

Studies on genetic variability, heritability, correlation and path analysis in bitter gourd (*Momordica charantia* L.)

SUMMARY

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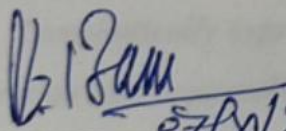
CERTIFICATE

This is to certify that the thesis entitled “**Studies on genetic variability, heritability, correlation and path analysis in bitter gourd (*Momordica charantia* L.)**” submitted for the degree of “**Doctor of Philosophy**” in the subject of **Horticulture** to the Babasaheb Bhimrao Ambedkar University, Lucknow is a bonafide research work carried out by **Mr. Som Prakash**, Enrollment No. **869/17** under my supervision and guidance during the periods of 2018-19 and 2019-20 and that no part of this thesis has been submitted for any other degree or diploma to this or any other university.

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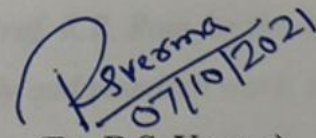
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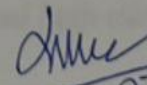
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DECLARATION

I **Som Prakash**, Enrollment No. **869/17**, hereby declare that thesis entitled "**Studies on genetic variability, heritability, correlation and path analysis in bitter gourd (*Momordica charantia* L.)**" submitted the thesis for the fulfillment of the requirements for the award of the degree of **Doctor of Philosophy in Horticulture**, Department of Applied Plant Science (Horticulture), School for Biosciences and Biotechnology, Babasaheb Bhimrao Ambedkar University (A Central University), Vidya Vihar, Rae Bareli Road, Lucknow (U.P.), India was carried out by me during the experimentation periods 2018-19 and 2019-20 are my own and original research work.

I do also hereby undertake that the thesis is essentially free from any kinds of plagiarism.

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ABSTRACT

The present investigation "Studies on genetic variability, heritability, correlation and path analysis in bitter gourd (*Momordica charantia* L.) using twenty genotypes of bitter gourd. The present investigation was carried out at Horticulture Research Farm-I of the Department of Applied Plant Science (Horticulture), School for Biosciences and Biotechnology, Babasaheb Bhimrao Ambedkar University, Vidya Vihar Raebareli Road, Lucknow- 226025 (U.P.), India during the summer seasons 2018-19 and 2019-20. The experimental material comprised of 20 bitter gourd genotypes obtained from various institutes. The experiment was laid out in Randomized Block Design and replicated thrice. Row-to-row and plant-to-plant distances were maintained as 2.5 m × 0.5 m. Each entry was grown in the plot size of 3.0 m x 2.0 m. Recommended agronomic practices were carried out basis across the cropping season to ensure optimum growth and development of plants. For optimal plants survival and flourishing, 1-2 healthy seedlings were maintained per pit. All total 15 physical characters and 6 chemical characters in the field as well as laboratory conditions were recorded viz., Node number to first staminate flowers, node number to first pistillate flowers, days to anthesis of first staminate flowers, days to anthesis of first pistillate flowers, days to first fruit harvest, vine length (m), fruit length (cm), nodes per plant, number of branches per plant, number

of seeds per plant, fruit diameter (cm), number of fruits per plant, Seeds weight per fruit (g), average fruit weight (g), ascorbic acid (mg/100g), reducing sugar (%), non-reducing sugar (%), total sugars (%), total soluble solids ($^{\circ}$ Brix), titratable acidity (%) and marketable fruit yield per plant (kg).

The analysis of variance for design of experiment indicated highly significant differences among the genotypes for all the characters. Based on mean performance genotype Kalyanpur Barahmasi followed by Kashi Urvasi, Arka Harit, Selection-5 and Pusa hybrid-1 were found significantly superior for marketable fruit yield per plant. These genotypes also showed significantly high mean performance for some other characters. The estimates of phenotypic coefficients of variation (PCV) were higher than genotypic coefficient of variation (GCV) for all the characters. High magnitudes of variability were observed in case of marketable fruit yield per plant followed by average fruit weight, number of branches per plant, titratable acidity, total soluble solids, fruit diameter, non-reducing sugar and number of fruits per plant. While, total sugars, days to first fruit harvest, days to anthesis of first staminate flowers and ascorbic acid exhibited low variability. High heritability coupled with high genetic advance in per cent of mean were estimated for average fruit weight followed by total soluble solids, total sugars, days to anthesis of first pistillate flower, nodes per plant, non-reducing sugar, marketable fruit yield per plant, number of branches per plant, vine length, days to first fruit harvest, number of fruits per plant, fruit diameter which indicated opportunity for selection response. The most important trait, marketable fruit yield per plant had exhibited highly significant and positive phenotypic correlation with fruit length, reducing sugar, number of fruits per plant. While, it showed highly significant and negative correlation with ascorbic acid followed by days to anthesis of first pistillate flowers and total soluble solids and selection for traits with positive correlation. The higher magnitude of positive direct effect on marketable fruit yield per plant was exerted by fruit length, number of fruits plant, number of seeds per fruit, vine length, node number to first pistillate flowers, days to first fruit harvest and total sugars. The higher magnitude of negative direct effect on marketable fruit yield per plant were pronounced by days to anthesis of first pistillate flowers, ascorbic acid, number of branches per plant, reducing sugar and non-reducing sugar both at phenotypic and genotypic levels. All the twenty genotypes into five diverse clusters. Cluster I (9) had highest number of genotypes followed by cluster II (8), cluster III (1), cluster IV (1) and cluster V (1). The Inter-cluster values between cluster II and V followed by cluster II and IV, cluster IV and V, cluster II and III, cluster I and V, cluster I and II, cluster I and IV, cluster III and V and cluster I and III were very high. The

minimum inter-cluster D^2 values were recorded in case of cluster III and IV (155.11). Average fruit weight followed by total sugars, total soluble solids, days to anthesis of first pistillate flowers, titratable acidity contributed maximum toward total genetic divergence in available germplasm of bitter gourd.



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List of Abbreviations

S. No.	Abbreviation/symbol	Stands for
1.	%	Percentage
2.	&	And
3.	/	Per
4.	@	At the rate of
5.	0C	Degree celsius
6.	ANOVA	Analysis of variance
7.	df	Degree of freedom
8.	<i>et al.</i>	<i>et alii</i> (Co-authors)
9.	PCA	Principal component analysis
10.	Fig.	Figure
11.	RBD	Randomized Block Design
12.	i.e.	That is
13.	M.S.S.	Mean sum of square
14.	Max.	Maximum
15.	Min.	Minimum
16.	cm	Centimeter
17.	cm ²	Centimeter square
18.	m	Meter
19.	Mg	Milligram
20.	g	Gram
21.	kg	Kilogram
22.	No.	Number
23.	S	Significant
24.	NS	Non significant
25.	ml	Milliliter
26.	mm	Millimeter
27.	R.H.	Relative humidity

28.	S.Em \pm	Standard error of mean
29.	e.g.	For example
30.	LSD	Least significant difference
31.	N	Normal solution
32.	$^{\circ}$ Brix	Degree Brix
33.	fig	Figure
34.	Vitamin-C	Ascorbic acid
35.	Vs.	Versus
36.	Per se	As such with mean
37.	GCV	Genotypic coefficient of variation
38.	PCV	Phenotypic coefficient of variation
39.	C.V.	Coefficient of variation
40.	C.D.	Critical difference
41.	GA	Genetic advance per cent of mean
42.	$h^2_{(bs)}$	Heritability in broad sense
43.	R.E.	Residual effect
44.	D	Divergence
45.	SS	Sum of square
46.	MS	Mean of square

INTRODUCTION

Bitter gourd (*Momordica charantia* L.; $2n=2x=22$) is a commercial and medicinal vegetable belonging to the Cucurbitaceae family. It has become an annual as well as perennial herbaceous climber. Bitter melon, balsam pear and maidan apple are some of its other names (**Morton, 1967**). Being monoecious in nature. It is a highly cross pollinated crop. It is believed that the crop evolved in India. Eastern India as well as Southern China has been proposed as probable domesticated areas. China, Malaysia, North America and Tropical Africa are among the countries that grow it. Recently, it has been found that six species closely related to bitter gourd are found in India, of which four species in dioecious and two species monoecious in nature. *Momordica charantia* and *Momordica balsamina* are monoecious, while *Momordica dioica*, *Momordica sahyadrica*, *Momordica cochinchinensis* and *Momordica subangulata* are dioecious (**De Wilde and Duyfjer, 2002; Joseph, 2005; Joseph and Antony 2008**). Wild species of bitter gourd *Momordica charantia* var. *abbreviata*, an origin place of Asia, may be the progenitor to domesticated one (**Degener, 1947**).

Cucurbits occupy a significant place among the various vegetable crop groupings. Liberty Hyde Bailey developed the word "cucurbits" to describe cultivated Cucurbitaceae species (**Robinson and Decker, 1997**). In the Cucurbitaceae family, there are approximately 100 genera and 750 species that are virtually equitably distributed across the past and present countries (**Yamaguchi, 2012**). In India, there are 38 endemic species and an additional 38 non-endemic species in 34 genera, comprising 108 species. Due to the absence of explicit knowledge of their utility, untamed plant genetic resources with specific value to the local community and the global community are frequently overlooked during germplasm excursions and cumulative impacts. Despite the implementation of novel crops and superior varieties, wild species play a significant role, primarily in the forest and rural areas of the country, in which many people are able to collect and eat wild amassed crops for nourishment.

Bitter gourd ranks first among the cucurbits in terms of high nutritional value. The 100 g edible fruit part constitutes 83.2% water, 10.5% carbohydrates, 0.2–1.0% fat, 0.5-1.0% minerals, 1.7% fiber, 2.1 g protein, 2 mg iron, 23 mg calcium, 96 mg vitamin C, 38 mg phosphorus, 171 mg potassium, 2.40 mg sodium, 0.19 mg copper, 0.08 mg manganese, 0.46 mg zinc and 126 mg β carotene (**Gopalan et al. 1993**). Hypertension, ophthalmic problems, neuropathy and improper carbohydrate

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metabolism are just a few of the issues that may be avoided with frequent usage. It boosts the body's anti-infection systems. The bitter gourd is some kind of gourd that is used as a traditional remedy for diabetes. According to a study conducted, it includes hypoglycemia as well as an insulin-like component known as plant insulin that has been revealed to be extremely effective in reducing blood and urine sugar levels. Most diabetics undergo denutrition as a result of their undernutrition. It contains alkaloids *viz.*, momordicin and cucurbitacin while skeleton is rich in momordicosides are tetracyclic triterpenoides glycosides with cucurbitane **(Chandravandna and Chandra, 1990)**. Bitter gourd fruit is said to be cooling, carminative, aphrodisiac, stomachic, antipyretic, appetitising, antihelminthic, aphrodisiac and vermifuge competency **(Blatter *et al.* 1935)**. They are used as a viral infection for Human immunodeficiency virus (HIV) disease and as acytostatic in the treatment of some cancers. Owing to its implicit oxygen free radical with the scavenging action of fruit juice, it is also recognized for its antidiabetic effects **(Shreejayan and Rao, 1991)**.

It is a bitter gourd famed for its therapeutic qualities. It has antioxidant, antimicrobial, antibacterial, antiviral, antiulcerogenic and antihepatotoxic effects. According to ethno-medical accounts, *Momordica charantia* L. is utilised in ancient medicine to cure a variety of blood sugar, ulcers and other infections. While root extracts are used to treat defluxio, arthritis, leaf and stem decoctions are used to treat dysentery and gout. Consequently, *Momordica charantia* L. juice extracted solely from the fruit has often been exploited for medical purposes across the world. Similarly, the juice is derived from the fruit, leaves and roots. Sometimes, the fresh fruit is commonly used to treat injuries, allergies, parasites (such as worms), fever, hepatitis and measles. Bitter gourd extracts, which are also often used as vegetable insulin, contain antidiabetic, hypoglycemia and antioxidative properties that can help with diabetes therapy **(Behera *et al.* 2010)**.

The main objective of cucurbitaceous vegetable research in India, particularly bitter gourd research, is to boost efficiency on a brief premise by continuing to develop abiotic and biotic stress resistant varieties and hybrids with quantity and quality attributes. Crop yield can also be increased by using agro-techniques and plant protection measures that are standardized. There are about 60 species in the genus *Momordica*, among them the species *Momordica charantia* L. is predominantly cultivated. It's a monoecious, extensively cross-pollinated crop with a lot of diversity

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in most practically relevant characteristics. Fruits have the most obvious variations in terms of shape, size and colour.

India is the second largest producer of vegetables in the world next only to China, which shares about 15 percent of the world's vegetable production and about 5 percent of the total cropped area in the country. The current vegetable production level is over 187.47 million tonnes from an area of 10.43 million hectares. During 2018-19, the bitter gourd crop had area was 0.099 million hectares and production was 1.20 million tonnes (2018-19) all over India (**Anon. 2019**).

Despite the substantial output, the per capita per day supply of vegetables in the country could not exceed 175 g, which is less than the recommended dietary requirement (RDA) of 350 to 400 g for a balanced diet. By 2020, our country's vegetable consumption is expected to exceed 220 million tonnes. According to Indian Council of Medical Research (ICMR), a normal person should take 300 g of vegetables per day (125 g of leafy vegetables, 100 g of tubers and root crops and 75 g of other vegetables). Vegetable eating decreases cholesterol levels, protects against respiratory and intestinal diseases and prevents the buildup of carcinogenic chemicals in the human body.

The basic tool for identifying significant genotypes is germplasm evaluation. The large amount of natural diversity found in many features between genotypes implies that economic characteristics have a suitable place for development. The large variety increases the chances of identifying new forms.

The relationship between two variables between the various characters as well as the positive effect of yield may refer to traits on total yield production are essential for developing a breeding plan that includes the benefit of the novel population's implicit variability. Under various climatic conditions, phenotypic variability fluctuates, but genetic variability stays constant and is more helpful to a plant breeder for selection and hybridization.

In India, bitter gourd genetic modification has rarely been studied. The evaluation of variability in every crop species is a foundation for developing successful selective breeding, since the existent variation may be exploited to optimize cultivar yields when breeding techniques can be applied correctly. Climate sensitivity information alone may not be useful in identifying characteristics for

selection, but it is more accurate when combined with forecast genetic progression (Johnson *et al.* 1955).

Heritability is useful for determining the degree of characteristic inheritance from parents to offspring, whereas genetic advance is useful for determining the precise genetic diversity predicted under selection. Considering the relationship between characters and yield as well as among themselves. It is required for a reasonable selection of characters on which selection will be conducted for better yield. However, path analysis is a useful tool for determining the positive and negative effects of each character on yield, therefore the current study focused on the function of genetic factors in bitter gourd selection. Genetic diversity is an essential requirement for increasing crop productivity through breeding. A wide range of parent tends to help isolate better recombination hierarchical clustering in breeding programmes, which is influential in determining genetically dissimilar parents. In advanced generations, genetic diversity influences a cross's evolutionary basis for heterosis and the frequency of attractive progenies.

Yield is a complicated feature that is influenced by a number of yield contributing factors. Besides these above parameters. Mahalanobis D^2 analysis was also utilized which helped in the assessment of the contribution of every feature to overall diversity and genetic diversity among genotypes. The greater the genetic distance between two groups, the higher the odds of producing better hybrids and segregates through hybridization.

Keeping in view of the above facts in mind, the present investigation entitled “**Studies on genetic variability, heritability, correlation and path analysis in bitter gourd (*Momordica charantia* L.)**” was under taken during the *summer season* of 2018-19 and 2019-20 with the following objectives:

1. To investigate the variability, heritability and genetic advance for the quantitative characters,
2. To estimate correlation among the important economic traits,
3. To find out the direct and indirect effect of yield components by path analysis and
4. To evaluate the genetic divergence for yield and yield attributing traits.

REVIEW OF LITERATURE

To develop desirable genotype, the information about the environment and degree of the amount of genetic diversity in breeding materials as well as the level of environmental effect on characteristics, is extremely valuable. Bitter gourd has been the subject of much genetic, cytogenetic and breeding research in the past. A review of literature on the line of work will help the breeder; since the accessible literature for the current study of the bitter gourd (*Momordica charantia* L.) is very meager, therefore, the work done on few other cucurbits have been considered and reviewed under the following aspects:

2.1 Genetic variability, heritability and genetic advance,

2.2 Correlation studies and path coefficient analysis

2.3 Genetic divergence analysis.

2.1 Genetic variability, heritability and genetic advance in bitter gourd and other cucurbits

In a plant breeding programme, genetic diversity is the raw material on which selection operates to produce superior genotypes or varieties. The genetic variability for different characters present in breeding programmes or materials is methodically subjected to selection in order to change the genetic structure of plant characters and as a result of the plant as a whole, in order to develop improved genotypes with significantly greater marketable green fruit yield. The diversity used in breeding programmes comes from naturally occurring variations and wild relatives of crops, as well as artificially created strains and genetic stocks developed via human efforts.

The germplasm of a plant species is a store of variety for distinct characteristics arising from accessible natural or intentionally produced variations or strains. Improved strains, primitive cultivars, wild relatives, outdated cultures, unique genetic stocks, seeds pollen, vegetative components and so forth are all examples of germplasm.

The majority of germplasm collections have not been thoroughly assessed or screened for genetic diversity. A metric trait's total variability is split into genotypic and phenotypic variability. The evaluation of genetic variability for yield and its components is required before the crop may be improved to the desired level. There is both additive and non-additive variation in genotypic variability.

The idea of heritability is critical for determining whether phenotypic variations observed across people are due to genetic alterations or environmental influences. Heritability refers to the likelihood and magnitude of improvement that may be achieved by selection. It is a percentage-based metric that considers the ratio of genetic variation to overall phenotypic variance. This is a measure of genetic relationship between parents and progeny, and it is an index of character transmissibility from parents to offspring. Thus, changing the characteristics of the population through selection can be predicted only by knowing the degree of correspondence between phenotypic and breeding values.

Heritability has been defined by several people. Broad sense heritability is defined by **Lush (1948)** as the ratio of genetic variation to total phenotypic variance, whereas narrow sense heritability is defined by the ratio of additive genetic variance to total phenotypic variance. Because additive genetic variation is the only part of total variance that can be fixed, narrow sense heritability is more important in practice than wide sense heredity. In both a wide and limited sense, **Robinson *et al.* (1949)** challenged heredity. It is defined as "the ratio of total genotypic variation to total phenotypic variance" in a wide sense and "the ratio of additive genetic variance to total phenotypic variance" in a restricted meaning. They also divided heritability estimates into the following categories:

1. Low heritability (below to 40%)
2. Medium heritability (40 to 60%)
3. High heritability (61 to 80%)
4. Extremely High heritability (above 80%)

Several methods have been developed by many workers (**Mather, 1949; Warner, 1952; Kempthorne and Curnow, 1961; Crumpacker and Allard, 1962;**

Mather and Jinks, 1967) to estimate of the heritability in narrow sense.

The most relevant estimate is genetic progress, which is the increase in genotypic value in the new population compared to the base population. Expected genetic progress, according to **Comstock and Robinson (1952)** is determined by three factors:

- I. Genetic variability,
- II. Degree of the masking impact of environmental and interaction components of variability on genetic diversity
- III. Strength of selection.

Expected genetic advance in per cent of mean is the product of:

- I. Selection differential measured in terms of phenotypic standard deviation and
- II. The genetic coefficient of variability and square root of heritability ratio
(Johnson *et al.* 1955).

According to **Burton and de Vane (1953)**, the genetic gain that can be expressed for a particular character through selection is the product of its heritability, phenotypic standard deviation (p), and selection differential. Though heritability value indicates the relative effectiveness of selection based on phenotypic expression of a trait, genetic advance, as demonstrated by **Johnson *et al.* (1955)** is more useful in predicting the actual value of selection.

The following is a summary of the information pertaining to these characteristics:

Chowdhury and Sharma (2002) investigated 12 ridge gourd genotypes (*Luffa acutangula L.*). For all characteristics, the genetic coefficient of variation (GCV) was less than phenotypic coefficient of variation (PCV). Vine length, yield per hectare, and fruit weight all had high heritability, PCV, GCV and genetic advance values, showing that such features were characterised by positive gene effects.

Kutty and Dharamatti (2004) evaluated at 10 quantitative parameters in 40 bitter gourd genotypes. At both the phenotypic and genotypic levels, the results clearly indicate a lot of diversity in yield and its components. For number of fruits per vine,

fruit weight and total fruit production per plant, substantial heritability was observed together with strong genetic progress as a per cent of mean, showing the impacts of gene action for such as variables. Bitter gourd genotypes might be improved with the use of selection techniques. BLG-1, DWD-2, NRN-1, and IC 44418 were the most promising of the 40 genotypes.

Maurya *et al.* (2004) recorded for days to the first male flower, days to the first female flower, node number to the first female flower, days to the first fruit harvest, vine length, number of primary branches, fruit weight, fruit length, fruit diameter, number of fruits per plant, and early fruit yield per plant were all recorded. For all of the characteristics, analysis of variance revealed substantial variations between genotypes.

Ahmed and Mufti (2006) evaluated fifteen diverse genotypes of bitter gourd (Kalyan Sona, BGR-II, Barsati, Jaunpuri, Patna Karela, Baramasi Karela, Faizabadi, BGR-I, Preethi, SH-BG-2, SH-BG-2, Priya hybrid, SH-BG-3, SH-BG-4 and Local) for seven yield characters (length of vines, number of branches per vines, length of fruits, diameter of fruits, fruits number per vine, weight of fruits and fruit yield per plant) and five genetic traits (variation coefficients phenotypic and genotypic, heritability, genetic advance as a per cent of the mean. Preethi had the highest values for the majority of yield-related characteristics, including the maximum fruit yield (2.89 kg) and the highest number of fruits per plant (16.00) and fruit diameter (5.50 cm). In BGR-1, the highest fruit length and fruit weight were recorded. All of the traits were highly heritable, with significant phenotypic and genotypic variability factors. For branch number per plant, average fruit length, average fruit diameter, fruit number per plant and number of fruits per plant, strong genetic coefficient of variation and heritability estimations were linked with high genetic progress. The findings revealed that these traits are cumulative in nature and may be utilised to make good decisions. High heritability and modest genetic advancement were found in vine length and average fruit weight.

Bharathi *et al.* (2006) studied on 32 cultivars of spine gourd, the study examined genetic variations for 10 traits. For the characteristics investigated, analysis of variance indicated substantial variations between genotypes. Fruit weight, fruit length, and number of fruits per vine all had significant heritability and genetic gain, showing

the predominance of additive gene action for all these traits.

Narayan *et al.* (2006) carried out an experiment on 15 diverse genotype of bitter gourd (Kalyanpur Sona, BGR-II, Barsati, Jaunpuri, Patna Karela, Baramasi Karela, Faizabadi, BGR-1, Priya hybrid, SH-BG-3, SH-BG-4 and Local) for 7 yield characters (vine length, branches number per plant, length of fruit, diameter of fruit, number of fruits per plant, weight of fruits and total fruit yield per plant) and phenotypic as well as genotypic coefficients of variance, heritability and genetic advance are five genetic parameters. Preethi has the highest yielding relevant characteristics, like the maximum fruit yield (2.89 kg), the maximum number of fruits per plant (16.00) and the highest fruit diameter (5.50 cm). Because of the prevalence of non-additive gene activity, maximum fruit can be enhanced by heterosis breeding.

Singh (2006) conducted trial on 30 diverse genotypes of bitter gourd for 12 characters. Various genetic parameters were estimated. Based on average performance for yield attributes, analysis of variance for the experiment design revealed very statistically significant differences across genotypes for all variables. The yield per plant had the highest phenotypic coefficient of variability followed by the average fruit weight and number of fruits per plant.

Ahmed *et al.* (2006) evaluated 15 genotypes of bitter gourd (Kalyan Sona, BGR II, Barsati, Jampur, Patna Karela, Long Baramasi, Karela Faizabadi, BGRI, Preethi, SHBG 2, Priya hybrid, SHBG 3, SHBG 4 and Local) were evaluated for 7 yield characters (vine length, branches per plant, fruit length, diameter, number per plant, fruit weight and fruit yield per plant) and 5 genetic traits (phenotypic and genotypic coefficients of variation, heritability and genetic advance as per cent of mean) in Jammu and Kashmir, India during the Kharif season of 2003. Preethi had the highest values for the majority of yield-related characteristics, such as the highest number of fruits per plant (2.89 kg) and the maximum fruit number per plant (16.00) and fruit weight diameter (5.50 cm). In BGR1, the maximum fruit length and average fruit weight were recorded. All of the traits were highly heritable, with significant phenotypic as well as genotypic variability factors.

Raja *et al.* (2007) worked on 46 genotypes of bitter gourd for 14 quantitative characters for variability, heritability and genetic advance. MC-23 obtained from the maximum number of primary branches per vines, fruit yield per plot and fruit weight.

The number of female flowers per plant had the greatest PCV and GCV followed by fruit weight and the number of primary branches per vines, suggesting the amount of variability depending on these features. Number of female flowers per plant had the highest heritability and genetic gain followed by fruit weight, number of primary branches per plant, and marketable fruit production per plot, showing additive gene activity. Fruit girth was shown to have a medium heritability and minimal genetic variation.

Kumar *et al.* (2008) studied on variability, heritability, genetic advance, correlation and path analysis were investigated for fruit yield component attributes in twenty-five different cucumber genotypes. Days to anthesis first female flower, primary branches per plant, fruits per plant, node bearing female flowers per plant, fruit length, fruit weight and fruit yield per plant all showed a broad range of variability, as well as PCV and GCV estimations. Days until first female flower anthesis, main branches per plant, fruits per plant, fruit length and fruit diameter all had significant heritability and anticipated genetic gain and fruit yield per plant. Some features have additive gene impact, indicating that they are more stable for successful selection.

Yadav *et al.* (2008) conducted a study on variance analysis of 17 bitter gourd genotypes' characteristics, which revealed remarkable variations. The longest vine length was measured. Internodal length and the number of main branches per vine are both much larger. In JMC-4, the highest number of nodes was observed. In MC-84, the minimum number of days for the initial emergence of male flowers as well as the maximum fruit length, width, yield per vine, yield per plot and yield per hectare were all recorded. In GY-I, the maximum number of fruits per plant was observed.

Banik *et al.* (2009) studied genetic variability of 26 snake gourd genotype for 15 characters. The considerable variability was observed for the characters like Crop yield per plant, node number to first female and male bloom and primary vine length are all important factors to consider. Fruit yield per plant, vine length, and the number of initial male flower nodes had strong heritability and genetic gain. As a consequence of these findings, it appears that character selections based on the relevant characters will be highly effective.

Dey *et al.* (2009) worked on with 38 bitter gourd cultivars. For all 12 quantitative parameters of the variables, there was a broad range of variance. Among these

genotypes, two gynoecious lines namely, DBTG-201 and DBTG-202 were found promising with respect to earliness and yield and their related characters. For traits including fruit weight (g), fruit diameter (cm), flesh thickness (cm) and yield per plant. The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all of the characters assessed, showing that the environment has an impact on character expression. All of the variables had medium to high heritability. Considering parameters like fruit weight (g), flesh thickness (cm), yield per plant (g) and yield per plant (g), the highest heritability and genetic advancement were observed. The prevalence of additive gene action as well as the success of improvement by selection for all these economically prominent components are shown by the node of the first female flower.

Bahera et al. (2010) discussed on the origin and domestication, nutritional uses and medicinal properties of bitter gourd (*Momordica charantia* L.). The botanical (taxonomy, morphology and reproductive biology), horticultural (climate and soil, culture, sex expression and modification, harvest, seed production and pests and diseases) and breeding aspects (genetic variation and germplasm development, inheritance, character association, goals and cultivar development, breeding methods and biotechnology) of bitter gourd.

Devmore et al. (2010) evaluated on days to first male flower, nodal position for first male flower, days to first female flower, nodal position for first female flower, vine length, primary branches per vine, nodes number per vine, days to fruit development, days to first fruit harvest, fruits number per vine. Heritability and genetic progress as a percentage of mean, fruit length, vine length, fruit number per vine, days to first fruit harvest are all factors to consider. The number of nodes per vine and the number of major branches per vine would allow for selection in bitter gourd breeding for maximum fruit output.

Naik et al. (2012) studied on variability, heritability and genetic advance of five female clones of teasle gourd (*Momordica subangulata* Blume. Subsp. *renigera*) were investigated. The length of the main vine (m), the number of vines per plant, the number of leaves per plant, the fruit weight at marketable stage (g), the ovary diameter (mm), the number of seeds per fruit, the number of fruits per plant, and the yield per plant all had higher phenotypic coefficients of variation (kg). marketable

stage of average fruit weight (g), main vine length (m), ovary radius (mm), number of fruits per plant and number of vines per plant all had high heritability as well as genetic advance, revealing that all these characteristics were still under additive gene moderation and that simplified selection could be used to improve these teasle gourd traits.

Pandey *et al.* (2012) tested with 30 genotypes of sponge gourd to evaluate 11 yield components. High to moderate heritability as well as genetic advance was estimated for the characters *viz.*, average fruit length, number of fruits per plant, average fruit weight, diameter of fruits and length of vines, while, average fruit yield per vine had high heritability but moderate genetic advance and days to taken to anthesis of first female exhibited high heritability and genetic advance. The intervention of non-additive gene action was clearly indicated by the two characters in the anthesis of the first female flower and fruit yield. Apart from these two qualities, all of the variables described above have high heritability combined with high genetic advance, showing that additive gene action prevails and selection for all these parameters is dependable for the production of high producing sponge gourd cultivars.

Kumar *et al.* (2013) studied the mean performance, variability, heritability, genetic advance, correlation and path analysis for yield components traits of 20 sponge gourd genotypes. In all of the genotypes analyzed in the experiment, significant differences were detected for all of the characteristics. The total yield per vine had the most genotypic and phenotypic diversity followed by the number of seeds per fruit, average weight of fruit and total soluble solids. The number of seeds per fruit, the average weight of the fruit and the specific gravity of the fruit all indicated significant heritability and genetic advance. The average number of fruits per vine, average fruit weight and number of seeds per fruit were all shown to be positively associated with total yield per vine. The diameter of fruit, number of primary branches, number of fruits per vine, weight of fruit and total soluble solids all had positive direct effects on total fruit yield per vine, according to path coefficient analysis. As a result, it is proposed that all these characteristics be selected in order to increase sponge gourd yield per vine.

Yadav *et al.* (2013) worked on 13 diverse genotypes of bitter gourd were evaluated for genetic variability during 2007 and 2008 for 13 traits under Allahabad conditions.

The genotypes were planted at 1 m x 1 m distance for two summer season. The analysis of variance revealed a wide variation in yield component characteristics across all genotypes. Fruit weight, number of nodes per vine, days to the first appearance of female flower, days to the first appearance of male flower, fruit length and yield per vine had the highest range of variation followed by fruit weight, number of nodes per vine, days to the first appearance of female flower, days to the first appearance of male flower, and fruit length, with yield per vine having the smallest range of variation. The number of nodes per vine, internodal length, fruit breadth, and number of fruits per vine all exhibited significant and positive correlations with vine length. The number of main branches per vine was related in a significant way.

Kumari *et al.* (2015) observed on its most important yield determining feature is the quantity of fruits per vine followed by average fruit weight. As a result, these traits should be priority when select cultivars for bitter gourd production enhancement.

Ananthan and Krishnamoorthy (2017) carried out an experiment Investigate the mean performance of twenty ridge gourd cultivars collected from various parts of Tamil Nadu in terms of genetic variability, heritability, genetic advance, correlation and path analysis for yield components like first female flower node, days taken for first female flowering, number of fruits per plant, fruit length, fruit weight (g), fruit yield per plant (kg). For fruit yield per plant (31.55, 32.86, and 62.39), the genotypes had high levels of genotypic coefficient variation and phenotypic coefficient variation and genetic advance in per cent of the mean, respectively and the heritability was high (98 percent). Fruit weight (0.722 and 0.681), fruit diameter (0.426 and 0.393), number of fruits per plant (0.504 and 0.477), and first female flower node all contributed significantly to fruit yield per plant, according to phenotypic and genotypic correlation coefficients (0.467 and 0.428). The path analysis revealed that the number of fruits per plant had a positive significant direct effect on yield per plant (1.4792) followed by fruit weight (0.9346) and fruit weight direct effect (0.9346) as well as indirect effect (0.7220).

Singh *et al.* (2017) reported on 20 germplasm and main focus of this field trail was to estimate the component of variance, phenotypic and genotypic coefficient, heritability and genetic advance over mean for different growth, yield and quality parameters.

The maximum difference between PCV and GCV was reported for fruit yield per vine, while the other traits showed moderate to low PCV and GVC with very less difference between them. This indicated the influence of environmental factors on these parameters is very negligible. The maximum traits showed high to moderate heritability coupled with high to moderate genetic advance over mean except total soluble solids. This indicated these traits are suitable for direct selection and improvement.

Tyagi *et al.* (2018) recorded data on the 31 bitter gourd cultivars were used to investigate the variability, heritability and genetic advance of 12 quantitative characters. For all of the characters, analysis of variance revealed considerable variation between genotypes. The phenotypic coefficient of variation (PCV) estimations were greater than genotypic coefficient of variation (GCV), showing that variation is caused not just by genotypes, but also by environmental factors. fruit weight, fruit yield per vine, vine length and fruit length all had high PCV and GCV levels, showing that the traits have a lot of variation. That means there's significant potential by selection.

Maurya *et al.* (2018) worked on estimates of phenotypic and genotypic coefficient of variation were observed higher for number of fruit per plant followed by fruit yield per plant, vine length and node number of first staminate flower, fruit length whereas, average fruit weight, node number to anthesis of first pistillate flower and were moderate coefficient of variation. All of the characters had high heritability estimates, with the exception of days to anthesis of first pistillate flower, days to anthesis of first staminate flower, and node number of first pistillate flower, which had moderate heritability, and days to first fruit harvest and fruit diameter, which had low heritability. For the quantity of fruits per plant, high estimations of genetic advance as per cent of mean were reported.

Thakur *et al.* (2018) evaluated varieties suited to specific agro-ecological conditions. A study was undertaken to evaluate eight different genotypes of bitter gourd (*Momordica charantia* L.) in relation to yield and yield contributing traits. All genotypes showed relevant results for different traits. Among genotypes Prachi produced the most fruit per plant (21.78), fruit yield per plant (1.16 kg) and total fruit yield (16.44 Mt ha⁻¹) followed by Preeti, and these 2 genotypes had best results for

high yielding parameters, Whereas for earliness Polo-71 performed best for days to first male (31.83) and female flower (30.36).

Priyadharshini et al. (2018) reported that the bitter gourd genotype MCM-19 followed by MCM-22 and MCM-21 was reported to the most good potential genotype, with higher fruit yield per plant (0.72 kg) and other economic fruit yield attributes like as fruit length (5.51 cm), fruit circumference (6.47 cm), fruit weight (9.08 g), number of seeds per fruit (9.80) and 100 seed weight (10.59 g). The genotypes MCM-4 (5.90 °Brix) and MCM-21 (5.87 °Brix) had the highest maximum total soluble solids, while the genotypes MCM-26 (123.62 mg/100g) and MCM-22 (122.59 mg/100g) had the highest ascorbic acid levels.

Kumari et al. (2018) studied the yield constituent traits are less complicated to inherit and are impacted by environment to a lower degree, evaluating them solely on yield may restrict the improvement. Understanding the type and amount of variation in the available material, as well as the relationship between characteristics with yield and among themselves, are necessary for rational development of yield and its components. Although statistically proven by correlation coefficient, the effect of environmental factors on the characters is important for determining the influencing factors of the various characters on yield, it does not provide an actual description of the perceived significance of the direct and indirect effects of each of the characters on yield. The correlation coefficient was partitioned into direct and indirect effects using path coefficient analysis.

Alhariri et al. (2018) observed and revealed that the (-23.65%) heterosis for days to first harvest when compared to the mid parent and (-28.24%) when compared to the standard parent. Over the mid and standard parents, the hybrid PDMGy-201 S-2 demonstrated (-95.93%) and (-69.83%) sex ratio (male: female) heterosis, respectively. Fruit length (33.43 percent) over mid parent, fruit diameter (15.12 percent) over standard parent, and flesh thickness (54.88 percent) and (29.07 percent) over mid and standard parents, respectively, revealed greater heterosis in the monoecious hybrid S-54 S-57. Over the mid and standard parents, all 28 F₁ crosses showed substantial desirable heterosis in average fruit weight and yield per plant.

Mallikarjunarao et al. (2018) reported that the combining ability study indicated that all of the characters gca and sca variations were significant. Characters including flesh

thickness, T.S.S., Vitamin-C, iron content and fruit yield per vine were all affected by non-additive gene action. Pusa do Mausami for T.S.S. and Phule Green Gold for Vitamin-C, iron content, and fruit yield per vine. Hybrids improved Katahi x Preethi for flesh thickness, Preethi x Pusa Do Mausami for T.S.S., Thusi x Pusa Do Mausami for Vitamin-C and Phule Green Gold x Pusa Do Mausami for iron content and fruit yield per vine according to specific combining ability analysis.

Talukder *et al.* (2018) found that genetic parameters, fruit weight, yield per plant, and fruit length had high genotypic coefficient of variation (GCV), but nodes per vine, days to first male and female flowering had low genotypic coefficient of variation (GCV). In every case, the phenotypic coefficient of variation was larger than the genotypic coefficient of variation, indicating that there was a lot of diversity among the genotypes and that there was a lot of room for selection. G₉ and G₁₃ had the shortest vine length of 3.90 m, while G₈ had the longest vine length of 4.83 m.

Rahman *et al.* (2019) studied on the exception of branches per vine, estimates were obtained for all of the characteristics investigated, indicating that virtually all of the variables under investigation are largely under genetic influence. Fruit length, fruit width, fruit weight, and quantity of fruits per plant all had high heritability and genetic progress, indicating that additive genes regulate these characteristics. These four characteristics were shown to be key yield related variables in the current study and may be utilised for phenotypic selection in bitter gourd breeding programmes.

Pradhan *et al.* (2021) observed the fruit per vine⁻¹ (91.36 percent and 49.11 percent), fruit circumference (91.12 percent and 26.74 percent), number of seeds per fruit⁻¹ (89.85 percent and 38.21 percent), total green fruit yield (89.35 percent and 44.67 percent), sex ratio (88.10 percent and 63.38 percent), internodal length (87.82 percent and 46.83 percent), fruit length (87.82 percent and 46.43 percent). As a result, direct selection of these characteristics in bitter gourd has a lot of potential.

2.2 Correlation studies and path coefficient analysis

In vegetable breeding, understanding the type and size of the relationship between yield and yield components is of significant importance. Correlation coefficients are statistics that quantify the relationship and its extent between two or more variables. Correlation tests show that choosing one character leads to development of the other positively associated characters. Many of the characters have good or negative associations with other characters due to natural associations. The indirect correlation becomes more complicated as more factors are examined in table correlation.

The type and degree of link between any two quantifiable characteristics or variables may be determined using correlation coefficient analysis. It reduces complicated relationships between events to a basic kind of association, but it does not take into account the dependency of one variable on the other. **Galton (1889)** introduced the idea of correlation, which was developed by **Fisher (1918)** and **Wright (1921)**. Classifying into phenotypic, genotypic and environmental components greatly improves the usefulness of correlation estimations (**Burton, 1952**). Pleiotropy and gene linkage can cause genetic correlation, but phenotypic value is a non-additive mix of genetic and environmental connection. This study just shows the type of connection; it does not offer a precise picture of each component character's proportionate impact. A component character may not have a direct impact on a significant economic feature, but it may have an indirect impact through related characters.

As a result, understanding the direct and indirect effects of various traits on positive traits is critical for population improvement selection. The path coefficient determines the type of connection by dividing the correlation into direct and indirect effects (**Falconer, 1989**). The use of correlation between distinct characters can increase the efficiency of selection. The phenotypic correlation coefficient illustrates the amount of the observed relationship between two characters, which contains both hereditary and environmental factors, while the genotypic correlation coefficient shows the true (genetic) association between two characters and is most helpful in selection (**Johnson et al. 1955**).

Simple correlation analyses cannot distinguish between the direct contribution

of each component to the yield and the indirect influence it has through its connection with other components. This gap is filled by path coefficient analysis. **Wright (1921)** was the first to create and define it as a technique for genetic analysis that separates the connection of the components on yield from the indirect effects of the characteristics on yield through other components.

Path coefficient analysis is a standard partial regression coefficient that divides the correlation coefficient into direct and indirect effects, as well as measuring the direct and indirect contributions of numerous independent variables to the dependent variable. Correlation combined with route analysis would provide a better understanding of the cause and effect relationship between various characteristics. The following are the contributions of several cucurbit reviewers:

Sharma and Bhutani (2001) analyzed path coefficient in bitter melon and indicated that the number of fruits per plant had the greatest direct effect on production, followed by chlorophyll content, fruit length and fruit diameter. While vine length had the greatest indirect impact on production, it was followed by internodal length, average fruit weight, fruit diameter and fruit length via the number of fruits per plant.

Sharma and Bhutani (2001) reported positive correlation among first female flowering and fruits per plant, length of fruit, diameter of fruit with average fruit weight, maximum number of fruits per plant and average fruit weight with total yield per plant.

Shah and Kale (2002) evaluated correlation for yield component of 55 cultivars in ridge melon. Fruit weight per plant had a highly significantly positive relationship with fruit number per vine, fruit weight, number of female flowers per vine and vine length, showing significant relationship and dependent on these parameters for yield.

Dora et al. (2002) observed the except for the number of branches per plant, diameter of fruit, fruit length and days from fruit set to marketable maturity, all four parameters showed a moderate positive association with yield, with the exception of the number of branches per plant, which has a positive direct effect. As a result, fruit diameter, length and days from fruit set to marketable maturity can all be used to enhance production. In the case of features like the number of days it takes for the first bloom to develop, the weight of the fruit, and the number of nodes per plant in pointed

gourd, there is a positive direct and negative association with yield.

