fruit harvest	7.33	13.66	9.16	22.77	10.03	19.00	9.11
Number of fruits/ plants	12.00	19.66	15.11	18.42	10.51	32.00	12.36
Fruit weight (g)	48.33	71.83	64.07	10.38	9.33	80.00	17.30
Fruit length (cm)	11.40	18.06	15.10	14.15	13.83	95.00	27.85
Fruit diameter (cm)	9.56	13.36	11.52	11.50	11.37	97.00	23.15
100 seed weight (g)	14.96	20.93	18.02	9.98	8.91	79.00	16.40
Number of seed/fruits	15.33	21.00	18.07	11.09	5.72	26.00	6.08
Ascorbic acid (mg/100g)	61.93	87.33	72.68	10.82	10.31	90.00	20.24
β carotene content (mg/100g)	0.58	1.22	0.89	23.18	19.53	71.00	33.89
Fruit yield/plant (kg)	0.60	1.96	1.26	35.75	34.06	90.00	66.85

The genetic advance (GA) expressed as percentage of mean was very high (more than 20.00 %) for all characters under study except node number at first female flower appearance, days to 50% flowering, sex ratio, days to first fruit harvest, days to last fruit harvest, number of marketable fruit harvest, number of fruits per plant and number of seeds per fruit (Table- 3). In other words, numbers of primary branches per plant, fruit yield per plant and beta carotene content were characterized by high GCV, heritability and genetic advance. According to Panse (1957), such association was attributed to additive gene effects and selection based on these characters could be effective. Moderate heritability accompanied with moderate genetic advance for number of fruits per plant suggested that this character was less influenced by favourable environment effect rather than genotypes. Selection based on this character would also be effective but not as efficiently as first group. High heritability along with high genetic advance for the above characters was recorded by Gowda *et al.* (2017), Sidhu *et al*. (2017), Yadagiri *et al.* (2016), Iqbal *et al*. (2016) and Rani *et al.* (2015) in bitter gourd.

Low, heritability with genetic advance for node number at first female flower appearance, days to 50% flowering, sex ratio, days to first fruit harvest, days to last fruit harvest, number of marketable fruit harvest, and number of seeds per fruit revealed non-additive genetic control of these characters. Hence, direct selection will bring no or slow genetic improvement for these traits. In such case heterosis breeding would be effective for improvement of such traits.

The present findings supported by earlier reports suggested that selection would be rewarding for improvement of characters number of primary branches and fruit yield per plant and beta carotene content which exhibited very high GCV values, heritability estimates and genetic advance as percent of mean.

4.2.2 Character association

Information generated from the studies of character association serve as the most important indicator (plant character) that ought to be considered in selection programme. Such studies would also help us to know the suitability of multiple characters for indirect selection, because selection for one or more traits results in correlated response in several other traits (Searle, 1965). Association analysis of different morphological characters with fruit yield of bitter gourd genotypes and their inter-relationships were investigated through the study of both phenotypic and genotypic correlation co-efficients.

In the present study, twenty characters including vegetative characters, reproductive, fruit quality were recorded and their phenotypic and genotypic correlation co-efficient were analysed. The results are presented in Table-4 & Table-5. Phenotypic and genotypic correlation co-efficients, in general, agreed very closely indicating little influence of environment on the correlated response on most of the pair of fruit and fruit quality characters. Falconer (1988) put forward the proposition of environmental influence on correlated expression of the characters. Statistical significance of the phenotypic correlation coefficients between pair of characters (Table- 4) has been utilized to study the character associationship. In general, the genotypic correlations were higher than phenotypic correlations in most of the cases. These could occur when the genes governing two traits were similar and environmental factors played a small part in the expression of these traits. Out of twenty characters studied, vine length, number of primary branches, internode length, petiole length, peduncle length, days to last fruit harvest, number of marketable fruit harvest, number of fruits per plant, fruit weight, fruit length, fruit diameter, beta carotene content exhibited significantly positive correlations with fruit yield per plant at genotypic and phenotypic level. Besides, four characters namely, days to 50% flowering, sex ratio, days to first fruit harvest, 100seed weight, number of seeds per fruit also expressed positive but non-significant correlation with fruit yield per plant at genotypic and phenotypic level. Such positive associationship with fruit yield per plant in bitter gourd was recorded by Singh and Singh *et al.* (2015), Guptha *et al.* (2015), Pathak *et al*. (2014), the similar studies were reported by Bhave *et al.* (2003b), Dey *et al.* (2005), Islam *et al.* (2009) and Sundaram (2010) with similar association of fruit yield per vine with fruit diameter, whereas Mangal *et al.* (1981), Geetashri *et al.* (1995), Bhave *et al.* (2003a), Bhave *et al.* (2003b), Dey *et al.* (2005), Ram *et al.* (2006), Islam *et al*. (2009) and Sundaram (2010) reported similar association of fruit yield with number of fruits per plant. Geetashri *et al*. (1995), Bhave *et al.* (2003a), Bhave *et al.* (2003b) and Sundaram (2010) reported similar association of fruits per plant with vine length.

Ascorbic acid content exhibited negative correlation with fruit yield per plant.

Table-4: Association among twenty yield components in bitter gourd (Phenotypic Correlation)

	NPB	IL	PTL	NNFF	DA50%F	SR	PDL	DTFFH	DTLFH	NMFH	NFPP	FW	FL	FD	100SW	NSPF	AA	BC	FYPP
VL	0.5262**	0.7852**	0.5601**	-0.2333*	-0.0532	-0.2042*	0.5601**	0.0404	**0.2611****	0.4165**	0.4837**	0.3604**	0.5152**	0.3418**	0.1082	0.0726	0.0909	0.1701	**0.4314****
NPB	**1.0000**	0.6473**	0.5559**	-0.2233*	-0.1130	-0.0933	0.5559**	0.1004	0.0988	0.3135**	0.3729**	0.4895**	0.6255**	0.4667**	-0.0985	-0.2058*	-0.2544*	0.1122	**0.4811****
IL		**1.0000**	0.4733**	-0.1128	-0.0830	-0.1514	0.4733**	0.0168	0.2675**	0.2871**	0.3482**	0.3185**	0.4965**	0.2536*	0.0766	-0.0098	-0.1838	0.2210*	**0.4820****
PTL			**1.0000**	-0.2638**	-0.1235	-0.0956	1.0000**	0.0629	0.2964**	0.4088**	0.4261**	0.7790**	0.7599**	0.7265**	0.1953	-0.0181	0.0275	0.1726	**0.7420****
NNFF				**1.0000**	0.1422	0.2109*	-0.2638**	0.0685	-0.1082	-0.2971**	-0.2242*	-0.1797	-0.1264	-0.1626	-0.1548	-0.1078	-0.2437*	-0.1031	**-0.0809**
DA50%F					**1.0000**	0.2402*	-0.1235	-0.0592	-0.1101	-0.1250	-0.1611	0.0029	-0.1157	-0.0271	0.0050	0.0384	0.1806	-0.1888	**0.0307**
SR						**1.0000**	-0.0956	0.0036	-0.0566	-0.3182**	-0.4260**	0.0099	-0.1245	0.0742	0.1740	-0.1497	-0.0561	-0.2075*	**0.0626**
PDL							**1.0000**	0.0375	0.2964**	0.4088**	0.4261**	0.7790**	0.7599**	0.7265**	0.1953	-0.0181	0.0275	0.1726	**0.6548****
DTFFH								**1.0000**	0.0292	0.0368	-0.0375	0.1015	0.0515	0.0964	0.0565	-0.0323	-0.0066	-0.0307	**-0.0145**
DTLFH									**1.0000**	0.0185	-0.0002	0.2146*	0.1990*	0.2674**	0.3075**	0.1112	-0.0974	0.1075	**0.2995****
NMFH										**1.0000**	0.7523**	0.2756**	0.3594**	0.2695**	0.0118	0.0024	0.1426	0.1450	**0.2624****
NFPP											**1.0000**	0.2834**	0.4373**	0.2408*	-0.0470	0.0428	0.1024	0.0684	**0.2701****
FW												**1.0000**	0.7561**	0.7272**	0.0982	-0.1725	-0.0069	0.0895	**0.7090****
FL													**1.0000**	0.6282**	-0.0770	-0.1423	-0.1258	0.0901	**0.6699****
FD														**1.0000**	0.0694	-0.0524	-0.2391*	0.0306	**0.6431****
100SW															**1.0000**	0.0017	0.2132*	0.0052	**0.0974**
NSPF																**1.0000**	0.2105*	0.0362	**0.0018**
AA																	**1.0000**	0.0627	**-0.1899***
BC																		**1.0000**	**0.1573***

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

1.VL (cm)- Vine length (cm) ;2. NPB- Number of primary branches; 3. IL (cm)- Internode length (cm);4. PTL (cm)- Petiole length (cm);5. NNFF-Node no at first female flower appearance; 6. DA50%F- Days to 50% flowering ;7. SR- Sex ratio; 8. PDL (cm)- Peduncle length (cm); 9. DTFFH- Days to first fruit harvest; 10. DTLFH- Days to last fruit harvest; 11. NMFH-Number of marketable fruit harvest; 12. NFPP-Number of fruits/ plants;13. FW(g)- Fruit weight (g);14. FL(cm)- Fruit length (cm);15. FD (cm)- Fruit diameter (cm); 16. 100 SW (g)- 100 seed weight (g); 17. NSPF- Number of seed/fruits ;18. AA mg/100g - Ascorbic acid (mg/100g); 19. BC mg/100g- β carotene content (mg/100g) ; 20. FYPP-Fruit yield/plant (kg).

Table-5: Association among twenty yield components in bitter gourd (Genotypic Correlation)

	NPB	IL	PTL	NNFF	DA50%F	SR	PDL	DTFFH	DTLFH	NMFH	NFPP	FW	FL	FD	100SW	NSPF	AA	BC	FYPP
VL	0.5736**	0.8113**	0.5769**	-0.6096*	-0.1827	-0.3841*	0.5769**	-0.1039	0.3090*	0.9975**	0.8916**	0.4061**	0.5409**	**0.3508****	0.1316	0.1276	0.0989	0.2191	**0.4627****
NPB	**1.0000**	0.6939**	0.6116**	-0.5826*	-0.2935	-0.2679	0.6116**	-0.2448	0.1800	0.8686**	0.8315**	0.5835**	0.7039**	0.5216**	-0.1284	-0.2693*	-0.2927*	0.1926	**0.5698****
IL		**1.0000**	0.4840**	-0.2866	-0.3093	-0.2802	0.4840**	-0.0697	0.3605**	0.6992**	0.6454**	0.3577**	0.5070**	0.2649*	0.0775	0.0005	-0.2031	0.2667*	**0.5159****
PTL			**1.0000**	-0.6554**	-0.4228	-0.2356	1.0000**	-0.0600	0.3730**	0.9355**	0.7907**	0.8712**	0.7937**	0.7497**	0.2372	-0.0249	0.0089	0.2222	**0.7779****
NNFF				**1.0000**	0.4739	0.8084	-0.6554**	-0.2043	-0.2752	-1.2281**	-0.9958*	-0.5894	-0.2443	-0.4168	-0.1559	-0.2215	-0.6134*	-0.2388	**-0.2819***
DA50%F					**1.0000**	1.1567*	-0.4228	-0.6454	-0.0693	-1.0057	-0.8845	-0.0951	-0.2817	-0.1559	0.1262	0.3594	0.5178	-0.5853	**-0.0235**
SR						**1.0000**	-0.2356	-0.1075	-0.1823	-1.1132**	-0.8822**	0.0197	-0.2610	0.1966	0.4621	0.3221	-0.2141	-0.2641*	**0.0289**
PDL							**1.0000**	-0.0600	0.3733**	0.9355**	0.7907**	0.8712**	0.7037**	0.7497**	0.2372	-0.0249	0.0089	0.2222	**0.7259****
DTFFH								**1.0000**	-0.0570	-0.0827	-0.0269	-0.1772	-0.2699	-0.3116	-0.2377	0.7467	0.2706	-0.0609	**0.0252**
DTLFH									**1.0000**	0.2843	0.1113	0.3471	0.2561*	0.3567**	0.4595**	0.1282	-0.1463	0.2755	**0.4243****
NMFH										**1.0000**	1.0375**	0.8147**	0.9084**	0.5932**	-0.0535	-0.2594	0.2969	0.3564	**0.6157****
NFPP											**1.0000**	0.5884**	0.8059**	0.3867**	-0.0816	-0.2735	0.1388	0.1720	**0.5553****
FW												**1.0000**	0.8513**	0.8161**	0.1078	-0.2632	-0.0366	0.0969	**0.8079****
FL													**1.0000**	0.6496**	-0.1120	-0.2395	-0.1358	0.0979	**0.7141****
FD														**1.0000**	0.0832	-0.1232	**-0.2548***	0.0342	**0.6690****
100SW															**1.0000**	0.2351	0.26208	-0.0408	**0.1107**
NSPF																**1.0000**	0.3407*	0.0847	**0.0475**
AA																	**1.0000**	0.1016	**-0.2268***
BC																		**1.0000**	**0.2081***

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

1.VL (cm)- Vine length (cm) ;2. NPB- Number of primary branches; 3. IL (cm)- Internode length (cm);4. PTL (cm)- Petiole length (cm);5. NNFF-Node no at first female flower appearance; 6. DA50%F- Days to 50% flowering ;7. SR- Sex ratio; 8. PDL (cm)- Peduncle length (cm); 9. DTFFH- Days to first fruit harvest; 10. DTLFH- Days to last fruit harvest; 11. NMFH-Number of marketable fruit harvest; 12. NFPP-Number of fruits/ plants;13. FW(g)- Fruit weight (g);14. FL(cm)- Fruit length (cm);15. FD (cm)- Fruit diameter (cm); 16. 100 SW (g)- 100 seed weight (g); 17. NSPF- Number of seed/fruits ;18. AA mg/100g - Ascorbic acid (mg/100g); 19. BC mg/100g- β carotene content (mg/100g) ; 20. FYPP-Fruit yield/plant (kg).

There would be less likelihood of high yielding bitter gourd genotypes with more content of ascorbic acid in fruits.

The inter-relationships among the characters exhibited that thirteen correlation co-efficients were significant either in positive or negative direction. They also showed high genotypic correlations as well. The correlation analysis indicated the complex nature of relationships for the plant characters as for example, number of fruit per plant and fruit weight, fruit length, fruit diameter not only exhibited high positive correlation co-efficient with fruit yield per plant but they were also positively and significantly inter-related to each other. Hence, the selection on the basis of any of the significantly positive inter-related characters would be expected to give a desired correlated response in other characters.

Among the different traits studied, number of fruits per vine registered high, significant and positive correlation with fruit yield followed by number of primary branches, days to last fruit harvest, vine length and fruit flesh thickness. It suggests that these are the most important parameters of yield, so more weightage should be given to these characters in bitter gourd breeding programme.

4.2.3 Path co-efficient analysis

The complexity of character relationship among themselves and with fruit yield becomes evident from the discussion alone did not provide a comprehensive picture of relative importance of direct and indirect influences of each character to fruit yield, as these traits were the resultant product of combined effects of various factors complementing or counteracting. In the present study, the phenotypic correlation and genotypic coefficients were partitioned into direct and indirect effects to identify relative importance of yield components towards fruit yield of bitter gourd (Table-6 & Table-7).

At phenotypic level, fruit weight recorded high positive direct effects on fruit yield followed by petiole length. Based on the characters which had positive effects on fruit yield could be exploited for selection to improve bitter gourd as they are directly responding for selection.

The residual factor determines how best the casual factors account for the variability of the dependent factor, the yield per vine in this case. The residual effects were 0.4465 and 0.5399, which were of low magnitude at genotypic and phenotypic levels.

Table- 6: Phenotypic (P) path coefficient analysis [direct (bold) and indirect effects] of the yield contributing characters in bitter gourd

	VL	NPB	IL	PTL	NNFF	DA50%F	SR	PDL	DTFFH	DTLFH	NMFH	NFPP	FW	FL	FD	100SW	NSPF	AA	BC	Correlation with FYPP at phenotypic level
VL	**-0.0769**	-0.0405	-0.0604	-0.0431	0.0179	0.0041	0.0157	-0.0431	-0.0031	-0.0201	-0.0320	-0.0372	-0.0277	-0.0396	-0.0263	-0.0083	-0.0056	-0.0070	-0.0131	**0.4314****
NPB	-0.0325	**-0.0618**	-0.0400	-0.0344	0.0138	0.0070	0.0058	-0.0344	-0.0062	-0.0061	-0.0194	-0.0231	-0.0303	-0.0387	-0.0289	0.0061	0.0127	0.0157	-0.0069	**0.4811****
IL	0.1525	0.1257	**0.1941**	0.0919	-0.0219	-0.0161	-0.0294	0.0919	0.0033	0.0519	0.0557	0.0676	0.0618	0.0964	0.0492	0.0149	-0.0019	-0.0357	0.0429	**0.4820****
PTL	0.2300	0.2282	0.1943	**0.4106**	-0.1083	-0.0507	-0.0393	0.4106	0.0258	0.1217	0.1678	0.1749	0.3199	0.3120	0.2983	0.0802	-0.0074	0.0113	0.0709	**0.7420****
NNFF	-0.0095	-0.0091	-0.0046	-0.0107	**0.0406**	0.0058	0.0086	-0.0107	0.0028	-0.0044	-0.0121	-0.0091	-0.0073	-0.0051	-0.0066	-0.0063	-0.0044	-0.0099	-0.0042	**-0.0809**
DA50%F	-0.0061	-0.0129	-0.0095	-0.0141	0.0162	**0.1139**	0.0274	-0.0141	-0.0067	-0.0125	-0.0142	-0.0183	0.0003	-0.0132	-0.0031	0.0006	0.0044	0.0206	-0.0215	**0.0307**
SR	-0.0265	-0.0121	-0.0196	-0.0124	0.0274	0.0312	**0.1297**	-0.0124	0.0005	-0.0073	-0.0413	-0.0553	0.0013	-0.0162	0.0096	0.0226	-0.0194	-0.0073	-0.0269	**0.0626**
PDL	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	**0.0000**	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	**0.6548****
DTFFH	-0.0026	-0.0065	-0.0011	-0.0041	-0.0044	0.0038	-0.0002	-0.0041	**-0.0648**	-0.0019	-0.0024	0.0024	-0.0066	-0.0033	-0.0062	-0.0037	0.0021	0.0004	0.0020	**-0.0145**
DTLFH	0.0141	0.0053	0.0144	0.0160	-0.0058	-0.0059	-0.0031	0.0160	0.0016	**0.0540**	0.0010	0.0000	0.0116	0.0107	0.0144	0.0166	0.0060	-0.0053	0.0058	**0.2995****
NMFH	0.0197	0.0148	0.0136	0.0193	-0.0140	-0.0059	-0.0150	0.0193	0.0017	0.0009	**0.0473**	0.0356	0.0130	0.0170	0.0127	0.0006	0.0001	0.0067	0.0069	**0.2624****
NFPP	0.0062	0.0048	0.0044	0.0054	-0.0029	-0.0021	-0.0054	0.0054	-0.0005	0.0000	0.0096	**0.0127**	0.0036	0.0056	0.0031	-0.0006	0.0005	0.0013	0.0009	**0.2701****
FW	0.1131	0.1536	0.1000	0.2445	-0.0564	0.0009	0.0031	0.2445	0.0318	0.0674	0.0865	0.0889	**0.3139**	0.2373	0.2282	0.0308	-0.0541	-0.0022	0.0281	**0.7090****
FL	0.0486	0.0590	0.0468	0.0716	-0.0119	-0.0109	-0.0117	0.0716	0.0049	0.0188	0.0339	0.0412	0.0713	**0.0943**	0.0592	-0.0073	-0.0134	-0.0119	0.0085	**0.6699****
FD	-0.0010	-0.0013	-0.0007	-0.0021	0.0005	0.0001	-0.0002	-0.0021	-0.0003	-0.0008	-0.0008	-0.0007	-0.0021	-0.0018	**-0.0029**	-0.0002	0.0001	0.0007	-0.0001	**0.6431****
100SW	-0.0008	0.0007	-0.0006	-0.0014	0.0011	0.0000	-0.0013	-0.0014	-0.0004	-0.0023	-0.0001	0.0003	-0.0007	0.0006	-0.0005	**-0.0074**	0.0000	-0.0016	0.0000	**0.0974**
NSPF	0.0088	-0.0248	-0.0012	-0.0022	-0.0130	0.0046	-0.0181	-0.0022	-0.0039	0.0134	0.0003	0.0052	-0.0208	-0.0172	-0.0063	0.0002	**0.1207**	0.0254	0.0044	**0.0018**
AA	-0.0178	0.0498	0.0360	-0.0054	0.0477	-0.0354	0.0110	-0.0054	0.0013	0.0191	-0.0279	-0.0201	0.0013	0.0246	0.0468	-0.0418	-0.0412	**-0.1958**	-0.0123	**-0.1899***
BC	0.0123	0.0081	0.0159	0.0125	-0.0074	-0.0136	-0.0150	0.0125	-0.0022	0.0078	0.0105	0.0049	0.0065	0.0065	0.0022	0.0004	0.0026	0.0045	**0.0722**	**0.1573***

R SQUARE = 0.7085 RESIDUAL EFFECT = 0.5399.

1.VL (cm)- Vine length (cm) ;2. NPB- Number of primary branches; 3. IL (cm)- Internode length (cm);4. PTL (cm)- Petiole length (cm);5. NNFF-Node no at first female flower appearance; 6. DA50%F- Days to 50% flowering ;7. SR- Sex ratio; 8. PDL (cm)- Peduncle length (cm); 9. DTFFH- Days to first fruit harvest; 10. DTLFH- Days to last fruit harvest; 11. NMFH-Number of marketable fruit harvest; 12. NFPP-Number of fruits/ plants;13. FW(g)- Fruit weight (g);14. FL(cm)- Fruit length (cm);15. FD (cm)- Fruit diameter (cm); 16. 100 SW (g)- 100 seed weight (g); 17. NSPF- Number of seed/fruits ;18. AA mg/100g - Ascorbic acid (mg/100g); 19. BC mg/100g- β carotene content (mg/100g) ; 20. FYPP-Fruit yield/plant (kg).