Bhave *et al.* (2003) reported that at both genotypic and phenotypic levels, there was a positive and significant relationship between fruit yield per vine and flowering duration, harvesting span, fruit length, fruit breadth, fruit rind thickness, number of fruits per vine, average fruit weight, biological yield, dry matter, and harvesting index. In bitter gourd, green fruit production had a negative association with days to first flowering at both the genotypic and phenotypic levels. Harvesting duration, leaves per plant, fruit length, average fruit weight, seeds per fruit, fruit per vine, biological yield and bitter gourd quality were all found to have a positive significant direct impact on yield.

Goa-Shan (2004) studied on 15 agronomic characters of 21 Balsam pear cultivars for correlations and principal components. Correlation found that the early stage fruit yield was positive highly significantly correlated with the node order of the first female flower, blooming period of female flowers and fruit bearing number per plant, while the, the total yield was a strong and moderate correlation with the fruit bearing number per plant, early stage yield, rate of female flowers, node order of the first female flowers and blooming period of female flowers.

Dey *et al.* (2005) reported that the phenotypic correlation is more important than genotypic correlation. Fruit weight had the strongest positive association, followed by fruit quantity per plant, flesh thickness, days from fruit set to maturity, fruit index, fruit length, and fruit diameter. Fruit weight and quantity of fruits per plant have a significant and favourable direct impact on bitter gourd output. They found that fruit weight, number of fruits per plant, and node number of initial female flower appearance are the most dependable and reliable criteria for selection to enhance production, based on path analysis.

Kutty and Dharamatti (2005) worked on 40 divergent genotypes of bitter gourd (*Momordica charantia* L.) for correlation and path coefficient. Days to first female flowers opening, first female flowers node number, number of leaves at 50% flowering, days to first harvest, productive length of vine, number of seeds per fruit, fruit length, number of fruits per plant, total yield per plant, fruit weight, fruit fly infestation, and downy mildew incidence were all recorded. The most important traits contributing to yield per plant were the number of leaves at 50% flowering stage,

number of seeds per fruit, fruit length, number of fruits per plant, and fruit weight, all of which had very high direct effects, positive correlations, and high indirect effects through other economic characters.

Ram et al. (2006) studied in Uttar Pradesh, researchers analyzed the relationship between yield components in 26 varieties of bitter gourd (*Momordica charantia* L.). For all parameters, the genotypes differed considerably (number of days to germination, number of days to first female anthesis, number of days to first male flower anthesis, node to first male flower emergence, node to first female flower emergence, number of fruits per plant, fruit length, fruit diameter, plant height, average fruit weight, seed weight per fruit, and yield per plant). Number of days to male flower emergence had the largest coefficient of variation (44.87 percent), followed by seed weight per fruit (40.48 percent) and yield per plant (39.47 percent) fruit weight (30.97 percent) and fruit length (30.82 percent).

Singh et al. (2006) reported in bitter gourd, there was a positive and significant relationship between yield per plant and number of fruits per plant, but not with days to first male flower anthesis, days to first female flowers anthesis or fruit diameter.

Singh et al. (2006) evaluated in 30 diverse genotypes of bitter gourd for 12 characters. Various genetic parameters were estimated. Compared to the mean performance for yield components, analysis of variance for the design of the study revealed statistically significant differences between genotypes for all attributes. The yield per plant had the highest phenotypic coefficient of variation followed by the number of fruits per plant and the average fruit weight.

Sundaram and Vadivel (2007) observed to determine the relationship between yield related characteristics and yield, study examined 20 genotypes of bitter gourd (*Momordica charantia* L.) for 14 biometric traits in saline sodic soil. The number of female flowers per vine, the number of fruits per vine, the vine length and the fruit weight all exhibited a strong positive relationship with yield. The number of female flowers per vine and the quantity of fruits per vine had the strongest positive connection. The quantity of fruits per vine had the highest positive direct effect on output, whereas, the number of female flowers per vine had the highest negative direct effect on output, according to the path coefficient analysis. The number of female flowers produced per vine had the greatest indirect positive effect on yield via

the number of fruits produced per vine, indicating that the number of fruits per vine and the number of female flowers produced per vine could be considered primary yield factors in bitter gourd under salt stress and that selecting for these attributes would also yield the desired outcome.

Yadav *et al.* (2008) studied that the analysis of variance on 17 bitter gourd cultivar characteristics revealed significant differences. The highest vine length, the number of main branches per vine and the intermodal length were all recorded. The highest number of nodes was found in JMC-4. In MC-84, the minimum number of days for the initial emergence of male flowers as well as the maximum fruit length, fruit, width, fruit per vine, yield per plot and yield per hectare were much lower. GY-1 had the highest number of fruits per vine.

Yadav *et al.* (2010) reported on the fruit yield per plant was observed to have significant positive and correlation coefficient with days to first female flowers anthesis, vine length (m), number of primary branches per plant, length of fruit (cm), weight per fruit (kg) and number of fruits per plant whereas, the length of fruit (cm), weight per fruit (kg) and number of fruits per plant were also found to have a positive and direct effect on fruit per plant. As a result, a high focus was placed on fruit weight (kg) and quantity of fruits per plant in the selection programme for bottle gourd development in the future.

Sureja *et al.* (2010) observed the thirteen growth and average yield indicators, as well as fourteen quality traits, were assessed. For characteristics including days to fruit maturity, number of seeds per fruit, seeds weight per fruit, iron and zinc content, phenotypic and genotypic coefficients of variation were detected. Elevated estimates of genetic advance as a per cent of mean were found for yield per vine, number of fruits per vine, seeds weight per fruit, number of seeds per fruit, vitamin-C, iron and copper content as well as a high number of heritability, revealing that all these aspects are governed by additive genes and that prolonged selection would be beneficial in modifying the populations mean performance.

Kumar *et al.* (2011) evaluated for all characteristics, the phenotypic coefficient of variation (PCV) was greater than the genotypic coefficient of variation (GCV). Fruit yield per plant had the highest genotypic and phenotypic coefficients of variation, followed by fruit length and number of seeds per fruit. Fruit production per plant,

number of seeds per fruit, and fruit diameter all had strong heritability. In terms of fruit output per plant, there was a lot of genetic progress. As a result, selective breeding procedures may be used to increase these characteristics.

Singh *et al.* (2011) studied on 103 genotypes of sponge gourd were used to analyzed that the association and path analysis of ten quantitative yield traits. The genotypic correlations were greater than the phenotypic correlation coefficient for the most part, this implies that there is an underlying link between them. Fruit yield per plant was shown to be substantially and positively linked with fruit length, width, weight, and number of fruits per plant, but not with days to first male flower, days to first female bloom, or days to first harvest. The quantity of fruits had the greatest direct influence on fruit output per plant (0.858) followed by fruit weight (0.443).

Singh *et al.* (2012) worked on the path coefficient analysis of 10 yield relevant quantitative parameters, 110 cultivars of ridge gourd were examined. Genotypic correlations were larger than phenotypic correlations, indicating an underlying connection between them. Fruit yield per plant was shown to be highly and positively associated with fruit length, fruit diameter and fruit weight, but not with days to first female bloom and days to first harvest. Fruit weight (0.432) had the highest direct effect on fruit yield per plant followed by the number of nodes to first female flowers (0.102).

Huang *et al.* (2012) reported on research in bitter gourd (*Momordica charantia* L.) genetics and breeding, comprising fruit character inheritance, gynoeious breeding, sex differentiation, disease resistance breeding, haploid breeding, and novel variety selection. Also, it explains the current difficulties with bitter gourd breeding in China as well as future trends based on the current state of bitter gourd breeding.

Pandey *et al.* (2013) evaluated 30 sponge gourd genotypes including Pusa Chikni (national check) best suited to high yield and marketable character for 11 traits. Days to first marketable fruit harvest had a considerable and favourable relationship with days to first male flowers anthesis and days to first females flower anthesis. Average fruit weight, number of fruits per plant and days to first marketable fruit harvest all showed a positive direct effect on marketable fruit yield per plant, according to the path coefficient analysis. According to the findings, an ideal plant with days to first marketable fruit harvest, days to anthesis of first female flower, days to anthesis of

first male flower, higher average fruit weight, and maximum number of fruits per plant could aid in forming an attractive plant with high yield and remarkable marketable fruit yield per plant in sponge gourd.

Devi *et al.* (2013) examined to the degree of diversity in the population and to select genotypically diverse and commercially attractive genotypes for crop improvement, the study examined 50 genotypes of snake gourd (*Trichosanthes anguina* L.). For all of the characteristics studied, the phenotypic coefficient of variation was found to be somewhat greater than the genotypic coefficient of variation, showing that the apparent variation is not simply genetic, but also attributable to the effect of the growing environment on genotype expression.

Pathak *et al.* (2014) worked on days to first male and female flower anthesis and days to marketable maturity from anthesis, which are indicators of a higher proportion of additive genetic variance and, as a result, a high genetic gain from selection, and days to first male and female flower anthesis and days to marketable maturity from anthesis, indicated that non-additive gene effects were involved in the expression of these characters. The quantity of fruits per plant exhibited a strong positive association with yield, according to correlation analysis. The association was further divided into direct and indirect effects using path analysis. Fruit weight, number of fruits per plant and fruit length were shown to be directly associated with yield, suggesting that selection based on these characteristics would be more profitable.

Singh *et al.* (2014) found that fresh fruit yield per plant had the highest phenotypic and genotypic coefficients of variation followed by fruit length, fruit width and number of fruits per plant, showed highest genetic variability in all these traits. Fruit length, yield per plant, fruit diameter, fruit weight, branches per plant and seeds per fruit all had strong heritability and genetic gain as a per cent of mean, showing the potential influence of role of additive gene action.

Gupta *et al.* (2015) evaluated on 26 bitter gourd cultivars including check (Solan Hara) Examine the relationship between yield components as well as both direct and indirect effects on total marketable fruit yield. While, the correlation of different characters with yield is helpful for improvement and provides criteria for direct selection of component characters, improvement of yield attributing characters, which can also be superior as beaded curtain, must be considered while selecting for yield.

Average fruit weight (0.726), marketable fruits per vine (0.547) and seeds per fruit (0.377) all had a positive phenotypic correlation whereas, marketable fruits per vine (0.684), seeds per fruit (0.625) and average fruit weight (0.726) all had a negative phenotypic association (0.591) and The genotypically favourable relationship with total marketable fruit yield per hectare was seen at the node where the first female blossom emerges (0.338).

Khan *et al.* (2015) tested the variability in genotypes for yield characters, evaluation of genetic and environmental factors and character relationship and contribution to yield. There was a lot of considerable variance among the genotypes for all of the characters. For branches per vine, yield per plant and quantity of fruit per plant, significant genotypic coefficients of variation (GCV) were found, but days to first male and female flowering had low genotypic coefficients of variation (GCV).

Gupta *et al.* (2016) studied with twenty-six bitter gourd genotypes and all characteristics exhibited greater phenotypic coefficients of variation (PCV) than genotypic coefficients of variation (GCV), showing a strong relationship among genotype and phenotype. For branches per plant, the PCV and GCV were high, followed by fruit yield per plant and total marketable fruit production per hectare. Number of branches per plant had the highest heritability estimates, followed by fruit size and number of seeds per fruit, all of which showed non-additive gene activity and may be enhanced by hybridization. In terms of overall marketable fruit production per hectare, there was a lot of genetic gain.

Yadagiri *et al.* (2017) observed that twenty genotypes of bitter gourd were studied. the genotypes for all the traits. Correlation analysis revealed a significant positive correlation for yield between vine length (0.640), number of branches per vine (0.577), number of male flowers per vine (0.594), number of female flowers per vine (0.529), number of fruits per vine (0.649), length of fruit (0.724), weight of fruits (0.961), number of seeds per fruit (0.360), seeds weight per fruit (0.380).

Yadagiri *et al.* (2018) estimated to the path analysis separated the association into direct and indirect effects and calculated twenty genotypes of bitter gourd for assessing their performance. Harvest duration (0.004), vine length (0.030), number of seeds per fruit (0.045), and fruit length (0.094) were shown to be directly linked with

yield, implying that selection based on these features would be more profitable.

Talukder *et al.* (2018) reported that the Sher-e-Bangla Agricultural University experimental farms in Dhaka, 20 genotypes of bitter gourd (*Momordica charantia* L.) were evaluated. Between genotypes, there is significant variance in all of the characters. Fruit weight, yield per plant and fruit length all had significant genotypic coefficient of variation (GCV) when genetic factors were included. The phenotypic coefficient of variation was found to be higher than the genotypic coefficient of variation, showing a broad range of variation between genotypes and allowing for more selection options.

Kumar *et al.* (2018) evaluate the fifteen genotypes of bitter gourd to Weight per fruit had the most phenotypic and genotypic variation, as well as the greatest genetic gain. GA per cent of mean was assessed for fruit yield per plant (kg) and higher heritability for primary branches per plant, the highest of PCV and GCV.

Tyagi *et al.* (2018) studied on the genotypic correlation coefficient was found to be greater than the phenotypic correlation coefficients in investigations. This meant that the environment's suppression effect changed the phenotypic variation of these characters by lowering phenotypic correlation coefficients. At both the phenotypic and genotypic levels, path analysis revealed that average fruit weight (g) and quantity of fruits per plant had the highest direct effect on yield, indicating their relevance when applying selection for yield correlation in bitter gourd.

Maurya *et al.* (2018) reported on the estimates of genotypic and phenotypic coefficient of variations, number of fruits per plant followed by fruit yield per plant, vine length and node number of first staminate flowers and fruit length had higher. Whereas, average fruit weight, node number to anthesis of first pistillate flowers and fruit length had moderate coefficient of variations. All of the characters had high heritability with the exception of days to anthesis of first pistillate flowers, days to anthesis of first staminate flowers and node number of first pistillate flowers which had moderate heritability and days to first fruit harvest and fruit diameter which had low heritability.

Kumari *et al.* (2018) carried out the work to evaluate characters that are less complicated in inheritance and are less impacted by the environment are used to

assess the yield component characters. Although useful in determining the relative influence of the various characters, understanding the nature and magnitude of variation in the available material, and the association of characters with yield and among themselves, as well as the extent of environmental influence on the characters, which is statistically determined by the correlation coefficient, is necessary for rational improvement of yield and its components. The correlation coefficient was separated into direct and indirect effects using path coefficient analysis. It contributes to an understanding about how each independent character affects the dependent character.

Bhagat *et al.* (2018) conducted an investigation with 33 spine gourd cultivars were used to estimate genetic parameters, correlation, principal component analysis and cluster analysis. Fruit yield per plant was shown to have 43 significant positive relationships with number of initial blooming nodes, ovary length, single fruit weight and number of fruits per plant. The seven major principal component lines explained for 76.4 percent of the variance in the divergence across spine gourd genotypes, according to principal component analysis. Cluster-III had the most genotypes (12), whereas Cluster-I (11) had the fewest genotypes, Cluster-II (8) had the fewest genotypes and Cluster-IV had just two genotypes. The genotypes were divided into four groups based on main component scores in PCA and cluster analysis.

Kumar *et al.* (2018) observed that the genotypes, HABG-22, NDBT-07, NDBT-09, Meghana-2, Selection-5, Preethi, Phul Ujjwala, Priya, Nakhara, Pant Karela-1, Hirkani, VRBT-23, Pusa Vishesh, Pusa Ashaudhi, and Arka Harit were among the fifteen bitter gourd genotypes. It is apparent from the correlation coefficient and direct and indirect effects of fruit yield contributing parameters for bringing forth intended improvements in bitter gourd fruit yield. Direct selection factors include average fruit weight and fruits per vine.

Alekar *et al.* (2019) assessed that the vine length after harvest, number of primary branches per vine, number of fruits per vine, average fruit, fruit yield per vine, average fruit weight, average fruit length, yield tonnes per hectare Fruit yield per hectare exhibited a significantly positive association with yield components characters, according to correlation studies. Characters like the number of female

flowers per vine, the number of fruits per vine, the average weight of fruit, crop duration, average length of fruit and average diameter of fruit should be emphasized when identifying high producing genotypes.

Tiwari *et al.* (2021) reported for all traits, the phenotypic coefficient of variance was greater than the genotypic coefficient of variance in fifteen cultivars of bitter melon (*Momordica charantia* L.). Fruit yield per plant (g) and number of branches per plant had the highest genotypic coefficient of variation (GCV). Fruit yield (96.89 q/ha) was found to have a high heritability. The number of days till first harvest (61.00) revealed that modest heritability. Fruit yield (62.13 q/ha) had the highest genetic advance in per cent of the mean.

2.3 Genetic divergence analysis

Genetic diversity is an essential requirement with the purpose of improving the crop via breeding. In breeding programmes, using a variety of parent's aids in the isolation of superior individuals recombinant cluster analysis and meterologyph analysis which are useful in selecting genetically distant parents. In advance segregation generations, genetic diversity affects a cross's inherent heterosis capability and the probability of attractive progenies.

D^2 statistics developed by P.C. Mahalanobis (1928) offers a scale of biological population divergence and the comparative contribution for every component feature to the overall divergence. D^2 analysis is useful in identification of divergent parent for use in the hybridization programmes. The D^2 analysis is only possible by replicated data. In D^2 analysis the genetic diversity is depicted by the cluster representing number of groups in which a population can be classified on the basis of D^2 statistics.

Varalakshmi *et al.* (1994) studied on 58 genotypes and analyses for genetic divergence in ridge melon genotypes for 19 quantitative characters. Mahalanobis (D^2) statistic was applied to study genetic divergence and Tocher's method was used to form the clusters. 58 genotypes were divided into five groups, although there was no correlation among geographical distances and genetic divergence in general. Cluster averages for total plant, sex ratio, fruit number per plant, fruit weight, and yield per plant all showed significant variance. Cluster-III was the most divergent from the other clusters, according to the inter-cluster D^2 values. A crossing scheme is outlined

for the development of an early, high yielding cultivar.

Mathew *et al.* (2001) reported on the genetic diversity of 28 bottle gourd germplasm obtained from various districts of Kerala, India, was investigated. During 1998-99, Mahalanobis D^2 statistics were used to assess the genetic divergence of accessions. Accessions were classified into eight groups based on D^2 values of 17 yield associated characteristics. The clustering pattern revealed there was no relationship among geographical distribution of germplasm and genetic divergence for such attributes that contributed the most to genetic divergence number of fruits, average fruit weight, vine length, and fruit set per cent.

Badade *et al.* (2001) observed in a collection of 20 different bottle gourd cultivars, genetic divergence was investigated using Mahalanobis D^2 statistics for 7 quantitative characteristics, including yield per vine (*Lagenaria siceraria* L.). The cultivars differ widely in nearly every aspect and they were classified into ten groups based on D^2 value comparisons. Vine length, number of branches, proportion of female flowers, fruits per vine, length and diameter of fruit and yield per vine all showed significant variation within and between clusters.

Islam (2004) analyzed the using D^2 and canonical analysis, genetic divergence across 42 bottle gourd genotypes from Bangladesh was reported in 2000. Five clusters were formed from the germplasm. There was no immediate connection among both geographic origin and genetic diversity. Cluster I and Cluster IV had the highest inter-cluster distance, while Cluster III and Cluster IV had the smallest. The most major sources to overall genetic divergence were primary branches per plant, fruit length and weight, number of fruits and yield per plant. D^2 analysis produced results that were also validated by canonical analysis. The germplasm in clusters I and II, which are the most divergent, represent potential parents for hybridization programme.

Karuppaiah *et al.* (2005) studied divergent analysis in ridge gourd (*Luffa acutangula*) genetic divergence was evaluated in 12 genotypes of ridge gourd, Using the Mahalanobis D^2 method. The genotypes were divided into four groups: I (four genotypes), II (one genotype), III (three genotypes) and IV (four genotypes) (4 genotypes). Cluster-IV (LA-7, LA-9, LA-10, and LA-12) had the highest mean values for vine length (6.20 m), number of male flowers per plant (79.30), number of female flowers per plant (23.20), yield per plant (5.20 kg), single fruit weight (242.20g), fruit

length (29.40 cm), number of fruit per plant (24.10), number of seeds per fruit (52.30), fruit size index (173.20), fruit size index (173.20), and (18.60 g). As a result, LA-7, LA-9, LA-10, and LA-12 from Cluster IV should be included in the breeding effort.

Dey *et al.* (2007) observed in the 17 characters, investigators used 38 genotypes, including two potential gynoecious lines, to investigate genetic divergence in bitter gourd. Regardless of geographical difference, these genotypes were classified into six groups, demonstrating that geographic as well as genetic diversity are not related. Cluster IV was very large containing 17 genotypes including some of the commercially released cultivars, while cluster IV was represented by two gynoecious lines. Cluster II and IV had the greatest inter-cluster distance, whereas cluster II and VI had the smallest gap. Cluster IV outperformed cluster III in terms of yield and other desired qualities, indicating that these varied genotypes collection has the potential to provide fundamental material for future breeding programmes, since cluster III contained the majority of commercially marketed cultivars.

Sundaram and Vadivel (2007) found in the genetic divergence investigation, 22 bitter gourd genotypes collected from various geographical areas under saline soil indicated a high level of genetic variety, forming six clusters. There was no parallelism between geographical diversity and genetic diversity among the genotypes tested, according to the clustering pattern of genotypes. Cluster-I had the most genotypes, with 14 in total, whereas clusters V and VI each had only one genotype. Clusters IV and V, as well as clusters I and V, had the greatest inter-cluster distances.

Sundaram (2008) observed in the 22 genotypes of bitter gourd, study examined at the nature and magnitude of genetic divergence. The findings indicated a wide range of genetic variability. Tocher's method was used to divide the genotypes into six groups based on Mahalanobis D^2 statistics. The genotype clustering pattern indicated that genetic diversity was unaffected by geographical variety. Cluster I had the most genotypes of the six clusters, whereas clusters V and VI were mono-genotypic. Average fruit weight contributed the most to the divergence of the 14 quantitative characteristics investigated, contributing for 26.83 percent followed by yield of fruits per vine and fruit length. The ability to select parents for heterosis breeding based on intra-cluster mean performance for these characters, which are major contributors to

genetic diversity, was revealed by ranking genotypes based on intra-cluster mean performance for these characters, which are major contributors to genetic diversity.

Islam *et al.* (2010) studied on the Mahalanobis D^2 and principal component analysis were used to investigate the genetic divergence of twenty genotypes of bitter gourd. All genotypes undergoing investigation are divided into four groups. The cluster with the most genotypes, Cluster I had a total of ten. Cluster IV has the smallest number of genotypes. Cluster II had the greatest mean weight per fruit value. Inter-cluster distances were much greater than intra-cluster distances. Cluster I has the most intra cluster distance, whereas Cluster III has the smallest distance. The distance between clusters I and II was the greatest, while the gap between clusters II and IV was the smallest. Cluster II had the greatest intra cluster means for weight per fruit and five significant yield contributing characteristics. As a result, greater attention should be placed on the cluster for selecting varied genotypes as parents for crossing with cluster II genotypes, which may result in novel recombination with desirable characteristics. Taking into account all of the characters, the G_1 (Shaparan), G_5 (Rampali gaj), G_9 (Nabil), and G_{12} (Shaparan) (Nandita). For the future breeding programme, G_{14} (Eureca), G_{16} (Tia) and G_{19} (Maharaj) were identified.

Quamruzzaman *et al.* (2011) studied on the cluster analysis was performed on Bangladesh 20 local genotypes of sponge gourd. The genotypes were divided into five groupings, ranging from two genotypes in cluster IV to six genotypes in cluster III. The inter-cluster distance was always higher than the intra-cluster distance, indicating that the genotypes of disparate groups had more genetic variation. Cluster II and IV genotypes had the highest inter-cluster distance (22.353) followed by cluster I and II (15.819). While, genotypes of cluster I and V had the smallest (4.504). Cluster II had the maximum intra cluster number (0.803), owing to genetic divergence.

Yadav *et al.* (2011) evaluated the 30 genotypes of sponge gourd germplasm were grouped into VI cluster. For 11 characters, the various clusters revealed significant variations in intra-cluster group means. Cluster VI had the highest cluster mean for fruit output per plant, followed by Cluster III. The highest direct influence on fruit output per plant suggested that these qualities should be prioritized in the selection process. In divergence analysis, major cluster III comprised 13 genotypes of various origins, suggesting that there is no parallelism between genetic and geographic

diversity. As a result, activities among cluster members separated by large inter-cluster distances are likely to create desirable segregates.

Khule *et al.* (2012) reported on 30 genotypes of sponge gourd genotypes were examined and classified into four groups. In general, the clustering pattern suggested that geographical origin cannot be used as the primary criterion for genetic diversity, as genotypes from various origins were clustered together in a single cluster. Cluster IV (12 genotypes) had the most genotypes, followed by clusters II and III (7), while cluster I had four genotypes. Cluster II had the greatest intra-cluster separation (2.637). Cluster I and Cluster IV (5.080) had the greatest inter-cluster distances, followed by Cluster I and Cluster II (5.080). (4.726). The results showed that when selecting genotypes for hybridization from various clusters, inter and intra-cluster distances, cluster means for fruit production and its components should be considered. Marketable fruit production per plant (35.40), days to first male bloom (20.22), fruit length (18.62), and 100-seed weight (11.26) all contributed the most to overall genetic divergence, according to the study.

Kundu *et al.* (2012) observed that the some methods of genetic divergence like a PCA, PCO, CVA, Cluster analysis (CLSA) and Mahalanobis analysis were used to assess genetic divergence among 36 genotypes of bitter gourd (*Momordica charantia* L.). 36 genotypes were sorted into six remote groups using multivariate analysis based on 22 characteristics. PCA was also used to analyse the genetic diversity of 36 genotypes. 60.04 percent of the overall variance was accounted for by the first three components. The days to the first male flower opening, the number of primary branches per vine, the fruit production per vine, the days to green fruit maturity, and the seed weight per fruit mature seed width had the most impact on the divergence.

Resmi *et al.* (2012) evaluate on the genetic diversity of 33 bitter gourd genotypes from various geographical origins. The Mahalanobis statistic study revealed that there was no relationship among genotype frequency and genetic divergence depending on the clustering pattern. The completely distinct and improved lines were genetically differentiable, according to the cluster based on quantitative data. The grouping pattern based on variance in yield related characteristics was remarkable.

Singh *et al.* (2014) analyzed multivariate analysis based on cluster and principal component (PC) for yield and During the summers of 2011 and 2012, eleven

germplasm characteristics in 32 bitter gourd genotypes, including two checks, Pusa Do Mausami and Kalyanpur Sona. Cluster V (NDBT-12) and Cluster VI had the greatest average inter cluster distance (717.86). (NDBT-76). Fruit weight and fruit length each contributed 74% and 13% to genetic divergence, respectively. Cluster V had the highest mean values for fruits per plant, fruit weight (g), and fruit production per plant (kg), followed by Cluster II. The main 6 components (PC 1, PC 2, PC 3, PC 4, PC 5 and PC 6) contributed for 83.19 percent of the total variation, with proportionate contribution values of 23.88, 16.81, 13.28, 11.23, 9.38, and 8.61 percent, respectively, according to principal component analysis. The first PCA has a positive relationship with the number of nodes between the anthesis of the first staminate flowers and the days until first fruit harvest, but a negative relationship with fruit weight (g) and fruits per plant.

Ghosh *et al.* (2015) estimated the genetic diversity in different characteristics, such as fruit yield, between genotypes. Cluster II had the greatest cluster mean for vine length, nodes per vine, branches per vine, days to first male and female flowering, weight per fruit, and yield per plant, while days to first male and female flowering were the most relevant yield contributing feature. In terms of genetic distance, cluster mean for various characteristics and field performance, the genotypes G₂, G₅, G₁₄, G₁₅ from cluster II, genotypes G₁ and G₃ from cluster I, genotypes G₈ and G₉ from cluster III and genotypes G₁₀, G₁₁, G₁₃ from cluster IV are appropriate for future hybridization programme.

Kumari *et al.* (2017) reported on Mahalanobis D² statistics were used to investigate genetic divergence between 16 genotypes of bitter gourd (*Momordica charantia* L.) for 16 yield attribution traits. On the basis of D² value comparisons, the genotypes were divided into six groups. Cluster I had the most genotypes (6) followed by cluster II, cluster III and cluster IV (3 genotypes). While, cluster V had only one genotype. Cluster I (2411.503) had the maximum intra-cluster distance, while Cluster V had the minimum intra-cluster distance. Because of their better mean performance within group, genotypes from cluster I might be utilised as parental lines in a hybrid breeding programme. Cluster V and Cluster I had the largest inter cluster distance, indicating that the genotypes in these two groupings were more genetically diverse.

Tyagi *et al.* (2017) worked to identify the nature and degree of genetic diversity

between 31 genotypes of bitter gourd Tocher's technique divided all bitter gourd genotypes into six different groups based on D₂ values. Cluster IV has the most genotypes (seven), followed by cluster V. The distances between clusters were greater than the distances between clusters. Cluster III and VI had the greatest inter-cluster distance (58.37) followed by Cluster II and VI showing that members of these two clusters are genetically significantly different. Cluster I had the greatest intra-cluster distance (18.42) which was followed by Cluster V. In most biometric characteristics, clusters IV, III, and II outperformed clusters I and II. Vine length followed by fruit diameter and average fruit weight, contributed the most to genetic difference (34.41 percent) among some of the 12 variables investigated in bitter gourd. The ability to select parents for heterosis breeding was shown by ranking genotypes based on intra-cluster mean performance for the characters, which are important contributors to genetic diversity.

Maurya *et al.* (2018) evaluated the Mahalanobis D₂ statistics were used to analyse the thirty genotypes of bitter gourd. Thirty genotypes were divided into six non-overlapping groups. Cluster III contained the most genotypes (8), followed by cluster II (7), cluster V (6), cluster IV (5), and cluster I, VI (2), with just two genotypes in each cluster. Cluster VI had the largest intra-cluster distance (123.61), followed by cluster V (91.85), cluster I (69.08), and cluster II (62.75), and cluster IV (62.75). (47.92). Clusters III and VI had the greatest inter-cluster distance (231.577) which suggested that members of these two clusters are genetically very diverse to each other.

Angadi *et al.* (2018) analyzed the Tocher's technique was used to divide genotypes into ten groups based on Mahalanobis D₂ statistics. The genotype clustering pattern indicated that genetic diversity was unaffected by geographical variety. Cluster I had the highest number of genotypes among the ten clusters. The rind thickness contributed the most to the divergence among the 19 quantitative characteristics investigated, accounting for 35.01 percent, followed by fruit production per vine. The ability to select parents for heterosis breeding based on intra cluster mean performance for these characters, which are major contributors to genetic diversity, was revealed by ranking genotypes based on intra cluster mean performance for these characters, which are major contributors to genetic diversity.

Singh *et al.* (2019) revealed that cluster VI had the greatest mean values for vine length (m), node count per vine, primary branch count per plant, and fruit length (cm). Both in cluster I and VI, would provide a strong opportunity for crop enhancement through a hybrid breeding programme based on rational selection. Characters such as average fruit production per plant (41.27 percent), number of fruits per plant (11.38 percent), and node number to anthesis first staminate flowers (11.38 percent) contributed the most to genetic divergence and therefore had a significant influence in sponge gourd progress.

Singh *et al.* (2020) studied on clustering technique was used to arrange 40 bitter gourd genotypes into six groups. Cluster II had the most genotypes (19), followed by cluster II, which had 13 genotypes, and clusters III and IV, which each had three genotypes. Mono-genotypic clusters V and VI were discovered. The intra-cluster divergence and inter-cluster divergence were calculated. Intra-cluster divergence varied between 0.00 and 43.68. Cluster IV had the highest intra-cluster divergence (43.68), followed by Cluster II (41.32) and Cluster I (40.30). (38.85). Clusters V and VI exhibited the lowest intra-cluster divergence, with a value of 0.00. Clusters I and VI had the highest inter-cluster divergence (88.84), whereas clusters II and IV had the lowest divergence (51.97). Fruit yield per vine had the greatest mean value (2.22) in Cluster III. Cluster I, on the other hand, had the lowest mean value (0.71).

Materials
&
Methods

MATERIALS AND METHODS

The experiment of the present research work entitled “Studies on genetic variability, heritability, correlation and path analysis in bitter gourd (*Momordica charantia* L.)” was undertaken at the field of Horticulture Research Farm-I in front of Gautam Buddha Central Library, Department of Applied Plant Science (Horticulture), School for Biosciences and Biotechnology, Babasaheb Bhimrao Ambedkar University (A Central University), Vidya Vihar, Rae Bareli Road, Lucknow (U.P.), India during the summer season of 2018-19 and 2019-20, respectively. The details materials used method followed and the technique adopted during the period of experimentation have been described here under:

3.1 Experimental site and climatic condition:

The field experiment was conducted at Horticultural Research Farm-I in front of Gautam Buddha Central Library, Department of Applied Plant Science (Horticulture), School for Biosciences and Biotechnology, Babasaheb Bhimrao Ambedkar University (A Central University), Vidya Vihar, Rae Bareli Road, Lucknow-226 025 (U.P.), India was undertaken during the summer season 2018-2019 and 2019-2020. Geographically, Lucknow is situated at 26° 76' North latitude, 80° 92' East longitudes and elevation of 123 meters above mean sea level (MSL). The climate of the experimental site is subtropical with maximum temperature ranging from 19°C to 40°C in summer and 5.5°C to 19°C in winter and relative humidity ranging from 60-90% in different seasons of the year. In general, the climate of Lucknow is characterized as sub-tropical climate with hot and dry summer season and cold winter. The average annual rainfall is 750 mm and 72.5 percent relative humidity in the year. Meteorological data during the experimental period has been given in Table-3.1.

Table-3.1.A Weekly meteorological parameters during the cropping period experimentation 2018-19 (Feb. 2018 to July 2018)

Periods 2018-19		Standard weeks	Mean temperature (°C)		Relative Humidity (%)	Wind Velocity (Km/hr)	Total Rainfall (mm)
Month	Date	Weeks	Max.	Min.			
Feb.-	12-18	07	23.6	10.4	73.5	2.3	0.0
Mar. 2018	19-25	08	26.4	11.3	67.5	3.6	0.0
	26-04	09	23.6	9.5	71.0	2.9	0.0
	05-11	10	27.5	10.9	63.0	4.4	0.0
	12-18	11	30.5	13.1	54.0	4.1	0.0
Apr. 2018	19-25	12	32.1	15.0	49.0	5.5	0.0
	26-01	13	34.7	17.0	51.0	3.9	0.0
	02-08	14	35.6	18.3	54.5	3.0	0.0
	09-15	15	38.1	21.4	48.0	3.2	0.0
Apr.- May 2018	16-22	16	34.3	18.7	49.5	4.7	0.0
	23-29	17	40.0	23.9	39.0	3.1	0.0
	30-06	18	40.3	22.8	38.0	3.9	0.0
	07-13	19	42.3	25.3	26.0	6.7	0.0
May- June 2018	14-20	20	39.1	23.2	37.5	5.1	0.0
	21-27	21	41.5	24.7	35.5	5.6	0.8
	28-03	22	41.9	24.2	44.0	3.7	0.0
	04-10	23	40.1	25.4	50.5	2.4	2.0
June- July 2018	11-17	24	40.9	26.6	49.0	5.7	0.0
	18-24	25	36.5	25.7	61.0	4.6	0.6
	25-01	26	39.5	26.3	61.0	3.3	0.6

Source: ICAR-Indian Institute of Sugarcane Research, Lucknow, (U.P.)

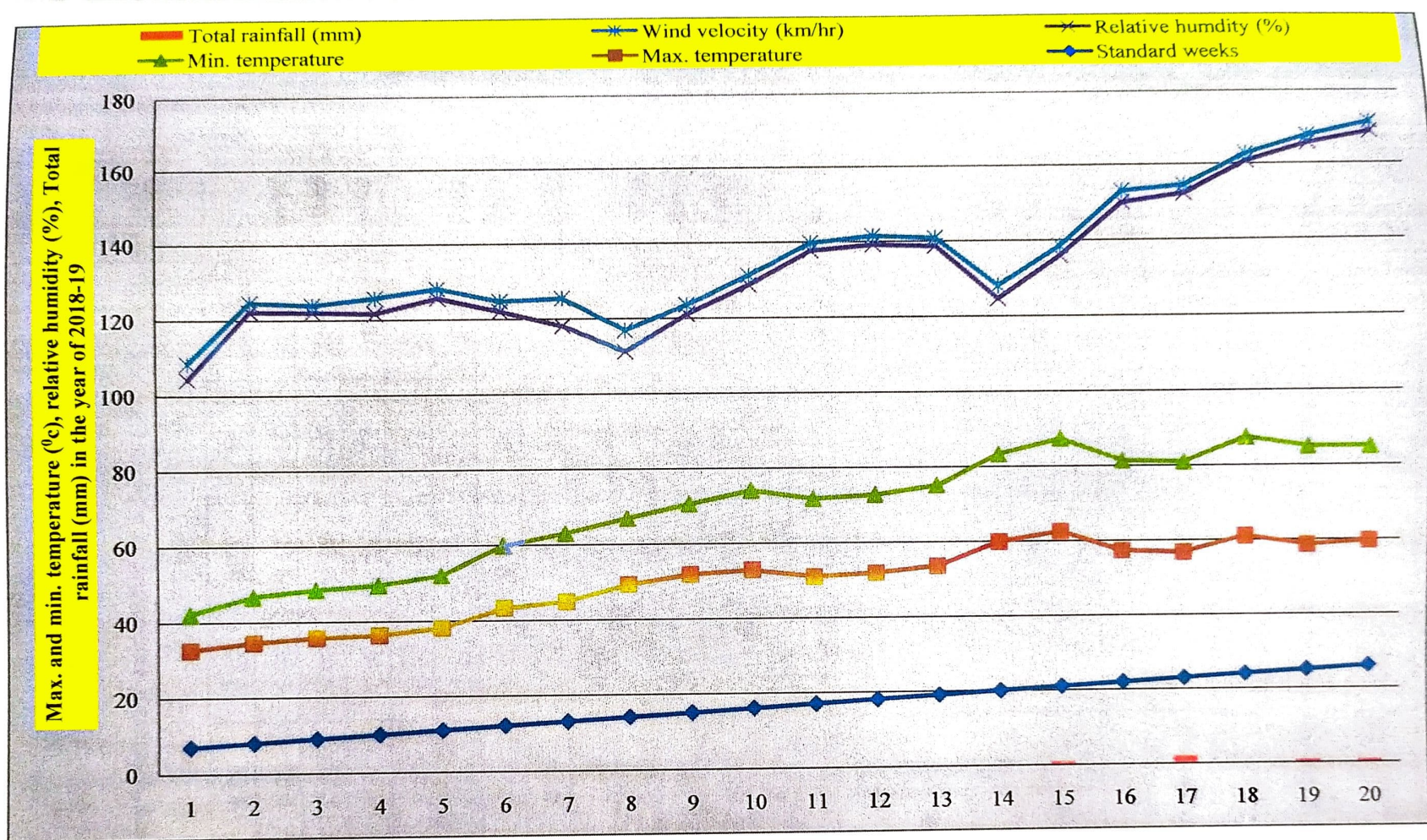


Fig-1. Weekly meteorological parameters during the cropping period of experimentation 2018-19 (Feb. 2018 to July 2018)

Table-3.1.B Weekly meteorological parameters during the cropping period experimentation 2019-20 (Feb. 2019 to July 2019)

Periods 2019-20		Standard weeks	Mean temperature (°C)		Relative Humidity (%)	Wind Velocity (Km/hr)	Total Rainfall (mm)
Month	Date	Weeks	Max.	Min.			
Feb.-	12-18	07	25.6	9.5	62.1	4.3	0.0
2019	19-25	08	26.5	12.1	75.5	2.5	9.2
	26-04	09	26.7	12.7	73.6	1.9	0.2
	05-11	10	26.3	13.2	72.1	4.1	24.8
	Mar.-	12-18	11	27.0	14.0	73.6	2.5
2019	19-25	12	31.2	16.5	62.3	2.7	0.0
	26-01	13	31.8	18.1	55.1	7.4	4.8
	02-08	14	35.2	17.6	44.3	5.7	0.0
	Apr.-	09-15	15	36.8	18.7	50.5	2.5
2019	16-22	16	36.8	21.1	54.7	2.6	3.0
	23-29	17	33.9	20.8	65.9	2.1	11.0
	30-06	18	33.8	20.8	66.5	2.3	16.4
	May-	07-13	19	34.5	21.5	63.6	2.2
2019	14-20	20	39.8	23.4	41.3	3.5	0.0
	21-27	21	41.5	24.7	48.7	2.6	0.0
	28-03	22	35.3	24.0	68.6	3.1	54.0
	June-	04-10	23	33.7	24.2	71.3	2.2
2019	11-17	24	37.0	26.4	73.3	2.0	3.8
	18-24	25	33.6	26.3	80.6	2.0	14.4
	25-01	26	33.6	25.3	83.6	2.7	26.0

Source: ICAR-Indian Institute of Sugarcane Research, Lucknow, (U.P.)