Table-7: Genotypic (G) path coefficient analysis [direct (bold) and indirect effects] of the yield contributing characters in bitter gourd

	VL	NPB	IL	PTL	NNFF	DA50%F	SR	PDL	DTFFH	DTLFH	NMFH	NFPP	FW	FL	FD	100SW	NSPF	AA	BC	Correlation with FYPP at genotypic level
VL	**0.4440**	0.2546	0.3602	0.2561	-0.2707	-0.0811	-0.1705	0.2561	-0.0461	0.1372	0.4429	0.3959	0.1803	0.2401	0.1557	0.0584	0.0567	0.0439	0.0973	**0.4627****
NPB	0.1352	**0.2357**	0.1635	0.1441	-0.1373	-0.0692	-0.0631	0.1441	-0.0577	0.0424	0.2047	0.1960	0.1375	0.1659	0.1229	-0.0303	-0.0635	-0.0690	0.0454	**0.5698****
IL	-0.1770	-0.1514	**-0.2181**	-0.1056	0.0625	0.0675	0.0611	-0.1056	0.0152	-0.0786	-0.1525	-0.1408	-0.0780	-0.1106	-0.0578	-0.0169	-0.0001	0.0443	-0.0582	**0.5159****
PTL	0.5453	0.5781	0.4575	**0.9452**	-0.6195	-0.3997	-0.2227	0.9452	-0.0567	0.3526	0.8843	0.7473	0.8234	0.7503	0.7086	0.2242	-0.0235	0.0084	0.2100	**0.7779****
NNFF	-0.0161	-0.0154	-0.0076	-0.0173	**0.0264**	0.0125	0.0213	-0.0173	-0.0054	-0.0073	-0.0324	-0.0263	-0.0155	-0.0064	-0.0110	-0.0041	-0.0058	-0.0162	-0.0063	**-0.2819***
DA50%F	-0.0162	-0.0260	-0.0274	-0.0375	0.0420	**0.0887**	0.1026	-0.0375	-0.0572	-0.0061	-0.0892	-0.0784	-0.0084	-0.0250	-0.0138	0.0112	0.0319	0.0459	-0.0519	**-0.0235**
SR	-0.0692	-0.0483	-0.0505	-0.0424	0.1457	0.2084	**0.1802**	-0.0424	-0.0194	-0.0328	-0.2006	-0.1589	0.0035	-0.0470	0.0354	0.0833	0.0580	-0.0386	-0.0476	**0.0289**
PDL	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	**0.0000**	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	**0.7259****
DTFFH	-0.0066	-0.0155	-0.0044	-0.0038	-0.0129	-0.0408	-0.0068	-0.0038	**0.0632**	-0.0036	-0.0052	-0.0017	-0.0112	-0.0171	-0.0197	-0.0150	0.0472	0.0171	0.0039	**0.0252**
DTLFH	0.0570	0.0332	0.0665	0.0689	-0.0508	-0.0128	-0.0336	0.0689	-0.0105	**0.1846**	0.0525	0.0205	0.0641	0.0473	0.0659	0.0848	0.0237	-0.0270	0.0509	**0.4243****
NMFH	0.0963	0.0838	0.0675	0.0903	-0.1185	-0.0970	-0.1074	0.0903	-0.0080	0.0274	**0.0965**	0.1001	0.0786	0.0877	0.0572	-0.0052	-0.0250	0.0286	0.0344	**0.6157****
NFPP	-0.4131	-0.3853	-0.2990	-0.3663	0.4614	0.4098	0.4087	-0.3663	0.0125	-0.0516	-0.4807	**-0.4633**	-0.2726	-0.3734	-0.1792	0.0378	0.1267	-0.0643	-0.0797	**0.5553****
FW	0.1828	0.2627	0.1610	0.3921	-0.2653	-0.0428	0.0089	0.3921	-0.0798	0.1562	0.3667	0.2648	**0.4501**	0.3832	0.3673	0.0485	-0.1185	-0.0165	0.0436	**0.8079****
FL	-0.0474	-0.0617	-0.0444	-0.0696	0.0214	0.0247	0.0229	-0.0696	0.0237	-0.0225	-0.0796	-0.0706	-0.0746	**-0.0877**	-0.0569	0.0098	0.0210	0.0119	-0.0086	**0.7141****
FD	-0.1940	-0.2885	-0.1465	-0.4147	0.2306	0.0863	-0.1088	-0.4147	0.1724	-0.1973	-0.3281	-0.2139	-0.4514	-0.3593	**-0.5532**	-0.0460	0.0682	0.1410	-0.0189	**0.6690****
100SW	-0.0341	0.0333	-0.0201	-0.0615	0.0404	-0.0327	-0.1198	-0.0615	0.0616	-0.1191	0.0139	0.0211	-0.0279	0.0290	-0.0216	**-0.2593**	-0.0610	-0.0679	0.0106	**0.1107**
NSPF	0.0004	-0.0008	0.0000	-0.0001	-0.0006	0.0010	0.0009	-0.0001	0.0021	0.0004	-0.0007	-0.0008	-0.0008	-0.0007	-0.0004	0.0007	**0.0029**	0.0010	0.0002	**0.0475**
AA	-0.0267	0.0792	0.0549	-0.0024	0.1659	-0.1401	0.0579	-0.0024	-0.0732	0.0396	-0.0803	-0.0375	0.0099	0.0367	0.0689	-0.0709	-0.0922	**-0.2705**	-0.0275	**-0.2268***
BC	0.0023	0.0020	0.0028	0.0023	-0.0025	-0.0062	-0.0028	0.0023	0.0006	0.0029	0.0038	0.0018	0.0010	0.0010	0.0004	-0.0004	0.0009	0.0011	**0.0105**	**0.2081***

R SQUARE = 0.8006 RESIDUAL EFFECT = 0.4465.

1.VL (cm)- Vine length (cm) ;2. NPB- Number of primary branches; 3. IL (cm)- Internode length (cm);4. PTL (cm)- Petiole length (cm);5. NNFF-Node no at first female flower appearance; 6. DA50%F- Days to 50% flowering ;7. SR- Sex ratio; 8. PDL (cm)- Peduncle length (cm); 9. DTFFH- Days to first fruit harvest; 10. DTLFH- Days to last fruit harvest; 11. NMFH-Number of marketable fruit harvest; 12. NFPP-Number of fruits/ plants;13. FW(g)- Fruit weight (g);14. FL(cm)- Fruit length (cm);15. FD (cm)- Fruit diameter (cm); 16. 100 SW (g)- 100 seed weight (g); 17. NSPF- Number of seed/fruits ;18. AA mg/100g - Ascorbic acid (mg/100g); 19. BC mg/100g- β carotene content (mg/100g) ; 20. FYPP-Fruit yield/plant (kg).

The set of characters identified as selection indices for fruit yield per plant based on the genetic variability parameters for the characters, their correlations and path coefficient analysis are fruit weight and petiole length.

4.3 Genetic diversity of genotypes through multivariate analysis

Mahalanobis (1936) developed the D^2 Statistic model to determine the divergence among population in terms of generalized group distance. It has been widely used in Psychometry and anthropometry for classificatory purpose. Later, it has been successfully exploited in plant breeding. Multivariate analysis is a powerful tool in qualifying the degree of divergence between biological populations (genetic distance) and to assess the relative contribution of different components to the total divergence. Although, Mahalanobis's generalized distance as a measure of genetic distance occupy a unique place in plant breeding yet, as it happens in biology, several problems under the influence of random unpredictable changes due to environment, evade the direct grip of the concept well proven is more exact fields like mathematical components. It suggests the measuring the genetic distance through multivariate analysis over environment, to fortify its reliability. Genetic divergence of bitter gourd using multivariate analysis was earlier studied by Gowda *et al.* (2017), Singh *et al.* (2015), Singh *et al*. (2013), Kundu *et al.* (2012), Laxuman *et al.* (2012) and Sundaram *et al*. (2010).

The present study aimed at analyzing the genetic divergence of 33 genotypes employing twenty important quantitative characters. Based on the degree of divergence (D^2 values) between any two genotypes a logical grouping of the genotypes with low D^2 value could be arrived at by Tocher's method as described by Rao (1952).

Based on the determination of divergence, all the 33 genotypes could meaningfully be grouped into 8 clusters (Table-8). Cluster II had 12 genotypes followed by cluster I had 9 genotypes, cluster v which comprised of 5 genotypes, cluster III had 3 genotypes. while cluster IV, VI, VII and VIII were monotypic. The monotypic genotypes in cluster IV, VI, VII and VIII indicated genotypes from those clusters might have originated across the geographical location in breeding programs. The grouping pattern of genotypes was observed to be random, indicating that geographical diversity and

Table-8: Clustering pattern of 33 genotypes of bitter gourd by Ward's method

Cluster	No. of genotypes	Genotypes with source of collection
I	9	IC-44438 (NBPGR, Thrissur), IC-599423(NBPGR, Thrissur), IC-599426(NBPGR, Thrissur), IC-599424(NBPGR, Thrissur), IC-68343(NBPGR, Thrissur), IC-45350(NBPGR, Thrissur), IC-32817(NBPGR, Thrissur), IC-68285, IC-398610(NBPGR, Thrissur).
II	12	IC-541448(NBPGR, Thrissur), IC-536670(NBPGR, Thrissur), Dhaka Karala(Local collection), IC-599420(NBPGR, Thrissur), IC-418486(NBPGR, Thrissur), IC-599421(NBPGR, Thrissur), IC-68236(NBPGR, Thrissur), IC-65787(NBPGR, Thrissur), IC-596983(NBPGR, Thrissur), IC-599428(NBPGR, Thrissur), K-85603 (TCR-76) (NBPGR, Thrissur), IC-45358(NBPGR, Thrissur).
III	3	K-68237(NBPGR, Thrissur), IC-599424(NBPGR, Thrissur), Don No-1(Local collection).
IV	1	IC-470557(NBPGR, Thrissur).
V	5	IC-467680(NBPGR, Thrissur), IC-427694(NBPGR, Thrissur), K-85608(NBPGR, Thrissur), IC-470565(NBPGR, Thrissur), IC-264699(NBPGR, Thrissur).
VI	1	Gangajali Karala (Local collection).
VII	1	IC-599429(NBPGR, Thrissur).
VIII	1	IC-596981(NBPGR, Thrissur).

Table-9: Average Inter and intra cluster D^2 values for eight clusters in 33 genotypes of bitter gourd

Cluster	I	II	III	IV	V	VI	VII	VIII
I	**7.41**	17.39	10.69	9.27	12.30	15.88	16.39	11.30
II		**8.05**	11.95	18.54	14.54	10.70	12.99	14.81
III			**6.94**	12.01	11.93	11.77	14.33	12.64
IV				**0.00**	16.81	16.13	19.86	11.78
V					**9.62**	16.20	12.00	12.38
VI						**0.00**	14.60	16.10
VII							**0.00**	12.23
VIII								**0.00**

Table-10: Mean values of eight clusters for yield and its contributing characters

Cluster Number	VL (cm)	NPB	IL (cm)	PTL (cm)	NNFF	DA50%F	SR	PDL (cm)	DTFFH	DTLFH
	1	2	3	4	5	6	7	8	9	10
Cluster -1	196.44	11.26	5.39	4.89	14.78	41.81	8.11	4.71	67.93	110.04
Cluster -2	238.42	15.42	7.07	6.75	14.58	41.33	8.08	6.11	68.14	113.67
Cluster -3	236.56	12.56	6.31	5.73	15.44	42.56	7.81	4.99	68.22	108.33
Cluster -4	216.33	9.33	7.30	4.40	16.33	42.33	7.83	4.67	67.00	110.67
Cluster -5	186.33	11.27	4.63	6.14	14.60	41.53	8.19	5.97	68.07	112.07
Cluster -6	214.33	16.67	7.80	5.50	16.67	42.67	8.30	6.23	70.33	114.67
Cluster -7	165.33	15.67	5.67	6.03	16.00	41.33	8.37	4.33	67.33	105.67
Cluster -8	196.33	10.00	5.77	4.57	15.00	41.67	8.43	4.23	70.00	112.67
% Contribution towards divergence	13.45%	0.19%	11.55%	3.41%	0.00%	0.00%	0.00%	1.70%	0.00%	0.57%
Times Ranked 1st	71	1	61	18	0	0	0	9	0	3

Cluster Number	NMFH	NFPP	FW(g)	FL (cm)	FD (cm)	100 SW (g)	NSPF	AA mg/100g	BC mg/100g	FYPP
	11	12	13	14	15	16	17	18	19	20
Cluster -1	8.48	14.19	57.74	12.64	10.12	18.21	18.15	76.41	0.92	0.91
Cluster -2	10.11	16.47	68.53	16.73	12.61	18.13	18.03	69.94	0.94	1.64
Cluster -3	9.56	15.89	62.33	15.98	10.80	16.58	18.67	75.76	0.76	1.08
Cluster -4	8.33	13.00	53.67	11.40	9.57	17.50	18.33	73.37	0.92	0.63
Cluster -5	8.80	14.40	67.34	15.56	11.89	18.64	17.93	76.13	0.78	1.17
Cluster -6	8.00	15.00	67.00	17.20	10.53	19.17	17.00	63.60	1.01	1.97
Cluster -7	8.33	13.67	70.00	17.37	13.37	15.10	16.67	61.93	1.00	1.43
Cluster -8	7.33	12.00	58.00	12.27	12.63	18.83	19.00	64.90	0.77	0.77
% Contribution towards divergence	0.00%	0.00%	0.00%	10.98%	37.88%	1.70%	0.38%	11.55%	1.52%	5.11%
Times Ranked 1st	0	0	0	58	200	9	2	61	8	27

1.VL (cm)- Vine length (cm) ;2. NPB- Number of primary branches; 3. IL (cm)- Internode length (cm);4. PTL (cm)- Petiole length (cm);5. NNFF-Node no at first female flower appearance; 6. DA50%F- Days to 50% flowering ;7. SR- Sex ratio; 8. PDL (cm)- Peduncle length (cm); 9. DTFFH- Days to first fruit harvest; 10. DTLFH- Days to last fruit harvest; 11. NMFH-Number of marketable fruit harvest; 12. NFPP-Number of fruits/ plants;13. FW(g)- Fruit weight (g);14. FL(cm)- Fruit length (cm);15. FD (cm)- Fruit dimeter (cm); 16. 100 SW (g)- 100 seed weight (g); 17. NSPF- Number of seed/fruits ;18. AA mg/100g - Ascorbic acid (mg/100g); 19. BC mg/100g- β carotene content (mg/100g); 20. FYPP-Fruit yield/plant (kg).

genetic divergence were unrelated. Therefore, the selection of genotypes for hybridization should be based on genetic divergence rather than geographic diversity. Environmental influence on the composition of cluster was also recorded earlier in bitter gourd by Kutty and Dharmatti *et al.* (2005), Laxuman *et al.* (2012), Kundu *et al.* (2012), Singh *et al.* (2015), Gowda *et al.* (2017).

The intra- and inter-cluster distances among 33 genotypes presented in Table-9 revealed that cluster II had the most intra-cluster value (8.05) indicating genotypes included in the cluster were extremely diverse. Cluster IV, VI, VII and VIII showed the minimum intra-cluster value.

At the inter-cluster level, minimum values occurred between cluster I and IV indicating close relationship among genotypes in those clusters. The greatest inter-cluster values were between cluster IV and VII followed by the distance between cluster II and IV indicating genotypes in those clusters had the greatest divergence.

Cluster means of genotypes (Table-10) indicated mean values of clusters varied in magnitude for all characters. The maximum cluster mean was in cluster VI for number of primary branches, internode length, node number at female flower appearance, days to 50% flowering, peduncle length, days to first fruit harvest, days to last fruit harvest, 100 seed weight, beta carotene content, fruit yield per plant. The maximum mean in cluster II was for vine length, petiole length, number of marketable fruit harvest, number of fruits per plant. Cluster II had the lowest for node number at female flower appearance and days to 50% flowering. These clusters could be useful sources of genes for simultaneous improvement of fruit yield, fruit quality. A high yielding, early flowering type, with better fruit quality could be bred utilizing genotypes from cluster II and VI as parents.

The relative contribution of individual characters towards genetic divergence was computed in terms of number of times it ranked first (Table-10). Fruit diameter contributed the most towards genetic divergence followed by vine length, internode length, ascorbic acid content, fruit length, fruit yield per plant, petiole length, 100 seed weight, peduncle length, beta carotene content, days to first fruit harvest, number of seed per fruit and number of primary branches indicating the possibility for selection of these characters (Table-10).

Fig-1: Dendrogram showing the genetic divergence among bitter gourd accessions using mean values of 33 genotypes

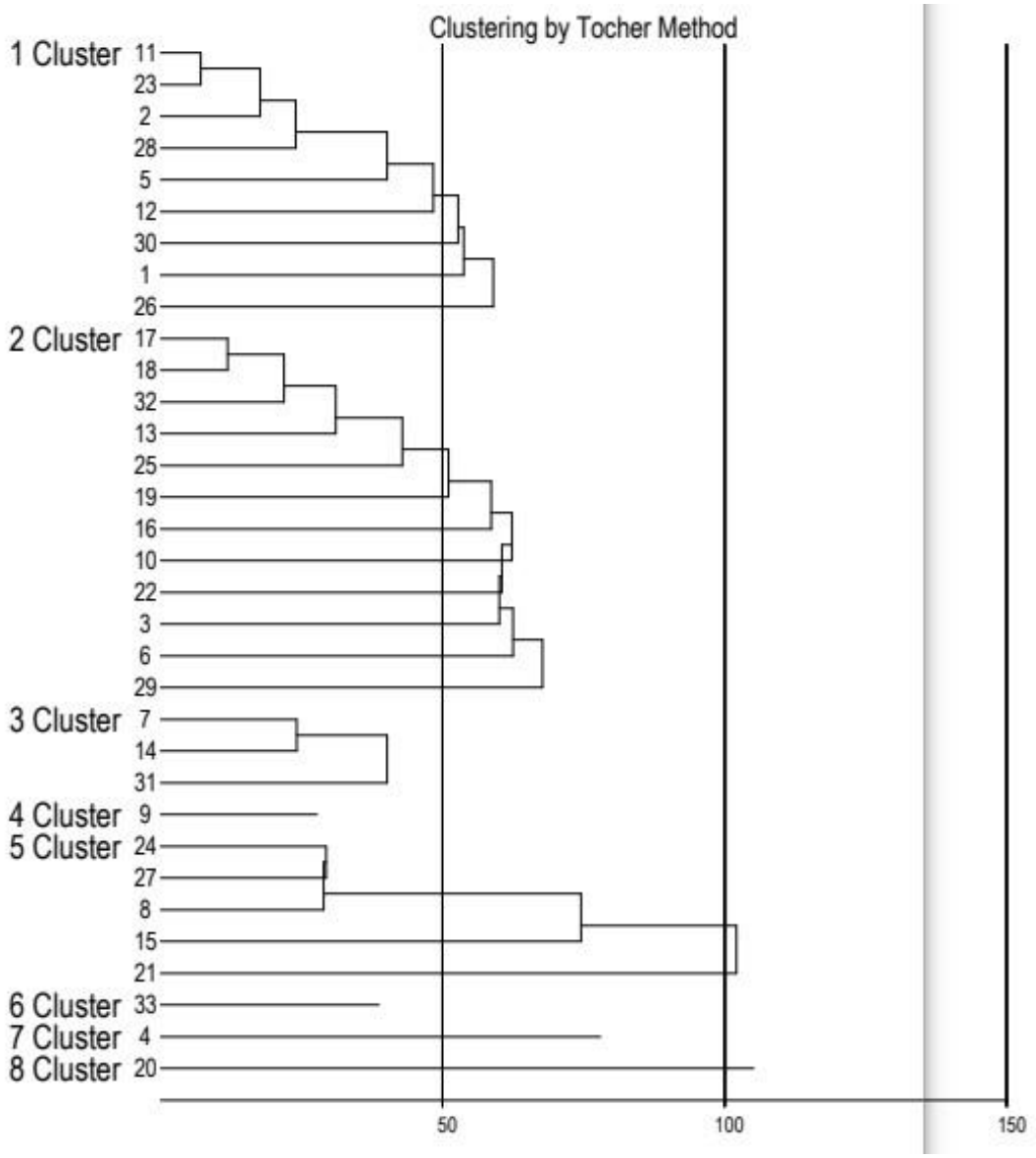

Fig-2: Parents used for hybridization programme

IC -599428

K-85603

IC- 65787

IC -541448

IC-596983

Gangajali Karala

High diversity occurred among bitter gourd genotypes along with strong relationships (Figure-1, Dendogram). Based on superior mean performance for agronomic characters (fruit yield per plant, etc.), genetic distances, clustering pattern and consumer preference characters (color, fruit shape, etc.), six promising and diverse inbred lines or varieties of bitter gourd viz IC-599428, K-85603, IC-65787, IC-541448, IC-596983 and Gangajali Karala were selected (Fig-2).

4.4 Genetic control of characters

The analysis of variance for combining ability based on Griffing's Model 1 and Method 2 exhibited significant component of GCA and SCA mean squares for fruit yield per plant along with all studied traits in F_1 generation (Table-11). This indicated that the inheritance of fruit yield per plant and most of the yield components, petiole length, days to 50% flowering, peduncle length, number of fruits per plant, fruit diameter traits were apparently controlled by both additive and non-additive gene action. The relative magnitude and importance of additive and non-additive variances in the genetic control of various characters were further revealed by σ^2gca/ σ^2sca. This reflected the preponderance of additive gene effects for petiole length, days to 50% flowering, peduncle length, number of fruits/plant and fruit diameter as their ratios were close to unity ($\geq$ 0.80) (Table-11). On the other hand, days to last fruit harvest was controlled by both additive and non-additive gene action as the ratio was $\geq$ 0.50 and < 0.80. In contrast, predictability ratios were < 0.50 for vine length, number of primary branches, internode length, node number at female flower appearance, sex ratio, number of marketable fruit harvest, fruit weight, fruit length, 100 seed weight, number of seed per fruit indicating non-additive genetic control for the conditioning of these traits. Similar non-additive gene action for yield and yield related characters were reported by Kumara *et al.* (2011), Gupta *et al.* (2006) and Bhave *et al.* (2004). Both additive and non-additive gene action for yield and yield related characters was reported by Mishra *et al*.(1994), Khattra *et al.* (1994a) Thangamani *et al*. (2011a) and Kushwaha and Karnwal (2011) in bitter gourd, while Singh *et al.* (2004) observed additive gene action for yield and yield related traits in bitter gourd.

While going through the nature of gene action governing twenty quantitative

Table-11: Analysis of variance for combining ability for twenty quantitative characters in bitter gourd

Source of variation	d.f	Mean sum of square									
		VL (cm)	NPB	IL (cm)	PTL (cm)	NNFF	DA50%F	SR	PDL (cm)	DTFFH	DTLFH
		1	2	3	4	5	6	7	8	9	10
GCA	**5**	999.410 **	1.206	0.215 **	0.766 **	0.659	0.447	0.651 **	0.766 **	14.962 **	7.706 *
SCA	**15**	1602.984 **	2.003 **	0.355 **	0.783 **	0.736	0.517	0.510 **	0.783 **	7.359 **	9.669 **
Error	**70**	19.713	0.526	0.018	0.045	0.589	1.110	0.019	0.045	1.447	2.564
σ^2gca		81.64	0.05	0.016	0.600	0.006	-0.055	0.053	0.600	1.126	4.290
σ^2sca		1583.27	1.477	0.336	0.738	0.147	-0.593	0.492	0.738	5.912	7.100
σ^2gca/ σ^2sca		0.05	0.03	0.04	0.81	0.04	0.93	0.10	0.81	0.19	0.60

Source of variation	d.f	Mean sum of square									
		NMFH	NFPP	FW(g)	FL (cm)	FD (cm)	100 SW (g)	NSPF	AA mg/100g	BC mg/100g	FYPP
		11	12	13	14	15	16	17	18	19	20
GCA	**5**	5.788 **	1.511	44.479 **	2.971 **	1.343 **	4.973 **	4.321 *	24.171 **	0.041 **	0.117 **
SCA	**15**	2.163 *	3.298 **	105.558 **	2.204 **	1.130 **	2.121 **	3.657 **	24.196 **	0.037 **	0.287 **
Error	**70**	0.954	1.273	1.569	0.068	0.029	0.043	1.410	3.169	0.004	0.012
σ^2gca		0.403	3.410	3.576	0.242	1.100	0.411	0.243	1.750	0.003	0.009
σ^2sca		1.209	3.740	10.398	2.136	1.101	2.078	2.247	21.027	0.033	0.274
σ^2gca/ σ^2sca		0.33	0.91	0.34	0.11	0.99	0.19	0.10	0.08	0.09	0.03

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

GCA - General combining ability, SCA- Specific combining ability σ^2gca - Variance due to GCA σ^2sca-Variance due to SCA

σ^2 gca/ σ^2 sca=1 additive & non additive gene action; σ^2 gca/ σ^2 sca>1 additive; σ^2 gca/ σ^2 sca<1 non additive gene action

1.VL (cm)- Vine length (cm) ;2. NPB- Number of primary branches; 3. IL (cm)- Internode length (cm);4. PTL (cm)- Petiole length (cm);5. NNFF-Node no at first female flower appearance; 6. DA50%F- Days to 50% flowering ;7. SR- Sex ratio; 8. PDL (cm)- Peduncle length (cm); 9. DTFFH- Days to first fruit harvest; 10. DTLFH- Days to last fruit harvest; 11. NMFH-Number of marketable fruit harvest; 12. NFPP-Number of fruits/ plants;13. FW(g)- Fruit weight (g);14. FL(cm)- Fruit length (cm);15. FD (cm)- Fruit diameter(cm); 16. 100 SW (g)- 100 seed weight (g); 17. NSPF- Number of seed/fruits ;18. AA mg/100g - Ascorbic acid (mg/100g); 19. BC mg/100g- β carotene content (mg/100g) ; 20. FYPP-Fruit yield/plant (kg).

traits, overwhelming response of non-additive gene action was observed for the control of vine length, number of primary branches, internode length, node number at female flower appearance, sex ratio, number of marketable fruit harvest, fruit weight, fruit length, 100 seed weight, number of seed per fruit. Hence, direct selection will bring no or slow genetic improvement for these traits. The successful breeding methods will be those that accumulate the genes to form superior gene constellations interacting in a favorable manner. The importance of non-additive gene action for the conditioning of most of traits in the present study indicates heterosis breeding to be the best possible option for improving these traits in bitter gourd. While a population improvement approach in the form of diallel selective mating (Jensen, 1970) or mass selection with concurrent random mating (Redden and Jensen, 1974) or restricted recurrent selection by intermating the most desirable segregates followed by selection (Shende *et al*., 2012) could be followed for the exploitation of both additive and non-additive gene action for days to last fruit harvest. Due to the predominance of additive gene action in petiole length, days to 50% flowering, peduncle length, number of fruits/plant and fruit diameter, selection of such trait should be done in later generation when the effects of non-additive gene action will be minimized and those of additive gene action effects will be fixed.

4.5 Identification of good general and specific combiners

No single parent was found to be a good general combiner for all the characters under study (Table-12). Among the parents, the maximum significant GCA effects in desired directions were recorded by the genitor IC- 65787 for fruit yield per plant, internode length, sex ratio, fruit weight, fruit diameter and beta carotene content. Next to IC- 65787, the genitor IC- 541448 also exhibited significant GCA effects for fruit yield per plant, number of marketable fruit harvest, days to first fruit harvest and fruit weight. Rest of the parents showed either negative or low magnitude of gca effects for fruit yield per plant but showed significant gca effects for vine length, internode length, sex ratio, days to first fruit harvest, number of marketable fruit harvest, fruit weight, fruit length, fruit diameter, 100 seed weight and ascorbic acid content by K-85603; for internode length, petiole length, sex ratio, peduncle length and numbers of seeds per fruit were recorded by the genitor IC-599428; for petiole length, peduncle length, days to first fruit harvest, days to last fruit harvest, fruit length and 100 seed weight by the genitor IC-596983 and for vine length and 100 seed weight by Gangajali Karala.

Table-12: Estimates of general combining ability of parents and specific combining ability of crosses for yield and its components in bitter gourd

Sl. No.	Genotype		VL (cm)	NPB	IL (cm)	PTL (cm)	NNFF	DA50%F	SR	PDL (cm)	DTFFH	DTLFH
			1	2	3	4	5	6	7	8	9	10
Parents												
1.	IC -599428		-8.824 **	-0.343	0.156 **	0.296 **	-0.028	0.269	0.376 **	0.296 **	-1.130 **	-0.676
2.	K-85603		6.231 **	0.380	0.090 *	-0.295 **	0.250	-0.065	0.182 **	-0.295 **	0.759 *	-1.176 **
3.	IC -65787		-4.741 **	-0.120	0.112 *	-0.237 **	-0.306	-0.204	-0.152 **	-0.237 **	0.259	0.407
4.	IC -541448		-2.407 *	0.380	-0.113 **	0.066	0.167	-0.093	-0.027	0.066	-1.324 **	0.074
5.	IC 596983		-5.713 **	-0.287	-0.094 *	0.271 **	-0.250	-0.120	-0.169 **	0.271 **	1.593 **	1.046 *
6.	Gangajali Karala		15.454 **	-0.009	-0.152 **	-0.101	0.167	0.213	-0.210 **	-0.101	-0.157	0.324
	S.E (m)		**1.170**	**0.191**	**0.035**	**0.056**	**0.202**	**0.278**	**0.036**	**0.056**	**0.317**	**0.422**
Crosses												
1.	IC -599428 × K-85603	1*2	-21.500**	0.833	0.733**	-0.133	0.333	0.667	-0.525**	-0.133	-0.167	-4.167**
2.	IC -599428 × IC -65787	1*3	10.000**	-1.000*	0.183	0.333*	0.833	0.258	-0.122	0.333*	0.167	-0.333
3.	IC -599428 × IC -541448	1*4	-0.333	-0.833	0.650**	0.283	-0.167	0.333	-0.420**	0.283	0.167	2.000
4.	IC -599428 × IC 596983	1*5	32.667**	2.167**	-0.017	0.817**	0.167	1.000	-0.310*	0.500	-0.833	-0.833
5.	IC -599428 × Gangajali Karala	1*6	24.333**	-1.000	-0.267*	-0.033**	-0.333	-0.833	-0.028	-0.033	0.500	3.000*
6	K-85603 × IC -65787	2*3	48.333**	-0.667	0.650**	1.250**	0.833	0.500	-0.418**	1.250**	-1.000	-9.833**
7	K-85603 × IC -541448	2*4	47.500**	-2.000**	-0.217*	-0.317	-0.333	0.667	-0.798**	-0.317	0.167	3.000*
8	K-85603 × IC 596983	2*5	-27.333**	0.333	0.050	-0.633**	0.667	-0.167	-0.030	-0.633**	3.500**	-0.667
9.	K-85603 × Gangajali Karala	2*6	24.833**	1.000**	0.317*	1.033**	-1.000	0.333	0.208*	1.033**	1.500	-0.667
10.	IC -65787 × IC -541448	3*4	7.500*	0.167	0.233*	0.500*	0.667	-0.167	0.033	0.500*	-1.000	-4.167**
11.	IC -65787 × IC 596983	3*5	-3.000	-0.167	0.183	0.717**	0.167	0.667	0.247*	0.717**	-0.833	0.231
12.	IC -65787 × Gangajali Karala	3*6	-7.167*	-0.500	-0.017	0.817**	-0.333	0.537	0.022	0.817**	-0.333	1.500
13.	IC -541448 × IC 596983	4*5	36.667**	1.833**	1.083**	0.917**	0.500	-0.500	0.133	0.917**	1.167	6.167**
14	IC -541448 × Gangajali Karala	4*6	17.667**	0.667	0.283*	-0.383*	0.250	0.667	-0.097	-0.383*	0.241	-6.167**

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

Sl. No.	Genotype		VL (cm)	NPB	IL (cm)	PTL (cm)	NNFF	DA50%F	SR	PDL (cm)	DTFFH	DTLFH
			1	2	3	4	5	6	7	8	9	10
15	IC 596983 × Gangajali Karala	5*6	0.167**	-0.333	0.083	-0.067	-0.333	1.000	0.083	-0.067	-4.333**	-1.333
Reciprocal crosses												
16	K-85603 × IC -599428	2*1	-25.481**	0.870	-0.254*	0.043	0.222	-0.519	-0.178	0.043	-0.037	-3.546**
17	IC -65787 × IC -599428	3*1	-29.009**	-0.463	0.141	0.618**	-0.389	0.954	-0.477**	0.618**	-1.204	-0.296
18	IC -541448 × IC -599428	4*1	12.657**	-0.463	0.066	-0.402*	0.139	0.509	0.800**	-0.402*	1.713	-2.296
19	IC 596983 × IC -599428	5*1	0.296	0.870	0.780**	0.676**	-0.444	-0.463	-0.611**	0.676**	-2.204	-0.102
20	Gangajali Karala × IC -599428	6*1	13.796**	0.426	0.121	0.215	-0.028	0.370	0.648**	0.215	0.380	3.120*
21	IC -65787 × K-85603	3*2	-2.731	1.815**	0.624**	-0.407*	1.333*	-0.546	0.347**	-0.407*	-2.593**	1.370
22	IC -541448 × K-85603	4*2	-10.231**	-0.352	-0.201*	0.456**	-0.639	-0.157	0.142	0.456**	-1.843*	1.204
23	IC 596983 × K-85603	5*2	-2.426	-1.352*	-0.520**	-0.832**	-0.222	0.537	0.829**	-0.832**	0.574	0.231
24	Gangajali Karala × K-85603	6*2	3.907	-0.630	0.038	0.540**	-0.639	0.204	-0.715**	0.540**	1.324	0.954
25	IC -541448 × IC -65787	4*3	47.407**	-1.685**	-0.340**	0.348*	0.250	-0.185	-0.199	0.348*	-0.509	1.454
26	IC 596983 × IC -65787	5*3	-8.787*	-0.685	-0.276**	0.393*	0.500	-0.324	0.240*	0.393*	3.074**	-1.019
27	Gangajali Karala × IC -65787	6*3	30.546**	0.037	0.249*	0.665**	-0.417	0.009	0.143	0.665**	-2.343*	-3.463**
28	IC 596983 × IC -541448	5*4	15.880**	0.815	-0.018	0.256	-0.639	0.065	-0.031	0.256	-1.009	3.148*
29	Gangajali Karala ×IC -541448	6*4	-40.287**	0.370	0.374**	-0.538**	0.444	-0.769	0.060	-0.538**	0.241	-1.796
30	Gangajali Karala × IC 596983	6*5	34.185**	0.704	0.055	-0.094	0.528	0.259	0.178	-0.094	1.657	0.398
SE(m)			2.668	0.436	0.081	0.127	0.461	0.633	0.083	0.127	0.723	0.962

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

1.VL (cm)- Vine length (cm) ;2. NPB- Number of primary branches; 3. IL (cm)- Internode length (cm);4. PTL (cm)- Petiole length (cm);5. NNFF-Node no at first female flower appearance; 6. DA50%F- Days to 50% flowering ;7. SR- Sex ratio; 8. PDL (cm)- Peduncle length (cm); 9. DTFFH- Days to first fruit harvest; 10. DTLFH- Days to last fruit harvest;

Table-12 Conti…

Sl. No.	Genotype		NMFH	NFPP	FW(g)	FL (cm)	FD (cm)	100 SW (g)	NSPF	AA mg/100g	BC mg/100g	FYPP
			11	12	13	14	15	16	17	18	19	20
Parents												
1.	IC -599428		-1.046 **	-0.417	-3.572 **	-0.907 **	-0.439 **	-0.402 **	0.713 *	0.516	-0.019	-0.031
2.	K-85603		0.676 *	0.417	0.729 *	0.579 **	0.367 **	1.045 **	-0.176	1.569 **	-0.058 **	-0.165 **
3.	IC -65787		0.065	0.000	1.568 **	-0.114	0.397 **	-0.799 **	-0.204	0.871	0.112 **	0.121 **
4.	IC -541448		0.704 **	0.361	1.407 **	0.132	-0.069	-0.282 **	-0.009	-0.210	0.002	0.074 *
5.	IC 596983		0.176	0.028	0.564	0.182 **	0.008	0.176 **	-0.926 **	-2.550 **	-0.022	-0.009
6.	Gangajali Karala		-0.574 *	-0.389	-0.696 *	0.128	-0.264 **	0.262 **	0.602	-0.197	-0.015	0.010
S.E (m)			**0.257**	**0.297**	**0.330**	**0.069**	**0.045**	**0.055**	**0.313**	**0.469**	**0.017**	**0.029**
Crosses												
1.	IC -599428 × K-85603	1*2	-1.167	-2.667*	-1.233	1.442**	1.017**	0.583**	-0.833	-2.367	0.178**	0.133
2.	IC -599428 × IC -65787	1*3	-0.593	0.944	-9.333**	-1.100**	0.400*	-1.133**	0.315	-1.515	0.008	0.006
3.	IC -599428 × IC -541448	1*4	-1.000	0.833	8.017**	0.550*	0.617**	0.117	-0.833	-5.818**	0.082	0.400**
4.	IC -599428 ×IC 596983	1*5	0.333	1.167	-3.492**	-1.483**	-0.683**	2.033**	-0.833	-1.940	0.042	-0.217*
5.	IC -599428 × Gangajali Karala	1*6	-1.667**	-1.333	0.583	0.458*	-0.050	0.500**	1.833*	-3.583*	-0.172**	0.583**
6	K-85603 × IC -65787	2*3	0.167	-0.167	-12.000**	-1.508**	0.217	0.033	-0.167	-0.850	-0.058	-0.117
7	K-85603 × IC -541448	2*4	-0.167	2.333*	8.133**	1.983**	0.767**	-1.133**	-0.167	-4.290**	0.068	-0.283**
8	K-85603 × IC 596983	2*5	-2.000**	-1.333	-7.750**	-1.817**	-0.417**	-0.333*	-1.333	-0.182	-0.098*	0.283**
9.	K-85603 × Gangajali Karala	2*6	-0.333	-0.833	1.850	0.733**	0.617**	-1.100**	-0.167	1.530	-0.187**	-0.083
10.	IC -65787 × IC -541448	3*4	-1.833**	-1.167	2.333*	0.400*	-0.133	-1.567**	-1.333	4.153*	0.073	0.333**
11.	IC -65787 × IC 596983	3*5	0.667	1.333	3.550**	-0.150	1.233**	2.433**	1.333	4.922**	-0.085	0.333**
12.	IC -65787 × Gangajali Karala	3*6	1.500**	0.500	-3.917**	-0.683**	-0.233	-1.617**	-0.667	6.532**	-0.197**	-0.267**
13.	IC -541448 × IC 596983	4*5	0.500	0.667	2.817*	-0.383	0.083	1.000**	-1.667	-2.485	-0.060	-0.117

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

Sl. No.	Genotype		NMFH	NFPP	FW(g)	FL (cm)	FD (cm)	100 SW (g)	NSPF	AA mg/100g	BC mg/100g	FYPP
			11	12	13	14	15	16	17	18	19	20
14.	IC -541448 × Gangajali Karala	4*6	1.167	0.667	-3.267**	-0.667**	0.983**	-1.833**	1.704	-4.090*	-0.092	-0.300**
15.	IC 596983 × Gangajali Karala	5*6	3.000**	1.500	16.333**	1.717**	-1.167**	2.433**	-0.157	-3.060*	0.183**	-0.317**
Reciprocal crosses												
16	K-85603 × IC -599428	2*1	0.852	0.194	2.483*	0.499*	0.250	1.821**	-1.935	-1.458	0.033	0.709**
17	IC -65787 × IC -599428	3*1	0.630	0.944	-1.922*	-0.500*	0.369**	-0.818**	-0.074	-6.581**	0.233**	-0.077**
18	IC -541448 × IC -599428	4*1	1.167	0.417	4.056**	0.437*	0.286*	-0.651**	-0.102	1.827	0.029	0.170*
19	IC 596983 × IC -599428	5*1	1.185	1.417	-0.760	0.454*	-0.092	-1.193**	-0.519	0.598	-0.030	-0.130
20	Gangajali Karala × IC -599428	6*1	-1.398	-1.333	0.758	0.583**	0.881**	0.521**	-0.713	4.922**	-0.080	0.051
21	IC -65787 × K-85603	3*2	-0.593	-2.056*	9.776**	1.989**	0.147	0.035	0.315	-0.253	-0.102*	0.006
22	IC -541448 × K-85603	4*2	0.500	0.417	3.571**	0.751**	-0.469**	-0.048	0.787	5.968**	-0.182**	-0.180*
23	IC 596983 × K-85603	5*2	0.796	0.417	0.031	-0.332	-0.564**	0.260	0.870	0.083	-0.044	-0.296**
24	Gangajali Karala × K-85603	6*2	0.880	2.333**	-5.643**	-1.461**	0.208	0.041	-0.157	-2.892*	0.084	0.018
25	IC -541448 × IC -65787	4*3	1.167	1.000	-9.568**	-0.872**	0.033	-0.070	1.648	-0.804	0.180**	-0.549**
26	IC 596983 × IC -65787	5*3	1.074	1.167	-4.508**	-0.772**	-0.878**	0.305	-2.102*	2.037	-0.061	0.001
27	Gangajali Karala × IC -65787	6*3	-1.009	-0.917	-6.215**	-0.685**	1.128**	-0.565**	1.704	1.564	-0.203**	0.215*
28	IC 596983 × IC -541448	5*4	-0.398	-0.528	-0.747	-0.151	1.006**	0.288	-0.296	-3.431*	-0.053	0.465**
29	Gangajali Karala × IC -541448	6*4	0.352	-0.778	-10.071**	-1.047**	-1.056**	0.902**	-1.157	-5.193**	-0.064	0.229**
30	Gangajali Karala ×IC 596983	6*5	-0.954	0.056	6.539**	1.319**	-0.217**	-1.723**	1.426	-1.216	0.158**	0.295**
SE(m)			**0.587**	**0.678**	**0.753**	**0.157**	**0.102**	**0.125**	**0.714**	**1.070**	**0.038**	**0.066**

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

11. NMFH-Number of marketable fruit harvest; 12. NFPP-Number of fruits/ plants;13. FW(g)- Fruit weight (g);14. FL(cm)- Fruit length (cm);15. FD (cm)- Fruit diameter (cm); 16. 100 SW (g)- 100 seed weight (g); 17. NSPF- Number of seed/fruits ;18. AA mg/100g - Ascorbic acid (mg/100g); 19. BC mg/100g- β carotene content (mg/100g) ; 20. FYPP-Fruit yield/plant (kg).

Table-13: *Per se* performance of parents and F_1 hybrids with respect of twenty **characters in bitter gourd**

Sl. No.	Parents/Hybrid	VL (cm)	NPB	IL (cm)	PTL (cm)	NNFF	DA50%F	SR	PDL (cm)	DTFFH	DTLFH
Parents		1	2	3	4	5	6	7	8	9	10
1.	IC -599428	253.000	13.000	5.667	6.433	14.333	40.000	8.177	6.433	70.333	110.667
2.	K-85603	292.333	15.333	6.700	6.600	14.333	40.667	7.547	6.600	75.333	106.333
3.	IC -65787	196.000	15.667	6.033	4.900	12.000	40.000	7.250	4.900	75.333	111.667
4.	IC -541448	212.667	17.000	6.100	7.000	14.667	40.667	6.780	7.000	70.000	107.333
5.	IC 596983	192.333	14.000	6.000	7.133	13.667	40.000	6.663	7.133	72.333	108.333
6.	Gangajali Karala	231.667	14.000	5.067	6.000	14.333	40.667	6.873	6.000	69.667	110.333
Crosses											
1.	IC -599428 × K-85603	193.33	16.67	6.93	6.90	14.67	40.00	7.46	6.90	70.67	99.33
2.	IC -599428 × IC -65787	210.33	13.00	6.80	8.00	14.00	41.33	7.23	8.00	69.33	108.00
3.	IC -599428 × IC -541448	244.00	13.67	6.97	7.23	14.00	41.33	8.34	7.23	70.67	108.00
4.	IC -599428 × IC 596983	261.33	17.33	7.03	8.23	13.33	41.00	6.89	8.23	68.67	108.33
5.	IC -599428 × Gangajali Karala	287.67	14.00	6.07	7.37	13.67	40.33	8.39	7.37	70.33	114.67
6	K-85603 × IC -65787	290.00	16.33	7.03	7.30	16.00	40.00	7.57	7.30	68.67	99.67
7	K-85603 × IC -541448	284.00	13.33	5.77	6.90	13.33	40.67	7.11	6.90	69.00	112.00
8	K-85603 × IC 596983	213.67	14.00	5.73	5.50	14.33	40.67	8.42	5.50	77.67	108.33
9.	K-85603 × Gangajali Karala	293.33	15.67	6.50	8.17	12.67	41.00	7.07	8.17	74.67	108.33
10.	IC -65787 × IC -541448	290.67	13.67	6.10	7.67	14.67	39.67	7.26	7.67	68.67	106.67
11.	IC -65787 × IC 596983	220.67	13.67	6.13	8.13	14.00	40.33	7.77	8.13	75.33	109.33
12.	IC -65787 × Gangajali Karala	277.00	14.33	6.40	8.13	13.00	40.33	7.41	8.13	68.67	107.67
13.	IC -541448 × IC 596983	287.33	17.67	7.07	8.50	13.67	39.67	7.51	8.50	71.67	119.33