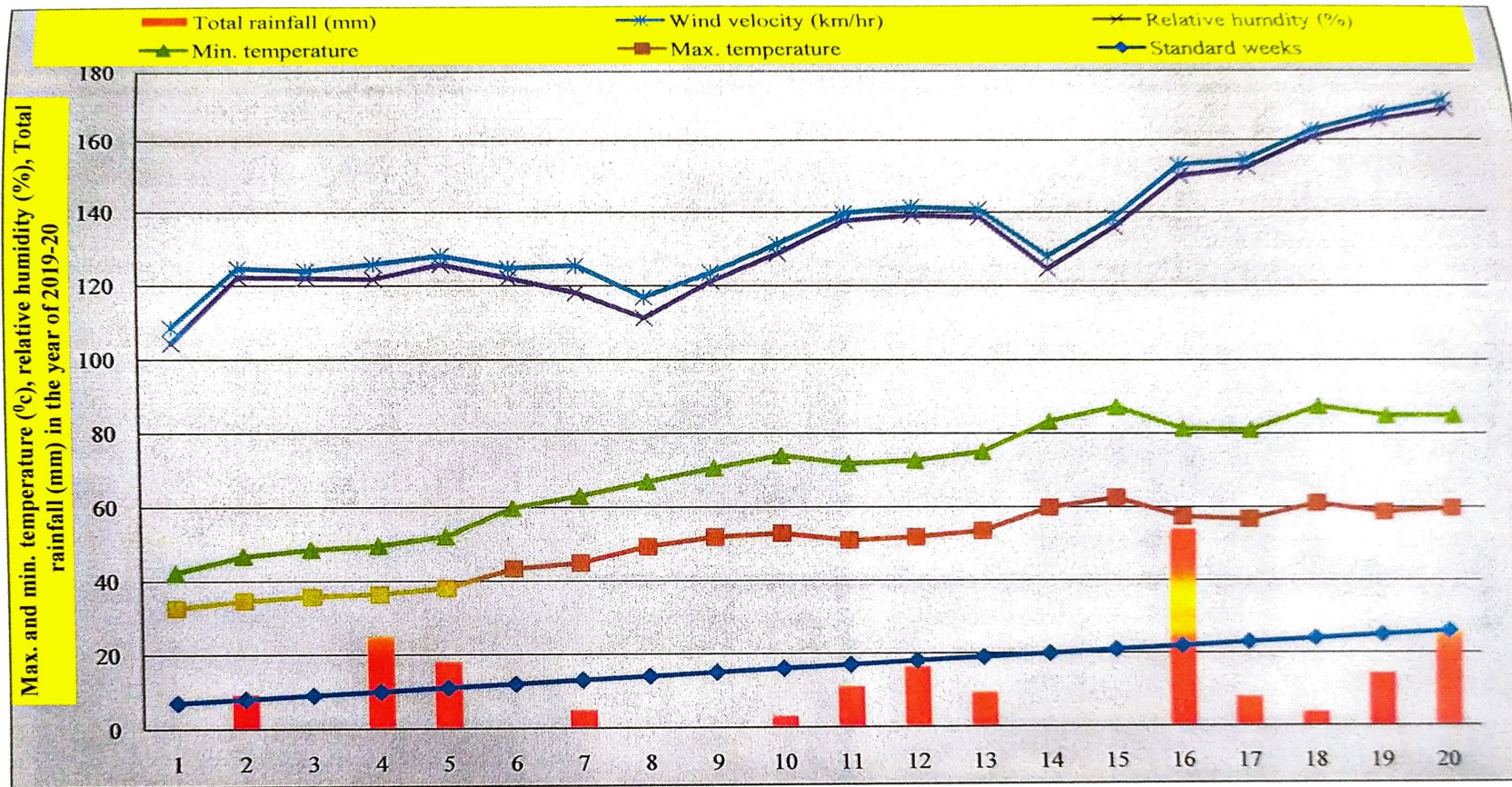


Fig-2. Weekly meteorological parameters during the cropping period of experimentation 2019-20 (Feb. 2019 to July 2019)



Fig.-1: Preparation of layout of experimental field



Fig.-2: Complete layout plan of experimental field

3.2 Soil status of experiment area:

The soil of experimental field is sandy clay loam and slightly alkaline in nature with the soil pH 8.2. The physical and chemical properties of soil have been presented in Table 3.2.

Table 3.2 Physical and chemical properties of soil:

A. Physical properties of soil			
S. No.	Soil Particle	Percentage	Method of Determination
1	Sand	34.50	Hydrometer method (Block, 1965)
2	Silt	50.20	
3	Clay	15.30	
4	Texture class	Sandy loam	Triangular method (Sigmoid, 1928)
B. Chemical properties of soil			
S. No.	Component	Amount	Method of determination
1	Available N ₂ (Kg/ha)	110.50	Kjeldahl's method (A.O.A.C., 1980)
2	Available P ₂ O ₅ (Kg/ha)	40.50	Olsen's method (Jackson, 1983)
3	Available K ₂ O (Kg/ha)	190.40	Flame photometer (Jackson, 1983)
4	Organic carbon (%)	0.12	Rapid titration method (Jackson, 1983)
5	pH	8.6	Glass electrode, pH meter (Jackson, 1983)
6	E.C (1:1)	0.26	Conductivity meter (Jackson, 1983)
7	E.S.P.	14.80	Conductivity meter (Jackson, 1983)



Fig.-3: A general view of planting of bitter gourd genotypes



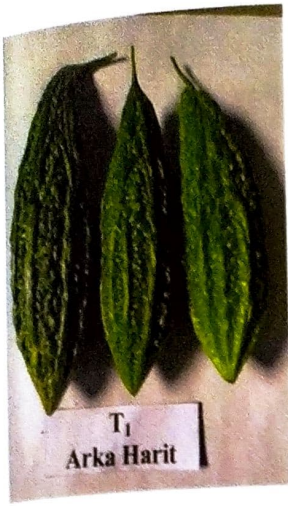
Fig.-3.1: Planting work of seedlings in the experimental field

3.3 Experimental material:

The experimental materials for the present investigation comprised of twenty genotypes of bitter gourd collected from different sources. The details of the materials are given in the Table 3.3.

Table-3.3: List of genotypes and their source of collection

S. No	Symbol	Genotype	Institute
1.	G ₁	Arka Harit	IIHR, Bangalore
2.	G ₂	Pusa Vishesh	IARI Pusa, New Delhi
3.	G ₃	Narendra Brarahmasi-1	N.D.U.A.&T, Kumarganj, Ayodhya
4.	G ₄	Kalyanpur Sona	C.S.A.U.A.&T, Kanpur
5.	G ₅	Pusa Hybrid-1	IARI Pusa, New Delhi
6.	G ₆	Sagar	VNR Seeds Private Limited
7.	G ₇	Kalyanpur Barahmasi	C.S.A.U.A.&T, Kanpur
8.	G ₈	Kashi Urvasi	IIVR, Varanasi
9.	G ₉	Arka Sujat	IIHR, Bangalore
10.	G ₁₀	Amanshri	IIVR, Varanasi
11.	G ₁₁	Meghana-2	IIVR, Varanasi
12.	G ₁₂	US-475	Nunhems Seeds Private Limited
13.	G ₁₃	Pusa Hybrid-2	IARI Pusa, New Delhi
14.	G ₁₄	Narendra Barahmasi-2	N.D.U.A.&T, Kumarganj, Ayodhya
15.	G ₁₅	Selection-5	IIVR, Varanasi
16.	G ₁₆	VRBT-23	IIVR, Varanasi
17.	G ₁₇	UDIT-008	Noble Seeds Private Limited
18.	G ₁₈	Ultima-1405	Noble Seeds Private Limited
19.	G ₁₉	US-484	Nunhems Seeds Private Limited
20.	G ₂₀	MC-23	IIVR, Varanasi



T₁
Arka Harit



T₂
Pusa Vishesh



T₃
Narendra
Barahmasi-1



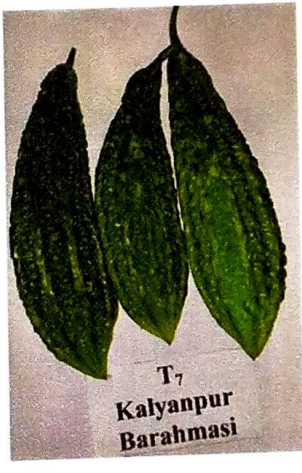
T₄
Kalyanpur
Sona



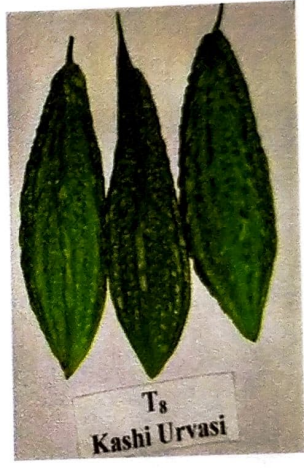
T₅
Sagar



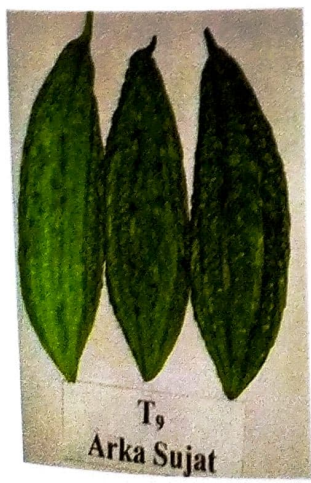
T₆
Pusa Hybrid-1



T₇
Kalyanpur
Barahmasi



T₈
Kashi Urvasi



T₉
Arka Sujat



T₁₀
Amanshri



T₁₁
Meghana-2



T₁₂
US-475

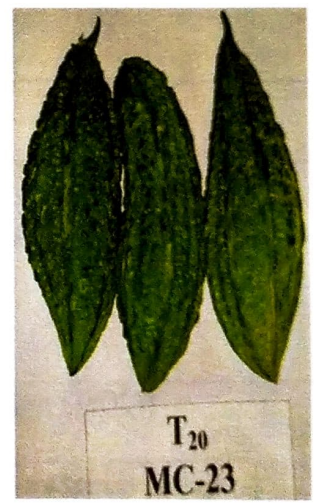
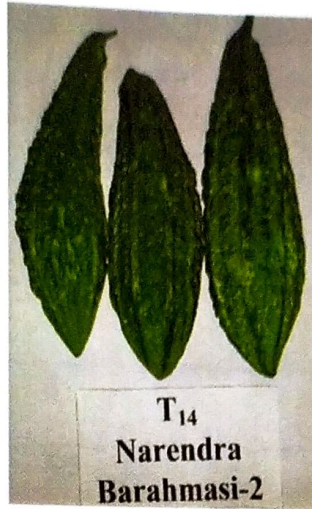


Fig.-4: A general view of different genotypes of bitter gourd

3.4 Details of Experimental Layout:

Location	Horticulture Research Farm-I in front of Gautam Buddha Central Library
Name of crop	Bitter gourd (<i>Momordica charantia</i> L.)
Season	Summer seasons (2018-19 and 2019-20)
Planting time	12 February 2018-19 and 2019-20
Number of genotypes	20
Replication	3
Total plots	60
Spacing (row to row x plant to plant)	2.5 m x 0.5 m
Gross plot size	3.20 m x 2.20 m
Net plot size	3.0 m (L.) x 2.0 m (W.)
Irrigation channel	0.5 m
Number of plants per plot	12
Total number of plants in entire experimental field	720
Design	Randomized Block Design (RBD)
Irrigation	At 5-7 days interval and as when required
Weed control	Hand weeding and hoeing at 20 days interval.
Crop duration	110-120 days.



Fig.-5: A general view of flowering and fruiting stages of bitter melon genotypes



Fig.-6: View of fruits weight (g) of bitter melon being recorded in lab.

Layout of the Experimental field:

R₁, R₂, R₃:

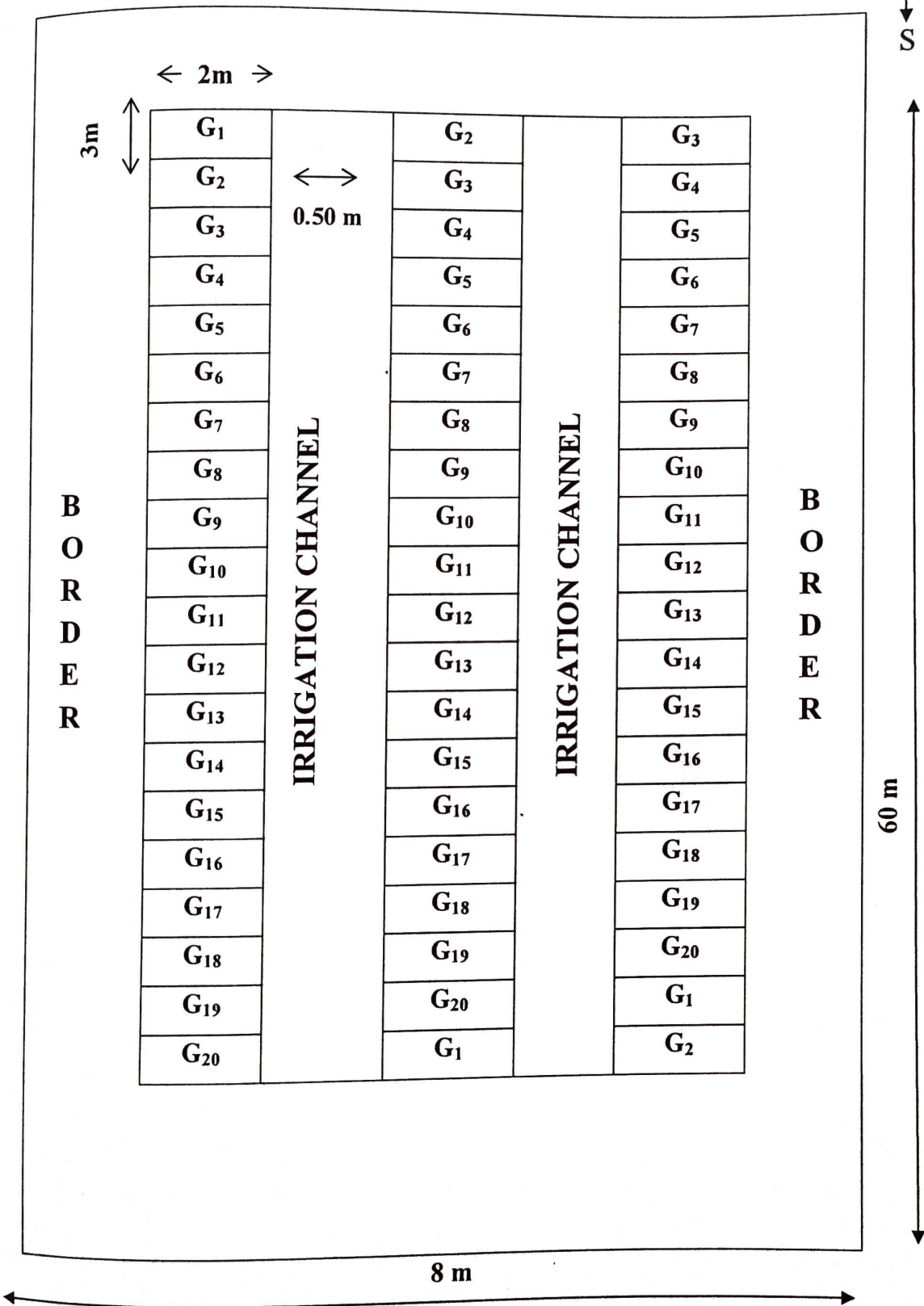
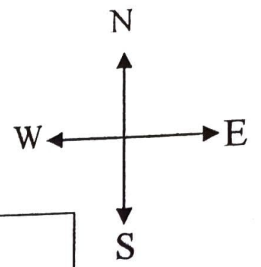




Fig.-7: View of fruit diameter (cm) being recorded on bitter gourd in lab.



Fig.-8: A general view of fruits length (cm) of bitter gourd is being measured in lab.

3.5 Agronomical practices:

Field preparation:

The experimental field was ploughed well up to depth 15-20 cm with the help of harrow and Power tiller and exposed to sun for at least 15 days for killing the weeds and eggs of insect- pest. Again two ploughing followed by planking was done to obtain fine tilth. Required area was marked and prepare according to the layout plan.

Manure and Fertilizers:

The recommended dose of fertilizers was applied to the experimental field i.e. 20:15:15. NPK per meter square was applied before planting in experimented field and half dose of nitrogen, full dose of phosphorus and potash was thoroughly mixed in the soil at the time of preparation of bed. The remaining half dose of nitrogen was applied one month after sowing of plant crops.

Irrigation, weeding and hoeing:

After 15 days planting of plant following light watering was done for better establishment of all plants. After establishment of plants field was irrigated at 7-10 days interval throughout the cropping period. Bitter gourd crop is a shallow rooted crop; therefore, shallow hoeing were done twice manually for weed control.

After care:

After establishment of plants uniform cultural operations were performed regularly in each plot to maintain the plants in proper health. The control measure for insect pest and disease were also taken from time to time.

Plant protection measure:

To protect the damping off in early stage of the crop. Soil drenching with carbendazim at the rate of 0.2% was done one week before sowing and seed treatment with Thiram pre sowing of the seed. To protect from Powdery mildew and Root-knot



Fig.-9: A general view of vine length (m) of bitter gourd

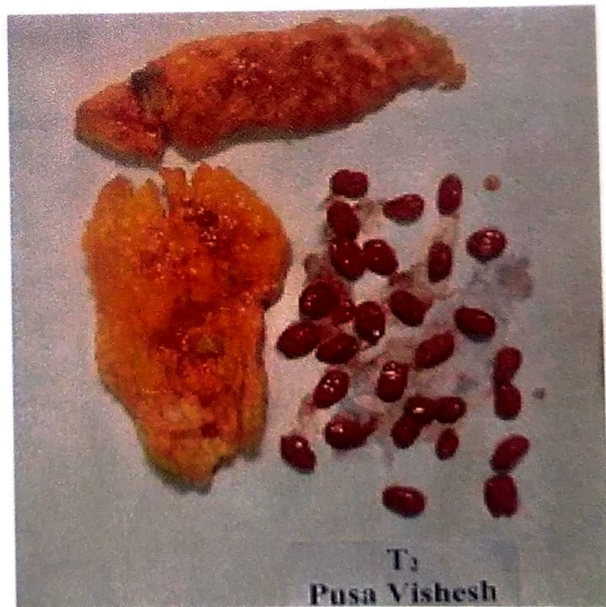
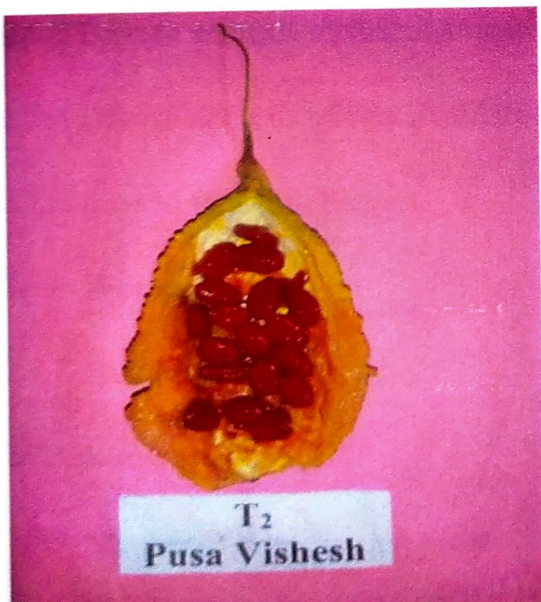


Fig.-10: A general view of number of seeds per fruit of bitter gourd

nematode field was treated with thimet 10 G @ 12 kg of granules per hectare while for the red pumpkin beetle of the crop was also sprayed with carboxyl @ 0.5%.

Harvesting:

Bitter gourd took about 100-120 days for maturity. The crop was ready to harvest, when, the immature fruit of the crop. Harvesting of crop was done in morning hours by hand picking.

3.6 Observations were recorded:

Observations were recorded on five randomly selected plants from each genotype in each replication. The observations recorded on the five plants were summed up and divided by five to get mean value. The procedure is described under the respective sub-heads:

3.7 Physical characters:

3.7.1. Node number to first staminate flowers

3.7.2. Node number to first pistillate flowers

3.7.3. Days to anthesis of first staminate flowers

3.7.4. Days to anthesis of first pistillate flowers

3.7.5. Days to first fruit harvest

3.7.6. Vine length (m)

3.7.7. Fruit length (cm)

3.7.8. Nodes per plant

3.7.9. Number of branches per plant

3.7.10. Number of seeds per fruit

3.7.11. Fruit diameter (cm)

3.7.12. Number of fruits per plant

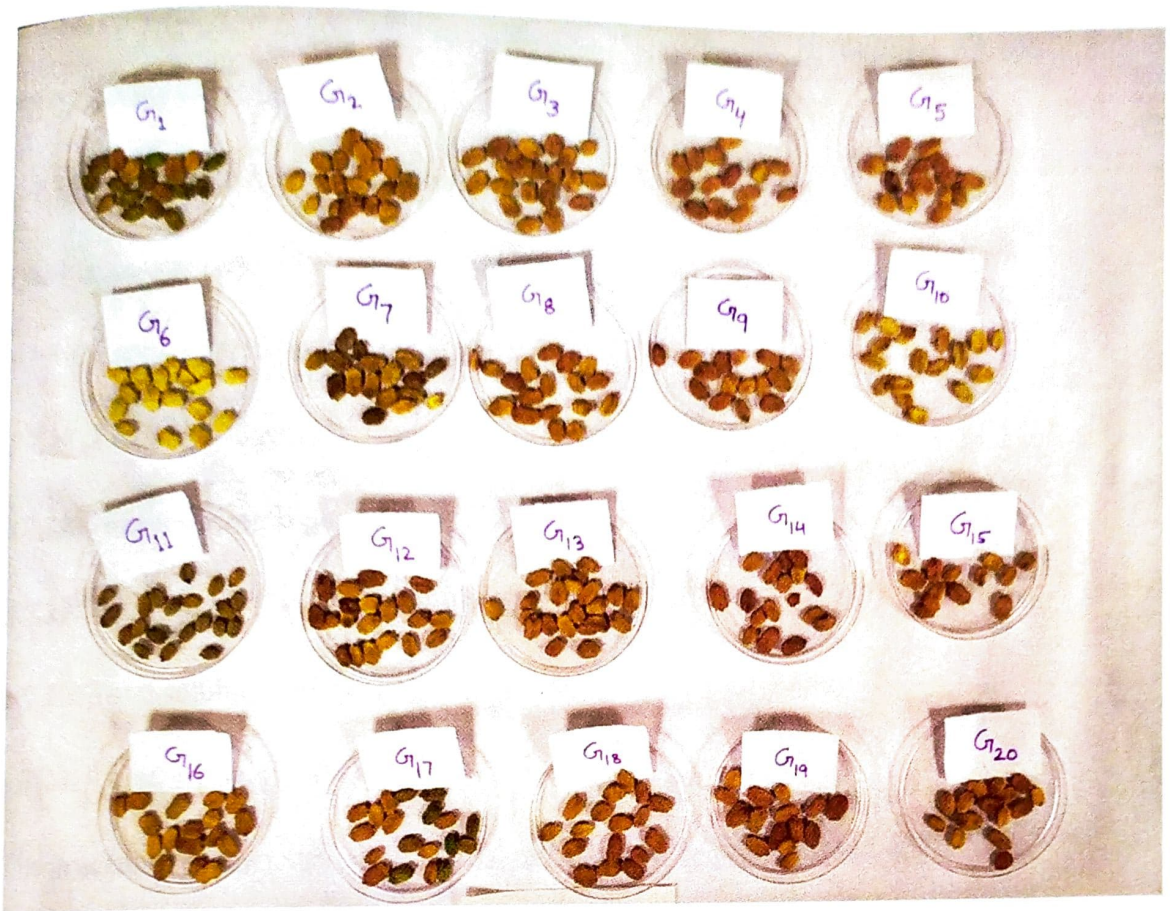


Fig.-10.1: An overview of number of seeds per fruit recorded in different genotypes of bitter gourd



Fig.-11: Showing seeds weight per fruit (g)

3.7.13. Average fruit weight (g)

3.7.14. Seeds weight per fruit (g)

3.7.15. Marketable fruit yield per plant (kg)

Quality characters:

3.7.16. Ascorbic acid (mg/100g)

3.7.17. Reducing sugar (%)

3.7.18. Non-reducing sugar (%)

3.7.19. Total sugars (%)

3.7.20. Total soluble solids (T.S.S.) ⁰Brix

3.7.21. Titratable acidity (%)

The procedure of observations on different characters is described below.

3.7.1 Node number to first staminate flowers

The node number from the base of the plant at which first staminate flower opened was recorded as the node number to first staminate flowers.

3.7.2 Node number to first pistillate flowers

The node number from the base of the plant at which first pistillate flower opened was recorded as the node number to first pistillate flowers.

3.7.3 Days to anthesis of first staminate flowers

The number of days taken from sowing of seed to the opening of first staminate flower on a plant was recorded as days to anthesis of first staminate flowers.

3.7.4 Days to anthesis of first pistillate flowers

The number of days taken from sowing of seed to the opening of first pistillate flower on a plant was recorded as days to anthesis of first pistillate flowers.



Fig.-12: Showing of variability of fruits in bitter gourd genotypes



Fig.13: View of samples of fruit juices in various genotypes of bitter gourd

3.7.5 Days to first fruit harvest

It was recorded as number of days taken from the date of sowing to the date of first picking of marketable fruits from a plant of each plot.

3.7.6 Vine length (m)

The vine length of the plant was measured in meter from the ground level to the tip of the vine of plants of a plot at the time of last picking and divided it by number of plants per plot to get average vine length.

3.7.7 Fruit length (cm)

Fruit length of marketable fruits was measured on five randomly selected fruits from plants of a plot in each replication at the third and six picking of the fruits and length of each fruits was measured from perpendicular distance between the points of attachment of the stalk and the blossom end with the help of measuring tape in centimeters. The average fruit length was derived by summing of the length of all five fruits and dividing it by five.

3.7.8 Nodes per plant

All the nodes of plant were counted separately and summed at last harvesting of the crop and mean values were worked out.

3.7.9 Number of branches per plant

Total numbers of branches of each plant of a plot were counted at the time of last picking and mean value was worked out.

3.7.10 Number of seeds per fruit

The fruits were cuts opened and the total number of seeds per fruit was counted and recorded with the help of five randomly selected plants in each replication.

3.7.11 Fruit diameter (cm)

Diameter of fruits was recorded on same five fruits from plants of a plot in each replication on which fruit length was measured. The measurement of fruit diameter at the middle portion of the fruit was taken with the help of vernier calipers and the average

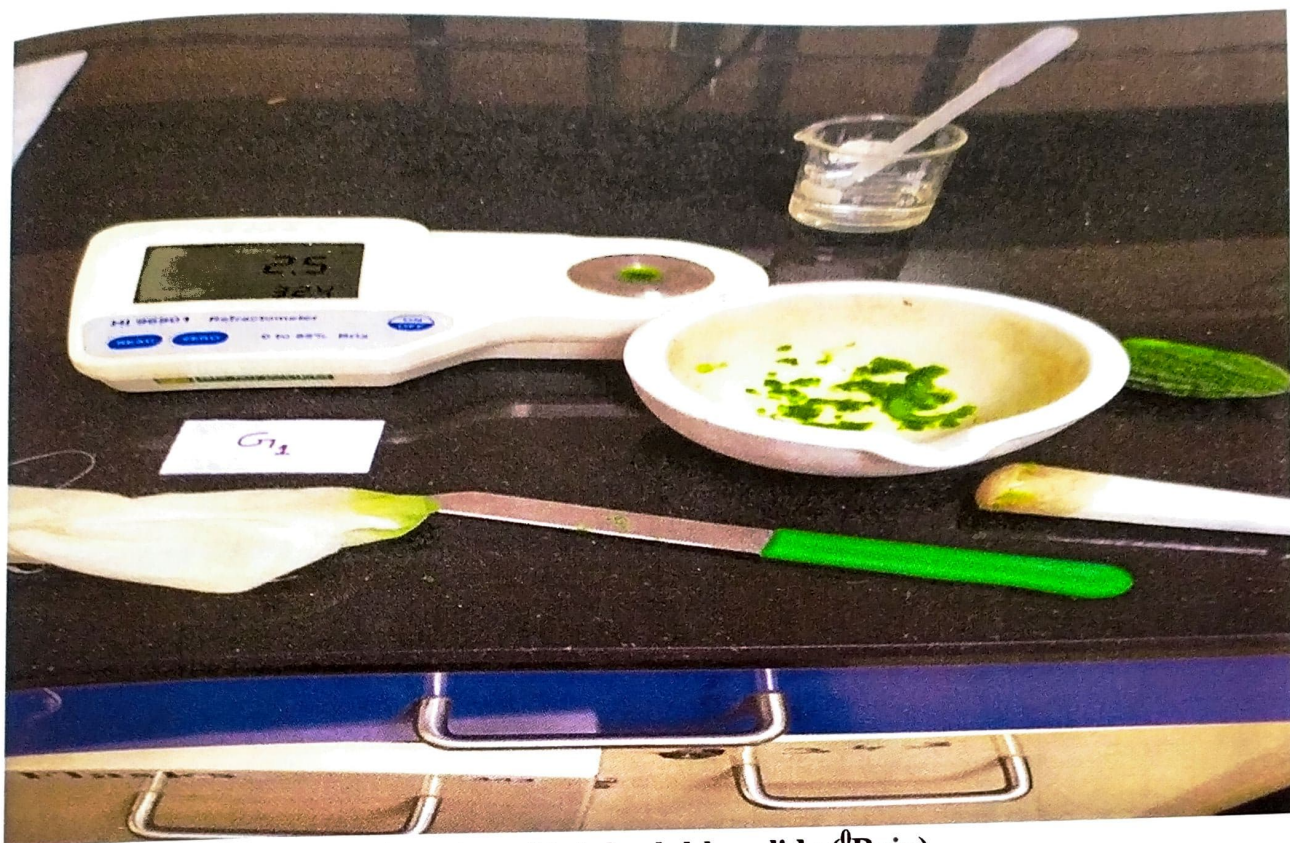


Fig.-14: Estimation of total soluble solids ($^{\circ}$ Brix)

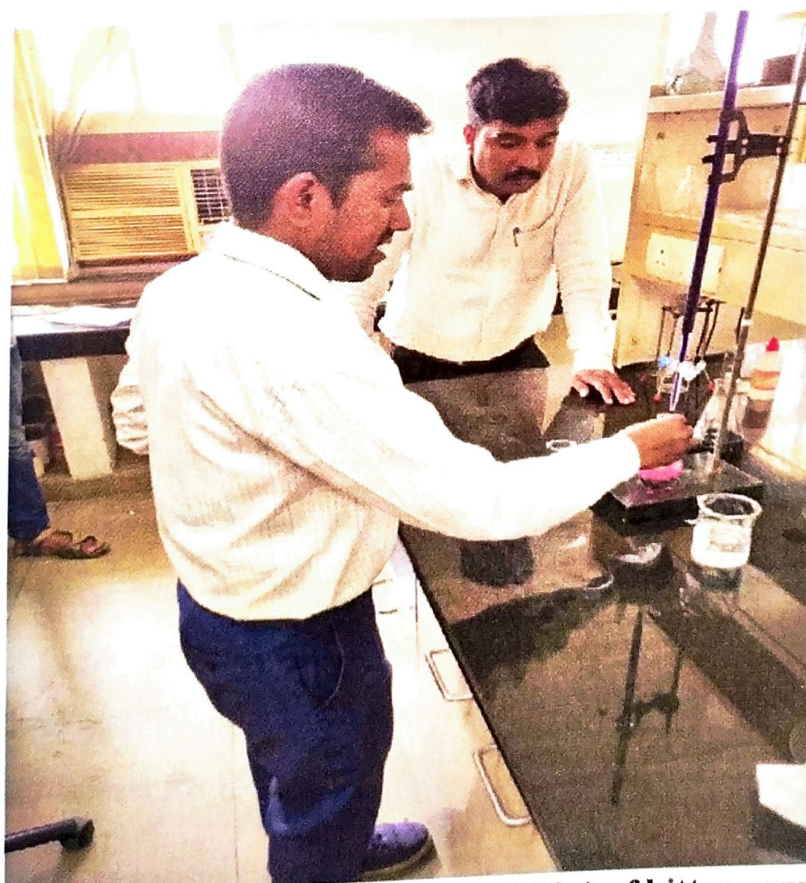


Fig.-15: Estimation of ascorbic acid (mg/100g) of bitter gourd fruits

fruit diameter was derived by summing of the diameter of all five fruits and dividing it by five.

3.7.12 Number of fruits per plant

Number of marketable fruits was counted at each picking and summed up for all the pickings for a plot. Number of fruits per plant was calculated after dividing total number of fruits in a plot by total number of plants in a plot.

3.7.13 Seeds weight per fruit (g)

The weight of randomly selected fruits is taken and then total numbers of seeds per fruit weights were calculated.

3.7.14 Average fruit weight (g)

Average weight of fruits was recorded on same five fruits of a plot in each replication on which fruit length and fruit diameters was measured and the average fruit weight was derived by summing of the individual weight of all five fruits and dividing it by five.

3.7.15 Marketable fruit yield per plant (kg)

The marketable fruit yield of all the pickings was recorded in kilogram for each plot and divided by total number of plants (6) to obtain fruit yield per plant (kg).

Quality characters

3.7.16 Ascorbic acid (mg/100g)

For determining the ascorbic acid, 5g fruit sample was crushed in pestle and mortar with 3 percent Metaphosphoric acid and filtered through muslin cloth in 50 ml volumetric flask. Then volume was made up of 50 ml with 3% HPO₃ (Metaphosphoric acid) solution. Then 5 ml aliquot was titrated against 2,6-dichlorophenol indophenol dye solution (A.O.A.C., 2000). The end point was marked by appearance of light pink colour which persisted at least for 15 second.

Preparation of 3% Metaphosphoric solution:

3% Metaphosphoric solution was made by dissolving exactly 30g of Metaphosphoric acid in 80 ml of acetic acid and adding to it 500 ml. distilled water and the volume made up to 1000 ml. filter the solution and store it.

Preparation of Dye solution:

50 mg of 2,6-dichlorophenol indophenol dye and 42 mg of sodium bicarbonate accurately on a balance. Dissolved both in 150 ml of distilled water. Heated the solution gently on water bath to make homogenous and raised the volume to 200 ml after cooling at room temperature. Transfer the solution in an air-tight brown container and stored in refrigerator.

$$\text{Dye Factor} = \frac{0.5}{\text{Titrate volume of standard ascorbic acid}}$$

The ascorbic acid content was expressed by mg/100g and calculated with the help of following formula:

$$\text{Ascorbic acid (mg/100g)} = \frac{\text{Titrate value} \times \text{Dye factor} \times \text{Volume made up} \times 100}{\text{Aliquot of extract taken for estimation} \times \text{Volume of sample taken for estimation}}$$

3.7.17 Reducing sugar (%)

10 ml fruit sample was taken and crushed with small amount of distilled water. The volume made up 100 ml with distilled water. 5 ml aliquot was taken into separate conical flask and 5 ml of each Fehling's solution A and B were mixed with aliquot. Thereafter, mixture was heated and titrated against 1 percent glucose (Dextrose) to the end point of brick colour appearance. A blank sample was also titrated against 1 percent glucose. The calculation for reducing sugar was expressed as percent.

$$\text{Reducing sugar (\%)} = \frac{\text{Blank titrate value} - \text{Aliquot value} \times \text{Volume made up}}{\text{Aliquot taken for estimation} \times \text{Weight of sample}} \times 100$$

3.7.18 Non-reducing sugar (%)

Non-reducing sugar was calculated by deducting the quantity of reducing sugar and multiplied by 0.95. The results were expressed by percent.

$$\text{Non-reducing sugar (\%)} = \text{Total sugar (\%)} - \text{reducing sugar (\%)} \times 0.95$$

3.7.19 Total sugars (%)

Sum of reducing sugar and non-reducing sugar was expressed in as total sugars.

$$\text{Total sugars (\%)} = \text{Reducing sugar} + \text{non-reducing sugar}$$

3.7.20 Total soluble solids (T.S.S. °Brix)

To determine the T.S.S of bitter gourd fruits were selected (10g), bitter gourd fruits were, hence were crushed to form a homogenized sample and then the juice was extracted through muslin cloth. The extract was used for determination of T.S.S. in °Brix by using digital refractometer. Few drops of juice were placed on the surface of refractometer. The reading was noted by revolving the eye piece at room temperature.

3.7.21 Titratable acidity (%)

Known quantity of the fruit pulp (5g) was mixed with small amount of distilled water and filtered through muslin cloth. Then volume was made up to 100 ml. Five ml aliquot was taken for titration against 0.1 N sodium hydroxide (NaOH) solution using 1-2 drops phenolphthalein as indicator. The results were calculated using following formula and expressed as percent acid per 100g fruit (Ranganna, 2010).

$$\text{Titrateable acidity (\%)} = \frac{\text{Titrateable value} \times \text{Normality of alkali} \times 64 \times \text{volume made up}}{\text{Aliquote taken} \times \text{volume of sample} \times 1000} \times 100$$

3.8 Statistical Analysis

The experimental data was compiled by taking the mean value of the 20 genotypes of bitter gourd for yield and its component traits from all the three replications. Then it was subjected to the following statistical analysis:

3.8.1. Analysis of variance for R.B.D. (Panse and Sukhatme, 1984).

3.8.2 Estimation of coefficient of variation (Burton and de Vane, 1952).

3.8.3. Estimation of heritability (Hanson *et al.*, 1963).

3.8.4. Genetic advance in per cent of mean (Johnson *et al.* 1955).

3.8.5. Estimation of correlation (Searle, 1961).

3.8.6. Path coefficient analysis (Dewey and Lu, 1959).

3.9.7. Genetic divergence (Mahalanobis, 1928).

3.9.1 Analysis of variance:

The analysis of variance for the design of experiment was carried out according to the procedure outlined by Panse and Sukhatme (1984). The significance of differences among treatment means was tested by 'F' test. To test the hypothesis $H_0: t_1 = t_2 = \dots = t_n$, the fixed effect model for the analysis of variance for Randomized Block Design is given below:

$$Y_{ij} = \mu + t_i + b_j + e_{ij}$$

Where,

Y_{ij} = Yield of i^{th} in the j^{th} replication

μ = General mean

t_i = Effect of the i^{th} entry ($i=1,2,\dots$)

b_j = Effect of the j^{th} replication ($j=1,2,\dots$)

e_{ij} = Environment effect.

3.9 ANOVA for the experiment:

Source of variation	Degree of freedom	Mean sum of Squares	F ratio
Replication	$r-1$	MSR	MSR/MSE
Treatments	$t-1$	MST	MST/MSE
Error	$(r-1) \times (t-1)$	MSE	
Total	$(rt-1)$		

Where,

r = Number of replications

t = Number of treatments

MSR = Mean square due to replications

MST = Mean square due to treatments

MSE = Mean square due to error

The mean square due to replications and treatments were tested against corresponding error mean square and the calculated 'F' value was compared with table value of 'F' at $P=0.005$ and $P=0.01$.

The mean, standard error, critical difference and coefficients of variation were calculated as follows:

3.9.1.1 Mean:

The mean value of each character was worked out by dividing the totals by corresponding number of observations.

$$m = \frac{\sum X_{ij}}{N}$$

Where,

X_{ij} = Any observation in i^{th} genotype and j^{th} replication,

N = Total number of observations.

3.9.1.2 Standard Error (S.E.):

The standard errors (SEm \pm) for genotypes were calculated with the help of mean square due to error from the analysis of variance table by the following formula:

$$\text{S. E. } m \pm = \sqrt{\frac{\text{MSE}}{r}}$$

Where,

MSE = mean of squares due to error

r = number of replication

3.9.1.3 Critical difference:

Critical difference was calculated to find out the superiority of one variety over the other by following formula.

$$\text{C. D.} = \sqrt{\frac{2\text{MSE}}{r}} \times \text{t value at 5\% and 1\% error d. f}$$

Where,

$$\text{SE}(d) = \sqrt{\frac{2 \times \text{variance due to error}}{\text{no. of replication}}}$$

t = Table value of 't' distribution at error d.f. on P < 0.05 and 0.01.

3.9.1.4 Coefficient of variation (C.V.):

$$\text{C. V. (\%)} = \frac{\sqrt{\text{MSE}}}{\bar{X}} \times 100$$

Where,

\bar{X} = General mean

3.9.1.5. Range :

Difference of Lower value and Higher value of mean values for each characters were arranged to measure the range of variation for the characters.

3.9.1.6. Estimation of variance:

The mean square for error was subtracted from the mean squares due to genotypes and the difference was divided by number of replications for obtaining the genotypic variance, which was calculated according to the method suggested by **Burton (1952)**. Environmental variance is the mean squares due to error. Phenotypic variance was calculated by adding genotypic variance and environmental variance, which was suggested by **Burton and de Vane (1952)**.

$$\text{Environmental variance } (\sigma^2_e) = \text{M.S.E.}$$

$$\text{Genotypic variance } (\sigma^2_g) = \frac{\text{M.S.T.} - \text{M.S.E.}}{r}$$

$$\text{Phenotypic variance } (\sigma^2_p) = \sigma^2_g + \sigma^2_e$$

Where,

M.S.T. is genotypes/ varieties mean square

M.S.E. is error mean square and

r is number of replications

3.9.2 Estimation of coefficient of variation:

The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were computed following **Burton and de Vane, (1952)**.

$$\text{GCV}(\%) = \frac{\text{Genotypic coefficient of variation}}{\text{Mean}} \times 100$$

$$\text{PCV}(\%) = \frac{\text{Phenotypic coefficient of variation}}{\text{Mean}} \times 100$$

3.9.3. Estimation of heritability:

Heritability in broad sense (h^2_{bs}) was calculated using the formula suggested by **Burton and de Vane (1953)**.

$$h^2_{bs} = \frac{\sigma^2_g}{\sigma^2_g + \sigma^2_e} \text{ or } \frac{\sigma^2_g}{\sigma^2_p}$$

$$h^2_{bs} (\%) = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where,

h^2 = Heritability

3.9.4. Genetic advance in per cent of mean:

Genetic advance (GA) was estimated by the method suggested by **Johnson et al. (1955)**.

$$GA = K \cdot \frac{\sigma^2_g}{\sigma^2_p} \cdot \sigma_p$$

Where,

K = Selection differential at 5% selection intensity (2.06).

σ_p = Phenotypic standard deviation

(GA%) = Genetic advance in percent of mean

3.9.5. Estimation of correlation:

The correlations between different characters at genotypic (g) and phenotypic (p) levels were worked out between characters as suggested by **Searle (1961)**.

i) Phenotypic correlation coefficient between characters X and Y

$$r_{xy(p)} = \frac{\text{Cov}_{xy(p)}}{\sqrt{\text{Var. X (p)} \cdot \text{Var. Y (p)}}$$

ii) Genotypic correlation between characters X and Y

$$r_{xy(g)} = \frac{\text{Cov}_{xy(g)}}{\sqrt{\text{Var. X (g)} \cdot \text{Var. Y (g)}}$$

Where,

r_{xy} = Correlation coefficients between X and Y.

Covariance XY = Co-variance between characters X and Y

Var. X = Variance for X character

Var. Y = Variance for Y character

The significance of phenotypic correlation coefficients was tested against (n-2) degrees of freedom at 5% and 1% probability level. Where, n is the number of genotypes on which the observations were recorded.

3.9.6 Path-coefficient analysis:

Path-coefficient analysis was carried out according to Dewey and Lu (1959). Yield per plant was assumed to be dependent variable (effect) which is influenced by all the characters, the independent variable (causes), directly as well as indirectly through other characters. The variation in total yield per plant unexplained by the 12 causes was presumed to be contributed by residual factor (x) which is uncorrelated with other factors. Path-coefficients were estimated by solving the following simultaneous equations indicating the basic relationship between correlation and path-coefficient. The equations used are as follows:

$$r_{iy} = P_{iy} + \sum_{j=1}^{11} r_{iy} P_{jy} \text{ for } r_{ij} = 1, 2, \dots, 12.$$

$$r_{iy} = P_{iy} + \sum_{j=1}^{11} r_{iy} P_{jy} \text{ for } r_{ij} = 1.$$

The above equation can be written in the form of matrix.

$$[A]_{11 \times 1} = [B]_{11 \times 1} [C]_{11 \times 1}$$

Where,

A is column vector of correlations r_{iy}

B is the correlation matrix of r_{ij} , and

C is the column vector of direct effects, P_{iy}

Residual factor was calculated as follows:

$$P_{xy} = \sqrt{1 - R^2}$$

Where,

$$R^2 = \sum_j P_{iy} r_{iy}$$

The r_{ij} 's i.e., $r_{1,2}$ to $r_{10,11}$ denote correlations between all possible combinations of independent characters P_{1y} to P_{11y} denote direct effect of various characters on character y.

r_{iy} = Correlation coefficient between i^{th} and y character.

p_{iy} = Direct effect of i^{th} character on Y.

3.7.7 Genetic divergence:

The genetic divergence of twenty genotypes was worked out by using Mahalanobis (1928) D^2 statistics. Twenty one quantitative and qualitative characters in bitter gourd were included for these analyses.

The calculation of D^2 values involved following steps:

I. A set of uncorrelated linear combinations (y, s) was obtained by pivotal condensation of the common dispersion matrix of set of correlated variables (x, s). The common dispersion matrix was arranged with the help of error mean squares and mean sum of products.

II. Using the relationship between y, s and x, s the mean values of different characters and (X1 to X13 in okra) were transferred in to the mean values of a set of uncorrelated linear combinations (Y1 to Y13) in okra.

III. The ' D^2 ' values between i^{th} and j^{th} genotypes for k^{th} characters in calculated as under.

$$D^2 = K (Y_{it} - Y_{jt})$$

Where, $t = 1$

IV. The 'K' components and D^2_{ij} for each combination were ranked in descending order of magnitude.

V. These ranks were added up for each component D^2_{ij} over combinations of i and j the total ranks were obtained.

VI. **Group constellation:** The D^2 values were arranged in an increasing order of magnitude. The grouping of the strains in to different clusters was done using Tocher's method. The two most closely associated groups were chosen and third group was found which had the smaller average D^2 value from the first two. Similarly the fourth was chosen to have the smallest average D^2 from the first three and so on. The D^2 value did not fit within with the former group and was, therefore, taken as another cluster.

VII. **Intra and inter-cluster distance:** The intra-cluster D^2 was calculated as the sum of $n(n-1)/2$ genotypes within a cluster divided by total number of combinations. All possible D^2 values between the groups of two clusters were added and then divided by $n_1 \times n_2$ for computing inter-cluster distance.

*Experimental
Findings*

EXPERIMENTAL FINDINGS

The present investigation entitled “**Studies on genetic variability, heritability, correlation and path analysis in bitter gourd (*Momordica charantia* L.)**” was carried out with twenty genotypes of bitter gourd during *summer season* of 2018-19 and 2019-20 at Horticulture Research Farm-I, Babasaheb Bhimrao Ambedkar University (A Central University), Vidya Vihar, Rae Bareli Road, Lucknow (U.P.), India. For deriving the results in all the observations, they were summarized and the findings of the experiments have also been described. The data with regards to different parameters were compiled and statistically analyzed in order to draw the valid conclusion and are presented in the following orders:

- 4.1 Analysis of variance for different characters,
- 4.2 Mean performance of the genotypes,
- 4.3 Genetic variability, heritability and genetic advance,
- 4.4 Genotypic and phenotypic correlations,
- 4.5 Path analysis and
- 4.6 Estimation of genetic divergence (**Mahalanobis D^2**)

4.1 Analysis of variance for different characters:

The analysis of variance for twenty genotypes for all the twenty one characters (15 physical characters and 6 chemical characters in field as well as laboratory condition) were subjected to analysis of variance to test the significance of differences among the genotypes. Analysis of variance also showed that the mean square due to the genotypes were highly significant for all the twenty one characters at indicating that genotypes differed significantly and genetic improvement is possible by selection. The selected materials for the present investigations has got a lot of variations in it, because of that it was thought necessary and essential for all the aspects of growth, yield, quality and genetically investigation. The analysis of variance was highly significant for all the characters under study (**Table-4.1**).

Table-4.1.A: Analysis of variance (mean square) for twenty one characters in bitter gourd (2018-19)

S. No	Characters	Source of variation		
		Replication	Treatments	Error
	Degree of freedom	2	19	38
		2018-19		
1.	Node no. to 1 st staminate flowers	2.21	11.96**	1.32
2.	Node no. to 1 st pistillate flowers	2.81	16.43**	1.65
3.	Days to anthesis of 1 st staminate flowers	0.52	56.50**	0.98
4.	Days to anthesis of 1 st pistillate flowers	2.24	108.75**	0.74
5.	Days to 1 st fruit harvest	1.85	102.67**	3.55
6.	Vine length (m)	0.27	1.83**	0.13
7.	Fruit length (cm)	0.67	33.44**	1.77
8.	Nodes per plant	18.15	261.26**	1.85
9.	No. of branches per plant	5.06	69.27**	1.36
10.	No. of seeds per fruit	4.01	47.31**	1.49
11.	Fruit diameter (cm)	0.11	5.87**	0.49
12.	No. of fruits per plant	2.06	24.71**	1.43
13.	Seeds weight per fruit (g)	0.05	0.66**	0.31
14.	Average fruit weight (g)	21.21	1753.84**	12.46
15.	Ascorbic acid (mg/100g)	2.91	84.22**	2.42
16.	Reducing sugar (%)	0.02	0.03**	0.07
17.	Non-reducing sugar (%)	0.00	0.04**	0.00
18.	Total sugars (%)	0.02	0.09**	0.01
19.	T.S.S (^o Brix)	0.07	2.56**	0.03
20.	Titrateable acidity (%)	0.09	0.02**	0.04
21.	Marketable fruit yield per plant (kg)	0.38	2.60**	0.69

*and** significant at 5% and 1% probability levels, respectively

Table-4.1.B: Analysis of variance (mean square) for twenty one characters in bitter gourd (2019-20)

S. No	Characters	Source of variation		
		Replication	Treatments	Error
	Degree of freedom	2	19	38
		2019-20		
1.	Node no. to 1 st staminate flowers	0.46	15.32**	1.64
2.	Node no. to 1 st pistillate flowers	3.75	14.98**	1.25
3.	Days to anthesis of 1 st staminate flowers	4.98	53.22**	1.77
4.	Days to anthesis of 1 st pistillate flowers	7.55	110.50**	1.26
5.	Days to 1 st fruit harvest	1.85	13.5.66**	3.00
6.	Vine length (m)	0.70	1.77**	0.25
7.	Fruit length (cm)	0.21	31.51**	0.80
8.	Nodes per plant	18.11	257.92**	1.45
9.	No. of branches per plant	3.21	71.24**	1.12
10.	No. of seeds per fruit	1.51	51.09**	0.95
11.	Fruit diameter (cm)	0.22	6.06**	0.41
12.	No. of fruits per plant	5.85	24.00**	1.32
13.	Seeds weight per fruit (g)	0.24	0.69**	0.25
14.	Average fruit weight (g)	8.01	1794.84**	7.05
15.	Ascorbic acid (mg/100g)	2.81	77.82**	1.74
16.	Reducing sugar (%)	0.08	0.04**	0.05
17.	Non-reducing sugar (%)	0.01	0.03**	0.02
18.	Total sugars (%)	0.05	0.08**	0.05
19.	T.S.S (⁰ Brix)	0.01	2.58**	0.01
20.	Titrateable acidity (%)	0.02	0.01**	0.02
21.	Marketable fruit yield per plant (kg)	0.64	2.41**	0.58

*and** significant at 5% and 1% probability levels, respectively

Table-4.1.C: Analysis of variance (mean square) for twenty one characters in bitter gourd (Pooled data)

S. No.	Characters	Source of variation		
		Replication	Treatments	Error
	Degree of freedom	2	19	38
		Pooled data		
1.	Node no. to I st staminate flowers	1.46	25.18**	1.48
2.	Node no. to I st pistillate flowers	6.16	30.35**	1.39
3.	Days to anthesis of I st staminate flowers	3.99	109.04**	1.25
4.	Days to anthesis of I st pistillate flowers	9.00	218.09**	1.04
5.	Days to I st fruit harvest	2.51	227.45**	4.79
6.	Vine length (m)	0.11	3.56**	0.08
7.	Fruit length (cm)	0.09	64.72**	1.08
8.	Nodes per plant	34.36	510.87**	2.98
9.	No. of branches per plant	8.11	140.04**	1.09
10.	No. of seeds per fruit	4.31	97.63**	1.14
11.	Fruit diameter (cm)	0.24	11.73**	0.41
12.	No. of fruits per plant	6.05	48.13**	1.23
13.	Seeds weight per fruit (g)	0.21	1.29**	0.25
14.	Average fruit weight (g)	27.47	3547.16**	8.11
15.	Ascorbic acid (mg/100g)	5.57	160.27**	2.03
16.	Reducing sugar (%)	0.02	0.07**	0.08
17.	Non-reducing sugar (%)	0.04	0.07**	0.04
18.	Total sugars (%)	0.07	0.19**	0.07
19.	T.S.S (^o Brix)	0.09	5.16**	0.01
20.	Titrateable acidity (%)	0.02	0.04**	0.01
21.	Marketable fruit yield per plant (kg)	1.02	4.99**	0.52

*and** significant at 5% and 1% probability levels, respectively

Table-4.2: Mean performance of twenty genotypes for twenty one characters in bitter gourd

S. No.	Characters Genotypes	Node no. to 1 st staminate flowers			Node no. to 1 st pistillate flowers			Days to anthesis of 1 st staminate flowers		
		1			2			3		
		2018-19	2019-20	Pooled	2018-19	2019-20	Pooled	2018-19	2019-20	Pooled
1.	Akra Harit	13.00	13.33	13.17	13.67	13.33	13.50	36.47	36.49	36.48
2.	Pusa Vishesh	15.00	15.33	15.17	16.67	16.33	16.50	36.84	36.77	36.81
3.	Narendra Barahmasi-1	12.33	11.67	12.00	13.33	12.67	13.00	34.26	34.19	34.23
4.	Kalyanpur Sona	14.00	13.00	13.50	13.00	12.33	12.67	42.64	42.40	42.52
5.	Pusa Hybrid-1	14.33	14.00	14.17	11.67	11.00	11.33	36.37	37.51	36.94
6.	Sagar	11.67	13.00	12.33	15.67	15.00	15.33	51.52	51.35	51.44
7.	Kalyanpur Barahmasi	12.33	10.33	11.33	12.67	14.00	13.33	41.98	41.84	41.91
8.	Kashi Urvasi	12.67	11.33	12.00	14.00	13.67	13.83	41.38	40.05	40.71
9.	Arka Sujat	12.00	11.67	11.83	12.00	10.00	11.00	42.84	43.68	43.26
10.	Amanshri	14.00	13.67	13.83	14.33	14.33	14.33	37.26	38.35	37.81
11.	Meghana-2	11.33	12.33	11.83	12.33	11.67	12.00	41.90	41.57	41.74
12.	US-475	9.00	8.33	8.67	11.00	10.33	10.67	42.55	42.34	42.45
13.	Pusa Hybrid-2	14.67	14.33	14.50	15.00	14.67	14.83	36.97	37.30	37.14
14.	Narendra Barahmasi-2	13.33	14.00	13.67	11.33	10.67	11.00	42.67	43.52	43.10
15.	Selection-5	11.33	12.00	11.67	7.67	8.00	7.83	36.17	36.50	36.33
16.	VRBT-23	13.67	12.67	13.17	10.67	10.33	10.50	33.85	33.52	33.68
17.	UDIT-008	13.00	12.33	12.67	9.33	9.67	9.50	34.86	35.82	35.34
18.	Ultima-1405	7.67	7.00	7.33	10.00	11.33	10.67	35.44	35.27	35.35
19.	US-484	13.33	10.67	12.00	10.33	12.00	11.17	42.20	41.53	41.86
20.	MC-23	8.67	7.33	8.00	9.00	8.67	8.83	41.60	40.60	41.10
	Mean	13.88	11.92	12.14	12.18	12.00	12.09	39.49	39.53	39.51
	C.V.	8.63	10.75	10.02	10.57	9.35	9.72	2.51	3.37	2.82
	S.E.	0.69	0.74	0.50	0.74	0.65	0.48	0.57	0.77	0.45
	C.D. at 5%	1.98	2.12	1.40	2.13	1.85	1.35	1.64	2.20	1.28
	Lowest	9.00	7.00	7.33	7.67	8.00	7.83	33.85	33.52	33.68
	Highest	20.00	15.33	15.17	16.67	16.33	16.50	51.52	51.35	51.44

Continued...

S. No.	Characters Genotypes	Days to anthesis of 1 st pistillate flowers			Days to 1 st fruit harvest			Vine length (m)		
		4			5			6		
		2018-19	2019-20	Pooled	2018-19	2019-20	Pooled	2018-19	2019-20	Pooled
1.	Akra Harit	40.95	41.28	41.11	46.00	41.33	43.67	5.67	5.54	5.60
2.	Pusa Vishesh	41.86	41.19	41.53	47.33	48.00	47.67	5.04	5.47	5.25
3.	Narendra Barahmasi-1	37.11	36.66	36.89	46.67	42.33	44.50	5.82	5.79	5.81
4.	Kalyanpur Sona	51.05	50.71	50.88	54.33	54.00	54.17	4.23	4.35	4.29
5.	Pusa Hybrid-1	36.48	36.70	36.59	56.33	56.00	56.17	4.85	4.55	4.70
6.	Sagar	49.36	49.19	49.27	47.33	45.33	46.33	5.61	5.51	5.56
7.	Kalyanpur Barahmasi	36.20	36.55	36.38	48.00	42.67	45.33	4.77	4.44	4.60
8.	Kashi Urvasi	42.46	42.15	42.30	65.00	62.00	63.50	5.58	5.47	5.53
9.	Arka Sujat	43.30	44.80	44.05	53.67	51.00	52.33	4.47	4.50	4.49
10.	Amanshri	35.83	36.12	35.97	53.00	52.00	52.50	3.24	3.26	3.25
11.	Meghana-2	43.32	46.68	45.00	54.67	46.33	50.50	4.57	4.53	4.55
12.	US-475	47.33	47.72	47.53	58.67	57.00	57.83	4.24	4.31	4.27
13.	Pusa Hybrid-2	42.57	42.23	42.40	48.00	47.33	47.67	3.46	3.48	3.47
14.	Narendra Barahmasi-2	36.06	36.36	36.21	54.00	53.67	53.83	4.79	4.64	4.71
15.	Selection-5	54.74	55.37	55.06	62.00	61.67	61.83	5.72	5.58	5.65
16.	VRBT-23	41.77	41.43	41.60	54.00	53.00	53.50	4.40	4.65	4.53
17.	UDIT-008	50.59	50.25	50.42	60.00	61.33	60.67	3.36	3.27	3.32
18.	Ultima-1405	44.89	45.30	45.10	61.33	54.00	57.67	5.00	4.67	4.84
19.	US-484	32.43	32.76	32.60	59.67	61.00	60.33	4.50	4.36	4.43
20.	MC-23	37.16	37.70	37.43	48.00	46.00	47.00	5.37	5.43	5.40
	Mean	42.27	42.56	42.42	53.90	51.80	52.85	4.73	51.80	4.71
	C.V.	2.04	2.64	2.40	3.50	3.35	4.15	7.74	3.35	5.79
	S.E.	0.50	0.65	0.42	1.09	1.00	0.89	0.21	1.00	0.11
	C.D. at 5%	1.43	1.86	1.17	3.12	2.87	2.51	0.61	2.87	0.31
	Lowest	32.43	32.76	32.60	46.00	41.33	43.67	3.24	41.33	3.25
	Highest	54.74	55.37	55.06	65.00	62.00	63.50	5.82	62.00	5.81

S. No.	Characters Genotypes	Fruit length (cm)			Nodes per plant			No. of branches per plant		
		7			8			9		
		2018-19	2019-20	Pooled	2018-19	2019-20	Pooled	2018-19	2019-20	Pooled
1.	Akra Harit	16.56	16.53	16.54	66.33	63.33	64.83	14.00	13.67	13.83
2.	Pusa Vishesh	15.73	15.66	15.70	58.67	56.67	57.67	21.33	21.00	21.17
3.	Narendra Barahmasi-1	19.54	20.20	19.87	48.00	46.33	47.17	16.67	16.33	16.50
4.	Kalyanpur Sona	22.67	22.21	22.44	72.00	72.33	72.17	17.00	16.67	16.83
5.	Pusa Hybrid-1	21.24	21.19	21.22	48.67	48.00	48.33	15.00	15.33	15.17
6.	Sagar	22.85	22.95	22.90	61.33	61.33	61.33	15.67	15.33	15.50
7.	Kalyanpur Barahmasi	21.87	22.19	22.03	65.67	62.33	64.00	20.00	19.67	19.83
8.	Kashi Urvasi	21.33	20.86	21.10	55.33	55.00	55.17	21.67	21.33	21.50
9.	Arka Sujat	14.67	15.00	14.83	73.33	72.67	73.00	21.33	21.67	21.50
10.	Amanshri	20.22	20.25	20.24	42.33	41.67	42.00	25.00	24.67	24.83
11.	Meghana-2	22.29	22.23	22.26	64.67	63.00	63.83	11.00	10.33	10.67
12.	US-475	17.00	17.19	17.10	64.33	63.00	63.67	22.33	22.00	22.17
13.	Pusa Hybrid-2	13.33	14.48	13.91	55.00	52.33	53.67	17.67	19.00	18.33
14.	Narendra Barahmasi-2	16.26	15.93	16.09	52.67	52.67	52.67	9.00	8.67	8.83
15.	Selection-5	24.35	24.44	24.40	40.33	41.33	40.83	20.67	19.00	19.83
16.	VRBT-23	21.67	21.54	21.60	57.00	47.33	52.17	23.67	24.00	23.83
17.	UDIT-008	21.55	21.56	21.56	63.67	61.67	62.67	22.67	22.33	22.50
18.	Ultima-1405	23.92	23.97	23.95	55.33	55.67	55.50	8.33	8.00	8.17
19.	US-484	17.99	17.32	17.65	56.67	52.00	54.33	21.00	20.67	20.83
20.	MC-23	15.62	15.60	15.61	44.67	44.00	44.33	20.33	20.67	20.50
	Mean	19.53	19.57	19.55	57.30	55.63	56.47	18.22	18.02	18.12
	C.V.	6.82	4.58	5.31	2.37	2.16	3.06	6.41	5.90	5.77
	S.E.	0.77	0.52	0.42	0.79	0.70	0.71	0.67	0.61	0.43
	C.D. at 5%	2.20	1.48	1.19	2.25	1.99	1.98	1.93	1.76	1.20
	Lowest	13.33	14.48	13.91	40.33	41.33	40.83	8.33	8.00	8.17
	Highest	24.35	24.44	24.40	73.33	72.67	73.00	25.00	24.67	24.83

Continued...

S. No.	Characters Genotypes	No. of seeds per fruit			Fruit diameter (cm)			No. of fruits per plant		
		10			11			12		
		2018-19	2019-20	Pooled	2018-19	2019-20	Pooled	2018-19	2019-20	Pooled
1.	Akra Harit	21.00	20.33	20.67	5.63	5.29	5.46	15.33	14.67	15.00
2.	Pusa Vishesh	17.67	17.33	17.50	4.66	4.51	4.58	20.00	20.33	20.17
3.	Narendra Barahmasi-1	16.00	16.33	16.17	7.48	6.15	6.81	14.00	14.33	14.17
4.	Kalyanpur Sona	19.67	19.33	19.50	6.02	5.89	5.95	13.33	13.67	13.50
5.	Pusa Hybrid-1	18.33	19.00	18.67	7.35	7.69	7.52	15.00	15.33	15.17
6.	Sagar	20.33	20.67	20.50	5.92	5.88	5.90	12.33	12.67	12.50
7.	Kalyanpur Barahmasi	28.00	28.33	28.17	9.50	9.35	9.42	16.33	16.00	16.17
8.	Kashi Urvasi	20.00	20.33	20.17	5.00	4.99	5.00	13.00	13.33	13.17
9.	Arka Sujat	26.33	26.67	26.50	6.67	6.97	6.82	12.67	14.33	13.50
10.	Amanshri	21.33	21.00	21.17	7.67	7.83	7.75	18.67	18.33	18.50
11.	Meghana-2	25.00	24.67	24.83	6.38	6.30	6.34	14.67	15.00	14.83
12.	US-475	30.67	31.33	31.00	8.15	8.48	8.31	12.67	13.00	12.83
13.	Pusa Hybrid-2	20.67	18.67	19.67	5.88	5.87	5.87	16.00	15.67	15.83
14.	Narendra Barahmasi-2	27.67	27.00	27.33	3.51	3.55	3.53	11.33	10.67	11.00
15.	Selection-5	22.33	21.67	22.00	7.59	7.39	7.49	12.67	11.67	12.17
16.	VRBT-23	22.00	22.33	22.17	7.07	7.56	7.31	11.67	11.00	11.33
17.	UDIT-008	26.00	25.00	25.50	7.19	7.06	7.13	17.67	18.00	17.83
18.	Ultima-1405	19.33	17.67	18.50	4.49	4.76	4.63	9.00	9.33	9.17
19.	US-484	21.67	21.00	21.33	6.07	6.10	6.09	12.00	12.33	12.17
20.	MC-23	17.33	17.00	17.17	6.57	6.41	6.49	9.33	10.33	9.83
	Mean	22.07	21.78	21.93	6.44	6.40	6.42	13.88	14.00	13.94
	C.V.	5.53	4.49	4.86	10.87	10.11	9.92	8.63	8.22	7.92
	S.E.	0.70	0.56	0.44	0.40	0.37	0.26	0.69	0.66	0.45
	C.D. at 5%	2.02	1.62	1.22	1.16	1.07	0.73	1.98	1.90	1.27
	Lowest	16.00	16.33	16.17	3.51	3.55	0.26	9.00	9.33	9.17
	Highest	30.67	31.33	31.00	9.50	9.35	0.73	20.00	20.33	20.17

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S. No.	Characters Genotypes	Seeds weight per fruit (g)			Average fruit weight (g)			Ascorbic acid (mg/100g)		
		13			14			15		
		2018-19	2019-20	Pooled	2018-19	2019-20	Pooled	2018-19	2019-20	Pooled
1.	Akra Harit	3.18	3.18	3.18	71.33	72.00	71.67	82.67	83.00	82.83
2.	Pusa Vishesh	3.80	3.82	3.81	118.33	120.00	119.17	79.67	81.00	80.33
3.	Narendra Barahmasi-1	3.81	3.83	3.82	75.67	75.00	75.33	84.33	83.67	84.00
4.	Kalyanpur Sona	3.77	3.46	3.62	84.67	85.33	85.00	81.00	81.00	81.00
5.	Pusa Hybrid-1	3.25	3.27	3.26	87.00	88.33	87.67	93.00	93.33	93.17
6.	Sagar	3.21	3.23	3.22	55.33	54.67	55.00	87.67	85.00	86.33
7.	Kalyanpur Barahmasi	2.85	3.21	3.03	127.67	126.00	126.83	91.00	91.33	91.17
8.	Kashi Urvasi	3.76	3.92	3.84	66.33	65.33	65.83	79.33	80.33	79.83
9.	Arka Sujat	3.70	3.49	3.60	62.33	63.00	62.67	82.33	80.67	81.50
10.	Amanshri	3.50	3.50	3.50	61.67	62.00	61.83	95.67	95.33	95.50
11.	Meghana-2	3.22	2.89	3.05	115.00	116.33	115.67	90.00	91.00	90.50
12.	US-475	3.90	3.92	3.91	94.33	94.00	94.17	82.00	83.33	82.67
13.	Pusa Hybrid-2	3.53	3.51	3.52	110.00	110.67	110.33	91.33	91.00	91.17
14.	Narendra Barahmasi-2	3.18	3.20	3.19	56.33	55.33	55.83	85.67	86.00	85.83
15.	Selection-5	2.54	2.55	2.54	64.00	63.67	63.83	79.00	80.00	79.50
16.	VRBT-23	3.27	3.95	3.61	120.00	121.67	120.83	92.33	92.00	92.17
17.	UDIT-008	4.24	4.22	4.23	83.67	84.33	84.00	86.00	84.00	85.00
18.	Ultima-1405	2.62	2.64	2.63	62.00	62.33	62.17	94.67	94.00	94.33
19.	US-484	3.48	3.16	3.32	74.00	73.00	73.50	89.00	88.33	88.67
20.	MC-23	2.55	2.57	2.56	53.00	54.33	53.67	87.67	87.33	87.50
	Mean	3.37	3.38	3.37	82.13	82.37	82.25	86.72	86.58	86.65
	C.V.	16.76	14.94	14.66	4.30	3.22	3.46	1.80	1.53	1.64
	S.E.	0.33	0.29	0.20	2.04	1.53	1.16	0.90	0.76	0.58
	C.D. at 5%	0.93	0.83	0.57	5.84	4.39	3.26	2.57	2.18	1.63
	Lowest	2.54	2.55	2.54	53.00	54.33	53.67	79.00	80.00	79.50
	Highest	4.24	4.22	4.23	127.67	126.00	126.83	95.67	95.33	95.50

Continued...

S. No.	Characters Genotypes	Reducing sugar (%)			Non-reducing sugar (%)			Total sugars (%)		
		16			17			18		
		2018-19	2019-20	Pooled	2018-19	2019-20	Pooled	2018-19	2019-20	Pooled
1.	Akra Harit	0.79	0.77	0.78	0.55	0.56	0.55	1.34	1.31	1.32
2.	Pusa Vishesh	0.86	0.87	0.86	0.43	0.45	0.44	1.29	1.32	1.31
3.	Narendra Barahmasi-1	0.74	0.73	0.73	0.52	0.51	0.52	1.39	1.38	1.39
4.	Kalyanpur Sona	0.90	0.89	0.90	0.53	0.53	0.53	1.44	1.42	1.43
5.	Pusa Hybrid-1	0.77	0.76	0.77	0.54	0.56	0.55	1.32	1.33	1.33
6.	Sagar	0.93	0.95	0.94	0.62	0.63	0.62	1.61	1.60	1.61
7.	Kalyanpur Barahmasi	0.96	0.98	0.97	0.56	0.58	0.57	1.54	1.55	1.54
8.	Kashi Urvasi	0.84	0.85	0.84	0.33	0.34	0.34	1.17	1.19	1.18
9.	Arka Sujat	0.92	0.93	0.93	0.46	0.45	0.46	1.25	1.27	1.26
10.	Amanshri	0.97	0.99	0.98	0.72	0.73	0.73	1.71	1.72	1.72
11.	Meghana-2	0.70	0.74	0.72	0.46	0.47	0.46	1.16	1.21	1.18
12.	US-475	0.83	0.97	0.90	0.63	0.65	0.64	1.64	1.62	1.63
13.	Pusa Hybrid-2	0.71	0.72	0.72	0.42	0.42	0.42	1.36	1.35	1.36
14.	Narendra Barahmasi-2	0.79	0.75	0.77	0.53	0.53	0.53	1.49	1.48	1.48
15.	Selection-5	0.69	0.71	0.70	0.45	0.44	0.45	1.40	1.41	1.40
16.	VRBT-23	0.76	0.80	0.78	0.37	0.36	0.37	1.14	1.16	1.15
17.	UDIT-008	0.95	0.96	0.96	0.71	0.70	0.70	1.66	1.67	1.66
18.	Ultima-1405	0.77	0.81	0.79	0.51	0.55	0.53	1.52	1.53	1.53
19.	US-484	0.82	0.84	0.83	0.30	0.31	0.31	1.12	1.15	1.14
20.	MC-23	0.55	0.54	0.54	0.41	0.53	0.47	1.46	1.47	1.46
	Mean	0.81	0.83	0.82	0.50	0.51	0.51	1.40	1.41	1.40
	C.V.	3.28	2.75	3.63	2.80	3.50	4.17	2.26	1.72	1.91
	S.E.	0.02	0.01	0.01	0.01	0.01	0.01	0.02	0.01	0.01
	C.D. at 5%	0.04	0.04	0.03	0.02	0.03	0.02	0.05	0.04	0.03
	Lowest	0.55	0.54	0.54	0.30	0.31	0.31	1.12	1.15	1.14
	Highest	0.97	0.99	0.98	0.72	0.73	0.73	1.71	1.72	1.72

Continued...

S. No.	Characters Genotypes	T.S.S. (⁰ Brix)			Titratable acidity (%)			Marketable fruit yield per plant (kg)		
		19			20			21		
		2018-19	2019-20	Pooled	2018-19	2019-20	Pooled	2018-19	2019-20	Pooled
1.	Akra Harit	3.21	3.16	3.19	0.31	0.30	0.31	3.79	3.62	3.70
2.	Pusa Vishesh	2.63	2.56	2.60	0.27	0.26	0.26	2.42	2.45	2.43
3.	Narendra Barahmasi-1	3.37	3.39	3.38	0.27	0.27	0.27	2.25	2.59	2.42
4.	Kalyanpur Sona	2.52	2.48	2.50	0.14	0.13	0.14	2.94	2.96	2.95
5.	Pusa Hybrid-1	3.13	3.26	3.20	0.33	0.32	0.32	3.41	3.38	3.40
6.	Sagar	4.57	4.52	4.54	0.27	0.26	0.27	3.09	3.11	3.10
7.	Kalyanpur Barahmasi	2.57	2.54	2.55	0.16	0.15	0.16	5.23	5.26	5.25
8.	Kashi Urvasi	4.23	4.35	4.29	0.28	0.27	0.28	4.29	4.32	4.31
9.	Arka Sujat	3.23	3.26	3.25	0.33	0.32	0.33	1.60	1.62	1.61
10.	Amanshri	5.30	5.33	5.31	0.22	0.22	0.22	2.79	2.81	2.80
11.	Meghana-2	2.60	2.64	2.62	0.22	0.21	0.22	3.35	3.08	3.22
12.	US-475	4.87	4.79	4.83	0.16	0.16	0.16	2.21	2.24	2.23
13.	Pusa Hybrid-2	2.40	2.43	2.42	0.12	0.11	0.12	2.23	2.25	2.24
14.	Narendra Barahmasi-2	3.10	3.23	3.17	0.32	0.31	0.32	2.97	3.01	2.99
15.	Selection-5	5.20	5.25	5.23	0.32	0.29	0.31	3.65	3.45	3.55
16.	VRBT-23	2.70	2.73	2.72	0.17	0.16	0.17	1.73	1.75	1.74
17.	UDIT-008	3.57	3.67	3.62	0.25	0.24	0.25	2.97	2.83	2.90
18.	Ultima-1405	4.40	4.43	4.41	0.25	0.23	0.24	1.93	1.95	1.94
19.	US-484	3.70	3.72	3.71	0.24	0.22	0.23	2.76	2.73	2.74
20.	MC-23	3.77	3.87	3.82	0.23	0.22	0.23	1.61	1.65	1.63
	Mean	3.55	3.58	3.57	0.24	0.23	0.24	2.86	2.85	2.86
	C.V.	5.20	2.89	3.88	4.82	6.02	5.14	29.20	26.83	25.19
	S.E.	0.11	0.06	0.06	0.01	0.01	0.01	0.48	0.44	0.29
	C.D. at 5%	0.31	0.17	0.16	0.02	0.02	0.01	1.38	1.27	0.83
	Lowest	2.40	2.43	2.42	0.12	0.11	0.12	1.60	1.62	1.61
	Highest	5.30	5.33	5.31	0.33	0.32	0.33	5.23	5.26	5.25

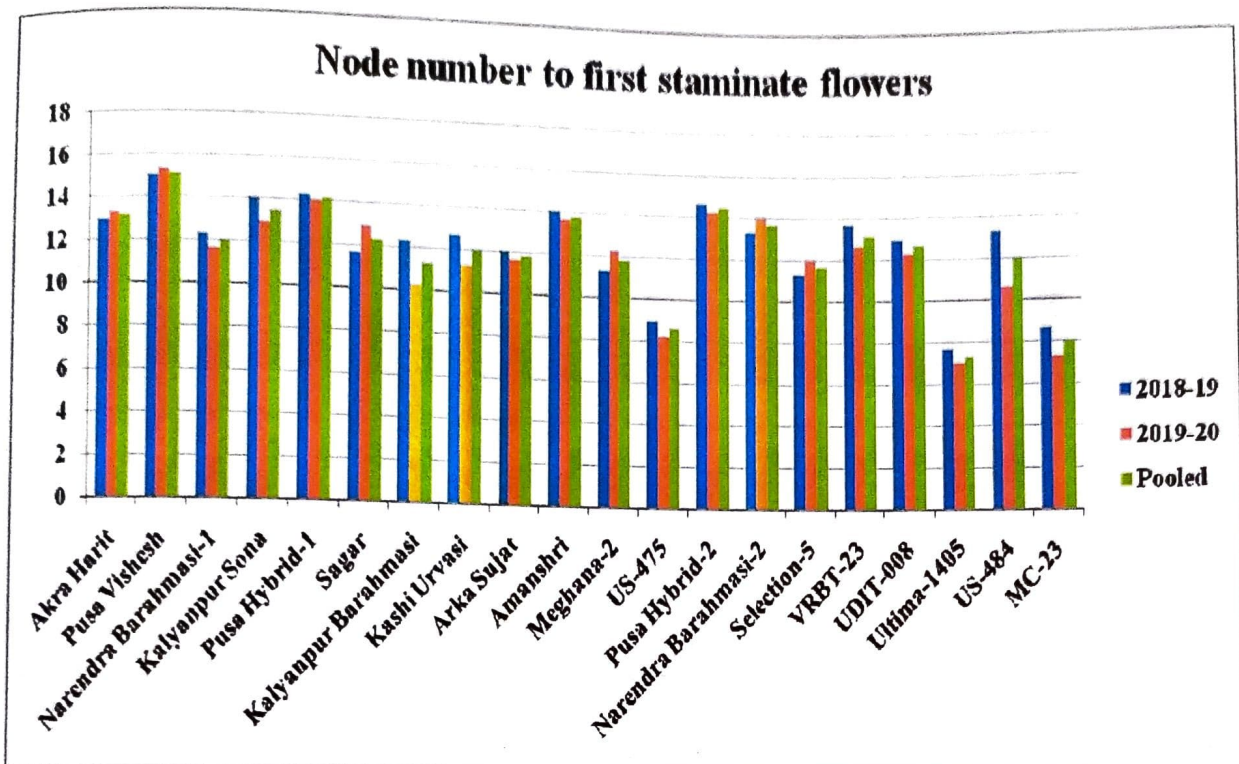


Fig 4.1: Justified node number to first staminate flowers of bitter gourd genotypes

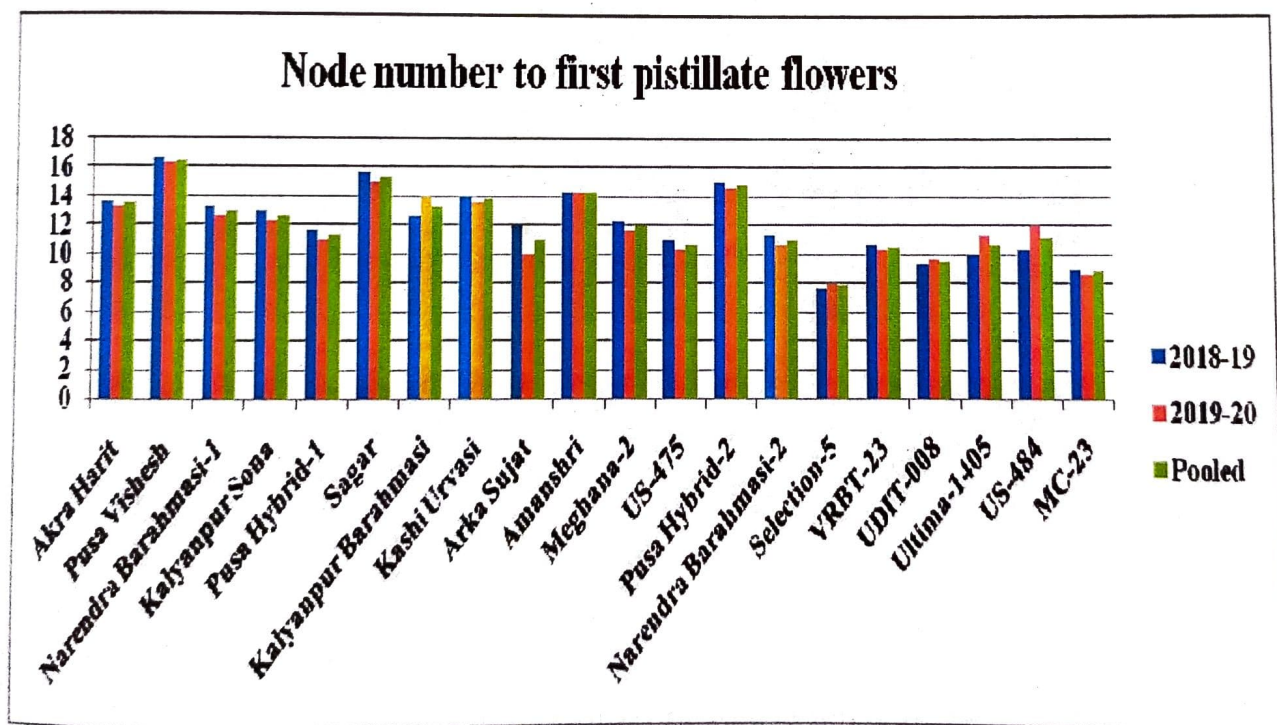


Fig 4.2: Justified node number to first pistillate flowers of bitter gourd genotypes

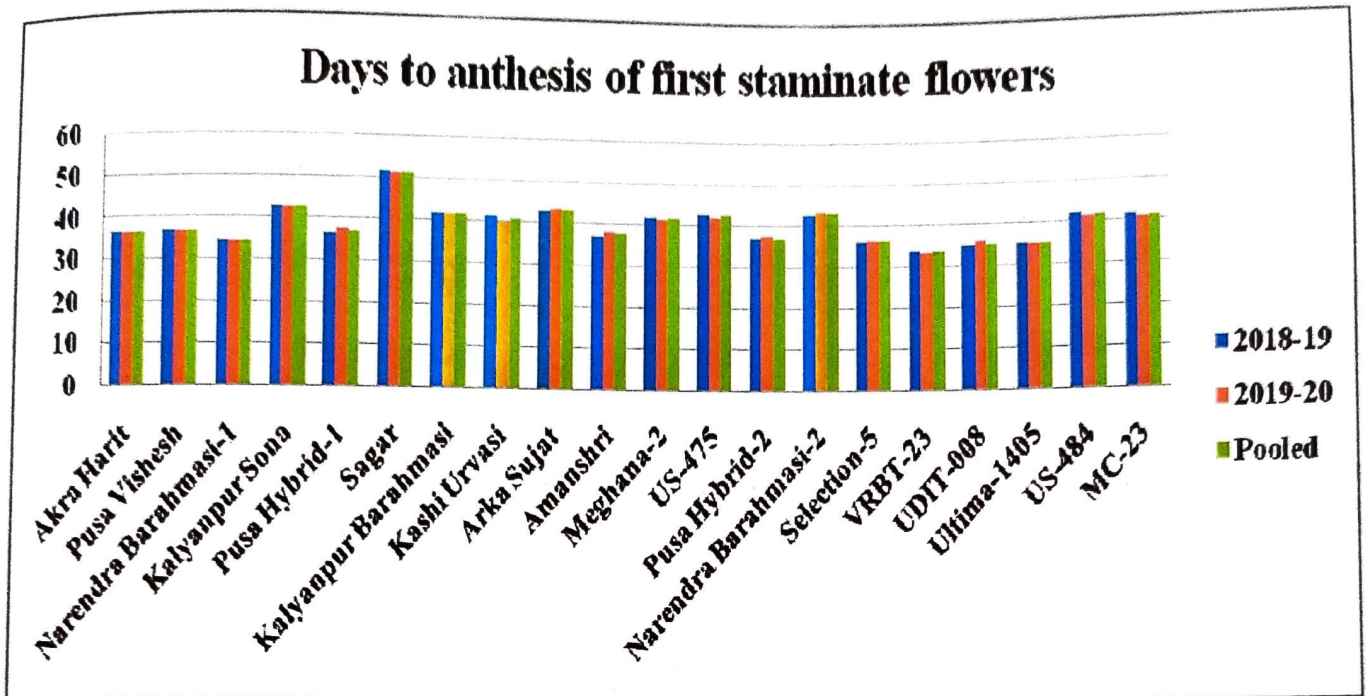


Fig 4.3: Justified days to anthesis of first staminate flowers of bitter gourd genotypes