Sl. No.	Hybrid	VL (cm)	NPB	IL (cm)	PTL (cm)	NNFF	DA50%F	SR	PDL (cm)	DTFFH	DTLH
		1	2	3	4	5	6	7	8	9	10
14	IC -541448 × Gangajali Karala	233.33	16.33	6.60	6.03	14.67	40.33	7.33	6.03	70.00	101.33
15.	IC 596983 × Gangajali Karala	287.00	15.00	6.10	7.00	14.00	41.67	7.49	7.00	70.00	109.33
Reciprocal crosses											
16	K-85603 × IC -599428	236.33	15.00	5.47	7.17	14.00	40.00	8.51	7.17	71.00	107.67
17	IC -65787 × IC -599428	190.33	15.00	6.43	7.33	12.33	41.33	7.48	7.33	69.00	108.67
18	IC -541448 × IC -599428	244.67	15.33	5.67	6.67	14.33	40.67	9.18	6.67	70.33	104.00
19	IC 596983 × IC -599428	196.00	13.00	7.07	8.23	13.00	39.00	7.51	8.23	70.33	110.00
20	Gangajali Karala × IC -599428	239.00	16.00	6.60	7.43	14.33	42.00	8.45	7.43	70.33	108.67
21	IC -65787 × K-85603	193.33	17.67	7.03	4.80	14.33	39.00	8.40	4.80	70.67	119.33
22	IC -541448 × K-85603	189.00	17.33	6.20	7.53	14.00	39.33	8.70	7.53	68.67	106.00
23	IC 596983 × K-85603	268.33	13.33	5.63	6.77	13.00	40.67	8.48	6.77	70.67	109.67
24	Gangajali Karala × K-85603	243.67	13.67	5.87	6.10	14.67	40.33	6.66	6.10	71.67	109.67
25	IC -541448 × IC -65787	275.67	13.33	5.63	6.67	13.33	40.00	7.20	6.67	70.67	115.00
26	IC 596983 × IC -65787	226.67	14.00	5.77	6.70	13.67	39.00	7.28	6.70	77.00	109.33
27	Gangajali Karala × IC -65787	291.33	15.33	6.43	6.50	13.67	40.33	7.37	6.50	69.33	104.67
28	IC 596983 × IC -541448	214.00	14.00	4.90	6.67	12.67	40.67	7.25	6.67	69.33	107.00
29	Gangajali Karala × IC -541448	198.00	15.00	6.03	6.80	14.67	39.00	7.53	6.80	70.00	113.67
30	Gangajali Karala × IC 596983	286.67	15.67	5.93	7.13	14.67	39.67	7.32	7.13	78.67	112.00
	General Mean	242.90	14.92	6.20	6.98	13.88	40.31	7.60	6.98	71.24	108.89
	S.E (m)	4.44	0.725	0.135	0.203	0.767	1.053	0.136	0.191	1.203	1.601
	CD (5%)	12.55	2.05	0.383	0.575	0.165	2.02	0.385	0.539	3.4	4.526

Table-13 Conti……

Sl. No.	Parents/Hybrid	NMFH	NFPP	FW(g)	FL (cm)	FD (cm)	100 SW (g)	NSPF	AA mg/100g	BC mg/100g	FYPP
Parents		11	12	13	14	15	16	17	18	19	20
1.	IC -599428	6.333	14.000	61.167	12.733	9.933	17.800	23.000	75.063	0.687	0.800
2.	K-85603	10.000	16.000	64.167	15.733	13.667	18.267	18.000	75.030	1.003	1.000
3.	IC -65787	10.333	16.333	88.500	16.633	12.500	17.800	16.333	79.120	1.087	2.233
4.	IC -541448	12.000	16.667	88.500	17.167	12.567	17.300	17.333	74.553	1.003	1.600
5.	IC 596983	8.667	14.000	73.500	15.867	13.267	20.700	17.000	70.170	0.897	1.233
6.	Gangajali Karala	11.000	16.333	86.167	17.567	11.033	19.633	18.333	75.760	0.983	0.800
Crosses											
1	IC -599428 × K-85603	9.33	14.00	71.33	17.63	13.70	21.33	16.00	71.60	1.04	2.23
2	IC -599428 × IC -65787	9.67	17.00	59.67	13.40	13.23	15.13	18.67	66.63	1.24	1.60
3	IC -599428 × IC -541448	9.00	17.67	82.83	16.23	12.90	17.07	18.00	69.65	1.00	2.20
4	IC -599428 × IC 596983	10.67	18.67	65.67	14.27	11.30	18.90	16.67	69.96	0.88	1.20
5	IC -599428 × Gangajali Karala	5.33	13.00	70.00	16.28	12.63	19.17	20.67	75.00	0.62	2.20
6	K-85603 × IC -65787	10.33	14.67	73.00	16.97	13.63	18.60	18.00	74.68	0.80	1.43
7	K-85603 × IC -541448	10.67	20.00	86.77	19.47	13.10	17.87	18.67	76.38	0.74	1.03
8	K-85603 × IC 596983	9.67	16.00	66.50	14.63	11.90	19.43	16.67	72.26	0.69	1.40
9	K-85603 × Gangajali Karala	10.67	18.00	69.17	16.00	13.43	18.53	18.33	73.35	0.73	1.37
10	IC -65787 × IC -541448	8.67	16.67	68.67	15.57	12.73	15.57	18.33	77.35	1.28	1.57
11	IC -65787 × IC 596983	12.00	19.00	74.10	15.17	13.27	20.40	16.33	78.62	0.85	2.03
12	IC -65787 × Gangajali Karala	10.00	15.67	63.67	14.67	13.53	15.57	19.67	82.11	0.61	1.67
13	IC -541448 × IC 596983	11.67	17.00	76.97	15.80	13.53	19.47	15.33	64.66	0.78	2.00

Table-13 Conti……

Sl. No.	Hybrid	NMFH	NFPP	FW(g)	FL (cm)	FD (cm)	100 SW (g)	NSPF	AA mg/100g	BC mg/100g	FYPP
		11	12	13	14	15	16	17	18	19	20
14	IC -541448 × Gangajali Karala	11.00	16.33	60.30	14.57	12.10	17.33	17.67	63.65	0.74	1.60
15	IC 596983 × Gangajali Karala	11.67	17.67	95.67	19.37	10.87	19.43	19.33	66.32	1.21	1.57
Reciprocal crosses											
16	K-85603 × IC -599428	11.67	19.33	73.80	14.75	11.67	20.17	17.67	76.33	0.69	1.97
17	IC -65787 × IC -599428	9.67	17.00	78.33	15.60	12.43	17.40	18.67	69.66	1.23	1.60
18	IC -541448 × IC -599428	11.00	16.00	66.80	15.13	11.67	16.83	19.67	81.29	0.84	1.40
19	IC 596983 × IC -599428	10.00	16.33	72.65	17.23	12.67	14.83	18.33	73.84	0.80	1.63
20	Gangajali Karala × IC -599428	8.67	15.67	68.83	15.37	12.73	18.17	17.00	82.16	0.97	1.03
21	IC -65787 × K-85603	10.00	15.00	97.00	19.98	13.20	18.53	18.33	76.38	0.92	1.67
22	IC -541448 × K-85603	11.00	15.33	70.50	15.50	11.57	20.13	19.00	84.96	0.60	1.60
23	IC 596983 × K-85603	13.67	18.67	82.00	18.27	12.73	20.10	19.33	72.62	0.88	0.83
24	Gangajali Karala × K-85603	11.33	19.67	65.47	14.53	12.20	20.73	18.67	70.29	1.11	1.53
25	IC -541448 × IC -65787	12.33	19.00	64.00	14.77	13.00	18.70	21.00	69.04	1.13	0.90
26	IC 596983 × IC -65787	10.67	16.33	67.00	15.47	10.80	15.53	13.67	68.78	1.02	1.37
27	Gangajali Karala × IC -65787	7.00	14.67	71.50	16.03	14.00	18.80	21.00	69.05	1.00	2.20
28	IC 596983 × IC -541448	9.33	15.67	71.33	16.57	13.37	17.47	18.67	69.63	0.90	2.23
29	Gangajali Karala × IC -541448	10.00	15.00	66.83	15.90	10.13	21.00	17.67	71.83	0.92	2.20
30	Gangajali Karala × IC 596983	5.67	14.67	63.00	15.93	13.20	14.57	19.33	72.44	0.85	2.20
	General Mean	10.01	16.47	72.92	16.02	12.50	18.28	18.23	73.33	0.90	1.58
	S.E (m)	0.977	1.128	1.252	0.261	0.169	0.207	1.187	1.78	0.064	0.11
	CD (5%)	2.761	3.189	3.54	0.737	0.477	0.585	3.356	5.031	0.18	0.312

1.VL (cm)- Vine length (cm) ;2. NPB- Number of primary branches; 3. IL (cm)- Internode length (cm);4. PTL (cm)- Petiole length (cm);5. NNFF-Node no at first female flower appearance; 6. DA50%F- Days to 50% flowering ;7. SR- Sex ratio; 8. PDL (cm)- Peduncle length (cm); 9. DTFFH- Days to first fruit harvest; 10. DTLFH- Days to last fruit harvest; 11. NMFH-Number of marketable fruit harvest; 12. NFPP-Number of fruits/ plants;13. FW(g)- Fruit weight (g);14. FL(cm)- Fruit length (cm);15. FD (cm)- Fruit diameter (cm); 16. 100 SW (g)- 100 seed weight (g); 17. NSPF- Number of seed/fruits ;18. AA mg/100g - Ascorbic acid (mg/100g); 19. BC mg/100g- β carotene content (mg/100g) ; 20. FYPP-Fruit yield/plant (kg).

The highest *per se* performance for fruit yield per plant along with fruit quality parameters was recorded in IC-65787 followed by IC-541448 (Table-13) and they were found most promising genitors because they produced the maximum frequency of high yielding hybrids with appreciable fruit nutritional qualities when crossed with other genitors. These two genitors could be identified as potential donors for future breeding in bitter gourd.

The significant gca effects for number of fruits per vine and average fruit weight were reported by Khattra *et al.* (2000). Sundaram (2006) and Thangamani *et al*. (2011a) reported the same association between *per se* performance and gca effects for days to first female flower appearance, fruit weight and fruit yield in bitter gourd.

Specific combining ability effects represent dominance and epistatic components of genetic variations which are not fixable but the crosses with high SCA effects involving good general combiner can be exploited in future breeding. The SCA effects for hybrids pertaining to twenty characters were given in Table-12. Significant SCA effects in desired direction were recorded in twenty-six crosses for fruit length; twenty four crosses for vine length; twenty three crosses for fruit weight; twenty two crosses for petiole length; twenty one crosses for fruit yield per plant and 100 seed weight; twenty crosses for fruit diameter and peduncle length; eighteen crosses for internode length; fifteen crosses for sex ratio; fourteen crosses for ascorbic acid content ; twelve crosses for beta carotene content ; eleven crosses for days to last fruit harvest; eight crosses for internode length; six crosses for days to first fruit harvest, five crosses for number of marketable fruit harvest; four crosses for number of fruits per plant ; two crosses for number of seeds per fruit and one cross for node number at first female flower appearance.

The reciprocal cross K-85603 × IC -599428 exhibited the maximum significant SCA effects in desired direction for fruit yield per plant (0.709**) along with 100 seed weight, fruit weight, and fruit length followed by the direct cross IC -599428 × Gangajali Karala which also expressed significant SCA effects in desired direction for fruit yield per plant (0.583**) along with number of seeds/fruit, 100-seed weight, fruit length, and vine length. None of the parents of these two crosses were good general combiner for fruit yield per plant with other desirable horticultural traits, indicating that these two hybrids would not produce desirable segregants in subsequent generations (Table-12).

Moreover, high significant SCA effects in desired direction for fruit yield per plant and other important horticultural traits were shown by seven crosses IC 596983 × IC -541448, IC-599428 × IC -541448, IC -65787 × IC -541448, IC -65787 × IC 596983, K-85603 × IC 596983, Gangajali Karala × IC -541448 and Gangajali Karala × IC 596983. Out of these seven crosses, five crosses involved either both parents or one of the parents as good general combiner(s) for fruit yield per plant and other desirable horticultural traits, suggesting further exploitation of these crosses in segregation generation to identify superior lines. The highest *per se* performance for fruit yield per (2.23 kg/plant) was recorded in two crosses IC 596983 × IC -541448 and IC -599428 × K-85603 followed by IC -599428 × IC -541448**,** IC -599428 × Gangajali Karala**,** Gangajali Karala × IC -65787 , Gangajali Karala × IC -65787, Gangajali Karala × IC 596983 (Table-13).

From the foregoing observations, it appeared that different cross combinations exhibited different SCA effects and only a few crosses showed consistently either positive or negative SCA effects for certain characters. Based on significant SCA effects and high *per se* performance, two cross combinations namely, IC 596983 × IC -541448 followed by IC -599428 × IC -541448 could be identified as good specific combiners for future breeding in bitter gourd. The significant sca effects were also reported by Singh *et al*. (2004), Bhave *et al*. (2004), Gupta *et al.* (2006), Sundharaiya and Venkatesan (2007), Gupta *et al*. (2006), Sundaram (2008b), Kumara *et al*. (2011), Thangamani *et al*. (2011a) and Laxuman *et al.* (2012a) for yield and yield contributing characters in bitter gourd utilizing different hybrid combinations.

Based on gca effects, the promising heterotic crosses involved four types of combinations namely, H $^{\times}$ H, H $^{\times}$ L, L $^{\times}$ H and L $^{\times}$ L, where H denotes significant GCA effect of parent in desired direction and L stands for non-significant GCA effect of the parent (Table-14). In the H $^{\times}$ H type cross combinations (K-85603 $^{\times}$ Gangajali Karala for vine length, petiole length; Gangajali Karala $^{\times}$ IC- 65787 for vine length, fruit diameters and number of seeds per fruit; IC- 541448 $^{\times}$ IC-596983 for number primary branches, internode length, peduncle length; IC- 596983 $^{\times}$ IC- 599428 for internode length;

Table-14: Overall performances of superior crosses based on Per se performance and sca effects for fourteen characters in bitter gourd

Cross	Per se performance	sca effect	GCA status
Vine length (cm)			
K-85603 x Gangajali karala	293.33	24.833**	H x H
Gangajali karala x IC- 65787	291.33	30.546**	H x H
Number of primary branches			
IC- 541448x IC-596983	17.67	1.833**	H x H
IC- 541448 x K-85603	17.33	-0.352	L x L
Internode length (cm)			
IC-596983 x IC-599428	7.07	0.780**	H x H
IC-541448 x IC- 596983	7.07	1.083**	H x H
Petiole length (cm)			
IC-599428 x IC- 596983	8.23	0.817**	H x H
K-85603 x Gangajali karala	8.17	1.033**	H x H
Node no at first female flower appearance			
K-85603 x IC-65787	16.00	0.833	H x H
IC- 65787 x IC- 541448	14.67	0.677	H x H
Days to 50% flowering			
Gangajali karala x IC- 599428	42.00	0.370	H x H
IC- 596983 x Gangajali karala	41.67	1.000	H x H
Sex ratio			
IC- 541448 x IC-599428	9.18	0.800**	H x H
IC-541448 x K-85603	8.70	0.142	H x L
Peduncle length (cm)			
IC-541448 x IC- 596983	8.50	0.917**	H x H
IC- 599428 x IC-596983	8.23	-0.310*	L x L
Days to first fruit harvest			
Gangajali karala x IC- 596983	78.67	1.657	H x H
K-85603 x IC- 596983	77.67	3.500**	H x H
Days to last fruit harvest			
IC-65787 x K-85603	119.33	1.370	H x H
IC- 599428 x Gangajali karala	114.67	3.000**	H x H

Cross	Per se performance	sca effect	GCA status
Number of marketable fruit harvest			
IC- 596983 x K-85603	13.67	0.796	H x H
IC- 541448 x IC- 65787	12.33	1.167	H x H
Number of fruits/ plants			
K- 85603 x IC- 541448	20.00	2.333**	H x H
K-85603 x IC-599428	19.33	0.194	H x H
Fruit weight (g)			
IC-65787 x K-85603	97.00	9.776**	H x H
IC- 596983 x Gangajali karala	95.67	1.500	H x H
Fruit length (cm)			
IC-65787 x K-85603	19.88	1.989**	H x H
K-85603 x IC- 541448	19.47	1.983**	H x H
Fruit diameter (cm)			
Gangajali karala x IC- 65787	14.00	1.128**	H x H
IC- 599428 x K-85603	13.70	1.017**	H x H
100 seed weight (g)			
IC- 599428 x K-85603	21.33	0.583**	H x L
Gangajali karala x IC-541448	21.00	0.902**	H x H
Number of seed/fruits			
IC- 541448 x IC- 65787	21.00	1.648	H x H
Gangajali karala x IC- 65787	21.00	1.704	H x H
Ascorbic acid (mg/100g)			
IC-541448 x K- 85603	84.96	5.968**	H x H
Gangajali karala x IC- 599428	82.16	4.922**	H x H
β carotene content (mg/100g)			
IC-65787 x IC- 541448	1.28	0.073	L x H
IC-599428 x IC- 65787	1.24	0.008	H x L
Fruit yield/plant (kg)			
IC- 596983 x IC- 541448	2.23	0.465**	H x H
IC- 599428 x K-85603	2.23	0.133	H x H

IC- 541448 × IC- 596983 for internode length, peduncle length; IC- 599428 × IC-5969983 for petiole length, peduncle length; IC-541448 × IC- 599428 for sex ratio; Gangajali Karala × IC-596983 for days to first fruit harvest ; IC- 65787 × K-85603 for days to last fruit harvest, fruit weight , fruit length; IC-599428 × Gangajali Karala for days to last fruit harvest; IC-596983 × K- 85603 for number of marketable fruit harvest; IC- 541448 × IC- 65787 for number of marketable fruit harvest and number of seeds per fruit; K- 85603 × IC- 541448 for number of fruits per plant and fruit length; K- 85603 × IC- 599428 for number of fruits per plant; IC- 599428 × K-85603 for fruit diameter and fruit yield per plant; Gangajali Karala × IC- 541448 for 100 seed weight; IC- 541448 × K-85603 for ascorbic acid content; IC-596983 × IC-541448 for fruit yield per plant; K-85603 × IC-65787 for node number at first female flower appearance; IC-65787 × IC-541448 for node no at first female flower appearance and beta carotene content; Gangajali Karala × IC- 599428 for days to 50% flowering and ascorbic acid content; IC-596983 × Gangajali Karala for days to 50% flowering and fruit weight; K- 85603 × IC-596983 for days to first fruit harvest), additive as well as additive × additive type of interactions were involved. These crosses would be very useful as desirable segregates would be fixed in early advance generation. On the other hand, crosses of H × L type (IC-541448 × K-85603 for sex ratio; IC-599428 × K-85603 for 100 seed weight ; IC-599428 × IC- 65787 for beta carotene content) or L × H type (IC-65787 × IC- 541448 for beta carotene content involved at least one parent with significant GCA effect which indicated that predominantly additive effect was present in good combiner and possibly complementary epistatic effect in poor combiner and these two gene actions acted in complementary fashion to maximize the expression as suggested by Salimath and Bahl (1985). In crosses involving L × L category (IC-541448 × K-85603 for number of primary branches; IC-599428 × IC-596983 for peduncle length), SCA effects seemed to have played a very important role and high performance was due to non-additive gene action (Bhutia *et al.*, 2015).

4.6 Variation among the parents and hybrids

Analysis of variance for parents and hybrids (Table-15) is the pre-requisite for the manifestation of heterosis for different characters. The variances due to parents and hybrids were found highly significant for all the traits under study except for node number at first female flower appearance and days to 50% flowering. The variance due

Table-15: Analysis of variance for twenty characters in 6 × 6 diallel cross (with reciprocals) in bitter gourd

Source of variation	Df	VL (cm)	NPB	IL (cm)	PTL (cm)	NNFF	DA50%F	SR	PDL (cm)	DTFFH	DTLFH
Replication	2	69.176	1.787	0.226	0.982	0.528	5.815	0.020	0.982	0.398	3.815
Treatment	35	4195.173 **	6.154 **	0.988 **	2.323 **	1.943	1.675	1.195 **	2.323 **	22.431 **	56.054 **
Parents	5	4375.067 **	6.233 **	0.871 **	1.998 **	2.889	0.400	0.988 **	1.998 **	20.633 **	13.156
Hybrids	29	4178.237 **	6.347 **	0.984 **	2.149 **	1.847	1.952	1.157 **	2.149 **	22.875 **	65.349 **
Parents vs hybrids	1	3786.852 **	0.185	1.689 **	8.996 **	0.000	0.007	3.329 **	8.996 **	18.519 *	0.980
Error	70	59.138	1.578	0.055	0.136	1.766	3.329	0.056	0.136	4.341	7.691

Mean sum of square											
Source of variation	Df	NMFH	NFPP	FW(g)	FL (cm)	FD (cm)	100 SW (g)	NSPF	AA mg/100g	BC mg/100g	FYPP
Replication	2	2.509	6.028	0.825	0.310	0.064	0.481	7.620	38.679	0.005	0.091
Treatment	35	9.732 **	9.245 ***	284.694 **	7.575 **	3.256 **	9.984 **	8.968 **	75.112 **	0.102 **	0.631 **
Parents	5	11.922 **	4.489	465.700 **	8.977 **	6.002 **	5.134 **	17.200 **	24.642 *	0.058 **	0.932 **
Hybrids	29	9.625 **	9.758 **	250.943 **	7.591 **	2.806 **	11.099 **	7.850 *	84.473 **	0.112 **	0.530 **
Parents vs hybrids	1	1.896	18.150 *	358.437 **	0.108	2.563 **	1.920 **	0.224	55.996 *	0.025	2.066 **
Error	70	2.862	3.818	4.707	0.204	0.086	0.128	4.230	9.507	0.012	0.037

* Significant at 5 per cent level ** Significant at 1 per cent level

1.VL (cm)- Vine length (cm) ;2. NPB- Number of primary branches; 3. IL (cm)- Internode length (cm);4. PTL (cm)- Petiole length (cm);5. NNFF-Node no at first female flower appearance; 6. DA50%F- Days to 50% flowering ;7. SR- Sex ratio; 8. PDL (cm)- Peduncle length (cm); 9. DTFFH- Days to first fruit harvest; 10. DTLFH- Days to last fruit harvest; 11. NMFH-Number of marketable fruit harvest; 12. NFPP-Number of fruits/ plants;13. FW(g)- Fruit weight (g);14. FL(cm)- Fruit length (cm);15. FD (cm)- Fruit diameter (cm); 16. 100 SW (g)- 100 seed weight (g); 17. NSPF- Number of seed/fruits ;18. AA mg/100g - Ascorbic acid (mg/100g); 19. BC mg/100g- β carotene content (mg/100g) ; 20. FYPP-Fruit yield/plant (kg).

to parents vs. hybrids was also significant for most of the characters except number of primary branches, days to 50% flowering, days to last fruit harvest, number of marketable fruit harvest, fruit length, number of seeds per fruit and beta carotene content equivalents indicate the presence of sufficient amount of genetic variation and suggest the possibility of improvement for economic traits through hybridization followed by selection and heterosis breeding in bitter gourd . Genetic diversity of parents for a particular character can be determined through analysis of variance, which is created due to differential expression in genotypes for the particular character.

4.7 Manifestation of heterosis with per se performance for different characters

In the present investigation thirty cross combinations along with their six parents were studied for twenty characters to determine the manifestation of heterosis in them.

The *per se* performance of parents and crosses for eighteen characters were presented in Tables-13. The range and the magnitude of heterosis estimated over mid-parent (relative heterosis), better-parent (heterobeltiosis) and commercial check (standard heterosis) were presented in Tables-16. The estimates of heterosis expressed in percentage increase or decrease of hybrids over mid-parental, better parental and standard check values for twenty ss characters were described hereunder.

4.7.1 Vine length (cm)

Relative heterosis ranged from -0.29 (IC- 599428 × K-85603) to 42.25 per cent (IC-65787 × IC-541448) with eighteen hybrids registered positively significant relative heterosis. Heterobeltiosis ranged from -35.35% (IC- 541448 × IC-599428) to 36.68 % (IC 65787 × IC-541448) and nine of the hybrids exhibited significantly positive heterobeltiosis. Standard heterosis ranged from -20.92% (IC- 541448 × IC -599428) to 22.73% (K-85603 × Gangajali Karala) over standard heterosis. Among 30 hybrids, twelve hybrids exhibited significantly positive heterosis over standard check (Table-16).

4.7.2 Number of primary branches

Relative heterosis ranged from -18.37 (IC- 541448 × IC -65787) to 28.40% per cent (IC 599428 × IC-596983) with three hybrids registered positively significant relative heterosis. Heterobeltiosis ranged from -21.57% (K-85603 × IC -541448 and IC -

541448 × IC -65787) to 14.29% (Gangajali Karala × IC -599428) and only single of the hybrids exhibited significantly positive heterobeltiosis. Standard heterosis ranged from -18.75% (IC -599428 × IC-65787 and IC -596983 × IC -599428) to 10.42 % (IC -65787 × K-85603) and (IC-541448 × IC-596983) (Table-16). Among the hybrids, none of the hybrids exhibited significantly positive heterosis over standard check.

4.7.3 Internode length (cm)

Heterosis in negative direction is considered to be desirable for internodal length. Magnitude of heterosis over mid parent, better parent and commercial check was highly significant in both the directions. Maximum negative and significant heterosis over the mid parent was observed in the cross IC-596983 × IC-541448 (-19.01%), over the better parent is in the cross IC-596983 × IC-541448 (-19.67 %%) and over the commercial check is in the cross IC-596983 × IC-541448 (-25.76%% over) (Table-16). Out of thirty crosses, six crosses over mid parent and nine crosses over better parent showed significantly negative heterosis for internode length. Among hybrids fourteen crosses exhibited significantly negative heterosis over standard check

4.7.3 Petiole length (cm)

The maximum significant positive heterosis over mid-parent was observed in IC-65787 × Gangajali Karala (49.24%) followed by IC-599428 × IC-65787 (41.18%). The range of heterosis over mid-parental value was from 49.24% to -19.90%. The significant positive heterobeltiosis was recorded in IC-65787 × Gangajali Karala (35.56 %) followed by IC-599428 × IC-65787 (24.35%). The range of heterobeltiosis varied from 35.56% to -27.27% (Table-16). Significant positive standard heterosis was recorded in IC-541448 × IC-596983 (14.35%) followed by in IC-599428 × IC-596983 and IC-596983 × IC-599428 the range of standard heterosis varied from 14.35% to -35.43%.

4.7.4 Node number at female flower appearance

For node number at first female flower appearance, negative heterosis is desirable, as it indicates earliness in hybrids. Significant negative heterosis over mid parent was recorded in 2 crosses, ranging from -11.63% to 21.52 (Table-16). Significant positive heterosis was recorded for only one cross over mid parent for the cross K-85603 × IC-65787 (21.52%). Heterobeltiosis was none of the cross shown the significantly

positively and negatively. Maximum negative heterobeltiosis was for the cross IC-65787 × IC-599428 (-13.95%) and minimum for IC- 599428 × IC-65787, K-85603 × IC-599428 and IC-596983 × Gangajali Karala (-2.33%). Standard heterosis was none of the cross shown the significantly either positively or negatively. The standard heterosis ranging from Gangajali Karala × IC- 65787 (-4.10%) to Gangajali Karala × IC- 599428 (4.13%). These results are in support of earlier observations by Singh *et al*. (2000), Mohan (2005) and Thangamani *et al*. (2011b).

4.7.5 Days to 50 % flowering

The negative heterosis estimates which indicate earliness of the crop would be considered desirable. The positive heterosis for this character indicated that there is no scope of selection of early plant type. None of the hybrids exhibited either significant negative or significantly positive heterosis over mid-parent and better parent. the mid parent heterosis and for better parent ranging from 4.13% to -4.10% and 3.33% to -4.10% respectively (Table-16). Standard heterosis ranged from 1.59% to -7.14%. Among the hybrids, three hybrids exhibited significantly negative heterosis over standard check.

4.7.6 Sex ratio

Narrow sex ratio is desirable as it decreases ratio of number of male flowers to number of female flowers. Negative significant heterosis was recorded for 5 crosses ranging from -5.07% to -7.67% (Table-16). Significant and positive heterosis over mid parent was recorded for seventeen crosses, ranging from 7.42% (IC-54148 × Gangajali Karala) to 22.71% (IC-541448 × IC-599428). Heterosis over better parent was significantly positive ten crosses and Significant negative heterobeltiosis was recorded for seven crosses, with minimum for Gangajali Karala × IC-596983 (6.55%) and maximum for IC-599428 × IC-596983 (-15.70%). Standard heterosis was significantly positive for only one cross IC-541448 × IC-599428 (8.50%). Negatively significant standard heterosis was recorded for twenty-one crosses from IC-65787 × IC--596983(-8.01%) to Gangajali Karala × K-85603 (-21.22%).

Table 16: Estimates of heterosis over mid parent (MP), better parent (BP) and commercial check (CC)

	Crosses		Vine length (cm)			Number of primary branches			Internode length (cm)		
			MP(%)	BP(%)	CC(%)	MP(%)	BP(%)	CC(%)	MP(%)	BP(%)	CC(%)
1	1*2	IC -599428 × K-85603	-29.10 **	-33.87 **	-19.11 **	17.65 **	8.70	4.17	12.13 **	3.48	5.05
2	1*3	IC -599428 × IC -65787	-6.31 *	-16.86 **	-11.99 **	-9.30	-17.02 *	-18.75 **	16.24 **	12.71 **	3.03
3	1*4	IC -599428 × IC -541448	4.80 *	-3.56	2.09	-8.89	-19.61 **	-14.58 *	18.41 **	14.21 **	5.56
4	1*5	IC -599428 × IC 596983	17.37 **	3.29	9.34 **	28.40 **	23.81 **	8.33	20.57 **	17.22 **	6.57 *
5	1*6	IC -599428 × Gangajali Karala	18.71 **	13.70 **	20.36 **	3.70	0.00	-12.50	13.04 **	7.06 *	-8.08 **
6	2*3	K-85603 × IC -65787	18.77 **	-0.80	21.34 **	5.38	4.26	2.08	10.47 **	4.98	6.57 *
7	2*4	K-85603 × IC -541448	12.48 **	-2.85	18.83 **	-17.53 **	-21.57 **	-16.67 *	-9.90 **	-13.93 **	-12.63 **
8	2*5	K-85603 × IC 596983	-11.83 **	-26.91 **	-10.60 **	-4.55	-8.70	-12.50	-9.71 **	-14.43 **	-13.13 **
9	2*6	K-85603 × Gangajali Karala	11.96 **	0.34	22.73 **	6.82	2.17	-2.08	10.48 **	-2.99	-1.52
10	3*4	IC -65787 × IC -541448	42.25 **	36.68 **	21.62 **	-16.33 **	-19.61 **	-14.58 *	0.55	0.00	-7.58 *
11	3*5	IC -65787 × IC 596983	13.65 **	12.59 **	-7.67 **	-7.87	-12.77	-14.58 *	1.94	1.66	-7.07 *
12	3*6	IC -65787 × Gangajali Karala	29.54 **	19.57 **	15.90 **	-3.37	-8.51	-10.42	15.32 **	6.08	-3.03
13	4*5	IC -541448 × IC 596983	41.89 **	35.11 **	20.22 **	13.98 *	3.92	10.42	16.80 **	15.85 **	7.07 *
14	4*6	IC -541448 × Gangajali Karala	5.03 *	0.72	-2.37	5.38	-3.92	2.08	18.21 **	8.20 *	0.00
15	5*6	IC 596983 × Gangajali Karala	35.38 **	23.88 **	20.08 **	7.14	7.14	-6.25	10.24 **	1.67	-7.58 *
Reciprocal crosses											
16	2*1	K-85603 × IC -599428	-13.33 **	-19.16 **	-1.12	5.88	-2.17	-6.25	-11.59 **	-18.41 **	-17.17 **
17	3*1	IC -65787 × IC -599428	-15.22 **	-24.77 **	-20.36 **	4.65	-4.26	-6.25	9.97 **	6.63 *	-2.53
18	4*1	IC -541448 × IC -599428	5.08 *	-3.29	2.37	2.22	-9.80	-4.17	-3.68	-7.10 *	-14.14 **
19	5*1	IC 596983 × IC -599428	-11.98 **	-22.53 **	-17.99 **	-3.70	-7.14	-18.75 **	21.14 **	17.78 **	7.07 *
20	6*1	Gangajali Karala × IC -599428	-1.38	-5.53 *	0.00	18.52 **	14.29	0.00	22.98 **	16.47 **	0.00
21	3*2	IC -65787 × K-85603	-20.82 **	-33.87 **	-19.11 **	13.98 *	12.77	10.42	10.47 **	4.98	6.57 *
22	4*2	IC -541448 × K-85603	-25.15 **	-35.35 **	-20.92 **	7.22	1.96	8.33	-3.12	-7.46 *	-6.06 *
23	5*2	IC 596983× K-85603	10.73 **	-8.21 **	12.27 **	-9.09	-13.04	-16.67 *	-11.29 **	-15.92 **	-14.65 **
24	6*2	Gangajali Karala × K-85603	-7.00 **	-16.65 **	1.95	-6.82	-10.87	-14.58 *	-0.28	-12.44 **	-11.11 **
25	4*3	IC -541448 × IC -65787	34.91 **	29.62 **	15.34 **	-18.37 **	-21.57 **	-16.67 *	-7.14 *	-7.65 *	-14.65 **
26	5*3	IC 596983 × IC -65787	16.74 **	15.65 **	-5.16	-5.62	-10.64	-12.50	-4.16	-4.42	-12.63 **
27	6*3	Gangajali Karala × IC -65787	36.24 **	25.76 **	21.90 **	3.37	-2.13	-4.17	15.92 **	6.63 *	-2.53
28	5*4	IC 596983 × IC -541448	5.68 *	0.63	-10.46 **	-9.68	-17.65 **	-12.50	-19.01 **	-19.67 **	-25.76 **
29	6*4	Gangajali Karala × IC -65787	-10.88 **	-14.53 **	-17.15 **	-3.23	-11.76	-6.25	8.06 **	-1.09	-8.59 **
30	6*5	Gangajali Karala × IC 596983	35.22 **	23.74 **	19.94 **	11.90	11.90	-2.08	7.23 *	-1.11	-10.10 **
	*: Significant at p = 0.05, **: Significant at p = 0.01, MP = Mid parent, BP = Better parent and CC = Commercial check										

Table 16 conti….

S. No	Cross		Petiole length (cm)			Node no at first female flower appearance			Days to 50% flowering		
			MP(%)	BP(%)	CC(%)	MP(%)	BP(%)	CC(%)	MP(%)	BP(%)	CC(%)
1	1*2	IC -599428 × K-85603	5.88	4.55	-7.17	2.33	2.33	2.33	-0.83	-1.64	-4.76
2	1*3	IC -599428 × IC -65787	41.18 **	24.35 **	7.62	6.33	-2.33	-2.33	3.33	3.33	-1.59
3	1*4	IC -599428 × IC -541448	7.69	3.33	-2.69	-3.45	-4.55	-2.33	2.48	1.64	1.59
4	1*5	IC -599428 × IC 596983	21.38 **	15.42 **	10.76 **	-4.76	-6.98	-6.98	2.50	2.50	-2.38
5	1*6	IC -599428 × Gangajali Karala	18.50 **	14.51 **	-0.90	-4.65	-4.65	-4.65	0.00	-0.82	-3.97
6	2*3	K-85603 × IC -65787	26.96 **	10.61 *	-1.79	21.52 **	11.63	11.63	-0.83	-1.64	-4.76
7	2*4	K-85603 × IC -541448	1.47	-1.43	-7.17	-8.05	-9.09	-6.98	0.00	0.00	-3.17
8	2*5	K-85603 × IC 596983	-19.90 **	-22.90 **	-26.01 **	2.38	0.00	0.00	0.83	0.00	-3.17
9	2*6	K-85603 × Gangajali Karala	29.63 **	23.74 **	9.87 *	-11.63**	-11.63	-11.63	0.82	0.82	-2.38
10	3*4	IC -65787 × IC -541448	28.85 **	9.52 *	3.14	10.00	0.00	2.33	-1.65	-2.46	-5.56
11	3*5	IC -65787 × IC 596983	35.18 **	14.02 **	9.42 *	9.09	2.44	-2.33	0.83	0.83	-3.97
12	3*6	IC -65787 × Gangajali Karala	49.24 **	35.56 **	9.42 *	-1.27	-9.30	-9.30	0.00	-0.82	-3.97
13	4*5	IC -541448 × IC 596983	20.28 **	19.16 **	14.35 **	-3.53	-6.82	-4.65	-1.65	-2.46	-5.56
14	4*6	IC -541448 × Gangajali Karala	-7.18	-13.81 **	-18.83 **	1.15	0.00	2.33	-0.82	-0.82	-3.97
15	5*6	IC 596983 × Gangajali Karala	6.60	-1.87	-5.83	0.00	-2.33	-2.33	3.31	2.46	-0.79
Reciprocal crosses											
16	2*1	K-85603 × IC -599428	9.97 *	8.59	-3.59	-2.33	-2.33	-2.33	-0.83	-1.64	-4.76
17	3*1	IC -65787 × IC -599428	29.41 **	13.99 **	-1.35	-6.33	-13.95	-13.95	3.33	3.33	-1.59
18	4*1	IC -541448 × IC -599428	-0.74	-4.76	-10.31 *	-1.15	-2.27	0.00	0.83	0.00	-3.17
19	5*1	IC 596983 × IC -599428	21.38 **	15.42 **	10.76 **	-7.14	-9.30	-9.30	-2.50	-2.50	-7.14 *
20	6*1	Gangajali Karala × IC -599428	19.57 **	15.54 **	0.00	0.00	0.00	0.00	4.13	3.28	0.00
21	3*2	IC -65787 × K-85603	-16.52 **	-27.27 **	-35.43 **	8.86	0.00	0.00	-3.31	-4.10	-7.14 *
22	4*2	IC -541448 × K-85603	10.78 **	7.62	1.35	-3.45	-4.55	-2.33	-3.28	-3.28	-6.35
23	5*2	IC 596983× K-85603	-1.46	-5.14	-8.97 *	-7.14	-9.30	-9.30	0.83	0.00	-3.17
24	6*2	Gangajali Karala × K-85603	-3.17	-7.58	-17.94 **	2.33	2.33	2.33	-0.82	-0.82	-3.97
25	4*3	IC -541448 × IC -65787	12.04 **	-4.76	-10.31 *	0.00	-9.09	-6.98	-0.83	-1.64	-4.76
26	5*3	IC 596983 × IC -65787	11.36 *	-6.07	-9.87 *	6.49	0.00	-4.65	-2.50	-2.50	-7.14 *
27	6*3	Gangajali Karala × IC -65787	19.27 **	8.33	-12.56 **	3.80	-4.65	-4.65	0.00	-0.82	-3.97
28	5*4	IC 596983 × IC -541448	-5.66	-6.54	-10.31 *	-10.59**	-13.64	-11.63	0.83	0.00	-3.17
29	6*4	Gangajali Karala × IC -65787	4.62	-2.86	-8.52 *	1.15	0.00	2.33	-4.10	-4.10	-7.14 *
30	6*5	Gangajali Karala × IC 596983	8.63 *	0.00	-4.04	4.76	2.33	2.33	-1.65	-2.46	-5.56
	*: Significant at p = 0.05, **: Significant at p = 0.01, MP = Mid parent, BP = Better parent and CC = Commercial check										

Table 16 conti….

S. No	Crosses		Sex ratio			Peduncle length (cm)			Days to first fruit harvest		
			MP(%)	BP(%)	CC(%)	MP(%)	BP(%)	CC(%)	MP(%)	BP(%)	CC(%)
1	1*2	IC -599428 × K-85603	-5.07 *	-8.72 **	-11.68 **	5.88	4.55	-7.17	-2.97	-6.19 **	0.47
2	1*3	IC -599428 × IC -65787	-6.22 **	-11.54 **	-14.40 **	41.18 **	24.35 **	7.62	-4.81 *	-7.96 **	-1.42
3	1*4	IC -599428 × IC -541448	11.48 **	1.96	-1.34	7.69	3.33	-2.69	0.71	0.47	0.47
4	1*5	IC -599428 × IC 596983	-7.10 **	-15.70 **	-18.42 **	21.38 **	15.42 **	10.76 **	-3.74	-5.07 *	-2.37
5	1*6	IC -599428 × Gangajali Karala	11.54 **	2.65	-0.67	18.50 **	14.51 **	-0.90	0.48	0.00	0.00
6	2*3	K-85603 × IC -65787	2.28	0.27	-10.45 **	26.96 **	10.61 *	-1.79	-8.85 **	-8.85 **	-2.37
7	2*4	K-85603 × IC -541448	-0.79	-5.83 *	-15.90 **	1.47	-1.43	-7.17	-5.05 *	-8.41 **	-1.90
8	2*5	K-85603 × IC 596983	18.51 **	11.57 **	-0.36	-19.90 **	-22.90 **	-26.01 **	5.19 *	3.10	10.43 **
9	2*6	K-85603 × Gangajali Karala	-1.90	-6.27 *	-16.29 **	29.63 **	23.74 **	9.87 *	2.99	-0.88	6.16 *
10	3*4	IC -65787 × IC -541448	3.54	0.18	-14.04 **	28.85 **	9.52 *	3.14	-5.50 **	-8.85 **	-2.37
11	3*5	IC -65787 × IC 596983	11.74 **	7.22 **	-8.01 **	35.18 **	14.02 **	9.42 *	2.03	0.00	7.11 **
12	3*6	IC -65787 × Gangajali Karala	4.93 *	2.21	-12.31 **	49.24 **	35.56 **	9.42 *	-5.29 *	-8.85 **	-2.37
13	4*5	IC -541448 × IC 596983	11.78 **	10.82 **	-11.08 **	20.28 **	19.16 **	14.35 **	0.70	-0.92	1.90
14	4*6	IC -541448 × Gangajali Karala	7.42 **	6.69 *	-13.21 **	-7.18	-13.81 **	-18.83 **	0.24	0.00	-0.47
15	5*6	IC 596983 × Gangajali Karala	10.66 **	8.97 **	-11.36 **	6.60	-1.87	-5.83	-1.41	-3.23	-0.47
Reciprocal crosses											
16	2*1	K-85603 × IC -599428	8.29 **	4.12	0.75	9.97 *	8.59	-3.59	-2.52	-5.75 *	0.95
17	3*1	IC -65787 × IC -599428	-3.07	-8.56 **	-11.52 **	29.41 **	13.99 **	-1.35	-5.26 *	-8.41 **	-1.90
18	4*1	IC -541448 × IC -599428	22.71 **	12.23 **	8.60 **	-0.74	-4.76	-10.31 *	0.24	0.00	0.00
19	5*1	IC 596983 × IC -599428	1.26	-8.11 **	-11.08 **	21.38 **	15.42 **	10.76 **	-1.40	-2.76	0.00
20	6*1	Gangajali Karala × IC -599428	12.29 **	3.34	0.00	19.57 **	15.54 **	0.00	0.48	0.00	0.00
21	3*2	IC -65787 × K-85603	13.58 **	11.35 **	-0.55	-16.52 **	-27.27 **	-35.43 **	-6.19 **	-6.19 **	0.47
22	4*2	IC -541448 × K-85603	21.50 **	15.33 **	3.00	10.78 **	7.62	1.35	-5.50 **	-8.85 **	-2.37
23	5*2	IC 596983× K-85603	19.35 **	12.37 **	0.36	-1.46	-5.14	-8.97 *	-4.29 *	-6.19 **	0.47
24	6*2	Gangajali Karala × K-85603	-7.67 **	-11.79 **	-21.22 **	-3.17	-7.58	-17.94 **	-1.15	-4.87 *	1.90
25	4*3	IC -541448 × IC -65787	2.59	-0.74	-14.83 **	12.04 **	-4.76	-10.31 *	-2.75	-6.19 **	0.47
26	5*3	IC 596983 × IC -65787	4.65	0.41	-13.85 **	11.36 *	-6.07	-9.87 *	4.29 *	2.21	9.48 **
27	6*3	Gangajali Karala × IC -65787	4.32	1.61	-12.82 **	19.27 **	8.33	-12.56 **	-4.37 *	-7.96 **	-1.42
28	5*4	IC 596983 × IC -541448	7.81 **	6.88 *	-14.24 **	-5.66	-6.54	-10.31 *	-2.58	-4.15	-1.42
29	6*4	Gangajali Karala × IC -65787	10.25 **	9.51 **	-10.93 **	4.62	-2.86	-8.52 *	0.24	0.00	-0.47
30	6*5	Gangajali Karala × IC 596983	8.20 **	6.55 *	-13.33 **	8.63 *	0.00	-4.04	10.80 **	8.76 **	11.85 **
	*: Significant at p = 0.05, **: Significant at p = 0.01, MP = Mid parent, BP = Better parent and CC = Commercial check										

Table 16 Conti….