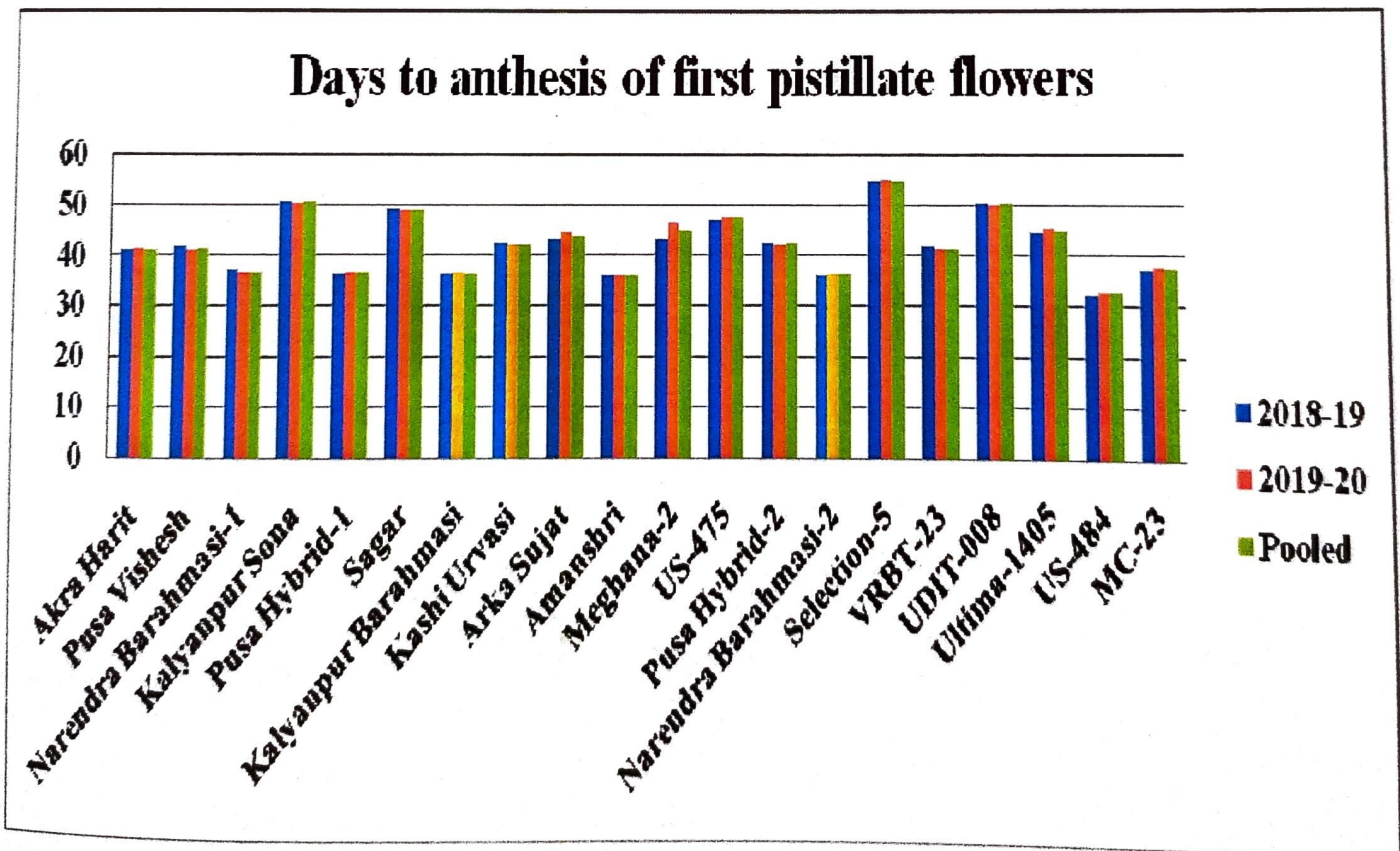


Fig 4.4: Justified days to anthesis of first pistillate flowers of bitter gourd genotypes

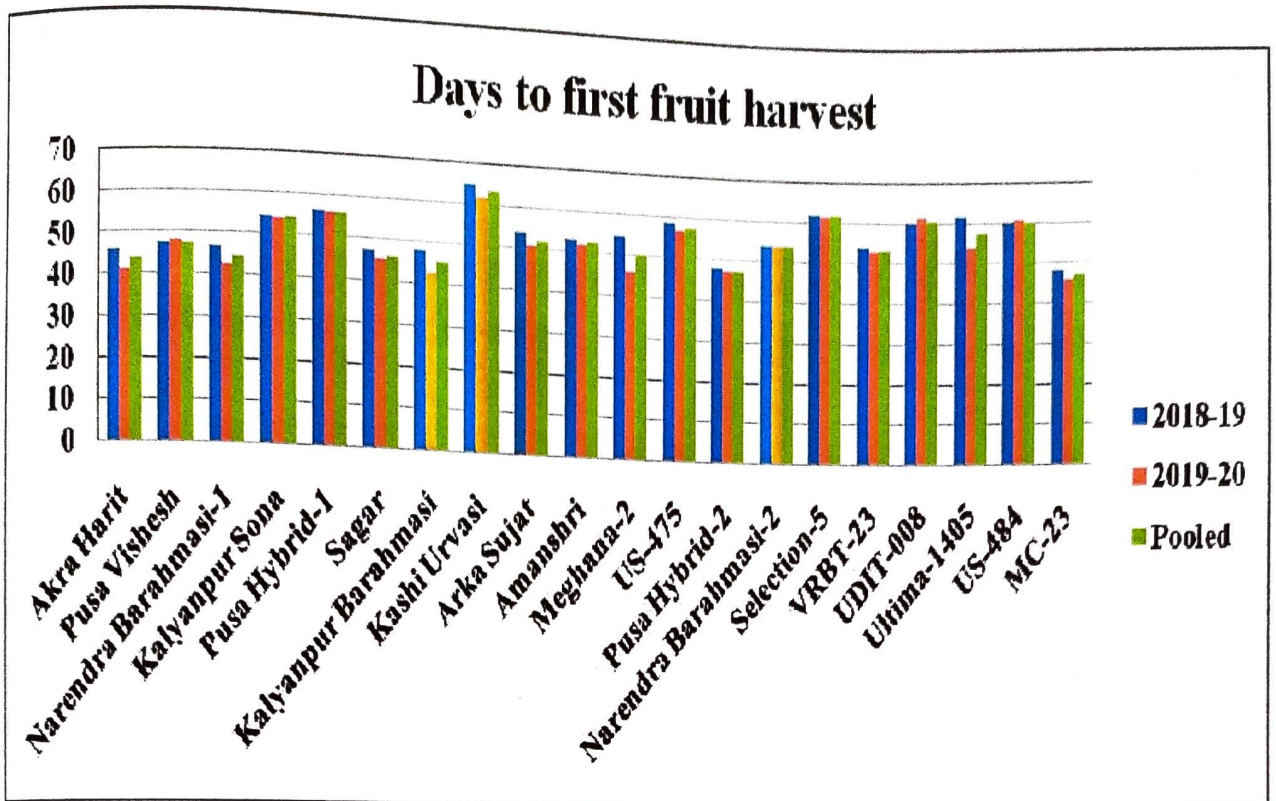


Fig 4.5: Justified days to first fruit harvest of bitter gourd genotypes

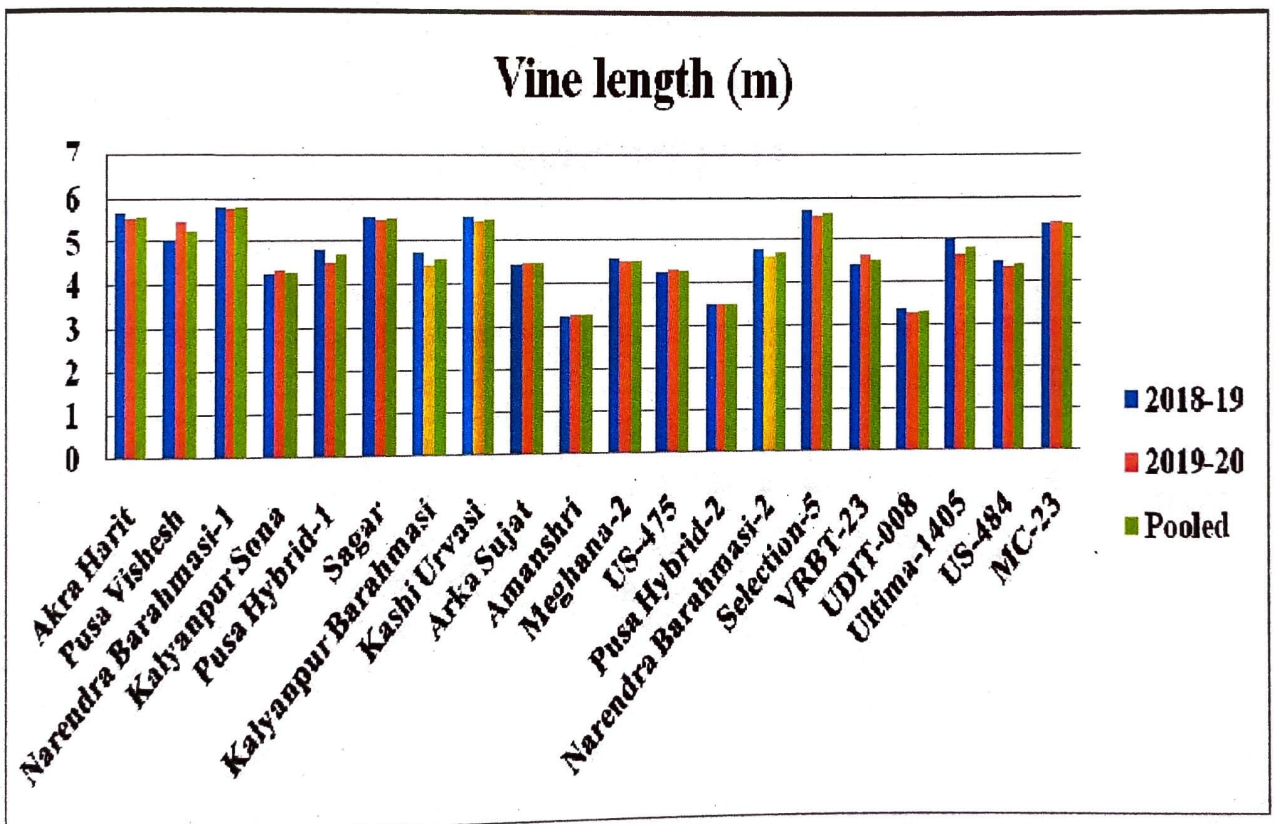


Fig 4.6: Justified vine length (m) of bitter gourd genotypes

Fruit length (cm)