S. No	Crosses		Days to last fruit harvest			Number of marketable fruit harvest			Number of fruits/ plants		
			MP(%)	BP(%)	CC(%)	MP(%)	BP(%)	CC(%)	MP(%)	BP(%)	CC(%)
1	1*2	IC -599428 × K-85603	-8.45 **	-10.24 **	-8.59 **	14.29	-6.67	7.69	-6.67	-12.50	-10.64
2	1*3	IC -599428 × IC -65787	-2.85	-3.28	-0.61	16.00	-6.45	11.54	12.09	4.08	8.51
3	1*4	IC -599428 × IC -541448	-0.92	-2.41	-0.61	-1.82	-25.00 *	3.85	15.22	6.00	12.77
4	1*5	IC -599428 × IC 596983	-1.07	-2.11	-0.31	42.22 *	23.08	23.08	33.33 **	33.33 **	19.15
5	1*6	IC -599428 × Gangajali Karala	3.77 *	3.61	5.52 **	-38.46 **	-51.52 **	-38.46 *	-14.29	-20.41 *	-17.02
6	2*3	K-85603 × IC -65787	-8.56 **	-10.75 **	-8.28 **	1.64	0.00	19.23	-9.28	-10.20	-6.38
7	2*4	K-85603 × IC -541448	4.84 *	4.35 *	3.07	-3.03	-11.11	23.08	22.45 **	20.00 *	27.66 **
8	2*5	K-85603 × IC 596983	0.93	0.00	-0.31	3.57	-3.33	11.54	6.67	0.00	2.13
9	2*6	K-85603 × Gangajali Karala	0.00	-1.81	-0.31	1.59	-3.03	23.08	11.34	10.20	14.89
10	3*4	IC -65787 × IC -541448	-2.59	-4.48 *	-1.84	-22.39 *	-27.78 *	0.00	1.01	0.00	6.38
11	3*5	IC -65787 × IC 596983	-0.61	-2.09	0.61	26.32 *	16.13	38.46 *	25.27 **	16.33	21.28 *
12	3*6	IC -65787 × Gangajali Karala	-3.00	-3.58	-0.92	-6.25	-9.09	15.38	-4.08	-4.08	0.00
13	4*5	IC -541448 × IC 596983	10.66 **	10.15 **	9.82 **	12.90	-2.78	34.62 *	10.87	2.00	8.51
14	4*6	IC -541448 × Gangajali Karala	-6.89 **	-8.16 **	-6.75 **	-4.35	-8.33	26.92	-1.01	-2.00	4.26
15	5*6	IC 596983 × Gangajali Karala	0.00	-0.91	0.61	18.64	6.06	34.62 *	16.48	8.16	12.77
Reciprocal crosses											
16	2*1	K-85603 × IC -599428	-0.77	-2.71	-0.92	42.86 **	16.67	34.62 *	28.89 **	20.83 *	23.40 *
17	3*1	IC -65787 × IC -599428	-2.25	-2.69	0.00	16.00	-6.45	11.54	12.09	4.08	8.51
18	4*1	IC -541448 × IC -599428	-4.59 *	-6.02 **	-4.29 *	20.00	-8.33	26.92	4.35	-4.00	2.13
19	5*1	IC 596983 × IC -599428	0.46	-0.60	1.23	33.33 *	15.38	15.38	16.67	16.67	4.26
20	6*1	Gangajali Karala × IC -599428	-1.66	-1.81	0.00	0.00	-21.21	0.00	3.30	-4.08	0.00
21	3*2	IC -65787 × K-85603	9.48 **	6.87 **	9.82 **	-1.64	-3.23	15.38	-7.22	-8.16	-4.26
22	4*2	IC -541448 × K-85603	-0.78	-1.24	-2.45	0.00	-8.33	26.92	-6.12	-8.00	-2.13
23	5*2	IC 596983× K-85603	2.17	1.23	0.92	46.43 **	36.67 **	57.69 **	24.44 **	16.67	19.15
24	6*2	Gangajali Karala × K-85603	1.23	-0.60	0.92	7.94	3.03	30.77	21.65 *	20.41 *	25.53 *
25	4*3	IC -541448 × IC -65787	5.02 **	2.99	5.83 **	10.45	2.78	42.31 **	15.15	14.00	21.28 *
26	5*3	IC 596983 × IC -65787	-0.61	-2.09	0.61	12.28	3.23	23.08	7.69	0.00	4.26
27	6*3	Gangajali Karala × IC -65787	-5.71 **	-6.27 **	-3.68	-34.38 **	-36.36 **	-19.23	-10.20	-10.20	-6.38
28	5*4	IC 596983 × IC -541448	-0.77	-1.23	-1.53	-9.68	-22.22	7.69	2.17	-6.00	0.00
29	6*4	Gangajali Karala × IC -65787	4.44 *	3.02	4.60 *	-13.04	-16.67	15.38	-9.09	-10.00	-4.26
30	6*5	Gangajali Karala × IC 596983	2.44	1.51	3.07	-42.37 **	-48.48 **	-34.62 *	-3.30	-10.20	-6.38
	*: Significant at p = 0.05, **: Significant at p = 0.01, MP = Mid parent, BP = Better parent and CC = Commercial check										

Table 16 Conti…..

S. No	Crosses		Fruit weight (g)			Fruit length (cm)			Fruit diameter (cm)		
			MP(%)	BP(%)	CC(%)	MP(%)	BP(%)	CC(%)	MP(%)	BP(%)	CC(%)
1	1*2	IC -599428 × K-85603	13.83 **	11.17 **	3.63	23.89 **	12.08 **	14.75 **	16.10 **	0.24	7.59 **
2	1*3	IC -599428 × IC -65787	-20.27 **	-32.58 **	-13.32 **	-8.74 **	-19.44 **	-12.80 **	17.98 **	5.87 **	3.93 *
3	1*4	IC -599428 × IC -541448	10.69 **	-6.40 **	20.34 **	8.58 **	-5.44 *	5.64 *	14.67 **	2.65	1.31
4	1*5	IC -599428 × IC 596983	-2.48	-10.66 **	-4.60	-0.23	-10.08 **	-7.16 **	-2.59	-14.82 **	-11.26 **
5	1*6	IC -599428 × Gangajali Karala	-4.98 *	-18.76 **	1.69	7.48 **	-7.31 **	5.97 *	20.51 **	14.50 **	-0.79
6	2*3	K-85603 × IC -65787	-4.37 *	-17.51 **	6.05 *	4.84 *	2.00	10.41 **	4.20 **	-0.24	7.07 **
7	2*4	K-85603 × IC -541448	13.67 **	-1.96	26.05 **	18.34 **	13.40 **	26.68 **	-0.13	-4.15 *	2.88
8	2*5	K-85603 × IC 596983	-3.39	-9.52 **	-3.39	-7.38 **	-7.77 **	-4.77	-11.63 **	-12.93 **	-6.54 **
9	2*6	K-85603 × Gangajali Karala	-7.98 **	-19.73 **	0.48	-3.90 *	-8.92 **	4.12	8.77 **	-1.71	5.50 **
10	3*4	IC -65787 × IC -541448	-22.41 **	-22.41 **	-0.24	-7.89 **	-9.32 **	1.30	1.60	1.33	0.00
11	3*5	IC -65787 × IC 596983	-8.52 **	-16.27 **	7.65 **	-6.67 **	-8.82 **	-1.30	2.98	0.00	4.19 *
12	3*6	IC -65787 × Gangajali Karala	-27.10 **	-28.06 **	-7.51 **	-14.23 **	-16.51 **	-4.56	15.01 **	8.27 **	6.28 **
13	4*5	IC -541448 × IC 596983	-4.98 *	-13.03 **	11.82 **	-4.34 *	-7.96 **	2.82	4.77 **	2.01	6.28 **
14	4*6	IC -541448 × Gangajali Karala	-30.95 **	-31.86 **	-12.40 **	-16.12 **	-17.08 **	-5.21 *	2.54	-3.71	-4.97 **
15	5*6	IC 596983 × Gangajali Karala	19.83 **	11.03 **	38.98 **	15.85 **	10.25 **	26.03 **	-10.56 **	-18.09 **	-14.66 **
Reciprocal crosses											
16	2*1	K-85603 × IC -599428	17.77 **	15.01 **	7.22 **	3.63	-6.25 **	-4.01	-1.13	-14.63 **	-8.38 **
17	3*1	IC -65787 × IC -599428	4.68 *	-11.49 **	13.80 **	6.24 **	-6.21 **	1.52	10.85 **	-0.53	-2.36
18	4*1	IC -541448 × IC -599428	-10.73 **	-24.52 **	-2.95	1.23	-11.84 **	-1.52	3.70 *	-7.16 **	-8.38 **
19	5*1	IC 596983 × IC -599428	7.90 **	-1.16	5.54 *	20.51 **	8.61 **	12.15 **	9.20 **	-4.52 *	-0.52
20	6*1	Gangajali Karala × IC -599428	-6.56 **	-20.12 **	0.00	1.43	-12.52 **	0.00	21.46 **	15.41 **	0.00
21	3*2	IC -65787 × K-85603	27.07 **	9.60 **	40.92 **	23.48 **	20.14 **	30.04 **	0.89	-3.41	3.66
22	4*2	IC -541448 × K-85603	-7.64 **	-20.34 **	2.42	-5.78 **	-9.71 **	0.87	-11.82 **	-15.37 **	-9.16 **
23	5*2	IC 596983× K-85603	19.13 **	11.56 **	19.13 **	15.61 **	15.13 **	18.87 **	-5.45 **	-6.83 **	0.00
24	6*2	Gangajali Karala × K-85603	-12.90 **	-24.02 **	-4.89	-12.71 **	-17.27 **	-5.42 *	-1.21	-10.73 **	-4.19 *
25	4*3	IC -541448 × IC -65787	-27.68 **	-27.68 **	-7.02 **	-12.62 **	-13.98 **	-3.90	3.72 *	3.45	2.09
26	5*3	IC 596983 × IC -65787	-17.28 **	-24.29 **	-2.66	-4.82 *	-7.01 **	0.65	-16.17 **	-18.59 **	-15.18 **
27	6*3	Gangajali Karala × IC -65787	-18.13 **	-19.21 **	3.87	-6.24 **	-8.73 **	4.34	18.98 **	12.00 **	9.95 **
28	5*4	IC 596983 × IC -541448	-11.93 **	-19.40 **	3.63	0.30	-3.50	7.81 **	3.48 *	0.75	4.97 **
29	6*4	Gangajali Karala × IC -65787	-23.47 **	-24.48 **	-2.91	-8.45 **	-9.49 **	3.47	-14.12 **	-19.36 **	-20.42 **
30	6*5	Gangajali Karala × IC 596983	-21.09 **	-26.89 **	-8.47 **	-4.69 *	-9.30 **	3.69	8.64 **	-0.50	3.66
	*: Significant at p = 0.05, **: Significant at p = 0.01, MP = Mid parent, BP = Better parent and CC = Commercial check										

Table 16 Conti…..

S. No	Crosses		100 seed weight (g);			Number of seed/fruits			Ascorbic acid (mg/100g);		
			MP(%)	BP(%)	CC(%)	MP(%)	BP(%)	CC(%)	MP(%)	BP(%)	CC(%)
1	1*2	IC -599428 × K-85603	18.30 **	16.79 **	17.43 **	-21.95 **	-30.43 **	-5.88	-4.59	-4.61	-12.86 **
2	1*3	IC -599428 × IC -65787	-14.98 **	-14.98 **	-16.70 **	-5.08	-18.84 *	9.80	-13.57 **	-15.79 **	-18.91 **
3	1*4	IC -599428 × IC -541448	-2.75	-4.12 *	-6.06 **	-10.74	-21.74 **	5.88	-6.89 *	-7.21 *	-15.23 **
4	1*5	IC -599428 × IC 596983	-1.82	-8.70 **	4.04 *	-16.67 *	-27.54 **	-1.96	-3.65	-6.79 *	-14.85 **
5	1*6	IC -599428 × Gangajali Karala	2.40	-2.38	5.50 **	0.00	-10.14	21.57 *	-0.55	-1.01	-8.72 **
6	2*3	K-85603 × IC -65787	3.14 *	1.82	2.39	4.85	0.00	5.88	-3.11	-5.62	-9.11 **
7	2*4	K-85603 × IC -541448	0.47	-2.19	-1.65	5.66	3.70	9.80	2.12	1.79	-7.04 *
8	2*5	K-85603 × IC 596983	-0.26	-6.12 **	6.97 **	-4.76	-7.41	-1.96	-0.47	-3.69	-12.05 **
9	2*6	K-85603 × Gangajali Karala	-2.20	-5.60 **	2.02	0.92	0.00	7.84	-2.71	-3.18	-10.73 **
10	3*4	IC -65787 × IC -541448	-11.30 **	-12.55 **	-14.31 **	8.91	5.77	7.84	0.67	-2.24	-5.86
11	3*5	IC -65787 × IC 596983	5.97 **	-1.45	12.29 **	-2.00	-3.92	-3.92	5.33	-0.63	-4.31
12	3*6	IC -65787 × Gangajali Karala	-16.83 **	-20.71 **	-14.31 **	13.46	7.27	15.69	6.03 *	3.78	-0.06
13	4*5	IC -541448 × IC 596983	2.46	-5.96 **	7.16 **	-10.68	-11.54	-9.80	-10.64 **	-13.27 **	-21.30 **
14	4*6	IC -541448 × Gangajali Karala	-6.14 **	-11.71 **	-4.59 **	-0.93	-3.64	3.92	-15.31 **	-15.98 **	-22.53 **
15	5*6	IC 596983 × Gangajali Karala	-3.64 **	-6.12 **	6.97 **	9.43	5.45	13.73	-9.11 **	-12.46 **	-19.29 **
Reciprocal crosses											
16	2*1	K-85603 × IC -599428	11.83 **	10.40 **	11.01 **	-13.82	-23.19 **	3.92	1.71	1.69	-7.10 *
17	3*1	IC -65787 × IC -599428	-2.25	-2.25	-4.22 *	-5.08	-18.84 *	9.80	-9.64 **	-11.96 **	-15.22 **
18	4*1	IC -541448 × IC -599428	-4.08 **	-5.43 **	-7.34 **	-2.48	-14.49	15.69	8.66 **	8.30 *	-1.06
19	5*1	IC 596983 × IC -599428	-22.94 **	-28.34 **	-18.35 **	-8.33	-20.29 **	7.84	1.69	-1.63	-10.13 **
20	6*1	Gangajali Karala × IC -599428	-2.94 *	-7.47 **	0.00	-17.74 *	-26.09 **	0.00	8.95 **	8.45 *	0.00
21	3*2	IC -65787 × K-85603	2.77	1.46	2.02	6.80	1.85	7.84	-0.91	-3.47	-7.04 *
22	4*2	IC -541448 × K-85603	13.21 **	10.22 **	10.83 **	7.55	5.56	11.76	13.59 **	13.23 **	3.40
23	5*2	IC 596983× K-85603	3.17 *	-2.90 *	10.64 **	10.48	7.41	13.73	0.03	-3.21	-11.61 **
24	6*2	Gangajali Karala × K-85603	9.41 **	5.60 **	14.13 **	2.75	1.82	9.80	-6.77 *	-7.22 *	-14.45 **
25	4*3	IC -541448 × IC -65787	6.55 **	5.06 **	2.94	24.75 **	21.15 *	23.53 *	-10.14 **	-12.74 **	-15.97 **
26	5*3	IC 596983 × IC -65787	-19.31 **	-24.96 **	-14.50 **	-18.00 *	-19.61	-19.61	-7.86 **	-13.07 **	-16.29 **
27	6*3	Gangajali Karala × IC -65787	0.45	-4.24 **	3.49 *	21.15 *	14.55	23.53 *	-10.84 **	-12.73 **	-15.96 **
28	5*4	IC 596983 × IC -541448	-8.07 **	-15.62 **	-3.85 *	8.74	7.69	9.80	-3.77	-6.60	-15.25 **
29	6*4	Gangajali Karala × IC -65787	13.72 **	6.96 **	15.60 **	-0.93	-3.64	3.92	-4.43	-5.19	-12.58 **
30	6*5	Gangajali Karala × IC 596983	-27.77 **	-29.63 **	-19.82 **	9.43	5.45	13.73	-0.72	-4.39	-11.84 **
	*: Significant at p = 0.05, **: Significant at p = 0.01, MP = Mid parent, BP = Better parent and CC = Commercial check										

Table 16 Conti….

S. No	Crosses		β carotene content (mg/100g)			Fruit yield/plant (kg)		
			MP(%)	BP(%)	CC(%)	MP(%)	BP(%)	CC(%)
1	1*2	IC -599428 × K-85603	23.47 *	3.99	7.93	148.15 **	123.33 **	116.13 **
2	1*3	IC -599428 × IC -65787	40.23 **	14.42	28.62 **	5.49	-28.36 **	54.84 **
3	1*4	IC -599428 × IC -541448	18.74 *	0.00	3.79	83.33 **	37.50 **	112.90 **
4	1*5	IC -599428 × IC 596983	11.16	-1.86	-8.97	18.03	-2.70	16.13
5	1*6	IC -599428 × Gangajali Karala	-25.35 **	-36.61 **	-35.52 **	175.00 **	175.00 **	112.90 **
6	2*3	K-85603 × IC -65787	-23.13 **	-26.07 **	-16.90	-11.34	-35.82 **	38.71 *
7	2*4	K-85603 × IC -541448	-26.25 **	-26.25 **	-23.45 *	-20.51	-35.42 **	0.00
8	2*5	K-85603 × IC 596983	-27.72 **	-31.56 **	-28.97 **	25.37 *	13.51	35.48 *
9	2*6	K-85603 × Gangajali Karala	-26.17 **	-26.91 **	-24.14 *	51.85 **	36.67 *	32.26 *
10	3*4	IC -65787 × IC -541448	22.17 **	17.48 *	32.07 **	-18.26 *	-29.85 **	51.61 **
11	3*5	IC -65787 × IC 596983	-13.95	-21.47 *	-11.72	17.31 *	-8.96	96.77 **
12	3*6	IC -65787 × Gangajali Karala	-41.38 **	-44.17 **	-37.24 **	9.89	-25.37 **	61.29 **
13	4*5	IC -541448 × IC 596983	-18.25 *	-22.59 *	-19.66 *	41.18 **	25.00 *	93.55 **
14	4*6	IC -541448 × Gangajali Karala	-25.50 **	-26.25 **	-23.45 *	33.33 **	0.00	54.84 **
15	5*6	IC 596983 × Gangajali Karala	29.08 **	23.39 *	25.52 **	54.10 **	27.03 *	51.61 **
Reciprocal crosses								
16	2*1	K-85603 × IC -599428	-18.74 *	-31.56 **	-28.97 **	118.52 **	96.67 **	90.32 **
17	3*1	IC -65787 × IC -599428	38.35 **	12.88	26.90 **	5.49	-28.36 **	54.84 **
18	4*1	IC -541448 × IC -599428	-0.59	-16.28	-13.10	16.67	-12.50	35.48 *
19	5*1	IC 596983 × IC -599428	0.63	-11.15	-17.59	60.66 **	32.43 *	58.06 **
20	6*1	Gangajali Karala × IC -599428	15.77	-1.69	0.00	29.17	29.17	0.00
21	3*2	IC -65787 × K-85603	-11.96	-15.34	-4.83	3.09	-25.37 **	61.29 **
22	4*2	IC -541448 × K-85603	-39.87 **	-39.87 **	-37.59 **	23.08 *	0.00	54.84 **
23	5*2	IC 596983× K-85603	-7.02	-11.96	-8.62	-25.37 *	-32.43 *	-19.35
24	6*2	Gangajali Karala × K-85603	11.41	10.30	14.48	70.37 **	53.33 **	48.39 **
25	4*3	IC -541448 × IC -65787	8.13	3.99	16.90	-53.04 **	-59.70 **	-12.90
26	5*3	IC 596983 × IC -65787	3.19	-5.83	5.86	-21.15 **	-38.81 **	32.26 *
27	6*3	Gangajali Karala × IC -65787	-3.38	-7.98	3.45	45.05 **	-1.49	112.90 **
28	5*4	IC 596983 × IC -541448	-5.61	-10.63	-7.24	57.65 **	39.58 **	116.13 **
29	6*4	Gangajali Karala × IC -65787	-7.05	-7.97	-4.48	83.33 **	37.50 **	112.90 **
30	6*5	Gangajali Karala × IC 596983	-9.93	-13.90	-12.41	116.39 **	78.38 **	112.90 **
	*: Significant at p = 0.05, **: Significant at p = 0.01, MP = Mid parent, BP = Better parent and CC = Commercial check							

4.7.7 Peduncle length (cm)

The maximum significant positive heterosis over mid-parent was observed in IC-599428 × IC-65787 (41.18%) followed by K-85603 × Gangajali Karala (29.63%). The range of heterosis over mid-parental value was from 41.18% to -0.74%. The significant positive heterobeltiosis was recorded in IC-65787 × Gangajali Karala (35.56 %) followed by IC-599428 × IC-65787 (24.35%). The range of heterobeltiosis varied from 35.56% to -27.27%. the significant positive standard heterosis was recorded in IC-541448 × IC-596983 (14.35%) followed by in IC-599428 × IC-596983 (10.76%) and IC-596983 × IC-599428 (10.76%) the range of standard heterosis varied from 14.35% to -35.43% (Table-16).

4.7.8 Days to first fruit harvest

Heterosis in negative direction is considered to be desirable for days to first fruit harvest. The relative heterosis ranged from -8.85% to 10.80 % (Table-16). The range of heterobeltiosis was from -8.85% (K-85603 × IC-65787, IC-65787 × IC-541448, IC-65787 × Gangajali Karala and IC-541448 × IC-599428) to 8.76 % (Gangajali Karala × IC-596983). Significant negative relative heterosis and heterobeltiosis were exhibited by ten and fifteen hybrids, respectively. Standard heterosis over Gangajali Karala ranged from -2.37% (IC--599428 × IC-596983, K-85603 × IC-65787 and IC-65787 × Gangajali Karala) to 11.85% (Gangajali Karala × IC-596983). None of the hybrids showed significant standard heterosis in desirable direction. These results are in agreement with the earlier works of Singh *et al*. (2000), Laxuman (2005) and Jadav *et al.* (2009).

4.7.9 Days to last fruit harvest

Relative heterosis ranged from -8.56% (K-85603 × IC-65787) to 10.66% (IC-541448 × IC-596983) with five hybrids registered negatively significant and five hybrids exhibited positively significant relative heterosis. Heterobeltiosis ranged from -10.75% (K-85603 × IC-65787) to 10.15% (IC-541448 × IC-596983) and two hybrids exhibited significantly positive and six hybrids registered significantly negative heterobeltiosis. Standard heterosis ranged from 9.82% (IC-65787 × K-85603 and IC-541449 × IC-596983) to -8.59% (IC-599428 × K-85603). The five hybrids exhibited significantly positive and four hybrids exhibited the significantly negative heterosis over standard check (Table-16).

4.7.10 Number of marketable fruit harvest

The maximum significant positive heterosis over mid-parent was observed in IC-596983 × K-85603 (46.43%) followed by K-85603 × IC-599428 (42.86%). The range of heterosis over mid-parental value was from 46.43% to -42.37% (Tble-16). The significant positive heterobeltiosis was observed in IC-596983 × K-85603 (36.67%). The range of heterobeltiosis varied from 36.57% to -51.52%. Standard heterosis ranged from 57.69% to -38.46%. The hybrid IC-596983 × K-85603 (57.79%) exhibited the maximum standard heterosis followed by IC-541448 × IC-65787 (42.31%). The six hybrids exhibited significantly positive heterosis over standard check.

4.7.11 Number of fruits per plant

The maximum significant positive heterosis over mid-parent was observed in IC-599428 × IC-596983 (33.33%), IC- k-85603 × IC-599428 (38.89%) followed by IC-65787 × IC-596983 (25.27%). The range of heterosis over mid-parental value was from 33.33% to -14.29% (Table-16). The significant positive heterobeltiosis was observed IC-599428 × IC-596983(33.33%) followed by K-85603 × IC-599428 (28.89%). The range of heterobeltiosis varied from 33.33 % to –20.41. The significant positive standard heterosis was shown by K-85603 × IC- 541448 (27.66%) over Gangajali Karala (Table-16). Singh *et al.* (2000), Laxuman (2005), Jadav *et al*. (2009) and Thangamani *et al.* (2011b) also reported significant heterosis for number of fruits per vine.

4.7.12 Fruit weight (g)

Average fruit weight greatly contributed to yield per vine and for this trait positive heterosis is most desirable. Out of 30 crosses 10 crosses, exhibited positive significant heterosis over mid parent, ranging from 4.68% to 27.07% , maximum for the cross IC-65787 × K-85603 (27.07%) followed by IC-596983 × Gangajali Karala (19.83%) and the minimum for the cross IC-65787 × IC-599428(4.68%). Heterobeltiosis is significantly positive for six crosses, ranging from 9.60% to 15.01%, maximum heterobeltiosis for the cross K-85603 × IC-599428 (15.01%) to minimum for the cross IC-65787 × K-85603 (9.60). Heterobeltiosis ranging from -32.58% (IC-599428 × IC-65787) to 15.01% (K-85603 × IC-599428) was found for fruit weight (Table-16). Standard heterosis exhibited significantly negative for four crosses and nine crosses exhibited positively significantly standard heterosis from 5.54 % % (IC-596983 × IC-

599428) to 40.92%% (IC-65787 × K-85603). These results are in support of earlier results reported by Mohan *et al.* (2005), Sundaram (2008a), Jadav *et al.* (2009) and Thangamani *et al*. (2011b).

4.7.13 Fruit length

Fruit length, fruit diameter, average fruit weight and number of fruits per vine greatly contributed to yield per plant. For these traits, positive heterosis is highly desirable. Ten crosses recorded considerable positive and significant average heterosis. Maximum heterosis was recorded in the cross IC-599428 × K-85603 (23.89%) followed by IC-65787 × K-85603 (23.48%). Significantly minimum heterosis was recorded in K-85603 × IC-65787 (4.84%). Fifteen crosses exhibited negative and significant heterosis over their mid parent. The maximum significant positive heterobeltiosis was observed in IC-65787 × K-85603 (20.14%). The range of heterobeltiosis varied from 20.1% to -19.44%. Standard heterosis ranged from 30.04% to -12.80%. The hybrid IC-65787 × K-85603 (20.14%) exhibited the maximum positive significant heterosis over standard check (Table-16). These results are in conformity with the results of Sundaram (2008a), Thangamani *et al*. (2011) and Laxuman *et al*. (2012b).

4.7.14 Fruit diameter

The maximum significant positive heterosis over mid-parent was observed in Gangajali Karala x IC-599428 (21.46%) followed IC-599428 x Gangajali Karala (20.51%). The range of heterosis over mid-parental value was from 21.46%% to -16.17%. The maximum significant positive heterobeltiosis was observed in Gangajali Karala × IC-599428 (15.41%). The range of heterobeltiosis varied from 15.41% to -19.36%. Standard heterosis ranged from 9.95 % to -20.42%. The hybrid Gangajali Karala × IC-65787 (9.95%) exhibited the maximum standard heterosis (Table-16). These results are in support of earlier results reported by Tewari and Ram (1999), Mohan (2005), Thangamani *et al.* (2011b) and Laxuman *et al.* (2012b).

4.7.15 Seed index (100 seed weight)

Significant Positive heterosis over mid-parent was shown by 9 hybrids and 7 hybrids exhibited positive heterobeltiosis (Tables-16). The heterosis for seed index ranged from 18.30 % to -27.77% over mid-parent 16.79% to -29.63% % over better

parent. The maximum heterosis over mid-parent was observed in ic-599428 × K-85603 (18.30%) followed by Gangajali Karala × IC-65787 (13.72%). Maximum heterobeltiosis was recorded in IC-599428 × K-85603 (16.79%). The thirteen hybrids recorded significantly positive standard heterosis ranging from 17.43% to -19.82%. The hybrid IC- 599428 × K-85603 (17.43%) exhibited maximum heterosis over standard check.

4.7.16 No. of seeds per fruit

Out of 30 hybrids, 2 crosses revealed positive significant heterosis over mid-parent, one cross recorded heterobeltiosis and three crosses exhibited for standard heterosis this character (Tables-16). The heterosis for no of seed per fruit ranged from 24.75% to -21.95 % over mid-parent, 21.15 % to -30.43 % over better-parent and 23.53% to -19.61% over standard heterosis. The maximum significant heterosis over mid-parent was observed in was IC- 541448 × IC-65787 (24.75% %) followed by Gangajali Karala × IC-65787 (21.15 %). The maximum heterobeltiosis was shown by IC- 541448 × IC-65787 (21.15%) followed by Gangajali Karala × IC-65787 (14.55 %). The hybrids IC-541448 × IC- 65787 and Gangajali Karala × IC- 65787 (23.53%) exhibited maximum significant positive over standard check.

4.7.18 Ascorbic acid content (mg/100 g)

High levels of ascorbic acid in bitter gourd fruits provide health benefits for humans and also play an important role in several aspects of plant life. Heterosis in positive direction for this trait is desirable. The maximum significant heterosis over mid-parent was observed in IC-541448 × IC-599428 (13.59 %) followed by Gangajali Karala × IC-599428 (8.95%). The maximum heterobeltiosis was shown by IC-541448 × IC-599428 (13.23%). The range of heterosis for ascorbic acid content was from 13.59% to -15.31% over mid-parent and from 13.23% to -15.98 % over better parent (Table-16). The only hybrid IC-541448 × IC-599428 (3.40%) recorded positive heterosis over standard check.

4.7.19 β-carotene content (mg/100 g)

Bitter gourd fruits with high β-carotene content are suitable for specialty applications and provide a rich dietary source of provitamin A. β-carotene is an essential nutrient due to its retinoid activity and like other carotenoids is an antioxidant and may

protect against free radical damage. The role that β-carotene and vitamin A play in growth, reproduction, mortality and morbidity from infectious diseases has been reviewed (Ross, 1998; Tee, 1992).

Six hybrids exhibited positive significant heterosis over mid-parent, two hybrids showed positive significant heterosis over better-parent and four hybrids recorded positive significant over standard heterosis. The range of heterosis was from 40.23 % to -41.38 % over mid-parent, from 23.39 % to -44.17 % over better-parent and from 28.62% to -35.52% over standard heterosis (Table-16). Maximum significant positive heterosis over mid-parent was shown by IC-599428 × IC-65787 (40.23% %) followed by IC-65787 × IC-599428 (38.35 %). Maximum significant heterobeltiosis was recorded in IC-596983 x Gangajali Karala (23.39% %) followed by IC- 65787 × IC- 541448 (17.48%). The hybrid IC – 599428 × IC-65787 (28.62%) reported maximum significant positive heterosis over standard check followed by IC- 65787 × IC-599428 (26.90%) (Table-16).

4.7.20 Fruit yield per plant (kg)

High fruit yield is the primary criterion of growers for selection of hybrids. Out of 30 hybrids, seventeen hybrids exhibited positive significant over relative heterosis, twelve hybrids recorded positive significant over heterobeltiosis and twenty-five hybrids exhibited positive significance over standard heterosis. The range of heterosis for fruit yield was from 175.00% % to -53.04 % over mid-parent, from 175.00 % to -59.70 % over better-parent and from 116.13% to -19.35% over standard heterosis (Table-16). Maximum positive, significant, heterosis over mid-parent was shown by IC- 599428 × Gangajali Karala (175.00%) followed by IC- 599428 × K- 85603 (148.15%), K-85603 × IC-599428 (118.52%). Good crosses for this trait were IC-599428 × Gangajali Karala (175.00%) and IC- 599428 × K-85603 (123.33%). Hybrids IC- 599428 × K-85603 (116.13%), IC- 599428 × Gangajali Karala (112.90%), Gangajali Karala × IC-596983 (112.90%) recorded maximum standard heterosis over Gangajali Karala. On the basis of mean performance, the hybrids IC- 596983 × IC- 541448 and IC- 599428 × K-85603 was most promising and the top parent was K-65787 for fruit yield per plant. These results are in conformity with the results of Celine and Sirohi (1996), Mohan (2005), Sundaram (2008a), Jadav *et al*. (2009) and Thangamani *et al.* (2011b).

The study on heterosis revealed that crosses with significant relative heterosis in

desired direction were more as compared to crosses with significant heterobeltiosis for most characters under study. The significant difference between direct cross and reciprocal cross depicted that reciprocal effect was existed for most traits under study. Owing to the existing reciprocal effect, hybrid performance for related traits was dependent on the cross direction (Machida *et al*., 2010). Principally reciprocal differences are attributable to maternal and non-maternal effects in which maternal effect is caused by cytoplasmic genetic factors, while maternal effect is explained by the interaction between nuclear genes and cytoplasmic gene effects (Evans and Kemicle, 2001). In practical breeding terms, the choice of the female parent in a single cross hybrid may influence agronomic performance and yields in case major contribution of maternal effect instead of non-maternal effect is revealed. Reciprocal cross effects significantly impact heterosis (both mid-parent, better-parent and standard check) for most traits observed as positively strong linear correlation coefficient were revealed. Considering both high heterosis percentage and significant reciprocal effects on fruit yield and other desirable horticultural traits, superior hybrids were potentially derived from bitter gourd F_1 hybrids tested. This investigation suggests bitter gourd breeders should include reciprocal crosses in their any mating design since it is imperative for high-yielding oriented breeding.

It was also observed that crosses between parents of intermediate divergence classes showed comparatively higher magnitude of heterosis for fruit yield and other important traits than crosses between closely or distantly related parents. For yield attributes, some crosses were non-heterotic, which may be ascribed to cancellation of positive and negative effects exhibited by the parents involved in a cross combination and can also happen when the dominance is not unidirectional as observed by Gardner

Fig-3: Promising hybrid was identified on the basis of average values heterosis manifested, and relevance of sca effects. Commercial exploitation of this hybrid, after critical testing could be done

IC -599428

×

Gangajali Karala

IC-599428 X Gangajali Karala

Fig-4: Promising hybrid was identified on the basis of average values heterosis manifested, and relevance of sca effects. Commercial exploitation of this hybrid, after critical testing could be done

IC -599428

×

K-85603

IC-599428 X K-85603

and Eberhart (1966) and Mather and Jinks (1982). Heterosis is thought to be the result from the combined action and interaction of allelic and non-allelic factors and is usually closely and positively correlated with heterozygosity (Falconer and Mackay Trudy, 1986).

4.8 Identification of promising hybrid(s)

On the basis of sca effects, heterobeltiosis, standard manifested in them, and *per se* performance, two promising hybrids 'IC-599428 × Gangajali Karala and IC- 599428 × K-85603' were identified considering fruit yield per plant and other desirable horticultural traits (Fig-3 & Fig-4). These two hybrids could be exploited at commercial level after their critical evaluations in different Agro-climatic situations of West Bengal.

4. 9 Dominance estimates of characters

Potence ratio can be used to indicate the dominance of inherited traits, with values greater than ±1 indicating over-dominance, values between -1 and +1 revealing partial dominance, values of+1.0 indicating complete dominance and values of 0 indicating no dominance. Values of dominance estimates in 30 F1 crosses varied (Table-17). Dominance estimates of vine length indicated they were more than +1 in 12 crosses, between ±1 in 18 crosses, indicating over-dominance, partial dominance, respectively. Potence ratio of number of primary branches expressed over-dominance in 7 crosses, partial dominance in 18 hybrids, complete dominance in 2 crosses and no dominance in 3crosses, respectively. Internode length exhibited over dominance in 4 crosses, partial dominance in 25 cross and no dominance in 1 cross in inheritance of this trait. Seven crosses for petiole length indicated over dominance and partial dominance in 23 crosses. Node no at first female flower appearance exhibited over-dominance in 3 crosses, partial dominance in 20 crosses and no dominance in 7 crosses. For days to 50% flowering, Potence ratio was more than +1 in 2 crosses, between +1 to -1 in 16 crosses and 0 in 12 crosses indicating over-dominance, partial dominance, and no dominance, respectively. Sex ratio exhibited over dominance in 5 crosses and partial dominance in 25 hybrids in inheritance of this trait. Seven crosses for peduncle length indicated over dominance and partial dominance in 23 crosses. Days to first fruit harvest exhibited over-dominance in 11 crosses, partial dominance in 17 hybrids and no dominance in 2 crosses. Days to last

Table 17: Dominance estimates characters of F_1 generation in bitter gourd

S. No	crosses	VL (cm)	NPB	IL (cm)	PTL (cm)	NNFF	DA50%F	SR	PDL (cm)	DTFFH	DTLH
		1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**
1	IC -599428 × K-85603	-6241.09	11.68	1.54	0.12	0	-0.44	0.506	0.12	-21.63	79.48
2	IC -599428 × IC -65787	1615.38	-7.11	0.69	-7.15	-3.88	0	0.89	-7.15	-35.03	-6.33
3	IC -599428 × IC -541448	-900.75	-10.64	0.94	0.58	-0.33	1.32	-2.40	0.58	-0.33	6.66
4	IC -599428 × IC 596983	-4691.2	7.66	0.79	2.02	0.89	0	1.60	2.02	-10.65	5.46
5	IC -599428 × Gangajali Karala	-1934.33	1	-0.84	-0.99	0	-0.00	-2.25	-0.99	-0.43	-2.78
6	K-85603 × IC -65787	-8830.56	0.55	-0.88	-5.27	-13.22	0.44	-0.10	-5.27	0	-99.53
7	K-85603 × IC -541448	-5018.96	-9.45	0.75	0.08	-0.781	0	0.08	0.08	39.10	10.33
8	K-85603 × IC 596983	5732.6	1.77	0.86	-1.45	-0.43	-0.44	-2.32	-1.4	-23.02	3.98
9	K-85603 × Gangajali Karala	-3801.33	-2.67	-2.01	-2.24	0	0	0.18	-2.24	-24.59	-0.02
10	IC -65787 × IC -541448	2877.94	-7.10	0.00	7.22	7.12	-0.88	-0.23	7.22	42.62	24.53
11	IC -65787 × IC 596983	-194.37	3.87	-0.00	9.43	3.88	0	-0.95	9.43	-8.98	4.46
12	IC -65787 × Gangajali Karala	4505.91	1.67	-1.64	5.89	-0.77	-0.00	-0.26	5.89	43.40	8.88
13	IC -541448 × IC 596983	-3449.87	-13.02	-0.20	0.38	0.99	0.88	-0.18	0.38	2.34	22.99
14	IC -541448 × Gangajali Karala	424.194	-4.98	-2.10	0.94	-0.11	0	0.09	0.94	-0.11	-45.01
15	IC 596983 × Gangajali Karala	5900.1	0	-1.05	-0.98	0	1.78	0.30	-0.98	5.33	-0.01
Reciprocal crosses											
16	K-85603 × IC -599428	2858.44	-3.88	1.47	-0.21	0	0.44	0.81	-0.21	18.33	-7.19
17	IC -65787 × IC -599428	-3895.38	-3.55	-0.42	5.10	-3.90	0	-0.43	5.10	38.33	4.99
18	IC -541448 × IC -599428	954.80	-2.64	0.18	0.05	0.11	-0.44	4.75	0.05	0.10	-33.34
19	IC 596983 × IC -599428	-3235.55	1	-0.82	-2.02	-1.33	0	0.27	-2.02	4.01	2.33
20	Gangajali Karala × IC -599428	-142.22	0	1.47	1.05	0	-2.22	2.41	1.05	0.43	-1.22
21	IC -65787 × K-85603	-9794.47	-1.44	0.88	-3.23	5.42	-1.77	0.59	-3.23	0	-110.2
22	IC -541448 × K-85603	-10117.6	-3.87	-0.24	-0.58	0.33	0	2.35	-0.58	-42.62	1.66
23	IC 596983× K-85603	5199.4	-3.56	-1.00	0.10	-1.33	0.44	2.43	0.10	-18.97	-9.34
24	Gangajali Karala × K-85603	-2224.02	-2.65	-0.04	-0.24	0	0	-0.74	-0.24	-9.40	-10.69
25	IC -541448 × IC -65787	-2377.93	8.00	0.05	-3.02	0.01	0.44	0.17	-3.02	-21.29	47.67
26	IC 596983 × IC -65787	238.38	-2.77	-0.01	-3.05	-2.78	0	0.37	-3.05	19.00	-4.46
27	Gangajali Karala × IC -65787	-5528.14	1.65	1.70	-2.31	-2.34	0.00	0.232	-2.31	-35.92	-16.88
28	IC 596983 × IC -541448	467.68	-9	-0.23	0.10	-2.99	0.44	0.12	0.10	8.56	1.66
29	Gangajali Karala × IC -65787	918.34	-3	0.92	0.6	0.11	0	-0.13	0.6	0.11	-29.02
30	Gangajali Karala × IC 596983	-5874.14	0	0.73	1.27	-0.89	0.88	-0.23	1.27	40.89	-10.66

1.VL (cm)- Vine length (cm) ;2. NPB- Number of primary branches; 3. IL (cm)- Internode length (cm);4. PTL (cm)- Petiole length (cm);5. NNFF-Node no at first female flower appearance; 6. DA50%F- Days to 50% flowering ;7. SR- Sex ratio; 8. PDL (cm)- Peduncle length (cm); 9. DTFFH- Days to first fruit harvest; 10. DTLFH- Days to last fruit harvest;

Table -17 Conti….

S. No	Crosses	NMFH	NFPP	FW(g)	FL (cm)	FD (cm)	100 SW (g)	NSPF	AA mg/100g	BC mg/100g	FYPP
		11	12	13	14	15	16	17	18	19	20
1	IC -599428 × K-85603	8.53	-4	51.97	20.38	14.18	3.07	45	0.22	0.12	0.53
2	IC -599428 × IC -65787	10.69	8.55	-828.92	-10.00	10.33	0	13.28	-84.88	0.28	0.23
3	IC -599428 × IC -541448	-1.88	12.46	437.13	11.35	8.69	0.48	24.55	5.26	0.09	1.6
4	IC -599428 × IC 596983	14.79	0	-41.03	-0.18	-2.00	-2.03	39.96	25.99	0.03	0.15
5	IC -599428 × Gangajali Karala	-31.14	-10.10	-183.35	10.92	4.72	1.66	-0.032	-0.57	-0.12	0
6	K-85603 × IC -65787	0.10	-0.99	-162.22	1.41	-1.27	-0.52	-25	-19.59	-0.04	-0.45
7	K-85603 × IC -541448	-1.32	-20	507.90	8.66	0.03	-0.16	-1.33	-1.51	0	-0.32
8	K-85603 × IC 596983	-0.89	-4	-43.55	-0.31	1.25	-0.26	1.66	3.30	0.05	0.13
9	K-85603 × Gangajali Karala	0.34	1.22	-263.86	-2.38	-5.68	-1.14	0.10	-2.98	0.01	-0.188
10	IC -65787 × IC -541448	-8.32	-7.01	0	-1.42	0.02	1.98	2.99	-4.69	-0.03	0.43
11	IC -65787 × IC 596983	-8.33	-17.88	207	1.65	0.59	6.67	-0.44	-71.15	0.05	-0.59
12	IC -65787 × Gangajali Karala	-0.88	0	110.41	-4.53	-5.17	-11.53	9.34	-31.38	0.08	-0.43
13	IC -541448 × IC 596983	-8.90	-8.88	120.9	1.86	0.85	3.19	1.22	67.51	0.03	-0.42
14	IC -541448 × Gangajali Karala	1	0.11	126.13	-2.23	-0.92	-5.30	-0.32	-27.77	0.01	0.64
15	IC 596983 × Gangajali Karala	8.56	11.68	401.20	9.02	5.71	1.57	4.43	-74.29	0.046	-0.47
Reciprocal crosses											
16	K-85603 × IC -599428	-25.69	-17.32	-66.79	-3.10	0.97	-1.99	-28.3	0.08	0.09	-0.42
17	IC -65787 × IC -599428	-10.69	-8.55	-191.14	-7.15	-6.23	0	-13.28	60.29	-0.27	-0.23
18	IC -541448 × IC -599428	-20.78	-3.55	439.15	-1.59	-2.21	-0.72	-5.62	6.61	0.00	-0.32
19	IC 596983 × IC -599428	-11.67	0	-131.13	-18.36	-7.13	25.63	-20.04	11.97	-0.00	-0.53
20	Gangajali Karala × IC -599428	-0.03	-2.34	241.85	-2.12	-4.94	2.00	-34.22	-9.40	-0.07	0
21	IC -65787 × K-85603	0.11	0.77	-1005.76	-6.83	0.27	0.46	3.87	5.68	0.021	-0.13
22	IC -541448 × K-85603	0	1.33	283.89	2.72	-3.40	4.53	1.77	9.70	0	-0.36
23	IC 596983× K-85603	11.56	14.68	-245.76	-0.66	-0.58	-2.99	3.66	0.19	-0.01	0.13
24	Gangajali Karala × K-85603	-1.66	-2.33	426.66	7.77	-0.79	-4.86	-0.33	7.45	0.00	0.25
25	IC -541448 × IC -65787	-3.87	-1.67	0	2.27	-0.06	1.15	9.44	-71.21	0.01	-1.28
26	IC 596983 × IC -65787	3.89	5.42	-420	-1.19	3.19	21.57	-75.96	-104.98	0.01	-0.72
27	Gangajali Karala × IC -65787	4.89	0	-73.87	1.99	6.55	-0.30	3.11	-56.38	-0.00	1.95
28	IC 596983 × IC -541448	-6.68	0	-290.1	0.13	-0.63	10.40	1.00	-23.94	-0.01	0.59
29	Gangajali Karala × IC -65787	-3	0.77	-95.66	1.17	-5.12	-11.82	0.326	8.03	-0.00	1.6
30	Gangajali Karala × IC 596983	19.42	2.31	426.45	2.67	4.6	-11.94	-4.43	5.86	0.01	1.02

11. NMFH-Number of marketable fruit harvest; 12. NFPP-Number of fruits/ plants; 13. FW (g)- Fruit weight (g);14. FL(cm)- Fruit length (cm);15. FD (cm)- Fruit diameter (cm); 16. 100 SW (g)- 100 seed weight (g); 17. NSPF- Number of seed/fruits ;18. AA mg/100g - Ascorbic acid (mg/100g); 19. BC mg/100g- β carotene content (mg/100g) ; 20. FYPP-Fruit yield/plant (kg).

fruit harvest showed over-dominance and partial dominance for 14 and 16 crosses, respectively. Potence ratio of number of marketable fruit harvest expressed over-dominance in 8 crosses and partial dominance in 20 crosses and no dominance in single cross. Number of fruits per plant exhibited over dominance in 8 crosses, partial dominance in 17 crosses and no dominance in 5 crosses in inheritance of this trait. Fourteen crosses for fruit weight indicated over dominance and 14 crosses for partial dominance and two crosses in no dominance. Fruit length exhibited over-dominance in 14 crosses, partial dominance in 16 crosses. For fruit diameter, Potence ratio was more than +1 in 9 crosses indicating over-dominance and between +1 and -1 in 21 crosses. 100 seed weight exhibited over dominance in 12 crosses and partial dominance in 16 hybrids and absence of dominance in 2 crosses in inheritance of this trait. Twelve crosses for number of seed per fruit indicated over dominance in 14 crosses in partial dominance in 15 crosses and complete dominance in single cross. Ascorbic acid content exhibited over-dominance in 11 crosses and partial dominance in 19 crosses. Beta carotene showed over-dominance and no dominance for 26 and 4 crosses, respectively. Potence ratio of fruit yield per plant expressed over-dominance in 4 crosses and partial dominance in 24 crosses and no dominance in two crosses.

Different degrees of dominance i.e. complete, partial to over-dominance effects, and no dominance were involved in inheritance of studied traits. The manifestation of heterosis in most of the characters was of partial- to over-dominance in nature reflect the genetic basis of heterosis. There is little known about for the dominance reaction in inheritance of traits in bitter gourd. Preponderance of partial- to over-dominance effects in most of hybrids occurs in horticultural traits of bitter gourd (Saha *et al*., 2019).