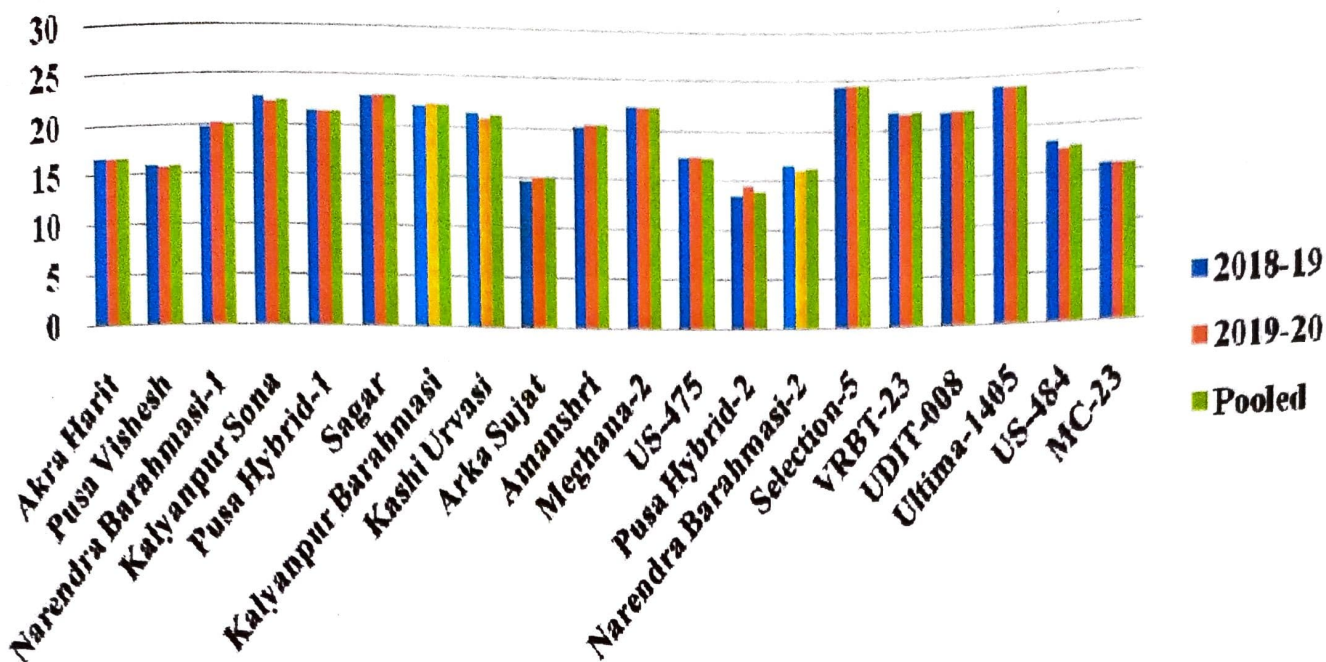


Fig 4.7: Justified fruit length (cm) of bitter gourd genotypes

Nodes per plant

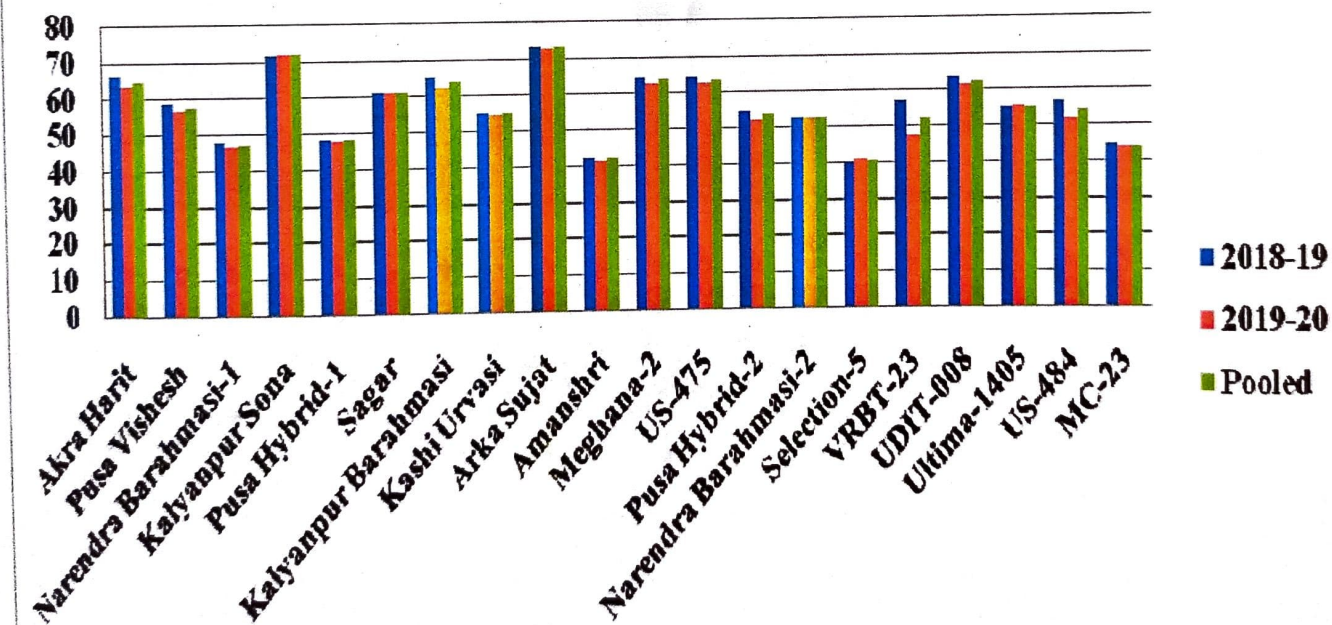


Fig 4.8: Justified nodes per plant of bitter gourd genotypes

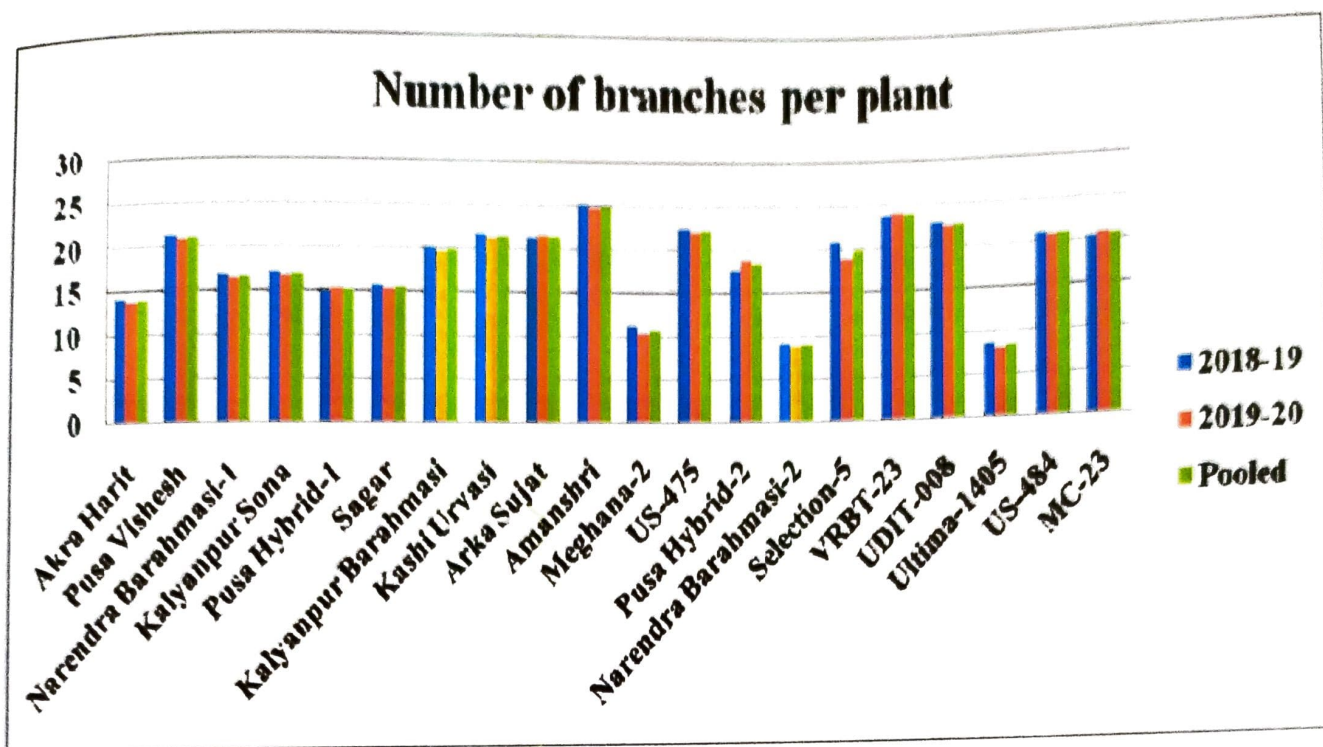


Fig 4.9: Justified number of branches per plant of bitter gourd genotypes

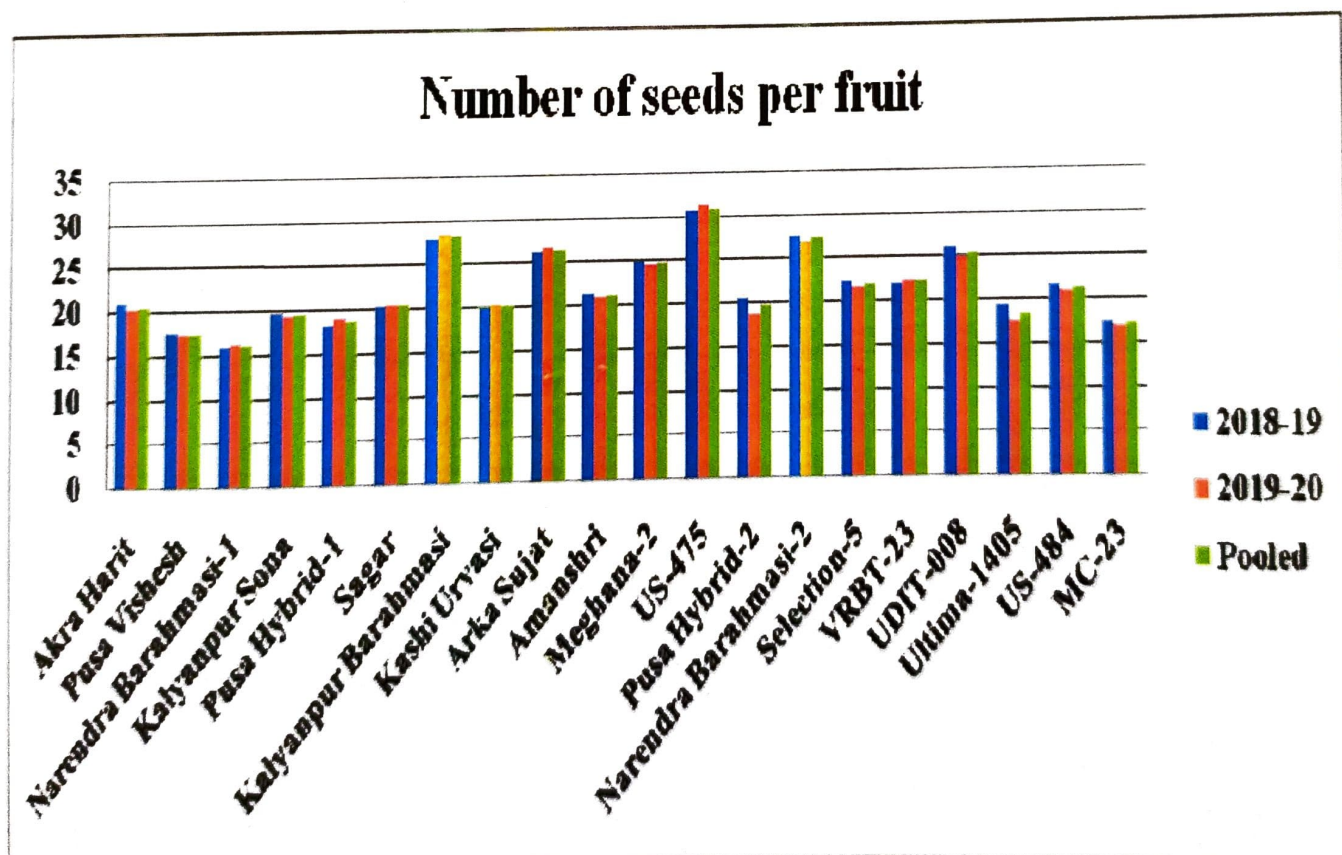


Fig 4.10: Justified number of seeds per plant of bitter gourd genotypes

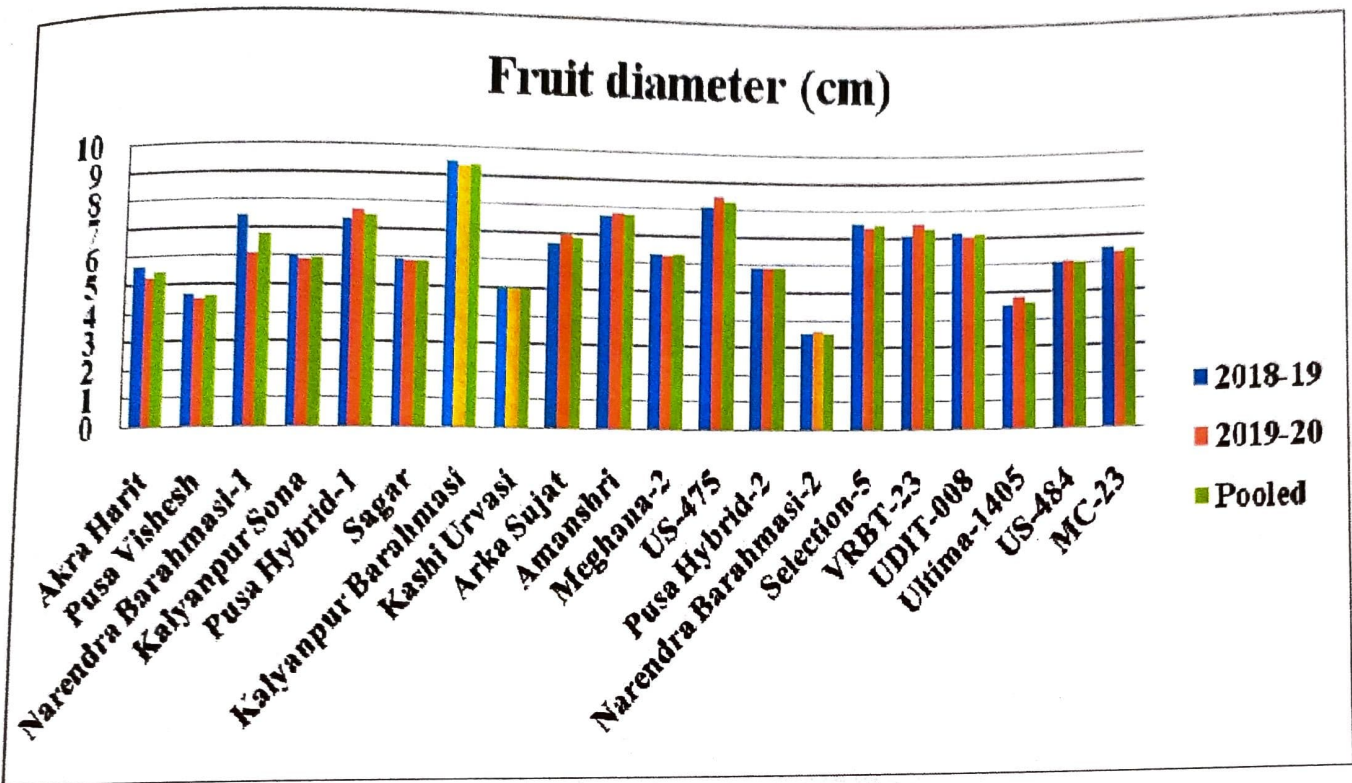


Fig 4.11: Justified fruit diameter (cm) of bitter gourd genotypes

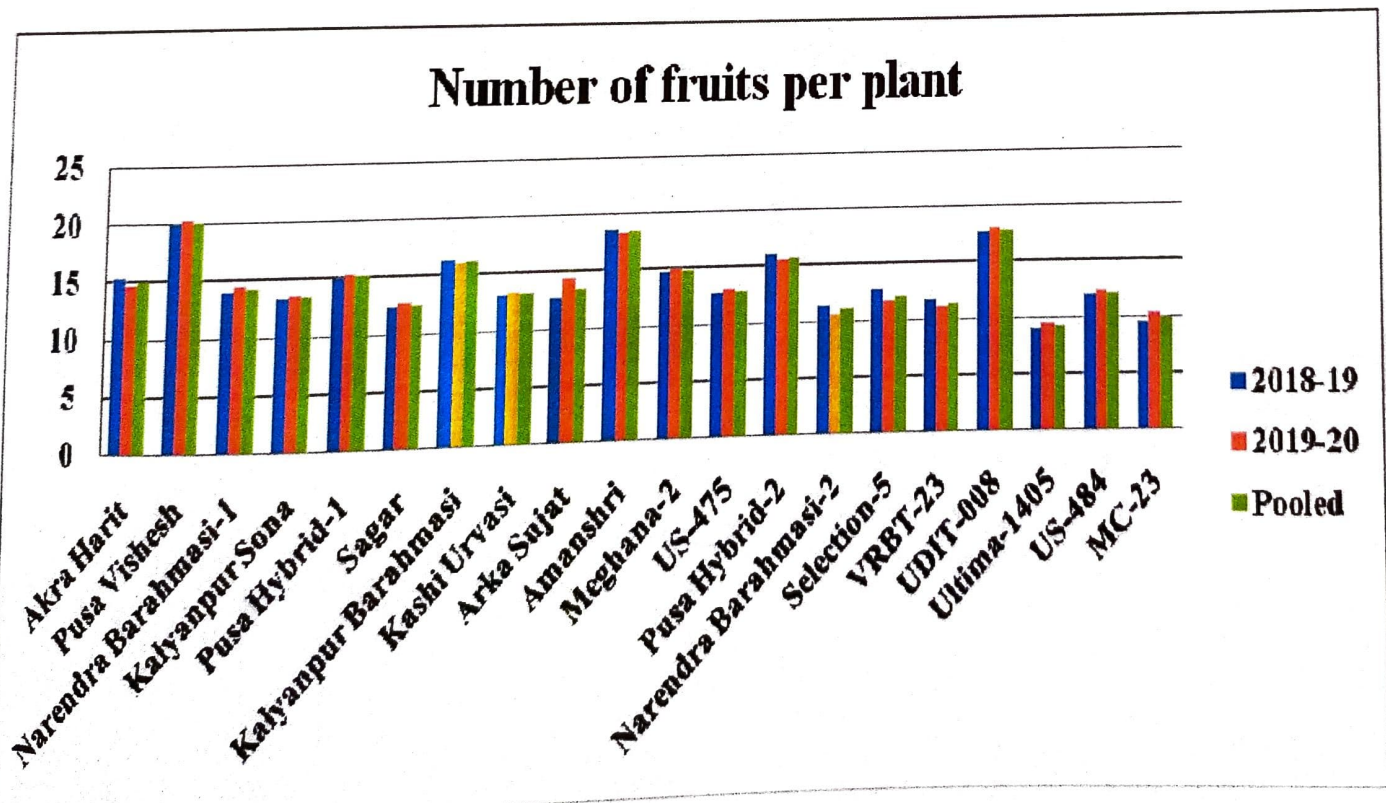


Fig 4.12: Justified number of fruits per plant of bitter gourd genotypes

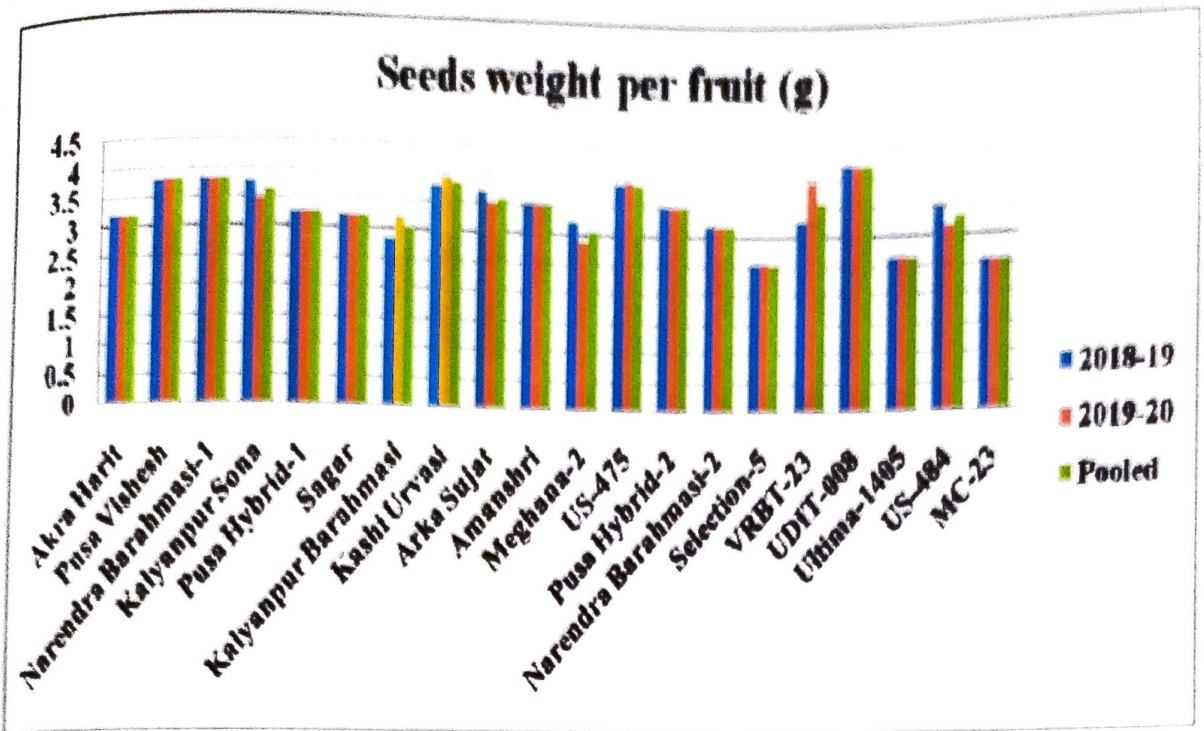


Fig 4.13: Justified seeds weight per fruit (g) of bitter gourd genotypes

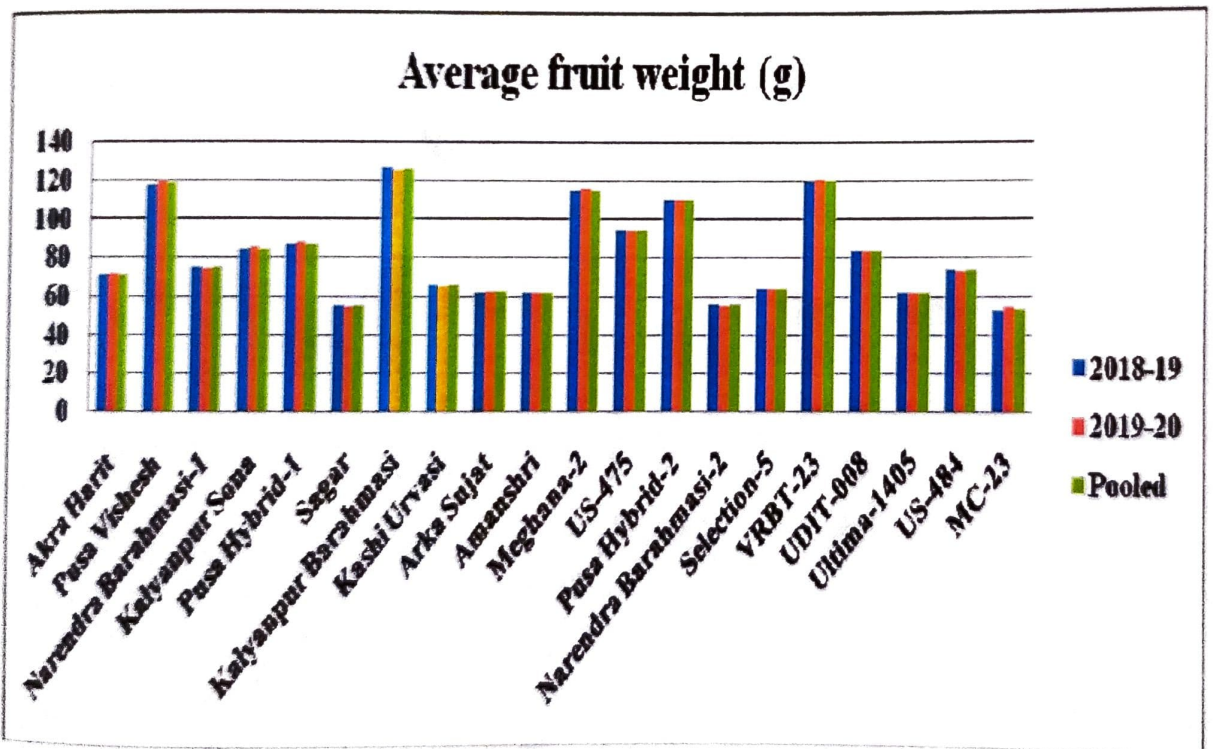


Fig 4.14: Justified average fruit weight (g) of bitter gourd genotypes

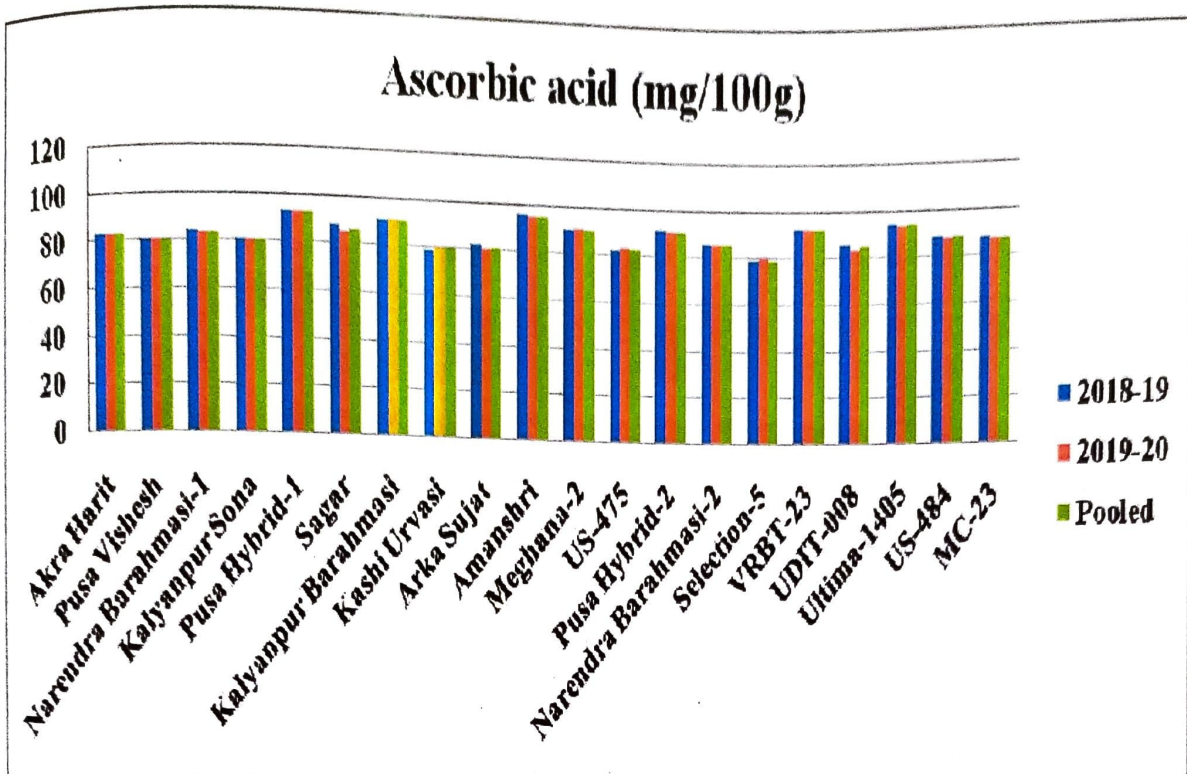


Fig 4.15: Justified ascorbic acid (mg/100g) of bitter gourd genotypes

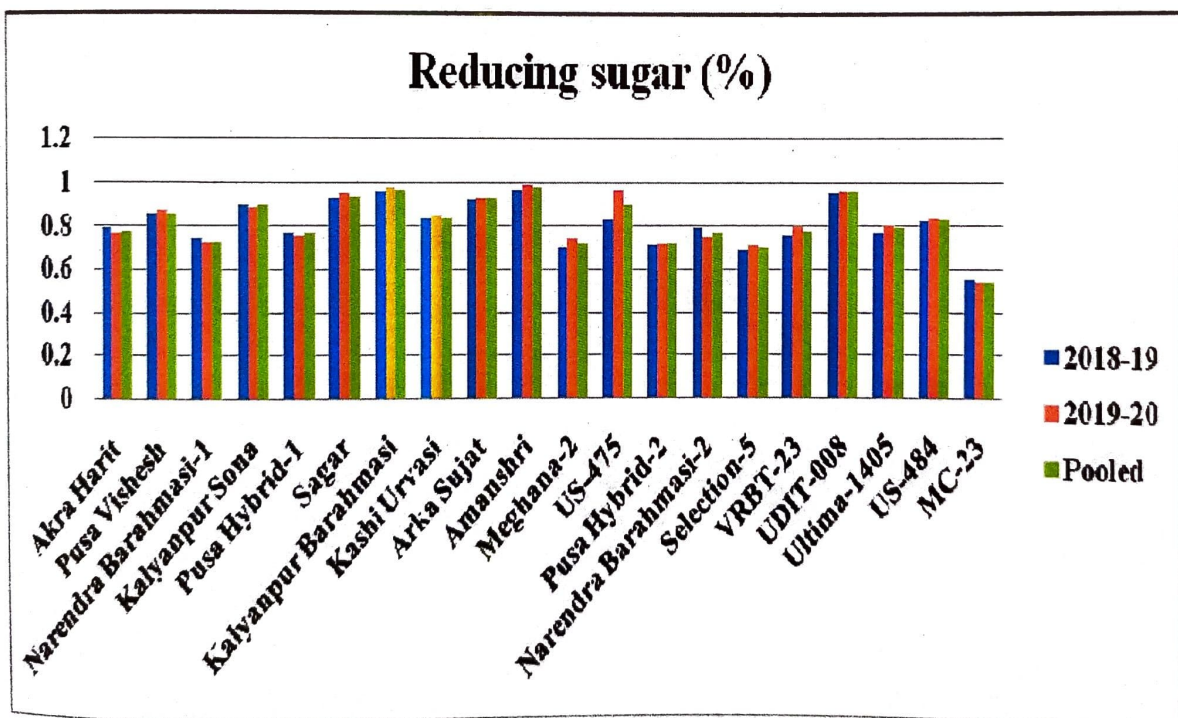


Fig 4.16: Justified reducing sugar (%) of bitter gourd genotypes

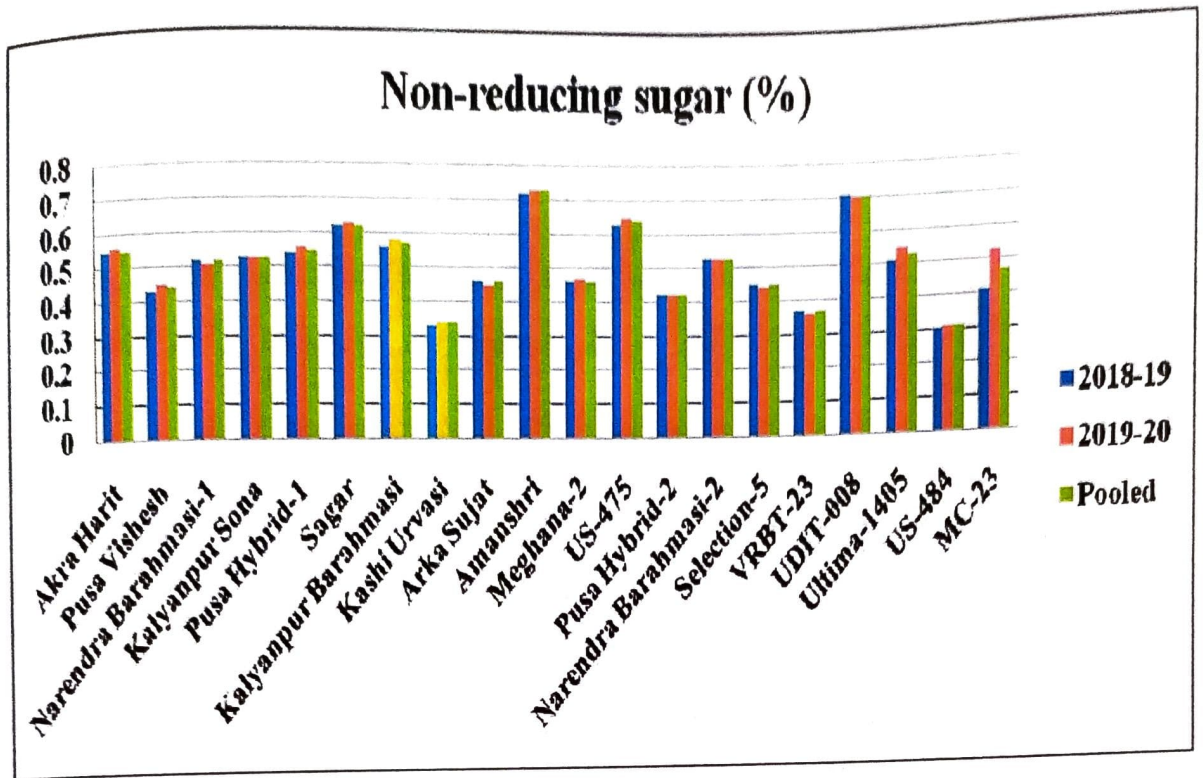


Fig 4.17: Justified non-reducing (%) of bitter gourd genotypes

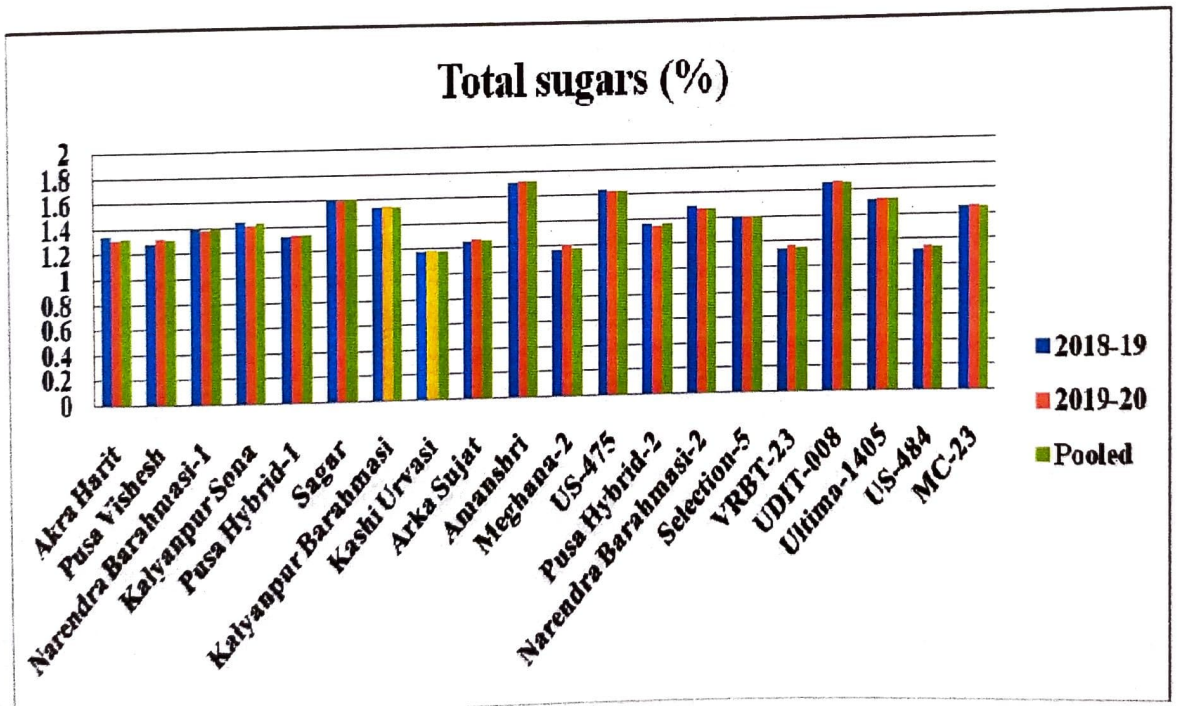


Fig 4.18: Justified total sugars (%) of bitter gourd genotypes

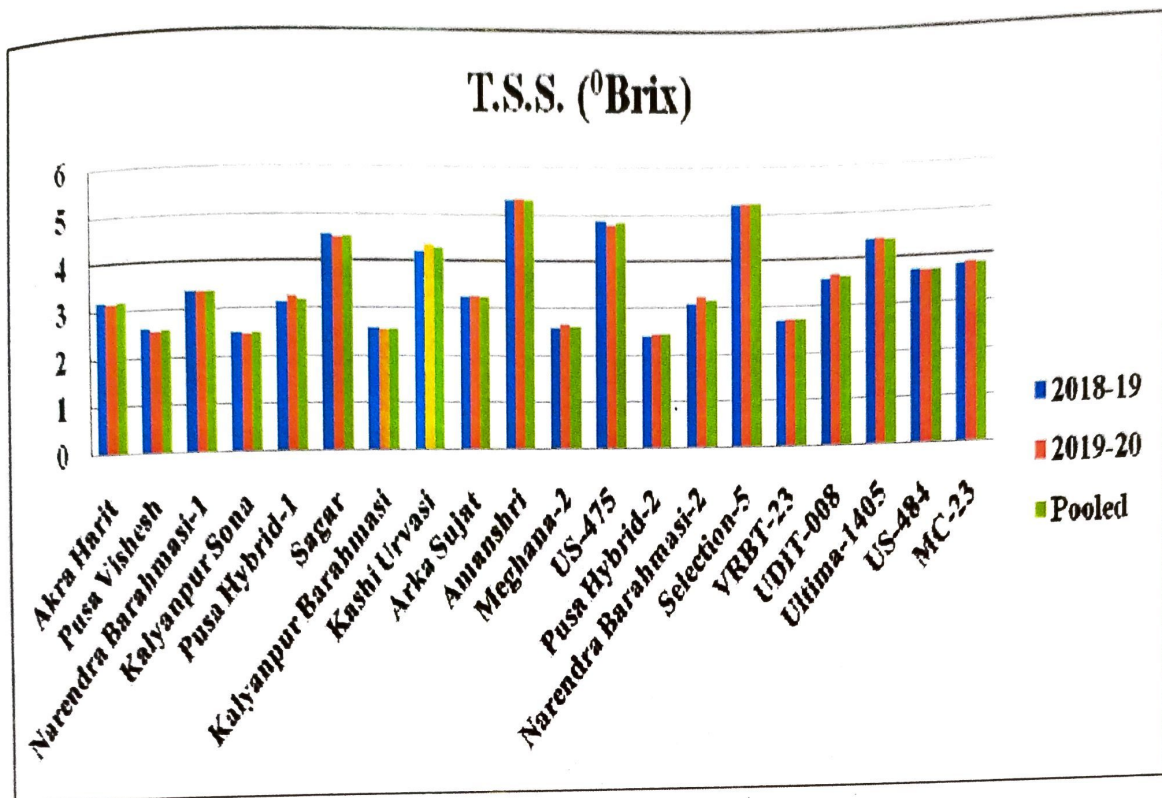


Fig 4.19: Justified T.S.S. ($^{\circ}$ Brix) of bitter gourd genotypes

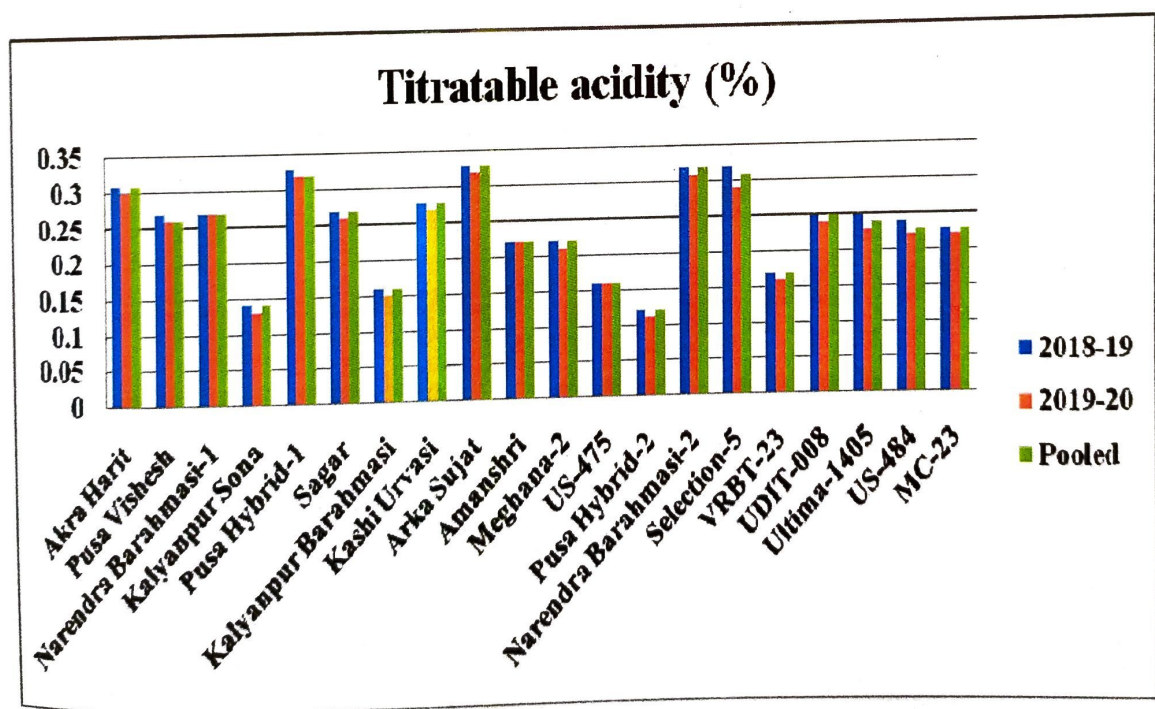


Fig 4.20: Justified titratable acidity (%) of bitter gourd genotypes

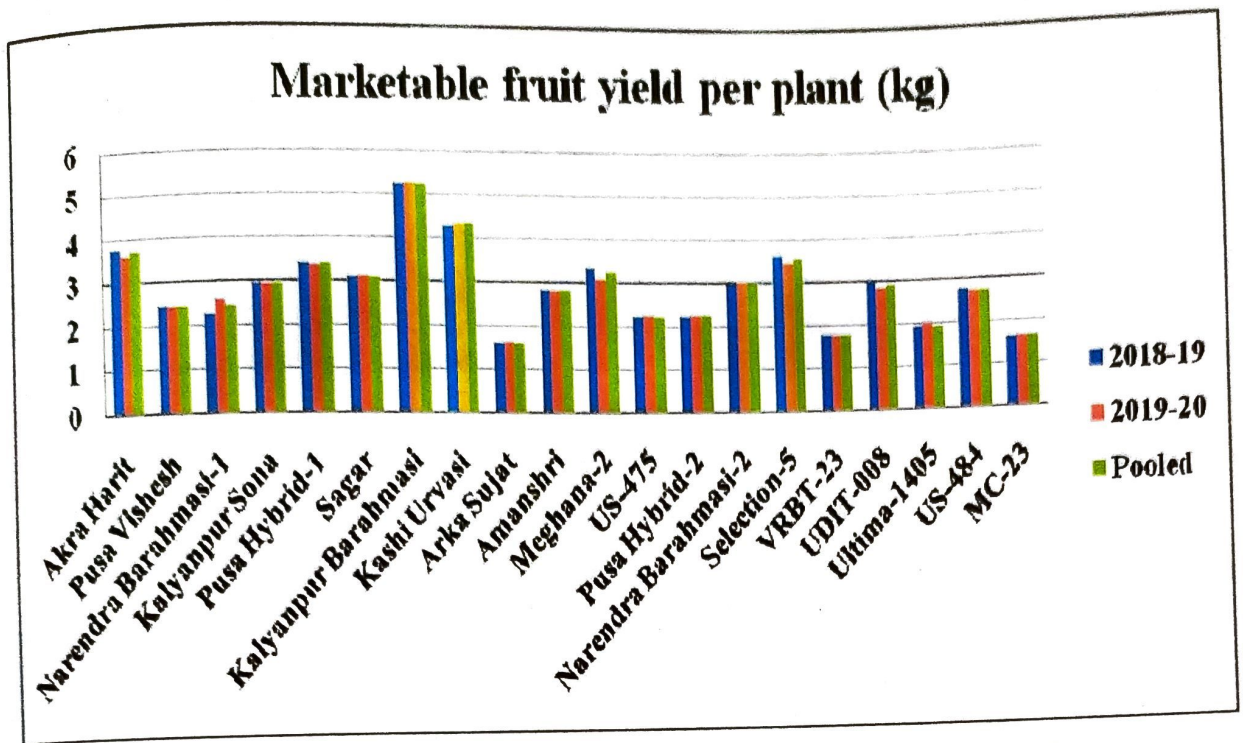


Fig 4.21: Justified marketable fruit yield per plant (kg) of bitter gourd genotypes

4.2 Mean performance of the genotypes:

The mean performance, range, standard error, and least significant differences of twenty genotypes for twenty on characters have been presented in the **Table-4.2** and graphically illustrated in Fig. 4.2.1 and the same is described characters wise in the following the paragraphs.

4.2.1

Node number to first staminate flowers

It is obvious from the data that the node number to first staminate flowers was found to vary from 7.33 (Ultima-1405) to 15.16 (Pusa Vishesh). The value of general mean (12.14) was recorded. The data clearly revealed that the best five entries among them are namely Pusa Vishesh (15.16) followed by Pusa hybrid-2 (14.50), Pusa hybrid-1 (14.16), Amanshri (13.83) and VRBT-23 (13.16) showed that the maximum node number to first staminate flowers. Whereas, Ultima-1405 (7.33) followed by MC-23 (8.00) and US-475 (8.66) which as the minimum were recorded in node number to first staminate flowers.

4.2.2

Node number to first pistillate flowers

It is explicit from the data observed on node number to first pistillate flowers ranged from 7.83 (Selection-5) to 16.50 (Pusa Vishesh). While, the general mean 12.09 was observed in five genotypes viz., Pusa Vishesh (16.50) followed by Sagar (15.33), Pusa Hybrid-2 (14.83), Amanshri (14.33) and Kashi Urvasi (13.83) respectively. The data clearly revealed that the maximum node number to first pistillate flowers. Whereas, Selection-5 (7.83) followed by MC-23 (8.83) and UDIT-008 (9.51) were found lower significant for node number to first pistillate flowers.

4.2.3

Days to anthesis of first staminate flowers

It is obvious from the data days to anthesis of first staminate flowers was found to range from 33.68 (VRBT-23) to 51.43 (Sagar). The grand mean for days to anthesis of first staminate flowers 39.50 was recorded. Out of twenty genotypes, overall of five best genotypes viz., Sagar (51.43) followed by Arka Sujat (43.26), Narendra Barahmasi-2

(43.10), Kalyanpur Sona (42.51) and US-475 (42.44) required in maximum in days to anthesis of first staminate flowers. Whereas, three genotypes viz., VRBT-23 (33.68) followed by Ultima-1405 (35.35), Narendra Barahmasi-1 (34.22) of lower days to anthesis of first staminate flowers.

4.2.4

Days to anthesis of first pistillate flowers

It is evident from the data that the days to anthesis of first pistillate flowers was found to range from 32.59 (US-484) to 55.05 (Selection-5). The grand mean for days to anthesis of first pistillate flowers was 42.41 recorded. Out of twenty genotypes, overall of five best genotypes viz., Selection-5 (55.05) followed by Kalyanpur Sona (50.88), UDIT-008 (50.42), Sagar (49.27) and US-475 (47.52) required in maximum in days to anthesis of first pistillate flowers. While, the three genotypes viz., US-484 (32.59) followed by Amanshri (35.97) and Narendra Barahmasi-2 (36.21) of lower days to anthesis of first pistillate flowers.

4.2.5

Days to first fruit harvest

It is explicated from the data recorded on days to first fruit harvest that varied from 43.66 (Arka Harit) to 63.51 (Kashi Urvasi). The general mean for days to first fruit harvest was 52.85. Out of twenty genotypes of best five genotypes viz., Kashi Urvasi (63.51) followed by Selection-5 (61.83), UDIT-008 (60.66), US-484 (60.33) and US-475(57.83). Three genotypes Arka Harit (4.66) followed by Narendra Barahmasi-1(44.51) and Kalyanpur Barahmasi (46.33) revealed significantly lesser days to first fruit harvest.

4.2.6

Vine length (m)

The data recorded on vine length clearly indicated that the highest and lowest value for vine length was observed in case of 3.25 m (Amanshri) and 5.80 m (Narendra Barahmasi-1) clearly indicated that the grand mean for vine length 4.71 m was recorded. Five best genotypes namely, Narendra Barahmasi-1(5.80 m) followed by Selection-5 (5.65 m), Arka Harit (5.60 m), Sagar (5.56 m) and Kashi Urvasi (5.52 m). While, the minimum vine

length was observed in Amanshri (3.25 m) followed by UDIT-008 (3.31 m) and Pusa Hybrid-2 (3.46 m).

4.2.7

Fruit length (cm)

It is conspicuous from the data recorded on the highest and lowest range values for fruit length was observed in case of 24.39 cm (Selection-5) and 13.09 cm (Pusa hybrid-2); respectively and grand mean for fruit length was 19.54 cm observed. Best five genotypes namely, Selection-5 (24.39 cm) followed by Ultima-1405 (23.94 cm), Sagar (22.90 cm), Kalyanpur Sona (22.44 cm) and Meghana-2 (22.26 cm). While, the minimum fruit length was observed in MC-23 (15.61 cm) followed by Arka Sujat (14.83 cm) and Pusa hybrid-2 (13.09 cm).

4.2.8

Nodes per plant

The data recorded on the nodes per plant revealed that the nodes per plant varied from 40.83 (Selection-5) to 73.00 (Arka Sujat). The general mean for nodes per plant 56.46 was observed. Out of twenty genotypes of best five genotypes viz., Arka Sujat (73.00) followed by Kalyanpur Sona (72.16), Arka Harit (64.83) Kalyanpur Barahmasi (64.00) and Meghana-2 (63.83). While, the three genotypes MC-23 (44.33) followed by Amanshri (42.00) and Selection-5 (40.83) was minimum value observed in nodes per plant.

4.2.9

Number of branches per plant

It is quite clear from the data recorded on number of branches per plant ranged from 8.16 (Ultima-1405) to 24.83 (Amanshri) with general mean 8.11 was recorded. Out of twenty genotypes, overall of five highest number of branches per plant genotypes viz., Amanshri (24.83) followed by VRBT-23 (23.83), UDIT-008 (22.50), US-475 (22.16) and Kashi Urvasi (21.50). Whereas, the lowest number of branches per plant was observed in Meghana-2 (10.66) followed by Narendra Barahmasi-2 (8.33) and Ultima-1405 (8.16).

4.2.10

Number of seeds per fruit

It is evident from the data that the number of seeds per fruit ranged from 16.16 (Narendra Barahmasi-1) to 31.00 (US-475) with general mean was 21.92 observed. Out of twenty genotypes, overall of five maximum numbers of seeds per fruit viz., US-475 (31.00) followed by Kalyanpur Barahmasi (28.16), Narendra Barahmasi-2 (27.33), Arka Sujat (26.50) and UDIT-1405 (25.50). Whereas, the minimum number of seeds per fruit was observed in Pusa Hybrid-1 (18.66) followed by MC-23 (17.16) and Narendra Barahmasi-1 (16.16).

4.2.11

Fruit diameter (cm)

The data recorded on fruit diameter showed that the general mean of the genotype for fruit diameter 6.42 cm was recorded. Whereas, it ranged from 4.62 cm (Ultima-1405) to 9.42 cm (Kalyanpur Barahmasi). Among the tests genotypes, five genotypes namely, Kalyanpur Barahmasi (9.42 cm) followed by US-475 (8.31 cm), Amanshri (7.75 cm), Pusa hybrid-1 (7.52 cm) and VRBT-23 (7.31 cm) showed higher significant genotypes. However, the minimum fruit diameter was recorded in this genotypes Narendra Barahmasi-2 (3.52 cm) followed by Narendra Barahmasi-1 (4.58 cm) and Ultima-1405 (4.62 cm).

4.2.12

Number of fruits per plant

It is conspicuous from the data that the number of fruits per fruit varied from 9.16 (Ultima-1405) to 20.16 (Pusa Vishesh) with the general mean 13.14 was recorded. Best five highest number of fruits per fruit of genotypes namely, Pusa Vishesh (20.16) followed by Amanshri (18.50), UDIT-008 (17.83), Kalyanpur Barahmasi (16.16) and Pusa hybrid-2 (15.83). While, the minimum number of fruits per fruit was noted in Narendra Barahmasi-2 (11.00) followed by MC-23 (9.83) and Ultima-1405 (9.16).

4.2.13

Seeds weight per fruit (g)

It is apparent from the data observed on seeds weight per fruit varied from 2.54 g (Selection-5) to 3.84 g (Kashi Urvasi) with the general mean 3.37 g was observed. Five maximum seeds weight per fruit of genotypes namely, Kashi Urvasi (3.84 g) followed by Pusa Vishesh (3.80 g), UDIT-008 (4.22 g), Pusa hybrid-2 (3.52 g) and Amanshri (3.50 g). Whereas, the minimum seeds weight per fruit was showed in Pusa Hybrid-1 (3.26 g) followed by MC-23 (2.56 g) and Selection-5 (2.54 g).

4.2.14

Average fruit weight (g)

It is lucid from the data showed that the average fruit weight ranged from 53.66 g (MC-23) to 126.83 g (Kalyanpur Barahmasi). While the general mean 82.25 g was noted. Best five highest average fruit weight genotypes namely, Kalyanpur Barahmasi (126.83 g) followed by VRBT-23 (120.83 g), Pusa Vishesh (119.16 g), Meghana-2 (115.66 g), Pusa Hybrid -2 (110.33 g). While, the minimum average fruit weight was observed in Narendra Barahmasi-2 (55.83 g) followed by Sagar (55.00) and MC-23 (53.66 g).

4.2.15

Ascorbic acid (mg/100g)

The data clearly revealed that the ascorbic acid (mg/100g) varied from 79.50 mg/100g (Narendra Barahmasi-2) to 95.50 mg/100g (Amanshri) with general mean 86.65 mg/100g was observed. The maximum ascorbic acid (mg/100g) was found in the genotypes namely, Amanshri (95.50 mg/100g) followed by Ultima-1405 (94.33 mg/100g), Pusa Hybrid-1 (93.16 mg/100g), VRBT-23 (92.16 mg/100g) and Pusa Hybrid-2 (91.16 mg/100g). While the minimum ascorbic acid (mg/100g) recorded in this genotypes Pusa Vishesh (80.33 mg/100g) followed by Kalyanpur Barahmasi (79.83 mg/100g) and Narendra Barahmasi-2 (79.50 mg/100g).

4.2.16 Reducing sugar (%)

It is quite clear from the data showed that the highest and lowest range from reducing sugar was observed in case of 0.54% (US-484) and 0.98% (Amanshri), respectively and grand mean of reducing sugar 0.82% was noted. The genotypes showed maximum reducing sugar, Amanshri (0.98%) followed by UDIT-008 (0.95%), US-475 (0.90%), Sagar (0.88%) and Kalyanpur Barahmasi (0.85%). While, the minimum reducing sugar was observed in Kashi Urvasi (0.81%) followed by VRBT-23 (0.78%) and US-484 (0.75%).

4.2.17 Non-reducing sugar (%)

It is evident from the data observed on the highest and lowest range from non-reducing sugar was observed in case of 0.30% (US-484) and 0.72% (Amanshri), respectively and grand mean of non-reducing sugar 0.50% was showed. The genotypes showed maximum non-reducing sugar, Amanshri (0.72%) followed by UDIT-008 (0.70%), US-475 (0.64%), Sagar (0.62%) and Kalyanpur Barahmasi (0.57%). However, the minimum non-reducing sugar was observed in VRBT-23 (0.36%) followed by Kashi Urvasi (0.33%) and US-484 (0.30%).

4.2.18 Total sugars (%)

It is explicated from the data recorded on the highest and lowest range from total sugars was observed in case of 1.13% (US-484) and 1.71% (Amanshri), respectively and grand mean of total sugars 1.40% was observed. The genotypes showed maximum total sugars, Amanshri (1.71%) followed by UDIT-008 (1.66%), US-475 (1.63%), Sagar (1.60%) and Kalyanpur Barahmasi (1.54%). Whereas, the minimum total sugars was observed in Kashi Urvasi (1.18%) followed by VRBT-23 (1.15%) and US-484 (1.13%).

4.2.19

Total soluble solids (T.S.S.) (^oBrix)

It is conspicuous from the data recorded on total soluble solids (^oBrix) varied from 5.31 ^oBrix (Amanshri) to 2.41 ^oBrix (Pusa Hybird-2) with general mean 3.56 ^oBrix was observed. Out of 20 genotypes none of the genotypes found significant for TSS all over best genotypes namely, Amanshri (5.31 ^oBrix) followed by Selection-5 (5.22 ^oBrix), US-

475 (4.83 °Brix), Sagar (4.54 °Brix) and Ultima-1405 (4.41 °Brix). While, the minimum TSS observed in this genotypes Narendra Barahmasi-1 (2.59 °Brix) followed by Kalyanpur Sona (2.50 °Brix) and Pusa Hybrid -2 (2.41 °Brix).

4.2.20

Titrateable acidity (%)

It is obvious from the data showed on titrateable acidity (%) ranged from 0.11% (Pusa Hybrid-2) to 0.32% (Pusa Hybrid-1) with the general mean 0.23% was recorded. Out of five maximum titrateable acidity (%) was found in Pusa Hybrid-1 (0.32%) followed by Narendra Barahmasi-2 (0.31%), Arka Harit (0.30%), Selection-5 (0.30%) and Kashi Urvasi (0.27%). While, the lowest titrateable acidity (%) was observed in Kalyanpur Barahmasi (0.15%) followed by Kalyanpur Sona (0.13%) and Pusa Hybrid-2 (0.11%).

4.2.21

Marketable fruit yield per plant (kg)

It is apparent from the data recorded on marketable fruit yield per plant (kg) varied from 1.61 kg (Arka Sujat) to 5.24 kg (Kalyanpur Barahmasi) with the general mean 2.85 kg was recorded. Out of twenty genotypes maximum marketable fruit yield of plant (kg) of the genotypes namely, Kalyanpur Barahmasi (5.24 kg) followed by Kashi Urvasi (4.30 kg), Arka Harit (3.70 kg), Selection-5 (3.55 kg) and Pusa hybrid-1 (3.39 kg). Whereas, the minimum marketable fruit yield per plant (kg) was found in VRBT-23 (1.73 kg) followed by MC-23 (1.63 kg) and Arka Sujat (1.61 kg) respectively.

4.3 Coefficient of variation, heritability and genetic advance as percent of mean for twenty one characters

4.3.1 Coefficient of variation:

The estimates of genotypic and phenotypic of variation for twenty one characters of bitter gourd genotypes have been presented in **Table-4.3**. Variability is helpful to measure the extent of variability present in particular character. It also provides measure to compare the variability present among various metric traits. The estimates of phenotypic coefficient of variation (PCV) were higher than genotypic coefficient variation (GCV) for all the characters.

The highest phenotypic as well as genotypic coefficient of variation were observed in marketable fruit yield per plant (39.36%) followed by average fruit weight (29.73%), number of branches per plant (27.18%), titratable acidity (27.06%), total soluble solids (26.21%), fruit diameter (23.58%), non-reducing sugar (22.26%) and number of fruits per plant (21.56%). Whereas, the node number to first staminate flowers (19.37), seeds weight per fruit (19.16%), number of seeds per fruit (18.92%), fruit length (17.48%) and vine length (17.15%) moderate coefficient of variation. While total sugars (12.58%), days to first fruit harvest (12.24%), days to anthesis of first staminate flowers (11.09%) and ascorbic acid (6.15%) had lowest coefficient of variation.

4.3.2 Heritability in broad sense per cent (h^2_{bs}):

The results of the coefficients of variation were followed by the data for heritability assessment in the genotype. All the data of the heritability in broad sense (h^2_{bs}) were presented in **Table-4.3**. The observed favourable in results which are described as follows:

The estimates of heritability in broad sense ranged from 41.5 percent (Seeds weight per fruit) to 98.6 percent (average fruit weight). High estimates of heritability (>80%) were recorded for different characters *viz.*, average fruit weight (98.6%) followed by total soluble solids (97.8%), total sugars (97.7%), days to anthesis of first pistillate flowers (97.2%), nodes per plant (96.6%), non-reducing sugar (96.5%), marketable fruit yield per plant (96.4%), number of branches per plant (95.5%), vine length (88.6%), days to first fruit harvest (88.5%), number of fruits per plant (86.5%) and fruit diameter (82.3%).

However, moderate heritability (>60% to <80%) was observed for node number to first pistillate flowers (77.7%) followed by node number to first staminate flowers (73.2%) and low heritability (<60%) was estimated for marketable fruit yield per plant (59.0%) followed by Seeds weight per fruit (41.5%).

4.3.3 Genetic advance in percent of mean:

Maximum value of genetic advance in per cent of mean was shown by average fruit weight (60.14%) while ascorbic acid exhibited minimum value (11.76%) for this parameter. The parameter which observed very high estimate value of genetic advance were average fruit weight (60.14%) followed by titratable acidity (53.73%), number of branches per plant (53.47%), total soluble solids (52.81%), marketable fruit yield per plant (47.87%), non-reducing sugar (44.25%), fruit diameter (39.97%) and number of fruits per plant (38.42%). The moderate genetic advance in per cent of mean was estimated in node number to first staminate flowers (29.24%) followed by days to anthesis of first pistillate flowers (28.80%), reducing sugar (26.91%), total sugars (25.33%), days to first fruit harvest (22.34%) and days to anthesis of first staminate flowers (21.35%) whereas showed Seeds weight per fruit (16.36%) followed by ascorbic acid (11.76%) lowest genetic advance in percent of mean. Higher magnitudes of genetic variability, heritability and genetic advance showing additive gene effect and good response to the selection of germplasm.

Table-4.3.A: Estimates of range, grand mean, and genotypic coefficient of variation (PCV, GCV), heritability in broad sense, genetic advance (GA) in percent of mean for twenty one characters in bitter melon (2018-19)

S. No	Characters	Range		Grand mean	Variations		Heritability in broad sense (%) (h^2_{bs})	Genetic advance	Genetic advance percent of mean
		Min.	Max.		PCV (%)	GCV (%)			
		2018-19							
1.	Node no. to 1 st staminate flowers	7.67	15.00	12.36	17.84	15.22	72.8	3.31	26.77
2.	Node no. to 1 st pistillate flowers	7.67	16.67	12.18	21.06	18.21	74.8	3.95	32.46
3.	Days to anthesis of 1 st staminate flowers	33.85	51.52	39.48	11.18	10.89	95.0	8.63	21.86
4.	Days to anthesis of 1 st pistillate flowers	32.43	54.74	42.27	14.34	14.19	98.0	12.23	28.94
5.	Days to 1 st fruit harvest	46.00	65.00	53.90	11.22	10.66	90.3	11.25	20.87
6.	Vine length (m)	3.24	5.82	4.73	17.67	15.88	80.8	1.39	29.41
7.	Fruit length (cm)	13.33	24.35	19.53	17.97	16.63	85.6	6.19	31.69
8.	Nodes per plant	40.33	73.33	57.30	16.40	16.22	97.9	18.95	33.07
9.	No. of branches per plant	8.33	25.00	18.21	26.89	26.11	94.3	9.51	52.25
10.	No. of seeds per fruit	16.00	30.67	22.06	18.55	17.71	91.1	7.68	34.82
11.	Fruit diameter (cm)	3.51	9.50	6.44	23.47	20.79	78.5	2.44	37.97
12.	No. of fruits per plant	9.00	20.00	13.88	21.84	20.06	84.4	5.27	37.96
13.	Seeds weight per fruit (g)	2.54	4.24	3.36	19.59	10.14	26.8	0.36	10.83
14.	Average fruit weight (g)	53.00	127.67	82.13	29.64	29.33	97.9	49.10	59.78
15.	Ascorbic acid (mg/100g)	79.00	95.67	86.71	6.28	6.02	91.8	10.30	11.88
16.	Reducing sugar (%)	0.55	0.97	0.81	13.62	13.22	94.2	0.21	26.43
17.	Non-reducing sugar (%)	0.30	0.72	0.50	22.52	22.35	98.4	0.23	45.68
18.	Total sugars (%)	1.12	1.71	1.40	12.90	12.70	96.9	0.36	25.76
19.	T.S.S. ($^{\circ}$ Brix)	2.40	5.30	3.55	26.38	25.86	96.1	1.85	52.23
20.	Titrateable acidity (%)	0.12	0.33	0.243	26.55	26.11	96.7	0.12	52.90
21.	Marketable fruit yield per plant (kg)	1.60	5.23	2.86	40.34	27.84	47.6	1.13	39.58

Table-4.3.B: Estimates of range, grand mean, phenotypic and genotypic coefficient of variation (PCV, GCV), heritability in broad sense, genetic advance (GA) in percent of mean for twenty one characters in bitter melon (2019-20)

S. No	Characters	Range		Grand mean	Variations		Heritability in broad sense (%) (h^2_{bs})	Genetic advance	Genetic advance percent of mean
		Min.	Max.		PCV (%)	GCV (%)			
		2019-20							
1.	Node no. to 1 st staminate flowers	7.00	15.33	11.91	20.90	17.92	73.5	3.77	31.66
2.	Node no. to 1 st pistillate flowers	8.00	16.33	12.00	20.12	17.82	78.4	3.90	32.51
3.	Days to anthesis of 1 st staminate flowers	33.52	51.35	39.52	11.00	10.47	90.6	8.12	20.54
4.	Days to anthesis of 1 st pistillate flowers	32.76	55.37	42.55	14.42	14.17	96.7	12.22	28.71
5.	Days to 1 st fruit harvest	41.33	62.00	51.80	13.26	12.83	93.6	13.25	25.58
6.	Vine length (m)	3.26	5.79	4.69	16.61	16.26	95.8	1.53	32.78
7.	Fruit length (cm)	14.48	24.44	19.56	16.98	16.35	92.7	6.34	32.44
8.	Nodes per plant	41.33	72.67	55.63	16.76	16.62	98.3	18.88	33.95
9.	No. of branches per plant	8.00	24.67	18.01	27.47	26.83	95.4	9.72	53.98
10.	No. of seeds per fruit	16.33	31.33	21.78	19.29	18.76	94.6	8.19	37.60
11.	Fruit diameter (cm)	3.55	9.35	6.40	23.69	21.42	81.8	2.55	39.92
12.	No. of fruits per plant	9.33	20.33	14.00	21.28	19.63	85.1	5.22	37.31
13.	Seeds weight per fruit (g)	2.55	4.22	3.37	18.72	11.29	36.4	0.47	14.04
14.	Average fruit weight (g)	54.33	126.00	82.36	29.81	29.63	98.8	49.99	60.69
15.	Ascorbic acid (mg/100g)	80.00	95.33	86.58	6.01	5.81	93.6	10.03	11.58
16.	Reducing sugar (%)	0.54	0.99	0.82	14.36	14.10	96.3	0.23	28.51
17.	Non-reducing sugar (%)	0.31	0.73	0.51	22.00	21.72	97.5	0.22	44.19
18.	Total sugars (%)	1.15	1.72	1.40	12.26	12.14	98.0	0.34	24.76
19.	T.S.S. ($^{\circ}$ Brix)	2.43	5.33	3.58	26.04	25.88	98.8	1.89	53.00
20.	Titratable acidity (%)	0.11	0.32	0.234	27.58	26.91	95.2	0.12	54.11
21.	Marketable fruit yield per plant (kg)	1.62	5.26	2.85	38.34	27.39	51.0	1.15	40.31

Table-4.3.C: Estimates of range, grand mean, phenotypic and genotypic coefficient of variation (PCV, GCV), heritability in broad sense, genetic advance (GA) in percent of mean for twenty one characters in bitter melon (Pooled data)

S. No	Characters	Range		Grand mean	Variations		Heritability in broad sense (%) (h^2_{bs})	Genetic advance	Genetic advance percent of mean
		Min.	Max.		PCV (%)	GCV (%)			
		Pooled data							
1.	Node no. to 1 st staminate flowers	7.33	15.16	12.14	19.37	16.58	73.2	3.55	29.24
2.	Node no. to 1 st pistillate flowers	7.83	16.50	12.09	20.60	18.16	77.7	3.99	32.99
3.	Days to anthesis of 1 st staminate flowers	33.68	51.43	39.50	11.09	10.72	93.5	8.44	21.37
4.	Days to anthesis of 1 st pistillate flowers	32.59	55.05	42.41	14.38	14.18	97.2	12.21	28.80
5.	Days to 1 st fruit harvest	43.66	63.50	52.85	12.24	11.52	88.5	11.80	22.34
6.	Vine length (m)	3.25	5.80	4.71	17.15	16.15	88.6	1.47	31.32
7.	Fruit length (cm)	13.90	24.39	19.54	17.48	16.65	90.8	6.39	32.69
8.	Nodes per plant	40.83	73.00	56.46	16.57	16.29	96.6	18.62	32.98
9.	No. of branches per plant	8.16	24.83	18.11	27.18	26.52	95.5	9.68	53.47
10.	No. of seeds per fruit	16.16	31.00	21.92	18.92	18.29	93.4	7.98	36.41
11.	Fruit diameter (cm)	3.52	9.42	6.42	23.58	21.39	82.3	2.56	39.97
12.	No. of fruits per plant	9.16	20.16	13.94	21.56	20.05	86.5	5.35	38.42
13.	Seeds weight per fruit (g)	2.54	4.22	3.37	19.16	12.33	41.5	0.55	16.36
14.	Average fruit weight (g)	53.66	126.83	82.25	29.73	29.5	98.6	49.69	60.41
15.	Ascorbic acid (mg/100g)	79.50	95.50	86.65	6.15	5.92	92.9	10.19	11.76
16.	Reducing sugar (%)	0.54	0.98	0.82	14.00	13.52	93.3	0.22	29.91
17.	Non-reducing sugar (%)	0.30	0.72	0.50	22.26	21.87	96.5	0.22	44.25
18.	Total sugars (%)	1.13	1.71	1.40	12.58	12.44	97.7	0.35	25.33
19.	T.S.S. (^o Brix)	2.41	5.31	3.56	26.21	25.92	97.8	1.88	52.81
20.	Titrateable acidity (%)	0.11	0.32	0.23	27.06	26.56	96.4	0.12	53.73
21.	Marketable fruit yield per plant (kg)	1.61	5.24	2.85	39.36	30.24	59.0	1.36	47.87

Table-4.4.A: Estimates of genotypic correlation coefficients between 20 different characters in bitter melon (2018-19)

S. No.	Characters	Node no. to 1 st staminate flowers	Node no. to 1 st pistillate flowers	Days to anthesis of 1 st staminate flowers	Days to anthesis of 1 st pistillate flowers	Days to 1 st fruit harvest	Vine length (m)	Fruit length (cm)
		1	2	3	4	5	6	7
1.	Node no. to 1 st staminate flowers	1.000	0.584**	-0.198	-0.234	-0.255*	-0.325*	-0.208
2.	Node no. to 1 st pistillate flowers		1.000	0.234	-0.168	-0.591**	0.008	-0.261*
3.	Days to anthesis of 1 st staminate flowers			1.000	0.084	-0.108	0.148	-0.030
4.	Days to anthesis of 1 st pistillate flowers				1.000	0.314*	0.016	0.413**
5.	Days to 1 st fruit harvest					1.000	-0.132	0.471**
6.	Vine length (m)						1.000	0.175
7.	Fruit length (cm)							1.000
8.	Nodes/plant							
9.	No. of branches/plant							
10.	No. of seeds/fruit							
11.	Fruit diameter (cm)							
12.	No. of fruits /plant							
13.	Seeds weight/fruit (g)							
14.	Average fruit weight (g)							
15.	Ascorbic acid (mg/100g)							
16.	Reducing sugar (%)							
17.	Non-reducing sugar (%)							
18.	Total sugars (%)							
19.	T.S.S. (^o Brix)							
20.	Titrateable acidity (%)							

S. No.	Characters	Nodes/ plant	No. of branches/ plant	No. of seeds/ fruit	Fruit diameter (cm)	No. of fruits/ plant	Seeds weight/ fruit (g)	Average fruit weight (g)
		8	9	10	11	12	13	14
1.	Node no. to I st staminate flowers	0.060	0.234	-0.161	-0.081	0.721**	0.714**	0.366**
2.	Node no. to I st pistillate flowers	0.264*	-0.016	-0.287*	-0.226	0.606**	0.522**	0.261*
3.	Days to anthesis of I st staminate flowers	0.370**	-0.116	0.291*	-0.106	-0.291*	-0.051	-0.253
4.	Days to anthesis of I st pistillate flowers	0.267*	0.039	0.145	0.015	-0.052	0.121	-0.044
5.	Days to I st fruit harvest	-0.101	0.100	0.241	-0.071	-0.306*	0.104	-0.216
6.	Vine length (m)	-0.193	-0.339**	-0.402**	-0.213	-0.427**	-0.644**	-0.322*
7.	Fruit length (cm)	-0.098	-0.135	-0.065	0.226	-0.129	-0.396**	-0.015
8.	Nodes/plant	1.000	-0.079	0.449**	-0.036	0.089	0.573**	0.329*
9.	No. of branches/plant		1.000	0.082	0.547**	0.352**	0.522**	0.163
10.	No. of seeds/fruit			1.000	0.283*	0.023	0.162	0.202
11.	Fruit diameter (cm)				1.000	0.256*	0.068	0.335**
12.	No. of fruits/plant					1.000	0.716**	0.491**
13.	Seeds weight/fruit (g)						1.000	0.272*
14.	Average fruit weight (g)							1.000
15.	Ascorbic acid (mg/100g)							
16.	Reducing sugar (%)							
17.	Non-reducing sugar (%)							
18.	Total sugars (%)							
19.	T.S.S. (^o Brix)							
20.	Titrateable acidity (%)							

Continued...