Chapter 5

SUMMARY AND CONCLUSION

CHAPTER-V

SUMMARY AND CONCLUSION

The salient findings of the present research programme on "Characterization, yield components and heterosis in bitter gourd (*Momordica charantia* L.)" and conclusions drawn there from the foregoing chapters were summarized here topic-wise

Study on mean performance of bitter gourd genotypes for different characters

Thirty-three bitter gourd genotypes collected from different sources were evaluated under following randomised block design with three replications during *autumn-winter* season, 2017-2018. All the genotypes under study exhibited wide range of variations in twenty-one qualitative traits and twenty quantitative traits. twenty quantitative traits namely, vine length (164.33 to 263.33cm), number of primary branches (9.33 to17.00), internode length (4.53 to 7.93cm), petiole length (4.26 to 7.60 cm), node number at which first female flower appearance (12.66 to 16.66), days to 50% flowering (39.00 to 44.66 days), sex ratio (7.30 to 8.86), peduncle length (4.23 to 7.13cm), days to first fruit harvest (65.66 to 70.33 days), days to last fruit harvest (105.66 to 118.66 days), number of marketable fruit harvest (7.33 to 13.66), number of fruits per plant (12.00 to 19.66), fruit weight (48.33 to 71.83g), fruit length (11.40 to 18.06cm), fruit diameter (9.56 to 13.36cm), number of seeds per fruit(15.33 to 21.00), 100 seed weight (14.96 to 20.93g), ascorbic acid content (61.93 to 87.33 mg/100g), ß-carotene content of fruit (0.58 to 1.22 mg/100g) and fruit yield per plant (0.60 to 1.96 kg). From the mean data it revealed that two genotypes Gangajali Karala and IC-541448 were found most promising in respect of fruit yield per plant and nutritional quality traits at the Gangetic plains of West Bengal. These two genotypes could be tested at the state and national levels before releasing as varieties.

Study on genetic variability and heritability of different characters

Different components of genetic variability of twenty growth and yield characters namely vine length , number of primary branches, inter node length, petiole length , node number at which first female flower appears, days to 50% flowering, sex ratio, peduncle length , days to first fruit harvest, days to last fruit harvest, number of marketable fruit harvest, number of fruits per plant, fruit weight , fruit length , fruit diameter , number of seeds per fruit, 100 seed weight , ascorbic acid content , ß-

carotene content of fruit and fruit yield per plant were determined employing total 33 genotypes evaluated in Randomized Block Design.

The differences between values of PCV and GCV were less for all the traits. High PCV and GCV estimates were observed for the traits number of primary branches, number of marketable fruit harvest, fruit yield per plant, β-carotene content mg/100g. High to moderate magnitude of GCV and PCV generally indicated ample scope for improvement through selection. The present findings clearly suggested the worth of vine length, number of primary branches, internode length, petiole length, peduncle length, number of marketable fruit harvest, number of fruits per plant, fruit length, fruit girth, beta carotene content and fruit yield per plant for the study of genetic variability in bitter gourd. The proportion of genotypic variation to phenotypic variation was very high (more than 90 %) for all characters except days to 50% flowering and days to last fruit harvest indicating that the traits are under genetic, rather than environmental control. Their use as important discriminatory variables for bitter gourd classification seems relatively reliable. Very high to moderate broad sense heritability were observed for all characters under study except days to 50% flowering (12.00%) , days to first fruit harvest (13.00%), node no at first female flower appearance (14.00%), number of marketable fruit harvest (19.00%) and number of seeds per fruit (26.00%).

The genetic advance (GA) expressed as percentage of mean was very high (more than 20.00 %) for all characters under study except node no at first female appearance, days to 50% flowering, sex ratio, days to first fruit harvest, days to last fruit harvest, number of marketable fruit harvest, number of fruits per plant and number of seeds per fruit. In other words, numbers of primary branches per plant, fruit yield per plant and beta carotene content were characterized by high GCV, heritability and genetic advance. According to Panse (1957), such association was attributed to additive gene effects and selection based on these characters could be effective. Moderate heritability accompanied with moderate genetic advance for number of fruits per plant suggested that this character was less influenced by favourable environment effect rather than genotypes. Selection based on this character would also be effective but not as efficiently as first group. Low, heritability with genetic advance for node number at first female flower appearance, days to 50% flowering, sex ratio, days to first fruit harvest, days to last fruit harvest, number of marketable fruit harvest, and number

of seeds per fruit revealed non-additive genetic control of these characters. Hence, direct selection will bring no or slow genetic improvement for these traits. In such case heterosis breeding would be effective for improvement of such traits.

The present findings supported by earlier reports suggested that selection would be rewarding for improvement of characters number of primary branches, fruit yield per plant and beta carotene content which exhibited very high GCV values, heritability estimates and genetic advance as percent of mean.

Study on character association and framing of important yield components

The inter-relationships among the characters exhibited that thirteen correlation co-efficient were significant either in positive or negative direction. They also showed high genotypic correlations as well. The correlation analysis indicated the complex nature of relationships for the plant characters as for example, number of fruit per plant and fruit weight, fruit length, fruit diameter not only exhibited high positive correlation co-efficient with fruit yield per plant but they were also positively and significantly inter-related to each other. Hence, the selection on the basis of any of the significantly positive inter-related characters would be expected to give a desired correlated response in other characters

Among the different traits studied, number of fruits per vine registered high, significant and positive correlation with fruit yield followed by number of primary branches, days to last fruit harvest, vine length and fruit flesh thickness. It suggests that these are the most important parameters for improvement of yield, so more weightage should be given to these characters in bitter gourd breeding programme. At phenotypic level, fruit weight recorded high positive direct effects on fruit yield followed by petiole length. Based on the characters which had positive effects on fruit yield could be exploited for selection to improve bitter gourd as they are directly responding for selection.

The residual factor determines how best the casual factors account for the variability of the dependent factor, the yield per vine in this case. The residual effects were 0.4465 and 0.5399, which were of low magnitude at genotypic and phenotypic levels, respectively. The set of characters identified as selection indices for fruit yield per plant based on the genetic variability parameters for the characters, their correlations and path coefficient analysis are fruit weight and petiole length.

Study on genetic divergence

The present study aimed at analysing genetic divergence of genotypes. Thirty-three genotypes of bitter gourd were subjected to Mahalnobis D^2 analysis and genotypes were grouped into seven clusters. The comparison of cluster means for different characters indicated considerable differences between clusters for all the characters. Out of the seven clusters, cluster- I was largest comprising 18 genotypes, followed by cluster- II comprising 12 genotypes, cluster -III with 9 genotypes, cluster - IV with 3 genotypes; and three other clusters were monotypic. Greater genetic divergence was found in clusters II, III and IV suggested exploitation of these clusters by inter-mating the genotypes in a definite breeding design to explore the fullest range of heterosis and to realize good recombinant lines.

The monotypic genotypes in cluster IV, VI, VII and VIII indicated genotypes from those clusters might have originated across the geographical location in breeding programs. The grouping pattern of genotypes was observed to be random, indicating that geographical diversity and genetic divergence were unrelated. Therefore, the selection of genotypes for hybridization should be based on genetic divergence rather than geographic diversity.

High diversity occurred among bitter gourd genotypes along with strong relationships. Based on superior mean performance for agronomic characters (fruit yield per plant, etc.), genetic distances, clustering pattern and consumer preference characters (color, fruit shape, etc.), six promising and diverse inbred lines or varieties of bitter gourd *viz*., IC-599428, K-85603, IC-65787, IC-541448, IC-596983 and Gangajali Karala were selected.

Genetic control of characters

A 6 x 6 full diallel mating design was followed to study gene action of 20 quantitative characters. The analysis of variance for combining ability based on Griffing's Model 1 and Method 2 exhibited significant component of GCA and SCA mean squares for fruit yield per plant along with all studied traits in F_1 generation. This indicated that the inheritance of fruit yield per plant and most of the yield components, petiole length, days to 50% flowering, peduncle length, number of fruits per plant, fruit diameter traits were apparently controlled by both additive and non-additive gene action. The relative magnitude and importance of additive and non-additive variances

in the genetic control of various characters were further revealed by σ^2gca/ σ^2sca. This reflected the preponderance of additive gene effects for petiole length, days to 50% flowering, peduncle length, number of fruits/plant and fruit diameter as their ratios were close to unity (> 0.80). On the other hand, days to last fruit harvest was controlled by both additive and non-additive gene action as the ratio was ≥ 0.50 and < 0.80. In contrast, σ^2gca/ σ^2sca ratios were < 0.50 for vine length, number of primary branches, internode length, node number at female flower appearance, sex ratio, number of marketable fruit harvest, fruit weight, fruit length, 100 seed weight and number of seed per fruit indicating non-additive genetic control for the conditioning of these traits.

Identification of good general- and specific-combiners

The highest *per se* performance along with significant gca effects for fruit yield per plant along with other desirable horticultural traits was recorded in IC-65787 and IC-541448, and they were found most promising genitors because they produced the maximum frequency of high yielding hybrids with appreciable fruit nutritional qualities when crossed with other genitors. These two genitors could be identified as potential donors for future breeding in bitter gourd. From the foregoing observations, it appeared that different cross combinations exhibited different SCA effects and only a few crosses showed consistently either positive or negative SCA effects for certain characters. Based on SCA effects and *per se* performance, one reciprocal cross IC-596983 × IC -541448 and a direct cross IC -599428 × IC -541448 could be identified as good specific combiners for future breeding in bitter gourd.

Manifestation of heterosis

The study on heterosis revealed that crosses with significant relative heterosis in desired direction were more as compared to crosses with significant heterobeltiosis for most characters under study. The significant difference between direct cross and reciprocal cross depicted that reciprocal effect existed for most traits under study. It also revealed that crosses between parents of intermediate divergence classes showed comparatively higher magnitude of heterosis for fruit yield and other important traits than crosses between closely or distantly related parents. On the basis of sca effects, heterobeltiosis, standard heterosis manifested in them, and *per se* performance, two outstanding hybrids 'IC-599428 × Gangajali Karala and IC- 599428 × K-85603' were identified considering fruit yield per plant and other desirable horticultural traits. These

two hybrids could be exploited at commercial level after their critical evaluations in different agro-climatic situations of West Bengal.

Dominance estimates of different characters

Different degrees of dominance i.e. complete, partial to over-dominance effects, and no dominance were involved in inheritance of studied traits. The manifestation of heterosis in most of the characters was of partial- to over-dominance in nature which reflected the genetic basis of heterosis.

Chapter 6

FUTURE SCOPE OF RESEARCH

CHAPTER-VI

FUTURE SCOPE OF RESEARCH

1. Evaluation of more number of genotypes to be done to identify nutritional aspects like high protein content, β carotene content, fiber, rich in vitamins, minerals and digestible fibre, etc

2. The promising hybrids 'IC-599428 × Gangajali Karala and IC- 599428 × K-85603' can further be tested in large scale yield trails (MLT's) before recommending for commercial cultivation.

3. Two parents IC-65787 and IC-541448 expressed high gca effects for yield per plant and yield related traits. Hence, these two parents can be utilized in commercial breeding programmes as good donors for improving fruit yield and yield contributing characters.

4. There is need to utilize local landrace diversity in hybridization programme for further exploitation of heterosis for fruit yield, nutritional quality and adaptability.

5. Germplasm used in current study may be utilized for disease and pest screening.

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APPENDIX

APPENDIX

The qualitative characters of plant morphology of the bitter gourd genotypes

S. No	Accessions	Early plant vigor	Plant growth habit	Stem pubescence	Stem shape	Twining tendency	Tendril branching
1	IC-68250	Good	Medium viny	Pubescent	Rounded	Spherical	Branched
2	IC-599426	poor	Short viny	Smooth	angular	Spherical	Unbranched
3	IC-599428	Good	Long viny	Pubescent	Rounded	Spherical	Branched
4	IC-599429	Good	Short viny	Pubescent	Rounded	Spherical	Branched
5	IC-68343	Low	Short viny	Smooth	Rounded	Spherical	Unbranched
6	K-85603 (TCR-76)	Good	Long viny	Pubescent	Rounded	Spherical	Branched
7	K-68237	Good	Medium viny	Pubescent	angular	Spherical	Branched
8	K-85608	Good	Short viny	Pubescent	Rounded	Spherical	Branched
9	IC-470557	poor	Medium viny	Smooth	Rounded	Spherical	Unbranched
10	IC-65787	Good	Medium viny	Pubescent	Rounded	Spherical	Branched
11	IC-44438	low	Short viny	Smooth	Rounded	Spherical	Unbranched
12	IC-45350	Good	Medium viny	Pubescent	angular	Spherical	Branched
13	IC-599420	Good	Medium viny	Pubescent	Rounded	Spherical	Branched
14	IC-599434	Poor	Medium viny	Smooth	Rounded	Spherical	Unbranched
15	IC-470565	poor	Short viny	Smooth	Rounded	Spherical	Branched
16	IC-68236	Good	Medium viny	Pubescent	angular	Spherical	Branched
17	IC-541448	Good	Medium viny	Pubescent	Rounded	Spherical	Branched

S. No	Accessions	Early plant vigor	Plant growth habit	Stem pubescence	Stem shape	Twining tendency	Tendril branching
18	IC-536670	Good	Medium viny	Pubescent	Rounded	Spherical	Branched
19	IC-599421	poor	Medium viny	Pubescent	Rounded	Spherical	Unbranched
20	IC-596981	low	Short viny	Pubescent	angular	Spherical	Unbranched
21	IC-264699	low	Short viny	Smooth	angular	Spherical	Branched
22	IC-596983	Good	Long viny	Smooth	Rounded	Spherical	Branched
23	IC-599423	Good	Short viny	Smooth	Rounded	Spherical	Branched
24	IC-467680	Good	Short viny	Smooth	Rounded	Spherical	Branched
25	IC-418486	Good	Medium viny	Pubescent	angular	Spherical	Branched
26	IC-398610	low	Medium viny	Pubescent	angular	Spherical	Unbranched
27	IC-427694	Good	Short viny	Smooth	Rounded	Spherical	Branched
28	IC-599424	Good	Short viny	Pubescent	Rounded	Spherical	Branched
29	IC-45358	Good	Long viny	Smooth	angular	Spherical	Branched
30	IC-32817	Good	Medium viny	Smooth	Rounded	Spherical	Branched
31	Don no-01	Good	Medium viny	Pubescent	Rounded	Spherical	Branched
32	Dhaka Karala	Good	Short viny	Pubescent	Rounded	Spherical	Branched
33	Gnaganjali Karala	Good	Medium viny	Pubescent	Rounded	Spherical	Branched

Table-18 Conti…….

S. No	Accession	Leaf margin	Leaf shape	Leaf size	Leaf pubescence	Sex type	Flower color	Peduncle separation from fruit
1	IC-68250	Deeply Lobed	obovate	Large	Pubescent	Monoecious	Creamy white	Easily
2	IC-599426	Shallow Lobed	obovate	Small	Smooth	Monoecious	Yellow	Easily
3	IC-599428	Deeply Lobed	obovate	Large	Pubescent	Monoecious	Orange	Easily
4	IC-599429	Deeply Lobed	obovate	Large	Pubescent	Monoecious	Orange	Easily
5	IC-68343	Shallow Lobed	obovate	Small	Pubescent	Monoecious	Yellow	Easily
6	K-85603 (TCR-76)	Deeply Lobed	obovate	Medium	Pubescent	Monoecious	Yellow	Easily
7	K-68237	Deeply Lobed	obovate	Large	Pubescent	Monoecious	Creamy white	Easily
8	K-85608	Deeply Lobed	obovate	Large	Pubescent	Monoecious	Creamy white	Easily
9	IC-470557	Shallow Lobed	obovate	Small	Pubescent	Monoecious	Creamy white	Difficult
10	IC-65787	Deeply Lobed	cordate	Large	Smooth	Monoecious	Yellow	Easily
11	IC-44438	Shallow Lobed	oblong	Small	Pubescent	Monoecious	Yellow	Easily
12	IC-45350	Deeply Lobed	obovate	Large	Pubescent	Monoecious	Yellow	Easily
13	IC-599420	Deeply Lobed	obovate	Large	Pubescent	Monoecious	Yellow	Easily
14	IC-599434	Shallow Lobed	obovate	Small	Pubescent	Monoecious	Creamy white	Easily
15	IC-470565	Shallow Lobed	obovate	Small	Pubescent	Monoecious	Orange	Easily
16	IC-68236	Deeply Lobed	obovate	Large	Pubescent	Monoecious	Orange	Difficult
17	IC-541448	Deeply Lobed	obovate	Large	Smooth	Monoecious	Creamy white	Difficult

S. No	Accession	Leaf margin	Leaf shape	Leaf size	Leaf pubescence	Sex type	Flower color	Peduncle separation from fruit
18	IC-536670	Deeply Lobed	obovate	Large	Smooth	Monoecious	Yellow	Easily
19	IC-599421	Shallow Lobed	obovate	Small	Pubescent	Monoecious	Creamy white	Easily
20	IC-596981	Shallow Lobed	obovate	Small	Pubescent	Monoecious	Yellow	Easily
21	IC-264699	Shallow Lobed	cordate	Small	Pubescent	Monoecious	Yellow	Easily
22	IC-596983	Deeply Lobed	oblong	Medium	Smooth	Monoecious	Yellow	Easily
23	IC-599423	Deeply Lobed	obovate	Large	Pubescent	Monoecious	Creamy white	Easily
24	IC-467680	Deeply Lobed	obovate	Large	Pubescent	Monoecious	Orange	Easily
25	IC-418486	Deeply Lobed	obovate	Large	Pubescent	Monoecious	Creamy white	Difficult
26	IC-398610	Shallow Lobed	obovate	Small	Pubescent	Monoecious	Creamy white	Difficult
27	IC-427694	Deeply Lobed	cordate	Medium	Pubescent	Monoecious	Creamy white	Easily
28	IC-599424	Deeply Lobed	oblong	Large	Pubescent	Monoecious	Gold	Easily
29	IC-45358	Deeply Lobed	obovate	Large	Smooth	Monoecious	Creamy white	Easily
30	IC-32817	Deeply Lobed	obovate	Large	Smooth	Monoecious	Creamy white	Easily
31	Don No-1	Deeply Lobed	obovate	Large	Pubescent	Monoecious	Gold	Easily
32	Dhaka Karala	Deeply Lobed	obovate	Large	Pubescent	Monoecious	Gold	Easily
33	Gnaganjali Karala	Deeply Lobed	obovate	Large	Pubescent	Monoecious	Creamy white	Difficult

Table-18 Conti…….

S. No	Accession	Fruit shape	Fruit surface	Nature of tubercles prominence	Blossom-end fruit shape	Fruit skin color at ripe stage	Fruit skin luster	Fruit bitterness	Seediness and Seed luster
1	IC-68250	Cylindrical	Warty	Non-conspicuous	oblong	Yellow	Glossy	Mild	Medium
2	IC-599426	Cylindrical	Tuberculate	conspicuous	ovate	Yellow	Glossy	Strong	Very less
3	IC-599428	Elongate flattened	Warty	Non-conspicuous	Spindle shaped	Yellow	Glossy	Strong	Medium
4	IC-599429	Elongate flattened	Warty	Non-conspicuous	Club shape	Yellow	Glossy	Strong	Many
5	IC-68343	Elongate flattened	Warty	Non-conspicuous	Spindle shaped	Yellow	Glossy	Mild	Very less
6	K-85603 (TCR-76)	Globular	Tuberculate	conspicuous	Spindle shaped	Yellow	Intermediate	Strong	Medium
7	K-68237	Oblong elliptical	Warty	Non-conspicuous	oblong	Yellow	Glossy	Strong	Medium
8	K-85608	Cylindrical	Warty	Non-conspicuous	oblong	Yellow	Glossy	Strong	Medium
9	IC-470557	Cylindrical	Warty	conspicuous	oblong	Orange	Glossy	Strong	Medium
10	IC-65787	Cylindrical	Warty	Non-conspicuous	oblong	Reddish orange	Intermediate	Mild	Very less
11	IC-44438	Cylindrical	Warty	Non-conspicuous	oblong	Reddish orange	Intermediate	Strong	Very less
12	IC-45350	Cylindrical	Warty	Non-conspicuous	oblong	Reddish orange	Glossy	Strong	Medium
13	IC-599420	Globular	Warty	Non-conspicuous	oblong	Yellow	Glossy	Strong	Medium
14	IC-599434	Oblong elliptical	Warty	Non-conspicuous	oblong	Orange	Glossy	Mild	Very less
15	IC-470565	Oblong elliptical	Tuberculate	conspicuous	Spindle shaped	Reddish orange	Glossy	Strong	Very less
16	IC-688236	Oblong elliptical	Tuberculate	conspicuous	ovate	Yellow	Glossy	Strong	Medium

S. No	Accession	Fruit shape	Fruit surface	Nature of tubercles prominence	Blossom-end fruit shape	Fruit skin color at ripe stage	Fruit skin luster	Fruit bitterness	Seediness and Seed luster
17	IC-541448	Cylindrical	Tuberculate	conspicuous	ovate	Yellow	Glossy	Mild	Many
18	IC-536670	Cylindrical	Warty	Non-conspicuous	oblong	Yellow	Intermediate	Strong	Medium
19	IC-599421		Tuberculate	conspicuous	oblong	Yellow	Glossy	Strong	Very less
20	IC-596981	Elongate	Warty	Non-conspicuous	oblong	Yellow	Glossy	Strong	Very less
21	IC-264699	Cylindrical	Warty	Non-conspicuous	Spindle shaped	Yellow	Glossy	Mild	Very less
22	IC-596983	Cylindrical	Warty	Non-conspicuous	Spindle shaped	Reddish orange	Glossy	Strong	Medium
23	IC-599423	Elongate flattened	Warty	Non-conspicuous	Spindle shaped	Reddish orange	Glossy	Strong	Medium
24	IC-467680	Dumbbell	Warty	Non-conspicuous	Spindle shaped	Reddish orange	Intermediate	Strong	Medium
25	IC-418486	Cylindrical	Tuberculate	conspicuous	oblong	Reddish orange	Intermediate	Strong	Medium
26	398610	Cylindrical	Tuberculate	conspicuous	oblong	Yellow	Intermediate	Mild	Very less
27	IC-427694	Globular	Tuberculate	conspicuous	oblong	Orange	Glossy	Strong	Medium
28	IC-599424	Elongate flattened	Tuberculate	conspicuous	oblong	Reddish orange	Glossy	Strong	Medium
29	IC-45358	Oblong elliptical	Warty	Non-conspicuous	oblong	Yellow	Glossy	Strong	Medium
30	IC-32817	Cylindrical	Warty	Non-conspicuous	ovate	Yellow	Glossy	Mild	Medium
31	Don No-1	Cylindrical	Warty	Non-conspicuous	ovate	Yellow	Intermediate	Strong	Many
32	Dhaka Karala	Elongate flattened	Warty	Non-conspicuous	oblong	Yellow	Glossy	Strong	Many
33	Gangajali Karala	Elongate flattened	Warty	Non-conspicuous	oblong	Yellow	Glossy	Strong	Many

Fig-5: **Overall view of Experimental plot**

Fig -6: Crossing programme in experimental block

Bagging operation should be done after pollination