S. No.	Characters	Ascorbic acid (mg/100g)	Reducing sugar (%)	Non-reducing sugar (%)	Total sugars (%)	T.S.S. (^o Brix)	Titrateable acidity (%)	Marketable fruit yield /plant (kg)
		15	16	17	18	19	20	21
1.	Node no. to I st staminate flowers	-0.031	0.369**	-0.068	-0.286*	-0.501**	-0.012	0.331**
2.	Node no. to I st pistillate flowers	-0.066	0.396**	0.087	-0.032	-0.278*	-0.143	0.213
3.	Days to anthesis of I st staminate flowers	-0.158	0.259*	0.030	0.122	0.116	-0.020	0.179
4.	Days to anthesis of I st pistillate flowers	-0.462**	0.102	0.222	0.235	0.243	-0.054	-0.005
5.	Days to I st fruit harvest	-0.104	0.056	-0.147	-0.108	0.449**	0.158	0.100
6.	Vine length (m)	-0.435**	-0.387**	-0.358**	-0.277*	0.129	0.542**	0.270*
7.	Fruit length (cm)	0.176	0.193	0.204	0.143	0.306*	0.010	0.516**
8.	Nodes/plant	-0.249	0.488**	0.081	-0.110	-0.468**	-0.246	0.094
9.	No. of branches/plant	-0.183	0.300*	-0.016	0.034	0.234	-0.236	-0.069
10.	No. of seeds/fruit	-0.057	0.373**	0.318*	0.253	0.035	-0.137	0.235
11.	Fruit diameter (cm)	0.183	0.186	0.358**	0.269*	0.137	-0.321*	0.295*
12.	No. of fruits /plant	-0.031	0.504**	0.393**	0.157	-0.213	-0.091	0.422**
13.	Seed weight/fruit (g)	-0.448**	0.753**	0.265*	0.038	-0.204	-0.196	-0.272*
14.	Average fruit weight (g)	0.153	0.076	-0.134	-0.267*	-0.637**	-0.590**	0.199
15.	Ascorbic acid (mg/100g)	1.000	-0.023	0.188	0.163	-0.046	-0.305*	-0.147
16.	Reducing sugar (%)		1.000	0.536**	0.374**	0.081	-0.046	0.384**
17.	Non-reducing sugar (%)			1.000	0.879**	0.320*	-0.002	0.150
18.	Total sugars (%)				1.000	0.474**	-0.132	0.042
19.	T.S.S. (^o Brix)					1.000	0.281*	-0.029
20.	Titrateable acidity (%)						1.000	0.137

*and** shows significant at 5% and 1%, respectively

Table-4.4.B: Estimates of genotypic correlation coefficients between 20 different characters in bitter gourd (2019-20)

S. No.	Characters	Node no. to I st staminate flowers	Node no. to I st pistillate flowers	Days to anthesis of I st staminate flowers	Days to anthesis of I st pistillate flowers	Days to I st fruit harvest	Vine length (m)	Fruit length (cm)
		1	2	3	4	5	6	7
1.	Node no. to I st staminate flowers	1.000	0.529**	-0.034	-0.042	-0.126	-0.134	-0.145
2.	Node no. to I st pistillate flowers		1.000	0.175	-0.292*	-0.465**	0.015	-0.122
3.	Days to anthesis of I st staminate flowers			1.000	0.123	-0.095	0.055	-0.077
4.	Days to anthesis of I st pistillate flowers				1.000	0.277*	0.033	0.438**
5.	Days to I st fruit harvest					1.000	-0.277*	0.232
6.	Vine length (m)						1.000	0.061
7.	Fruit length (cm)							1.000
8.	Nodes/plant							
9.	No. of branches/plant							
10.	No. of seeds/fruit							
11.	Fruit diameter (cm)							
12.	No. of fruits /plant							
13.	Seeds weight/fruit (g)							
14.	Average fruit weight (g)							
15.	Ascorbic acid (mg/100g)							
16.	Reducing sugar (%)							
17.	Non-reducing sugar (%)							
18.	Total sugars (%)							
19.	T.S.S. (^o Brix)							
20.	Titrateable acidity (%)							

Continued...

S. No.	Characters	Nodes/ plant	No. of branches/ plant	No. of seeds/ fruit	Fruit diameter (cm)	No. of fruits/ plant	Seeds weight/ fruit (g)	Average fruit weight (g)
		8	9	10	11	12	13	14
1.	Node no. to 1 st staminate flowers	0.007	0.051	-0.142	-0.235	0.652**	0.469**	0.263*
2.	Node no. to 1 st pistillate flowers	0.166	0.012	-0.298*	-0.265*	0.592**	0.391**	0.308*
3.	Days to anthesis of 1 st staminate flowers	0.465**	-0.135	0.387**	-0.039	-0.157	-0.229	-0.287*
4.	Days to anthesis of 1 st pistillate flowers	0.380**	-0.055	0.169	0.058	-0.084	-0.042	-0.033
5.	Days to 1 st fruit harvest	-0.138	0.259*	0.180	0.040	-0.171	0.223	-0.227
6.	Vine length (m)	-0.122	-0.256*	-0.360**	-0.351**	-0.352**	-0.349**	-0.239
7.	Fruit length (cm)	-0.072	-0.189	-0.049	0.281*	-0.160	-0.235	0.014
8.	Nodes/plant	1.000	-0.159	0.429**	-0.060	0.164	0.264*	0.179
9.	No. of branches/plant		1.000	0.119	0.581**	0.378**	0.648**	0.190
10.	No. of seeds/fruit			1.000	0.446**	-0.005	0.236	0.192
11.	Fruit diameter (cm)				1.000	0.215	0.176	0.351**
12.	No. of fruits /plant					1.000	0.609**	0.456**
13.	Seeds weight/fruit (g)						1.000	0.402**
14.	Average fruit weight (g)							1.000
15.	Ascorbic acid (mg/100g)							
16.	Reducing sugar (%)							
17.	Non-reducing sugar (%)							
18.	Total sugars (%)							
19.	T.S.S. (^o Brix)							
20.	Titrateable acidity (%)							

Continued...

S. No.	Characters	Ascorbic acid (mg/100g)	Reducing sugar (%)	Non-reducing sugar (%)	Total sugars (%)	T.S.S. (^o Brix)	Titrateable acidity (%)	Marketable fruit yield /plant (kg)
		15	16	17	18	19	20	21
1.	Node no. to I st staminate flowers	-0.091	0.128	-0.062	-0.197	-0.398**	0.184	0.243
2.	Node no. to I st pistillate flowers	0.092	0.371**	0.021	0.002	-0.254	-0.191	0.399**
3.	Days to anthesis of I st staminate flowers	-0.187	0.329*	0.151	0.194	0.104	0.029	0.203
4.	Days to anthesis of I st pistillate flowers	-0.464**	0.178	0.144	0.200	0.222	-0.077	-0.070
5.	Days to I st fruit harvest	-0.168	0.178	-0.183	-0.049	0.443**	0.099	-0.024
6.	Vine length (m)	-0.488**	-0.432**	-0.337**	-0.347**	0.068	0.474**	0.155
7.	Fruit length (cm)	0.187	0.204	0.177	0.192	0.290*	-0.037	0.472**
8.	Nodes/plant	-0.374**	0.512**	0.099	-0.010	-0.389**	-0.122	0.115
9.	No. of branches/plant	-0.149	0.340**	-0.051	0.031	0.163	-0.272*	-0.126
10.	No. of seeds/fruit	-0.074	0.510**	0.241	0.233	0.044	-0.101	0.224
11.	Fruit diameter (cm)	0.288*	0.363**	0.322*	0.274*	0.159	-0.334**	0.213
12.	No. of fruits /plant	-0.048	0.458**	0.299*	0.154	-0.256*	-0.034	0.278*
13.	Seeds weight/fruit (g)	-0.286*	0.680**	0.076	0.022	-0.236	-0.189	-0.078
14.	Average fruit weight (g)	0.244	0.146	-0.193	-0.264*	-0.661**	-0.573**	0.160
15.	Ascorbic acid (mg/100g)	1.000	-0.060	0.186	0.136	-0.049	-0.323*	-0.068
16.	Reducing sugar (%)		1.000	0.405**	0.404**	0.156	-0.153	0.285*
17.	Non-reducing sugar (%)			1.000	0.916**	0.342**	0.005	0.080
18.	Total sugars (%)				1.000	0.472**	-0.123	0.049
19.	T.S.S. (^o Brix)					1.000	0.286*	-0.035
20.	Titrateable acidity (%)						1.000	0.076

*and** significant at 5% and 1% respectively

Table-4.4.C: Estimates of genotypic correlation coefficients between 20 different characters in bitter melon (Pooled data)

S. No	Characters	Node no. to I st staminate flowers	Node no. to I st pistillate flowers	Days to anthesis of I st staminate flowers	Days to anthesis of I st pistillate flowers	Days to I st fruit harvest	Vine length (m)	Fruit length (cm)
		1	2	3	4	5	6	7
1.	Node no. to I st staminate flowers	1.000	0.567**	-0.124	-0.134	-0.171	-0.227*	-0.172
2.	Node no. to I st pistillate flowers		1.000	0.205*	-0.223*	-0.526**	0.018	-0.191
3.	Days to anthesis of I st staminate flowers			1.000	0.101	-0.110	0.105	-0.053
4.	Days to anthesis of I st pistillate flowers				1.000	0.309**	0.026	0.423**
5.	Days to I st fruit harvest					1.000	-0.225*	0.347**
6.	Vine length (m)						1.000	0.118
7.	Fruit length (cm)							1.000
8.	Nodes/plant							
9.	No. of branches/plant							
10.	No. of seeds/fruit							
11.	Fruit diameter (cm)							
12.	No. of fruits /plant							
13.	Seeds weight/fruit (g)							
14.	Average fruit weight (g)							
15.	Ascorbic acid (mg/100g)							
16.	Reducing sugar (%)							
17.	Non-reducing sugar (%)							
18.	Total sugars (%)							
19.	T.S.S. (^o Brix)							
20.	Titrateable acidity (%)							

Continued...

S. No.	Characters	Nodes/ plant	No. of branches/ plant	No. of seeds/ fruit	Fruit diameter (cm)	No. of fruits/ plant	Seeds weight/ fruit (g)	Average fruit weight (g)
		8	9	10	11	12	13	14
1.	Node no. to I st staminate flowers	0.015	0.137	-0.148	-0.159	0.676**	0.502**	0.310**
2.	Node no. to I st pistillate flowers	0.217*	0.001	-0.278**	-0.245*	0.593**	0.387**	0.280**
3.	Days to anthesis of I st staminate flowers	0.416**	-0.125	0.336**	-0.075	-0.223*	-0.123	-0.268**
4.	Days to anthesis of I st pistillate flowers	0.325**	-0.005	0.156	0.032	-0.068	0.047	-0.039
5.	Days to I st fruit harvest	-0.123	0.183	0.215*	-0.020	-0.236*	0.146	-0.228*
6.	Vine length (m)	-0.151	-0.294**	-0.381**	-0.280**	-0.384**	-0.421**	-0.279**
7.	Fruit length (cm)	-0.086	-0.160	-0.058	0.258**	-0.142	-0.253**	0.002
8.	Nodes/plant	1.000	-0.117	0.442**	-0.042	0.123	0.378**	0.256**
9.	No. of branches/plant		1.000	0.099	0.552**	0.363**	0.514**	0.176
10.	No. of seeds/fruit			1.000	0.367**	0.005	0.175	0.196*
11.	Fruit diameter (cm)				1.000	0.226*	0.077	0.338**
12.	No. of fruits/plant					1.000	0.589**	0.468**
13.	Seeds weight/fruit (g)						1.000	0.301**
14.	Average fruit weight (g)							1.000
15.	Ascorbic acid (mg/100g)							
16.	Reducing sugar (%)							
17.	Non-reducing sugar (%)							
18.	Total sugars (%)							
19.	T.S.S. (^o Brix)							
20.	Titrateable acidity (%)							

Continued...

S. No.	Characters	Ascorbic acid (mg/100g)	Reducing sugar (%)	Non-reducing sugar (%)	Total sugars (%)	T.S.S. (^o Brix)	Titratable acidity (%)	Marketable fruit yield /plant (kg)
		15	16	17	18	19	20	21
1.	Node no. to I st staminate flowers	-0.0670	0.240*	-0.0540	-0.239**	-0.444**	0.0940	0.251**
2.	Node no. to I st pistillate flowers	0.0130	0.388**	0.0530	-0.0150	-0.266**	-0.1570	0.264**
3.	Days to anthesis of I st staminate flowers	-0.1710	0.297**	0.0960	0.1570	0.1080	0.0040	0.1750
4.	Days to anthesis of I st pistillate flowers	-0.463**	0.1420	0.1840	0.215*	0.233*	-0.0630	-0.0330
5.	Days to I st fruit harvest	-0.1350	0.1320	-0.1640	-0.0760	0.453**	0.1340	0.0340
6.	Vine length (m)	-0.463**	-0.421**	-0.349**	-0.314**	0.1000	0.504**	0.1890
7.	Fruit length (cm)	0.1800	0.1940	0.1910	0.1640	0.294**	-0.0150	0.433**
8.	Nodes/plant	-0.314**	0.512**	0.0880	-0.0600	-0.433**	-0.1830	0.0970
9.	No. of branches/plant	-0.1630	0.326**	-0.0350	0.0340	0.197*	-0.254**	-0.0960
10.	No. of seeds/fruit	-0.0660	0.444**	0.280**	0.241*	0.0410	-0.1220	0.211*
11.	Fruit diameter (cm)	0.231*	0.266**	0.334**	0.267**	0.1460	-0.323**	0.223*
12.	No. of fruits/plant	-0.0310	0.476**	0.339**	0.1530	-0.235*	-0.0640	0.307**
13.	Seeds weight/fruit (g)	-0.323**	0.603**	0.1490	0.0170	-0.195*	-0.1720	-0.1220
14.	Average fruit weight (g)	0.196*	0.1120	-0.1650	-0.265**	-0.646**	-0.580**	0.1640
15.	Ascorbic acid (mg/100g)	1.000	-0.0450	0.1840	0.1490	-0.0470	-0.311**	-0.0970
16.	Reducing sugar (%)		1.000	0.476**	0.396**	0.1250	-0.1020	0.301**
17.	Non-reducing sugar (%)			1.000	0.902**	0.332**	0.0020	0.1060
18.	Total sugars (%)				1.000	0.471**	-0.1270	0.0410
19.	T.S.S. (^o Brix)					1.000	0.282**	-0.0290
20.	Titratable acidity (%)						1.000	0.0980

*and** significant at 5% and 1% respectively

Table-4.5.A: Estimates of phenotypic correlation coefficients between 20 different characters in bitter gourd (2018-19)

S. No	Characters	Node no. to I st staminate flowers	Node no. to I st pistillate flowers	Days to anthesis of I st staminate flowers	Days to anthesis of I st pistillate flowers	Days to I st fruit harvest	Vine length (m)	Fruit length (cm)
		1	2	3	4	5	6	7
1.	Node no. to I st staminate flowers	1.000	0.402**	-0.173	-0.184	-0.202	-0.281*	-0.135
2.	Node no. to I st pistillate flowers		1.000	0.215	-0.137	-0.476**	-0.035	-0.244
3.	Days to anthesis of I st staminate flowers			1.000	0.065	-0.093	0.145	-0.035
4.	Days to anthesis of I st pistillate flowers				1.000	0.289*	0.002	0.387**
5.	Days to I st fruit harvest					1.000	-0.113	0.388**
6.	Vine length (m)						1.000	0.156
7.	Fruit length (cm)							1.000
8.	Nodes/plant							
9.	No. of branches/plant							
10.	No. of seeds/fruit							
11.	Fruit diameter (cm)							
12.	No. of fruits /plant							
13.	Seeds weight/fruit (g)							
14.	Average fruit weight (g)							
15.	Ascorbic acid (mg/100g)							
16.	Reducing sugar (%)							
17.	Non-reducing sugar (%)							
18.	Total sugars (%)							
19.	T.S.S. (°Brix)							
20.	Titrateable acidity (%)							

Continued...

S. No.	Characters	Nodes/ plant	No. of branches/ plant	No. of seeds/ fruit	Fruit diameter (cm)	No. of fruits/ plant	Seeds weight/ fruit (g)	Average fruit weight (g)
		8	9	10	11	12	13	14
1.	Node no. to 1 st staminate flowers	0.037	0.226	-0.146	-0.057	0.563**	0.264*	0.311*
2.	Node no. to 1 st pistillate flowers	0.200	-0.012	-0.227	-0.224	0.453**	0.290*	0.211
3.	Days to anthesis of 1 st staminate flowers	0.361**	-0.115	0.268*	-0.106	-0.264*	-0.040	-0.238
4.	Days to anthesis of 1 st pistillate flowers	0.263*	0.045	0.133	0.008	-0.051	0.088	-0.045
5.	Days to 1 st fruit harvest	-0.104	0.068	0.250	-0.078	-0.270*	0.038	-0.215
6.	Vine length (m)	-0.158	-0.286*	-0.354**	-0.169	-0.345**	-0.280*	-0.274*
7.	Fruit length (cm)	-0.086	-0.101	-0.083	0.238	-0.113	-0.127	0.006
8.	Nodes/plant	1.000	-0.079	0.421**	-0.026	0.090	0.272*	0.323*
9.	No. of branches/plant		1.000	0.070	0.500**	0.335**	0.272*	0.168
10.	No. of seeds/fruit			1.000	0.262*	0.002	0.114	0.188
11.	Fruit diameter (cm)				1.000	0.213	-0.052	0.306*
12.	No. of fruits/plant					1.000	0.318*	0.451**
13.	Seeds weight/fruit (g)						1.000	0.130
14.	Average fruit weight (g)							1.000
15.	Ascorbic acid (mg/100g)							
16.	Reducing sugar (%)							
17.	Non-reducing sugar (%)							
18.	Total sugars (%)							
19.	T.S.S. (^o Brix)							
20.	Titrateable acidity (%)							

Continued...

S. No.	Characters	Ascorbic acid (mg/100g)	Reducing sugar (%)	Non-reducing sugar (%)	Total sugars (%)	T.S.S. (^o Brix)	Titratable acidity (%)	Marketable fruit yield /plant (kg)
		15	16	17	18	19	20	21
1.	Node no. to I st staminate flowers	-0.037	0.307*	-0.043	-0.242	-0.430**	0.003	0.116
2.	Node no. to I st pistillate flowers	-0.032	0.362**	0.086	-0.017	-0.245	-0.114	0.069
3.	Days to anthesis of I st staminate flowers	-0.157	0.223	0.043	0.115	0.101	-0.022	0.154
4.	Days to anthesis of I st pistillate flowers	-0.428**	0.107	0.216	0.227	0.243	-0.045	-0.018
5.	Days to I st fruit harvest	-0.093	0.038	-0.130	-0.106	0.426**	0.156	0.094
6.	Vine length (m)	-0.389**	-0.378**	-0.315*	-0.273*	0.120	0.497**	0.168
7.	Fruit length (cm)	0.149	0.147	0.187	0.120	0.264*	0.019	0.284*
8.	Nodes/plant	-0.241	0.465**	0.080	-0.106	-0.456**	-0.232	0.075
9.	No. of branches/plant	-0.163	0.290*	-0.013	0.042	0.221	-0.224	-0.087
10.	No. of seeds/fruit	-0.051	0.336**	0.302*	0.232	0.045	-0.139	0.173
11.	Fruit diameter (cm)	0.168	0.157	0.297*	0.245	0.130	-0.275*	0.130
12.	No. of fruits /plant	-0.020	0.443**	0.348**	0.149	-0.225	-0.083	0.204
13.	Seeds weight/fruit (g)	-0.220	0.307*	0.153	-0.027	-0.137	-0.099	-0.034
14.	Average fruit weight (g)	0.140	0.063	-0.130	-0.264*	-0.615**	-0.573**	0.137
15.	Ascorbic acid (mg/100g)	1.000	-0.008	0.172	0.154	-0.039	-0.271*	-0.087
16.	Reducing sugar (%)		1.000	0.508**	0.385**	0.082	-0.038	0.218
17.	Non-reducing sugar (%)			1.000	0.854**	0.313*	-0.001	0.097
18.	Total sugars (%)				1.000	0.451**	-0.127	0.021
19.	T.S.S. (^o Brix)					1.000	0.272*	-0.019
20.	Titratable acidity (%)						1.000	0.075

*and** shows significant at 5% and 1%, respectively

Table-4.5.B: Estimates of phenotypic correlation coefficients between 20 different characters in bitter melon (2019-20)

S. No.	Characters	Node no. to I st staminate flowers	Node no. to I st pistillate flowers	Days to anthesis of I st staminate flowers	Days to anthesis of I st pistillate flowers	Days to I st fruit harvest	Vine length (m)	Fruit length (cm)
		1	2	3	4	5	6	7
1.	Node no. to I st staminate flowers	1.000	0.351**	-0.044	-0.025	-0.068	-0.091	-0.115
2.	Node no. to I st pistillate flowers		1.000	0.106	-0.246	-0.401**	0.011	-0.102
3.	Days to anthesis of I st staminate flowers			1.000	0.109	-0.109	0.049	-0.056
4.	Days to anthesis of I st pistillate flowers				1.000	0.255*	0.036	0.417**
5.	Days to I st fruit harvest					1.000	-0.263*	0.224
6.	Vine length (m)						1.000	0.064
7.	Fruit length (cm)							1.000
8.	Nodes/plant							
9.	No. of branches/plant							
10.	No. of seeds/fruit							
11.	Fruit diameter (cm)							
12.	No. of fruits/plant							
13.	Seeds weight/fruit (g)							
14.	Average fruit weight (g)							
15.	Ascorbic acid (mg/100g)							
16.	Reducing sugar (%)							
17.	Non-reducing sugar (%)							
18.	Total sugars (%)							
19.	T.S.S. (^o Brix)							
20.	Titrateable acidity (%)							

Continued...

S. No.	Characters	Nodes/ plant	No. of branches/ plant	No. of seeds/ fruit	Fruit diameter (cm)	No. of fruits/ plant	Seeds weight/ fruit (g)	Average fruit weight (g)
		8	9	10	11	12	13	14
1.	Node no. to 1 st staminate flowers	-0.001	-0.006	-0.103	-0.179	0.464**	0.224	0.232
2.	Node no. to 1 st pistillate flowers	0.134	0.007	-0.242	-0.202	0.480**	0.172	0.253
3.	Days to anthesis of 1 st staminate flowers	0.440**	-0.127	0.347**	-0.030	-0.151	-0.130	-0.266*
4.	Days to anthesis of 1 st pistillate flowers	0.371**	-0.041	0.156	0.036	-0.063	-0.006	-0.033
5.	Days to 1 st fruit harvest	-0.141	0.236	0.177	0.032	-0.176	0.103	-0.221
6.	Vine length (m)	-0.123	-0.238	-0.351**	-0.321*	-0.312*	-0.208	-0.237
7.	Fruit length (cm)	-0.080	-0.185	-0.050	0.252	-0.144	-0.090	0.017
8.	Nodes/plant	1.000	-0.154	0.418**	-0.038	0.152	0.156	0.176
9.	No. of branches/plant		1.000	0.093	0.478**	0.365**	0.415**	0.185
10.	No. of seeds/fruit			1.000	0.419**	0.011	0.153	0.180
11.	Fruit diameter (cm)				1.000	0.144	0.042	0.311*
12.	No. of fruits/plant					1.000	0.400**	0.418**
13.	Seeds weight/fruit (g)						1.000	0.280*
14.	Average fruit weight (g)							1.000
15.	Ascorbic acid (mg/100g)							
16.	Reducing sugar (%)							
17.	Non-reducing sugar (%)							
18.	Total sugars (%)							
19.	T.S.S. (°Brix)							
20.	Titrateable acidity (%)							

Continued...

S. No.	Characters	Ascorbic acid (mg/100g)	Reducing sugar (%)	Non-reducing sugar (%)	Total sugars (%)	T.S.S. (°Brix)	Titratable acidity (%)	Marketable fruit yield /plant (kg)
		15	16	17	18	19	20	21
1.	Node no. to 1 st staminate flowers	-0.103	0.103	-0.048	-0.181	-0.333**	0.174	0.128
2.	Node no. to 1 st pistillate flowers	0.087	0.339**	0.021	0.010	-0.238	-0.162	0.227
3.	Days to anthesis of 1 st staminate flowers	-0.188	0.301*	0.144	0.188	0.102	0.029	0.110
4.	Days to anthesis of 1 st pistillate flowers	-0.446**	0.180	0.143	0.194	0.221	-0.059	-0.054
5.	Days to 1 st fruit harvest	-0.149	0.164	-0.170	-0.046	0.426**	0.086	-0.016
6.	Vine length (m)	-0.470**	-0.411**	-0.329*	-0.338**	0.064	0.455**	0.090
7.	Fruit length (cm)	0.175	0.188	0.170	0.182	0.283*	-0.062	0.276*
8.	Nodes/plant	-0.365**	0.494**	0.097	-0.009	-0.387**	-0.116	0.078
9.	No. of branches/plant	-0.140	0.335**	-0.044	0.032	0.160	-0.257*	-0.089
10.	No. of seeds/fruit	-0.063	0.481**	0.226	0.221	0.043	-0.098	0.170
11.	Fruit diameter (cm)	0.239	0.312*	0.271*	0.244	0.138	-0.324*	0.119
12.	No. of fruits/plant	-0.022	0.407**	0.270*	0.142	-0.235	-0.027	0.187
13.	Seeds weight/fruit (g)	-0.200	0.356**	0.056	-0.009	-0.128	-0.137	-0.007
14.	Average fruit weight (g)	0.227	0.137	-0.186	-0.260*	-0.649**	-0.559**	0.109
15.	Ascorbic acid (mg/100g)	1.000	-0.062	0.164	0.128	-0.049	-0.305*	-0.055
16.	Reducing sugar (%)		1.000	0.389**	0.405**	0.156	-0.146	0.186
17.	Non-reducing sugar (%)			1.000	0.896**	0.333**	0.011	0.074
18.	Total sugars (%)				1.000	0.466**	-0.122	0.033
19.	T.S.S. (°Brix)					1.000	0.273*	-0.023
20.	Titratable acidity (%)						1.000	0.088

*and** significant at 5% and 1% respectively

Table-4.5.C: Estimates of phenotypic correlation coefficients between 20 different characters in bitter melon (Pooled data)

S. No.	Characters	Node no. to I st staminate flowers	Node no. to I st pistillate flowers	Days to anthesis of I st staminate flowers	Days to anthesis of I st pistillate flowers	Days to I st fruit harvest	Vine length (m)	Fruit length (cm)
		1	2	3	4	5	6	7
1.	Node no. to I st staminate flowers	1.000	0.374**	-0.105	-0.099	-0.127	-0.183	-0.124
2.	Node no. to I st pistillate flowers		1.000	0.162	-0.190*	-0.436**	-0.013	-0.177
3.	Days to anthesis of I st staminate flowers			1.000	0.087	-0.101	0.099	-0.045
4.	Days to anthesis of I st pistillate flowers				1.000	0.271**	0.018	0.401
5.	Days to I st fruit harvest					1.000	-0.189	0.302
6.	Vine length (m)						1.000	0.113
7.	Fruit length (cm)							1.000
8.	Nodes/plant							
9.	No. of branches/plant							
10.	No. of seeds/fruit							
11.	Fruit diameter (cm)							
12.	No. of fruits/plant							
13.	Seeds weight/fruit (g)							
14.	Average fruit weight (g)							
15.	Ascorbic acid (mg/100g)							
16.	Reducing sugar (%)							
17.	Non-reducing sugar (%)							
18.	Total sugars (%)							
19.	T.S.S. (°Brix)							
20.	Titrateable acidity (%)							

Continued...

S. No.	Characters	Nodes/ plant	No. of branches/ plant	No. of seeds/ fruit	Fruit diameter (cm)	No. of fruits/ plant	Seeds weight/ fruit (g)	Average fruit weight (g)
		8	9	10	11	12	13	14
1.	Node no. to I st staminate flowers	0.017	0.102	-0.123	-0.121	0.510**	0.243*	0.268**
2.	Node no. to I st pistillate flowers	0.168	-0.003	-0.234*	-0.213*	0.466**	0.234*	0.232*
3.	Days to anthesis of I st staminate flowers	0.400**	-0.121	0.308**	-0.068	-0.209*	-0.084	-0.252**
4.	Days to anthesis of I st pistillate flowers	0.317**	0.001	0.145	0.022	-0.057	0.042	-0.039
5.	Days to I st fruit harvest	-0.123	0.158	0.210*	-0.019	-0.220*	0.071	-0.218*
6.	Vine length (m)	-0.141	-0.263**	-0.352**	-0.242*	-0.329**	-0.246**	-0.256**
7.	Fruit length (cm)	-0.083	-0.142	-0.067	0.245*	-0.128	-0.110	0.011
8.	Nodes/plant	1.000	-0.117	0.419**	-0.032	0.121	0.215*	0.249**
9.	No. of branches/plant		1.000	0.082	0.489**	0.350**	0.342**	0.177
10.	No. of seeds/fruit			1.000	0.342**	0.007	0.133	0.184*
11.	Fruit diameter (cm)				1.000	0.179*	-0.006	0.308**
12.	No. of fruits/plant					1.000	0.358**	0.435**
13.	Seeds weight/fruit (g)						1.000	0.204*
14.	Average fruit weight (g)							1.000
15.	Ascorbic acid (mg/100g)							
16.	Reducing sugar (%)							
17.	Non-reducing sugar (%)							
18.	Total sugars (%)							
19.	T.S.S. (^o Brix)							
20.	Titrateable acidity (%)							

Continued...

S. No.	Characters	Ascorbic acid (mg/100g)	Reducing sugar (%)	Non-reducing sugar (%)	Total sugars (%)	T.S.S. (^o Brix)	Titratable acidity (%)	Marketable fruit yield /plant (kg)
		15	16	17	18	19	20	21
1.	Node no. to I st staminate flowers	-0.071	0.195*	-0.045	-0.210*	-0.378**	0.094	0.122
2.	Node no. to I st pistillate flowers	0.024	0.350**	0.055	-0.005	-0.242**	-0.138	0.144
3.	Days to anthesis of I st staminate flowers	-0.172	0.263**	0.093	0.15	0.102	0.003	0.133
4.	Days to anthesis of I st pistillate flowers	-0.437**	0.145	0.179	0.211*	0.232*	-0.052	-0.035
5.	Days to I st fruit harvest	-0.122	0.107	-0.151	-0.074	0.425**	0.118	0.037
6.	Vine length (m)	-0.427**	-0.394**	-0.322**	-0.303**	0.093	0.477**	0.132
7.	Fruit length (cm)	0.162	0.167	0.179	0.149	0.273**	-0.02	0.280*
8.	Nodes/plant	-0.302**	0.480**	0.089	-0.059	-0.422**	-0.174	0.076
9.	No. of branches/plant	-0.152	0.313**	-0.029	0.037	0.191*	-0.240*	-0.088
10.	No. of seeds/fruit	-0.057	0.412**	0.264**	0.227*	0.044	-0.118	0.172
11.	Fruit diameter (cm)	0.203*	0.237**	0.284**	0.244**	0.134	-0.300**	0.125
12.	No. of fruits/plant	-0.021	0.424**	0.309**	0.145*	-0.230*	-0.055	0.196*
13.	Seeds weight/fruit (g)	-0.210*	0.331**	0.106	-0.018	-0.132	-0.117	-0.021
14.	Average fruit weight (g)	0.183*	0.101	-0.158	-0.262**	-0.632**	-0.566**	0.124
15.	Ascorbic acid (mg/100g)	1.000	-0.035	0.168	0.142	-0.044	-0.287**	-0.072
16.	Reducing sugar (%)		1.000	0.446**	0.394**	0.12	-0.094	0.202*
17.	Non-reducing sugar (%)			1.000	0.874**	0.323**	0.005	0.085
18.	Total sugars (%)				1.000	0.458**	-0.125	0.027
19.	T.S.S. (^o Brix)					1.000	0.272**	-0.021
20.	Titratable acidity (%)						1.000	0.082

*and** significant at 5% and 1% respectively

Table-4.6.A: Direct and indirect (path analysis) effects of 20 different characters on marketable fruit yield per plant (kg) at genotypic level in bitter melon (2018-19)

S. No	Characters	Node no. to I st staminate flowers	Node no. to I st pistillate flowers	Days to anthesis of I st staminate flowers	Days to anthesis of I st pistillate flowers	Days to I st fruit harvest	Vine length (m)	Fruit length (cm)
		1	2	3	4	5	6	7
1.	Node no. to I st staminate flowers	-4.567	-3.493	-0.297	-0.042	1.644	1.491	-0.044
2.	Node no. to I st pistillate flowers	-2.667	-5.982	0.350	-0.030	3.811	-0.038	-0.056
3.	Days to anthesis of I st staminate flowers	0.906	-1.402	1.495	0.015	0.699	-0.680	-0.006
4.	Days to anthesis of I st pistillate flowers	1.068	1.002	0.126	0.181	-2.023	-0.071	0.088
5.	Days to I st fruit harvest	1.164	3.534	-0.162	0.057	-6.451	0.603	0.100
6.	Vine length (m)	1.486	-0.050	0.222	0.003	0.849	-4.582	0.037
7.	Fruit length (cm)	0.949	1.559	-0.045	0.075	-3.036	-0.802	0.213
8.	Nodes/plant	-0.272	-1.579	0.553	0.048	0.651	0.885	-0.021
9.	No. of branches/plant	-1.070	0.096	-0.173	0.007	-0.646	1.552	-0.029
10.	No. of seeds/fruit	0.736	1.714	0.435	0.026	-1.552	1.842	-0.014
11.	Fruit diameter (cm)	0.370	1.353	-0.158	0.003	0.459	0.977	0.048
12.	No. of fruits /plant	-3.291	-3.624	-0.435	-0.009	1.973	1.958	-0.027
13.	Seeds weight/fruit (g)	-3.261	-3.120	-0.076	0.022	-0.674	2.952	-0.084
14.	Average fruit weight (g)	-1.674	-1.564	-0.379	-0.008	1.396	1.474	-0.003
15.	Ascorbic acid (mg/100g)	0.139	0.393	-0.237	-0.083	0.673	1.994	0.038
16.	Reducing sugar (%)	-1.684	-2.367	0.387	0.018	-0.364	1.772	0.041
17.	Non-reducing sugar (%)	0.311	-0.522	0.045	0.040	0.946	1.641	0.044
18.	Total sugars (°Brix)	1.308	0.191	0.183	0.042	0.699	1.271	0.030
19.	T.S.S. (°Brix)	2.289	1.664	0.173	0.044	-2.899	-0.593	0.065
20.	Titrateable acidity (%)	0.055	0.854	-0.029	-0.010	-1.022	-2.485	0.002

S. No.	Characters	Nodes/ plant	No. of branches/ plant	No. of seeds/ fruit	Fruit diameter (cm)	No. of fruits/ plant	Seeds weight/ fruit (g)	Average fruit weight (g)
		8	9	10	11	12	13	14
1.	Node no. to 1 st staminate flowers	-0.391	-1.441	0.334	-0.013	1.706	0.404	0.631
2.	Node no. to 1 st pistillate flowers	-1.731	0.099	0.594	-0.036	1.435	0.295	0.450
3.	Days to anthesis of 1 st staminate flowers	-2.425	0.712	-0.603	-0.017	-0.688	-0.029	-0.436
4.	Days to anthesis of 1 st pistillate flowers	-1.751	-0.241	-0.301	0.002	-0.122	0.068	-0.075
5.	Days to 1 st fruit harvest	0.661	-0.616	-0.499	-0.011	-0.724	0.059	-0.373
6.	Vine length (m)	1.267	2.084	0.833	-0.034	-1.012	-0.364	-0.554
7.	Fruit length (cm)	0.643	0.833	0.135	0.036	-0.305	-0.224	-0.026
8.	Nodes/plant	-6.559	0.487	-0.930	-0.006	0.211	0.324	0.567
9.	No. of branches/plant	0.519	-6.152	-0.171	0.088	0.834	0.295	0.280
10.	No. of seeds/fruit	-2.944	-0.507	-2.073	0.046	0.054	0.091	0.348
11.	Fruit diameter (cm)	0.235	-3.364	-0.586	0.161	0.607	0.039	0.578
12.	No. of fruits /plant	-0.583	-2.168	-0.047	0.041	2.368	0.405	0.846
13.	Seeds weight/fruit (g)	-3.756	-3.209	-0.335	0.011	1.695	0.566	0.469
14.	Average fruit weight (g)	-2.161	-1.000	-0.419	0.054	1.163	0.154	1.722
15.	Ascorbic acid (mg/100g)	1.634	1.128	0.117	0.029	-0.074	-0.253	0.264
16.	Reducing sugar (%)	-3.204	-1.848	-0.773	0.030	1.194	0.426	0.130
17.	Non-reducing sugar (%)	-0.532	0.100	-0.659	0.058	0.931	0.150	-0.231
18.	Total sugars (%)	0.720	-0.209	-0.524	0.043	0.373	0.021	-0.459
19.	T.S.S. (^o Brix)	3.070	-1.438	-0.072	0.022	-0.505	-0.115	-1.098
20.	Titrateable acidity (%)	1.616	1.454	0.283	-0.052	-0.215	-0.111	-1.016

Continued...

S. No.	Characters	Ascorbic acid (mg/100g)	Reducing sugar (%)	Non-reducing sugar (%)	Total sugars (%)	T.S.S. (^o Brix)	Titrateable acidity (%)	Correlation with marketable fruit yield /plant (kg)
		15	16	17	18	19	20	21
1.	Node no. to I st staminate flowers	0.148	3.449	0.070	1.972	-1.251	0.022	0.331**
2.	Node no. to I st pistillate flowers	0.318	3.702	-0.089	0.220	-0.694	0.264	0.213
3.	Days to anthesis of I st staminate flowers	0.766	2.420	-0.031	-0.843	0.289	0.036	0.179
4.	Days to anthesis of I st pistillate flowers	2.234	0.952	-0.228	-1.619	0.607	0.099	-0.005
5.	Days to I st fruit harvest	0.505	0.528	0.150	0.747	1.122	-0.293	0.100
6.	Vine length (m)	2.106	-3.618	0.367	1.910	0.323	-1.004	0.270*
7.	Fruit length (cm)	-0.851	1.807	-0.209	-0.982	0.763	-0.019	0.516**
8.	Nodes/plant	1.205	4.569	-0.083	0.756	-1.168	0.456	0.094
9.	No. of branches/plant	0.887	2.810	0.017	-0.234	0.583	0.437	-0.069
10.	No. of seeds/fruit	0.274	3.487	-0.326	-1.742	0.087	0.253	0.235
11.	Fruit diameter (cm)	-0.884	1.739	-0.366	-1.850	0.343	0.594	0.295*
12.	No. of fruits /plant	0.151	4.717	-0.403	-1.084	-0.532	0.168	0.422**
13.	Seeds weight/fruit (g)	2.166	7.040	-0.271	-0.259	-0.509	0.363	-0.272*
14.	Average fruit weight (g)	-0.741	0.708	0.138	1.837	-1.591	1.092	0.199
15.	Ascorbic acid (mg/100g)	-4.838	-0.211	-0.193	-1.120	-0.114	0.565	-0.147
16.	Reducing sugar (%)	0.109	9.355	-0.550	-2.577	0.203	0.085	0.384**
17.	Non-reducing sugar (%)	-0.909	5.018	-1.025	-6.058	0.799	0.003	0.150
18.	Total sugars (%)	-0.787	3.500	-0.901	-6.888	1.184	0.245	0.042
19.	T.S.S. (^o Brix)	0.220	0.760	-0.328	-3.266	2.497	-0.519	-0.029
20.	Titrateable acidity (%)	1.477	-0.427	0.002	0.910	0.700	-1.851	0.137

Residual effect: 1.0934

Bold values shows direct and normal values shows indirect effects

Table-4.6.B: Direct and indirect (path analysis) effects of 20 different characters on marketable fruit yield per plant (kg) at genotypic level in bitter gourd (2019-20)

S. No.	Characters	Node no. to I st staminate flowers	Node no. to I st pistillate flowers	Days to anthesis of I st staminate flowers	Days to anthesis of I st pistillate flowers	Days to I st fruit harvest	Vine length (m)	Fruit length (cm)
		1	2	3	4	5	6	7
1.	Node no. to I st staminate flowers	-1.9833	-1.1819	-0.0643	0.0164	0.2553	0.2125	-0.2450
2.	Node no. to I st pistillate flowers	-1.0492	-2.2342	0.3355	0.1139	0.9408	-0.0238	-0.2057
3.	Days to anthesis of I st staminate flowers	0.0666	-0.3919	1.9127	-0.0482	0.1929	-0.0878	-0.1296
4.	Days to anthesis of I st pistillate flowers	0.0834	0.6523	0.2361	-0.3902	-0.5615	-0.0523	0.7380
5.	Days to I st fruit harvest	0.2502	1.0386	-0.1823	-0.1083	-2.0236	0.4395	0.3912
6.	Vine length (m)	0.2660	-0.0335	0.1060	-0.0129	0.5612	-1.5849	0.1033
7.	Fruit length (cm)	0.2884	0.2727	-0.1471	-0.1709	-0.4698	-0.0971	1.6851
8.	Nodes/plant	-0.0133	-0.3704	0.8900	-0.1484	0.2800	0.1929	-0.1219
9.	No. of branches/plant	-0.1021	-0.0270	-0.2574	0.0215	-0.5238	0.4056	-0.3177
10.	No. of seeds/fruit	0.2809	0.6657	0.7401	-0.0660	-0.3643	0.5698	-0.0826
11.	Fruit diameter (cm)	0.4667	0.5914	-0.0749	-0.0228	-0.0811	0.5567	0.4733
12.	No. of fruits /plant	-1.2938	-1.3231	-0.2999	0.0329	0.3452	0.5578	-0.2691
13.	Seeds weight/fruit (g)	-0.9301	-0.8730	-0.4373	0.0163	-0.4504	0.5524	-0.3966
14.	Average fruit weight (g)	-0.5213	-0.6875	-0.5494	0.0129	0.4597	0.3786	0.0232
15.	Ascorbic acid (mg/100g)	0.1812	-0.2047	-0.3571	0.1812	0.3395	0.7726	0.3149
16.	Reducing sugar (%)	-0.2530	-0.8293	0.6295	-0.0694	-0.3595	0.6849	0.3430
17.	Non-reducing sugar (%)	0.1228	-0.0471	0.2881	-0.0563	0.3703	0.5348	0.2978
18.	Total sugars (%)	0.3913	-0.0048	0.3703	-0.0780	0.0982	0.5494	0.3227
19.	T.S.S. (^o Brix)	0.7902	0.5668	0.1990	-0.0866	-0.8958	-0.1085	0.4891
20.	Titrateable acidity (%)	-0.3654	0.4270	0.0553	0.0299	-0.2007	-0.7515	-0.0615

Continued...

S. No.	Characters	Nodes/ plant	No. of branches/ plant	No. of seeds/ fruit	Fruit diameter (cm)	No. of fruits/ plant	Seeds weight/ fruit (g)	Average fruit weight (g)
		8	9	10	11	12	13	14
1.	Node no. to I st staminate flowers	-0.0275	-0.0234	-0.0056	0.6148	1.3711	-0.1274	0.2021
2.	Node no. to I st pistillate flowers	-0.6803	-0.0055	-0.0118	0.6917	1.2448	-0.1061	0.2366
3.	Days to anthesis of I st staminate flowers	-1.9095	0.0611	0.0153	0.1024	-0.3296	0.0621	-0.2208
4.	Days to anthesis of I st pistillate flowers	-1.5605	0.0250	0.0067	-0.1525	-0.1775	0.0114	-0.0255
5.	Days to I st fruit harvest	0.5679	-0.1176	0.0071	-0.1047	-0.3586	-0.0604	-0.1747
6.	Vine length (m)	0.4994	0.1163	-0.0143	0.9180	-0.7398	0.0947	-0.1837
7.	Fruit length (cm)	0.2968	0.0857	-0.0019	-0.7339	-0.3357	0.0639	0.0106
8.	Nodes/plant	-4.1038	0.0723	0.0170	0.1576	0.3446	-0.0716	0.1375
9.	No. of branches/plant	0.6531	-0.4543	0.0047	-1.5176	0.7955	-0.1760	0.1459
10.	No. of seeds/fruit	-1.7595	-0.0542	0.0397	-1.1662	-0.0100	-0.0640	0.1477
11.	Fruit diameter (cm)	0.2475	-0.2638	0.0177	-2.6131	0.4523	-0.0478	0.2695
12.	No. of fruits/plant	-0.6729	-0.1719	-0.0002	-0.5622	2.1019	-0.1654	0.3509
13.	Seeds weight/fruit (g)	-1.0818	-0.2945	0.0093	-0.4601	1.2805	-0.2716	0.3091
14.	Average fruit weight (g)	-0.7339	-0.0862	0.0076	-0.9159	0.9593	-0.1092	0.7689
15.	Ascorbic acid (mg/100g)	1.5344	0.0677	-0.0029	-0.7528	-0.1015	0.0777	0.1877
16.	Reducing sugar (%)	-2.1000	-0.1542	0.0202	-0.9483	0.9626	-0.1847	0.1123
17.	Non-reducing sugar (%)	-0.4045	0.0233	0.0095	-0.8403	0.6290	-0.0206	-0.1484
18.	Total sugars (%)	0.0421	-0.0141	0.0092	-0.7158	0.3247	-0.0060	-0.2033
19.	T.S.S. (^o Brix)	1.5983	-0.0742	0.0017	-0.4146	-0.5371	0.0640	-0.5079
20.	Titrateable acidity (%)	0.4988	0.1237	-0.0040	0.8719	-0.0721	0.0514	-0.4408

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S. No.	Characters	Ascorbic acid (mg/100g)	Reducing sugar (%)	Non-reducing sugar (%)	Total sugars (%)	T.S.S. (^o Brix)	Titratable acidity (%)	Correlation with marketable fruit yield /plant (kg)
		15	16	17	18	19	20	21
1.	Node no. to I st staminate flowers	0.2093	0.3687	-0.1396	0.7601	0.1680	-0.1378	0.243
2.	Node no. to I st pistillate flowers	-0.2100	1.0729	0.0476	-0.0083	0.1070	0.1429	0.399**
3.	Days to anthesis of I st staminate flowers	0.4279	0.9512	0.3399	-0.7458	-0.0439	-0.0216	0.203
4.	Days to anthesis of I st pistillate flowers	1.0640	0.5138	0.3257	-0.7706	-0.0935	0.0573	-0.070
5.	Days to I st fruit harvest	0.3844	0.5135	-0.4129	0.1869	-0.1866	-0.0742	-0.024
6.	Vine length (m)	1.1171	-1.2491	-0.7613	1.3357	-0.0289	-0.3546	0.155
7.	Fruit length (cm)	-0.4282	0.5883	0.3987	-0.7379	-0.1224	0.0273	0.472**
8.	Nodes/plant	0.8567	1.4790	0.2224	0.0395	0.1642	0.0909	0.115
9.	No. of branches/plant	0.3416	0.9814	-0.1155	-0.1192	-0.0688	0.2037	-0.126
10.	No. of seeds/fruit	0.1700	1.4744	0.5431	-0.8975	-0.0184	0.0757	0.224
11.	Fruit diameter (cm)	-0.6602	1.0489	0.7255	-1.0554	-0.0669	0.2495	0.213
12.	No. of fruits/plant	0.1106	1.3236	0.6751	-0.5951	0.1077	0.0256	0.278*
13.	Seeds weight/fruit (g)	0.6559	1.9663	0.1715	-0.0847	0.0994	0.1414	-0.078
14.	Average fruit weight (g)	-0.5593	0.4223	-0.4355	1.0186	0.2785	0.4287	0.160
15.	Ascorbic acid (mg/100g)	-2.2915	-0.1722	0.4203	-0.5247	0.0208	0.2414	-0.068
16.	Reducing sugar (%)	0.1365	2.8903	0.9127	-1.5573	-0.0657	0.1147	0.285*
17.	Non-reducing sugar (%)	-0.4269	1.1693	2.2561	-3.5293	-0.1440	-0.0038	0.080
18.	Total sugars (%)	-0.3121	1.1682	2.0666	-3.8528	-0.1990	0.0921	0.049
19.	T.S.S. (^o Brix)	0.1130	0.4504	0.7707	-1.8181	-0.4216	-0.2137	-0.035
20.	Titratable acidity (%)	0.7399	-0.4433	0.0115	0.4745	-0.1205	-0.7478	0.076

Residual effect: 0.8133

Bold values shows direct and normal values indirect effects

Table- 4.6.C: Direct and indirect (path analysis) effects of 20 different characters on marketable fruit yield per plant (kg) at genotypic level in bitter melon (Pooled data)

S. No.	Characters	Node no. to I st staminate flowers	Node no. to I st pistillate flowers	Days to anthesis of I st staminate flowers	Days to anthesis of I st pistillate flowers	Days to I st fruit harvest	Vine length (m)	Fruit length (cm)
		1	2	3	4	5	6	7
1.	Node no. to I st staminate flowers	4.560	3.542	0.396	0.215	-1.190	-1.321	-0.148
2.	Node no. to I st pistillate flowers	2.587	6.243	-0.656	0.356	-3.663	0.107	-0.165
3.	Days to anthesis of I st staminate flowers	-0.564	1.280	-3.200	-0.161	-0.769	0.611	-0.046
4.	Days to anthesis of I st pistillate flowers	-0.613	-1.390	-0.322	-1.597	2.151	0.149	0.365
5.	Days to I st fruit harvest	-0.779	-3.284	0.353	-0.493	6.964	-1.310	0.300
6.	Vine length (m)	-1.033	0.114	-0.335	-0.041	-1.565	5.828	0.102
7.	Fruit length (cm)	-0.785	-1.192	0.170	-0.675	2.419	0.689	0.863
8.	Nodes/plant	0.069	1.357	-1.332	-0.519	-0.854	-0.881	-0.074
9.	No. of branches/plant	0.626	0.009	0.401	0.009	1.276	-1.714	-0.138
10.	No. of seeds/fruit	-0.674	-1.733	-1.076	-0.249	1.500	-2.219	-0.050
11.	Fruit diameter (cm)	-0.723	-1.532	0.239	-0.051	-0.136	-1.630	0.222
12.	No. of fruits/plant	3.081	3.703	0.712	0.109	-1.642	-2.240	-0.122
13.	Seeds weight/fruit (g)	2.288	2.414	0.394	-0.076	1.017	-2.453	-0.218
14.	Average fruit weight (g)	1.412	1.747	0.856	0.062	-1.585	-1.624	0.002
15.	Ascorbic acid (mg/100g)	-0.306	0.080	0.549	0.740	-0.943	-2.698	0.155
16.	Reducing sugar (%)	1.095	2.422	-0.949	-0.227	0.921	-2.453	0.167
17.	Non-reducing sugar (%)	-0.248	0.328	-0.308	-0.295	-1.140	-2.031	0.165
18.	Total sugars (%)	-1.091	-0.094	-0.502	-0.344	-0.528	-1.828	0.141
19.	T.S.S. (^o Brix)	-2.026	-1.660	-0.346	-0.372	3.151	0.583	0.254
20.	Titrateable acidity (%)	0.429	-0.978	-0.012	0.101	0.934	2.938	-0.013

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No.		8	9	10	11	12	13	14
1.	Node no. to 1 st staminate flowers	0.133	0.539	-0.553	-0.357	0.275	-1.093	-1.259
2.	Node no. to 1 st pistillate flowers	1.920	0.006	-1.040	-0.553	0.242	-0.843	-1.138
3.	Days to anthesis of 1 st staminate flowers	3.678	-0.492	1.260	-0.168	-0.091	0.268	1.088
4.	Days to anthesis of 1 st pistillate flowers	2.870	-0.021	0.584	0.073	-0.028	-0.103	0.158
5.	Days to 1 st fruit harvest	-1.083	0.720	0.807	-0.044	-0.096	-0.318	0.925
6.	Vine length (m)	-1.335	-1.155	-1.426	-0.630	-0.157	0.917	1.133
7.	Fruit length (cm)	-0.759	-0.629	-0.218	0.580	-0.058	0.552	-0.007
8.	Nodes/plant	8.835	-0.460	1.657	-0.095	0.050	-0.823	-1.041
9.	No. of branches/plant	-1.035	3.929	0.370	1.243	0.148	-1.120	-0.717
10.	No. of seeds/fruit	3.908	0.388	3.747	0.826	0.002	-0.381	-0.795
11.	Fruit diameter (cm)	-0.371	2.168	1.375	2.252	0.092	-0.169	-1.374
12.	No. of fruits/plant	1.083	1.426	0.019	0.508	0.407	-1.284	-1.902
13.	Seeds weight/fruit (g)	3.339	2.020	0.655	0.174	0.240	-2.179	-1.223
14.	Average fruit weight (g)	2.263	0.693	0.732	0.761	0.191	-0.656	-4.064
15.	Ascorbic acid (mg/100g)	-2.773	-0.639	-0.246	0.520	-0.013	0.704	-0.797
16.	Reducing sugar (%)	4.524	1.281	1.662	0.600	0.194	-1.314	-0.455
17.	Non-reducing sugar (%)	0.774	-0.137	1.050	0.751	0.138	-0.324	0.669
18.	Total sugars (%)	-0.533	0.133	0.902	0.601	0.062	-0.037	1.079
19.	T.S.S. (^a Brix)	-3.822	0.773	0.154	0.329	-0.096	0.426	2.627
20.	Titrateable acidity (%)	-1.619	-0.997	-0.457	-0.728	-0.026	0.375	2.357

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No.	Characters	Ascorbic acid (mg/100g)	Reducing sugar (%)	Non-reducing sugar (%)	Total sugars (%)	T.S.S. (°Brix)	Titrate acidity (%)	Correlation with marketable fruit yield /plant (kg)
		15	16	17	18	19	20	21
1.	Node no. to I st staminate flowers	-0.286	-2.105	0.117	-1.779	0.608	-0.042	0.251**
2.	Node no. to I st pistillate flowers	0.055	-3.401	-0.113	-0.112	0.364	0.069	0.264**
3.	Days to anthesis of I st staminate flowers	-0.731	-2.600	-0.207	1.168	-0.148	-0.002	0.1750
4.	Days to anthesis of I st pistillate flowers	-1.975	-1.246	-0.396	1.600	-0.319	0.028	-0.0330
5.	Days to I st fruit harvest	-0.577	-1.159	0.351	-0.564	-0.619	-0.059	0.0340
6.	Vine length (m)	-1.973	3.690	0.748	-2.332	-0.137	-0.222	0.1890
7.	Fruit length (cm)	0.767	-1.697	-0.410	1.220	-0.402	0.007	0.433**
8.	Nodes/plant	-1.338	-4.490	-0.188	-0.448	0.592	0.081	0.0970
9.	No. of branches/plant	-0.693	-2.858	0.075	0.252	-0.269	0.112	-0.0960
10.	No. of seeds/fruit	-0.280	-3.890	-0.602	1.790	-0.056	0.054	0.211*
11.	Fruit diameter (cm)	0.985	-2.336	-0.716	1.984	-0.200	0.143	0.223*
12.	No. of fruits/plant	-0.133	-4.176	-0.728	1.135	0.322	0.028	0.307**
13.	Seeds weight/fruit (g)	-1.377	-5.288	-0.319	0.126	0.267	0.076	-0.1220
14.	Average fruit weight (g)	0.835	-0.982	0.354	-1.974	0.884	0.256	0.1640
15.	Ascorbic acid (mg/100g)	4.262	0.394	-0.396	1.109	0.064	0.137	-0.0970
16.	Reducing sugar (%)	-0.191	-8.768	-1.023	2.942	-0.171	0.045	0.301**
17.	Non-reducing sugar (%)	0.786	-4.177	-2.147	6.708	-0.454	-0.001	0.1060
18.	Total sugars (%)	0.635	-3.469	-1.936	7.436	-0.644	0.056	0.0410
19.	T.S.S. (°Brix)	-0.199	-1.098	-0.712	3.499	-1.368	-0.125	-0.0290
20.	Titrate acidity (%)	-1.326	0.898	-0.005	-0.945	-0.386	-0.441	0.0980

Residual effect: -1.5186

Bold values shows direct and normal values indirect effects

Table-4.7.A: Direct and indirect (path analysis) effects of 20 different characters on marketable fruit yield per plant (kg) at phenotypic level in bitter melon (2018-19)

S. No	Characters	Node no. to I st staminate flowers	Node no. to I st pistillate flowers	Days to anthesis of I st staminate flowers	Days to anthesis of I st pistillate flowers	Days to I st fruit harvest	Vine length (m)	Fruit length (cm)
		1	2	3	4	5	6	7
1.	Node no. to I st staminate flowers	0.131	-0.010	-0.032	0.030	-0.047	-0.117	-0.031
2.	Node no. to I st pistillate flowers	0.052	-0.026	0.040	0.023	-0.112	-0.015	-0.055
3.	Days to anthesis of I st staminate flowers	-0.023	-0.006	0.184	-0.011	-0.022	0.061	-0.008
4.	Days to anthesis of I st pistillate flowers	-0.024	0.004	0.012	-0.165	0.068	0.001	0.088
5.	Days to I st fruit harvest	-0.026	0.012	-0.017	-0.048	0.234	-0.047	0.088
6.	Vine length (m)	-0.037	0.001	0.027	0.000	-0.027	0.417	0.035
7.	Fruit length (cm)	-0.018	0.006	-0.006	-0.064	0.091	0.065	0.226
8.	Nodes/plant	0.005	-0.005	0.066	-0.043	-0.024	-0.066	-0.020
9.	No. of branches/plant	0.030	0.000	-0.021	-0.007	0.016	-0.119	-0.023
10.	No. of seeds/fruit	-0.019	0.006	0.049	-0.022	0.059	-0.148	-0.019
11.	Fruit diameter (cm)	-0.007	0.006	-0.020	-0.001	-0.018	-0.071	0.054
12.	No. of fruits/plant	0.074	-0.012	-0.049	0.009	-0.063	-0.144	-0.026
13.	Seeds weight/fruit (g)	0.035	-0.007	-0.007	-0.015	0.009	-0.117	-0.029
14.	Average fruit weight (g)	0.041	-0.005	-0.044	0.008	-0.050	-0.114	0.001
15.	Ascorbic acid (mg/100g)	-0.005	0.001	-0.029	0.071	-0.022	-0.162	0.034
16.	Reducing sugar (%)	0.040	-0.009	0.041	-0.018	0.009	-0.158	0.033
17.	Non-reducing sugar (%)	-0.006	-0.002	0.008	-0.036	-0.030	-0.132	0.042
18.	Total sugars (%)	-0.032	0.000	0.021	-0.038	-0.025	-0.114	0.027
19.	T.S.S. (^o Brix)	-0.056	0.006	0.019	-0.040	0.100	0.050	0.060
20.	Titrateable acidity (%)	0.000	0.003	-0.004	0.008	0.037	0.207	0.004

Continued...

S. No.	Characters	Nodes/ plant	No. of branches/ plant	No. of seeds/ fruit	Fruit diameter (cm)	No. of fruits/ plant	Seeds weight/ fruit (g)	Average fruit weight (g)
		8	9	10	11	12	13	14
1.	Node no. to I st staminate flowers	-0.006	-0.068	-0.037	-0.009	0.243	-0.005	-0.010
2.	Node no. to I st pistillate flowers	-0.033	0.004	-0.058	-0.034	0.195	-0.006	-0.007
3.	Days to anthesis of I st staminate flowers	-0.059	0.034	0.069	-0.016	-0.114	0.001	0.007
4.	Days to anthesis of I st pistillate flowers	-0.043	-0.013	0.034	0.001	-0.022	-0.002	0.001
5.	Days to I st fruit harvest	0.017	-0.020	0.064	-0.012	-0.116	-0.001	0.007
6.	Vine length (m)	0.026	0.085	-0.090	-0.026	-0.149	0.005	0.009
7.	Fruit length (cm)	0.014	0.030	-0.021	0.036	-0.049	0.003	0.000
8.	Nodes/plant	-0.163	0.024	0.108	-0.004	0.039	-0.005	-0.010
9.	No. of branches/plant	0.013	-0.299	0.018	0.076	0.144	-0.005	-0.005
10.	No. of seeds/fruit	-0.068	-0.021	0.256	0.040	0.001	-0.002	-0.006
11.	Fruit diameter (cm)	0.004	-0.149	0.067	0.151	0.092	0.001	-0.010
12.	No. of fruits/plant	-0.015	-0.100	0.000	0.032	0.431	-0.006	-0.014
13.	Seeds weight/fruit (g)	-0.044	-0.081	0.029	-0.008	0.137	-0.019	-0.004
14.	Average fruit weight (g)	-0.053	-0.050	0.048	0.046	0.194	-0.003	-0.031
15.	Ascorbic acid (mg/100g)	0.039	0.049	-0.013	0.025	-0.009	0.004	-0.004
16.	Reducing sugar (%)	-0.076	-0.087	0.086	0.024	0.191	-0.006	-0.002
17.	Non-reducing sugar (%)	-0.013	0.004	0.077	0.045	0.150	-0.003	0.004
18.	Total sugars (%)	0.017	-0.013	0.059	0.037	0.064	0.001	0.008
19.	T.S.S. (^o Brix)	0.074	-0.066	0.012	0.020	-0.097	0.003	0.019
20.	Titrateable acidity (%)	0.038	0.067	-0.036	-0.042	-0.036	0.002	0.018

Continued...

S. No.	Characters	Ascorbic acid (mg/100g)	Reducing sugar (%)	Non-reducing sugar (%)	Total sugars (%)	T.S.S. (°Brix)	Titrateable acidity (%)	Correlation with marketable fruit yield /plant (kg)
		15	16	17	18	19	20	21
1.	Node no. to 1 st staminate flowers	0.004	0.056	0.005	-0.018	0.037	-0.001	0.116
2.	Node no. to 1 st pistillate flowers	0.004	0.066	-0.011	-0.001	0.021	0.021	0.069
3.	Days to anthesis of 1 st staminate flowers	0.017	0.041	-0.005	0.008	-0.009	0.004	0.154
4.	Days to anthesis of 1 st pistillate flowers	0.046	0.020	-0.026	0.017	-0.021	0.008	-0.018
5.	Days to 1 st fruit harvest	0.010	0.007	0.016	-0.008	-0.037	-0.028	0.094
6.	Vine length (m)	0.042	-0.069	0.038	-0.020	-0.010	-0.089	0.168
7.	Fruit length (cm)	-0.016	0.027	-0.023	0.009	-0.023	-0.003	0.284*
8.	Nodes/plant	0.026	0.085	-0.010	-0.008	0.040	0.042	0.075
9.	No. of branches/plant	0.018	0.053	0.002	0.003	-0.019	0.040	-0.087
10.	No. of seeds/fruit	0.006	0.061	-0.037	0.017	-0.004	0.025	0.173
11.	Fruit diameter (cm)	-0.018	0.029	-0.036	0.018	-0.011	0.049	0.130
12.	No. of fruits/plant	0.002	0.081	-0.043	0.011	0.020	0.015	0.204
13.	Seeds weight/fruit (g)	0.024	0.056	-0.019	-0.002	0.012	0.018	-0.034
14.	Average fruit weight (g)	-0.015	0.011	0.016	-0.019	0.053	0.103	0.137
15.	Ascorbic acid (mg/100g)	-0.107	-0.001	-0.021	0.011	0.003	0.049	-0.087
16.	Reducing sugar (%)	0.001	0.182	-0.062	0.028	-0.007	0.007	0.218
17.	Non-reducing sugar (%)	-0.018	0.093	-0.122	0.063	-0.027	0.000	0.097
18.	Total sugars (%)	-0.017	0.070	-0.104	0.073	-0.039	0.023	0.021
19.	T.S.S. (°Brix)	0.004	0.015	-0.038	0.033	-0.087	-0.049	-0.019
20.	Titrateable acidity (%)	0.029	-0.007	0.000	-0.009	-0.024	-0.180	0.075

Residual effect: 0.7810

Bold values shows direct and normal values shows indirect effects

Table-4.7.B: Direct and indirect (path analysis) effects of 20 different characters on marketable fruit yield per plant (kg) at phenotypic level in bitter gourd (2019-20)

S. No.	Characters	Node no. to I st staminate flowers	Node no. to I st pistillate flowers	Days to anthesis of I st staminate flowers	Days to anthesis of I st pistillate flowers	Days to I st fruit harvest	Vine length (m)	Fruit length (cm)
		1	2	3	4	5	6	7
1.	Node no. to I st staminate flowers	0.154	0.163	0.001	0.017	-0.006	0.013	-0.094
2.	Node no. to I st pistillate flowers	0.054	0.464	-0.002	0.166	-0.035	-0.002	-0.083
3.	Days to anthesis of I st staminate flowers	-0.007	0.049	-0.019	-0.074	-0.009	-0.007	-0.046
4.	Days to anthesis of I st pistillate flowers	-0.004	-0.114	-0.002	-0.674	0.022	-0.005	0.338
5.	Days to I st fruit harvest	-0.011	-0.186	0.002	-0.172	0.086	0.037	0.182
6.	Vine length (m)	-0.014	0.005	-0.001	-0.024	-0.023	-0.140	0.052
7.	Fruit length (cm)	-0.018	-0.047	0.001	-0.281	0.019	-0.009	0.812
8.	Nodes/plant	0.000	0.062	-0.008	-0.250	-0.012	0.017	-0.065
9.	No. of branches/plant	-0.001	0.003	0.002	0.028	0.020	0.033	-0.151
10.	No. of seeds/fruit	-0.016	-0.112	-0.007	-0.105	0.015	0.049	-0.041
11.	Fruit diameter (cm)	-0.028	-0.094	0.001	-0.024	0.003	0.045	0.204
12.	No. of fruits/plant	0.072	0.223	0.003	0.042	-0.015	0.044	-0.117
13.	Seeds weight/fruit (g)	0.035	0.080	0.002	0.004	0.009	0.029	-0.073
14.	Average fruit weight (g)	0.036	0.118	0.005	0.023	-0.019	0.033	0.014
15.	Ascorbic acid (mg/100g)	-0.016	0.041	0.004	0.301	-0.013	0.066	0.143
16.	Reducing sugar (%)	0.016	0.158	-0.006	-0.121	0.014	0.058	0.153
17.	Non-reducing sugar (%)	-0.007	0.010	-0.003	-0.096	-0.015	0.046	0.138
18.	Total sugars (%)	-0.028	0.005	-0.004	-0.131	-0.004	0.047	0.148
19.	T.S.S. (^o Brix)	-0.052	-0.111	-0.002	-0.149	0.037	-0.009	0.230
20.	Titrateable acidity (%)	0.027	-0.075	-0.001	0.040	0.007	-0.064	-0.050

Continued...

Table-4.7.B: Direct and indirect (path analysis) effects of 20 different characters on marketable fruit yield per plant (kg) at phenology level in bitter gourd (2019-20)

S. No.	Characters	Node no. to I st staminate flowers	Node no. to I st pistillate flowers	Days to anthesis of I st staminate flowers	Days to anthesis of I st pistillate flowers	Days to I st fruit harvest	Vine length (m)	Fruit length (cm)
		1	2	3	4	5	6	7
1.	Node no. to I st staminate flowers	0.154	0.163	0.001	0.017	-0.006	0.013	-0.094
2.	Node no. to I st pistillate flowers	0.054	0.464	-0.002	0.166	-0.035	-0.002	-0.083
3.	Days to anthesis of I st staminate flowers	-0.007	0.049	-0.019	-0.074	-0.009	-0.007	-0.046
4.	Days to anthesis of I st pistillate flowers	-0.004	-0.114	-0.002	-0.674	0.022	-0.005	0.338
5.	Days to I st fruit harvest	-0.011	-0.186	0.002	-0.172	0.086	0.037	0.182
6.	Vine length (m)	-0.014	0.005	-0.001	-0.024	-0.023	-0.140	0.052
7.	Fruit length (cm)	-0.018	-0.047	0.001	-0.281	0.019	-0.009	0.812
8.	Nodes/plant	0.000	0.062	-0.008	-0.250	-0.012	0.017	-0.065
9.	No. of branches/plant	-0.001	0.003	0.002	0.028	0.020	0.033	-0.151
10.	No. of seeds/fruit	-0.016	-0.112	-0.007	-0.105	0.015	0.049	-0.041
11.	Fruit diameter (cm)	-0.028	-0.094	0.001	-0.024	0.003	0.045	0.204
12.	No. of fruits/plant	0.072	0.223	0.003	0.042	-0.015	0.044	-0.117
13.	Seeds weight/fruit (g)	0.035	0.080	0.002	0.004	0.009	0.029	-0.073
14.	Average fruit weight (g)	0.036	0.118	0.005	0.023	-0.019	0.033	0.014
15.	Ascorbic acid (mg/100g)	-0.016	0.041	0.004	0.301	-0.013	0.066	0.143
16.	Reducing sugar (%)	0.016	0.158	-0.006	-0.121	0.014	0.058	0.153
17.	Non-reducing sugar (%)	-0.007	0.010	-0.003	-0.096	-0.015	0.046	0.138
18.	Total sugars (%)	-0.028	0.005	-0.004	-0.131	-0.004	0.047	0.148
19.	T.S.S. (^o Brix)	-0.052	-0.111	-0.002	-0.149	0.037	-0.009	0.230
20.	Titrateable acidity (%)	0.027	-0.075	-0.001	0.040	0.007	-0.064	-0.050

Continued...

S. No.	Characters	Nodes/ plant	No. of branches/ plant	No. of seeds/ fruit	Fruit diameter (cm)	No. of fruits/ plant	Seeds weight/ fruit (g)	Average fruit weight (g)
		8	9	10	11	12	13	14
1.	Node no. to I st staminate flowers	-0.001	-0.001	-0.045	0.003	0.049	-0.039	0.061
2.	Node no. to I st pistillate flowers	0.068	0.001	-0.106	0.003	0.051	-0.030	0.067
3.	Days to anthesis of I st staminate flowers	0.223	-0.023	0.152	0.000	-0.016	0.023	-0.070
4.	Days to anthesis of I st pistillate flowers	0.188	-0.008	0.069	-0.001	-0.007	0.001	-0.009
5.	Days to I st fruit harvest	-0.071	0.043	0.077	-0.001	-0.019	-0.018	-0.059
6.	Vine length (m)	-0.062	-0.043	-0.154	0.005	-0.033	0.037	-0.063
7.	Fruit length (cm)	-0.040	-0.034	-0.022	-0.004	-0.015	0.016	0.004
8.	Nodes/plant	0.507	-0.028	0.183	0.001	0.016	-0.027	0.047
9.	No. of branches/plant	-0.078	0.181	0.041	-0.007	0.039	-0.073	0.049
10.	No. of seeds/fruit	0.212	0.017	0.438	-0.006	0.001	-0.027	0.048
11.	Fruit diameter (cm)	-0.019	0.086	0.183	-0.014	0.015	-0.007	0.082
12.	No. of fruits/plant	0.077	0.066	0.005	-0.002	0.106	-0.070	0.111
13.	Seeds weight/fruit (g)	0.079	0.075	0.067	-0.001	0.043	-0.176	0.074
14.	Average fruit weight (g)	0.089	0.034	0.079	-0.004	0.044	-0.049	0.265
15.	Ascorbic acid (mg/100g)	-0.185	-0.025	-0.028	-0.003	-0.002	0.035	0.060
16.	Reducing sugar (%)	0.251	0.061	0.211	-0.005	0.043	-0.062	0.036
17.	Non-reducing sugar (%)	0.049	-0.008	0.099	-0.004	0.029	-0.010	-0.049
18.	Total sugars (%)	-0.005	0.006	0.097	-0.004	0.015	0.002	-0.069
19.	T.S.S. (^o Brix)	-0.196	0.029	0.019	-0.002	-0.025	0.022	-0.172
20.	Titratable acidity (%)	-0.059	-0.047	-0.043	0.005	-0.003	0.024	-0.148

Continued...

S. No.	Characters	Ascorbic acid (mg/100g)	Reducing sugar (%)	Non-reducing sugar (%)	Total sugars (%)	T.S.S. (°Brix)	Titrateable acidity (%)	marketable fruit yield /plant (kg)
		15	16	17	18	19	20	21
1.	Node no. to 1 st staminate flowers	0.043	-0.076	0.007	-0.058	-0.098	0.035	0.128
2.	Node no. to 1 st pistillate flowers	-0.037	-0.251	-0.003	0.003	-0.070	-0.032	0.227
3.	Days to anthesis of 1 st staminate flowers	0.079	-0.222	-0.020	0.060	0.030	0.006	0.110
4.	Days to anthesis of 1 st pistillate flowers	0.188	-0.133	-0.020	0.062	0.065	-0.012	-0.054
5.	Days to 1 st fruit harvest	0.063	-0.121	0.023	-0.015	0.125	0.017	-0.016
6.	Vine length (m)	0.198	0.304	0.045	-0.108	0.019	0.090	0.090
7.	Fruit length (cm)	-0.074	-0.139	-0.023	0.059	0.083	-0.012	0.276*
8.	Nodes/plant	0.154	-0.365	-0.013	-0.003	-0.114	-0.023	0.078
9.	No. of branches/plant	0.059	-0.248	0.006	0.010	0.047	-0.051	-0.089
10.	No. of seeds/fruit	0.027	-0.356	-0.031	0.071	0.013	-0.019	0.170
11.	Fruit diameter (cm)	-0.101	-0.231	-0.037	0.078	0.041	-0.064	0.119
12.	No. of fruits/plant	0.009	-0.301	-0.037	0.046	-0.069	-0.005	0.187
13.	Seed weight/fruit (g)	0.084	-0.263	-0.008	-0.003	-0.038	-0.027	-0.007
14.	Average fruit weight (g)	-0.096	-0.101	0.025	-0.084	-0.191	-0.111	0.109
15.	Ascorbic acid (mg/100g)	-0.421	0.046	-0.022	0.041	-0.014	-0.061	-0.055
16.	Reducing sugar (%)	0.026	-0.739	-0.053	0.130	0.046	-0.029	0.186
17.	Non-reducing sugar (%)	-0.069	-0.288	-0.137	0.288	0.098	0.002	0.074
18.	Total sugars (%)	-0.054	-0.300	-0.122	0.321	0.137	-0.024	0.033
19.	T.S.S. (°Brix)	0.020	-0.115	-0.046	0.150	0.294	0.054	-0.023
20.	Titrateable acidity (%)	0.128	0.108	-0.002	-0.039	0.080	0.199	0.088

Residual effect: 0.7664

Bold values shows direct and normal values indirect effects

Table-4.7.C: Direct and indirect (path analysis) effects of 20 different characters on marketable fruit yield per plant (kg) at phenotypic level in bitter gourd (Pooled data)

S. No	Characters	Node no. to I st staminate flowers	Node no. to I st pistillate flowers	Days to anthesis of I st staminate flowers	Days to anthesis of I st pistillate flowers	Days to I st fruit harvest	Vine length (m)	Fruit length (cm)
		1	2	3	4	5	6	7
1.	Node no. to I st staminate flowers	0.089	0.075	-0.007	0.036	-0.023	-0.041	-0.060
2.	Node no. to I st pistillate flowers	0.033	0.200	0.011	0.069	-0.078	-0.003	-0.086
3.	Days to anthesis of I st staminate flowers	-0.009	0.032	0.068	-0.032	-0.018	0.022	-0.022
4.	Days to anthesis of I st pistillate flowers	-0.009	-0.038	0.006	-0.363	0.048	0.004	0.194
5.	Days to I st fruit harvest	-0.011	-0.087	-0.007	-0.098	0.179	-0.042	0.146
6.	Vine length (m)	-0.016	-0.003	0.007	-0.007	-0.034	0.223	0.055
7.	Fruit length (cm)	-0.011	-0.035	-0.003	-0.145	0.054	0.025	0.485
8.	Nodes/plant	0.002	0.034	0.027	-0.115	-0.022	-0.031	-0.040
9.	No. of branches/plant	0.009	-0.001	-0.008	0.000	0.028	-0.058	-0.069
10.	No. of seeds/fruit	-0.011	-0.047	0.021	-0.053	0.038	-0.078	-0.032
11.	Fruit diameter (cm)	-0.011	-0.043	-0.005	-0.008	-0.003	-0.054	0.119
12.	No. of fruits /plant	0.045	0.093	-0.014	0.021	-0.039	-0.073	-0.062
13.	Seeds weight/fruit (g)	0.022	0.047	-0.006	-0.015	0.013	-0.055	-0.053
14.	Average fruit weight (g)	0.024	0.046	-0.017	0.014	-0.039	-0.057	0.005
15.	Ascorbic acid (mg/100g)	-0.006	0.005	-0.012	0.158	-0.022	-0.095	0.078
16.	Reducing sugar (%)	0.017	0.070	0.018	-0.053	0.019	-0.088	0.081
17.	Non-reducing sugar (%)	-0.004	0.011	0.006	-0.065	-0.027	-0.072	0.087
18.	Total sugars (%)	-0.019	-0.001	0.010	-0.077	-0.013	-0.068	0.072
19.	T.S.S. (°Brix)	-0.034	-0.048	0.007	-0.084	0.076	0.021	0.132
20.	Titrateable acidity (%)	0.008	-0.027	0.000	0.019	0.021	0.106	-0.010

Continued...

S. No.	Characters	Nodes/ plant	No. of branches/ plant	No. of seeds/ fruit	Fruit diameter (cm)	No. of fruits/ plant	Seeds weight/ fruit (g)	Average fruit weight (g)
		8	9	10	11	12	13	14
1.	Node no. to I st staminate flowers	0.001	-0.015	-0.043	-0.011	0.184	-0.023	-0.017
2.	Node no. to I st pistillate flowers	0.006	0.000	-0.083	-0.020	0.168	-0.023	-0.014
3.	Days to anthesis of I st staminate flowers	0.015	0.017	0.109	-0.006	-0.075	0.008	0.016
4.	Days to anthesis of I st pistillate flowers	0.012	0.000	0.051	0.002	-0.021	-0.004	0.002
5.	Days to I st fruit harvest	-0.005	-0.022	0.074	-0.002	-0.079	-0.007	0.014
6.	Vine length (m)	-0.005	0.037	-0.124	-0.022	-0.119	0.024	0.016
7.	Fruit length (cm)	-0.003	0.020	-0.024	0.023	-0.046	0.011	-0.001
8.	Nodes/plant	0.038	0.017	0.148	-0.003	0.044	-0.021	-0.016
9.	No. of branches/plant	-0.004	-0.143	0.029	0.045	0.126	-0.033	-0.011
10.	No. of seeds/fruit	0.016	-0.012	0.353	0.032	0.002	-0.013	-0.011
11.	Fruit diameter (cm)	-0.001	-0.070	0.121	0.092	0.065	0.001	-0.019
12.	No. of fruits /plant	0.005	-0.050	0.002	0.017	0.362	-0.035	-0.027
13.	Seeds weight/fruit (g)	0.008	-0.049	0.047	-0.001	0.129	-0.097	-0.013
14.	Average fruit weight (g)	0.010	-0.025	0.065	0.028	0.157	-0.020	-0.062
15.	Ascorbic acid (mg/100g)	-0.012	0.022	-0.020	0.019	-0.008	0.020	-0.011
16.	Reducing sugar (%)	0.018	-0.045	0.146	0.022	0.153	-0.032	-0.006
17.	Non-reducing sugar (%)	0.003	0.004	0.093	0.026	0.112	-0.010	0.010
18.	Total sugars (%)	-0.002	-0.005	0.080	0.023	0.053	0.002	0.016
19.	T.S.S. (°Brix)	-0.016	-0.027	0.016	0.012	-0.083	0.013	0.039
20.	Titrateable acidity (%)	-0.007	0.034	-0.042	-0.028	-0.020	0.011	0.035

Continued...

S. No.	Character	Ascorbic acid (mg/100g)	Reducing sugar (%)	Non-reducing sugar (%)	Total sugars (%)	T.S.S. (°Brix)	Titratable acidity (%)	Correlation with marketable fruit yield /plant (kg)
		15	16	17	18	19	20	21
1.	Node no. to I st staminate flowers	0.015	-0.027	0.005	-0.031	0.021	-0.006	0.122
2.	Node no. to I st pistillate flowers	-0.005	-0.049	-0.006	-0.001	0.013	0.009	0.144
3.	Days to anthesis of I st staminate flowers	0.037	-0.037	-0.009	0.022	-0.006	0.000	0.133
4.	Days to anthesis of I st pistillate flowers	0.095	-0.020	-0.018	0.031	-0.013	0.003	-0.035
5.	Days to I st fruit harvest	0.026	-0.015	0.015	-0.011	-0.024	-0.007	0.037
6.	Vine length (m)	0.093	0.055	0.033	-0.045	-0.005	-0.030	0.132
7.	Fruit length (cm)	-0.035	-0.023	-0.018	0.022	-0.015	0.001	0.280*
8.	Nodes/plant	0.066	-0.067	-0.009	-0.009	0.023	0.011	0.076
9.	No. of branches/plant	0.033	-0.044	0.003	0.005	-0.011	0.015	-0.088
10.	No. of seeds/fruit	0.012	-0.058	-0.027	0.033	-0.002	0.007	0.172
11.	Fruit diameter (cm)	-0.044	-0.033	-0.029	0.036	-0.007	0.019	0.125
12.	No. of fruits /plant	0.005	-0.059	-0.031	0.021	0.013	0.003	0.196*
13.	Seeds weight/fruit (g)	0.046	-0.046	-0.011	-0.003	0.007	0.007	-0.021
14.	Average fruit weight (g)	-0.040	-0.014	0.016	-0.039	0.035	0.035	0.124
15.	Ascorbic acid (mg/100g)	-0.218	0.005	-0.017	0.021	0.002	0.018	-0.072
16.	Reducing sugar (%)	0.008	-0.140	-0.045	0.058	-0.007	0.006	0.202*
17.	Non-reducing sugar (%)	-0.037	-0.062	-0.101	0.129	-0.018	0.000	0.085
18.	Total sugars (%)	-0.031	-0.055	-0.089	0.148	-0.025	0.008	0.027
19.	T.S.S. (°Brix)	0.010	-0.017	-0.033	0.068	-0.055	-0.017	-0.021
20.	Titratable acidity (%)	0.063	0.013	-0.001	-0.018	-0.015	-0.062	0.082

Residual effect: 0.7971

Bold values shows direct and normal values shows indirect effects

4.5 Correlation coefficient:

The phenotypic and genotypic correlation coefficient computed among the twenty one characters under study had been presented in Table- 4.4 and 4.5 respectively.

In general, genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients, suggesting therefore, a strong inherent relationship in different pairs of characters in bitter gourd genotypes. The most important character marketable fruit yield per plant had exhibited highly significant and positive phenotypic correlation with fruit length (0.280*) followed by reducing sugar (0.202*), number of fruits per plant (0.196*) whereas positive and non significant number of seeds per fruit (0.172) followed by node number first pistillate flowers (0.144), days to anthesis of first staminate flowers (0.133), fruit diameter (0.125) and seeds weight per fruit (0.124) and negative correlation with ascorbic acid (-0.072) followed by days to anthesis of first pistillate flowers (-0.035) and total soluble solids (-0.021).

The data recorded on node number to first staminate flowers showed highly significant and positive correlation with number of fruits per plant (0.510**) followed by node number to first pistillate flowers (0.374**) and average fruit weight (0.268**) while the positive non significant seeds weight per fruit (0.243) followed by reducing sugar (0.195) number of branches per plant (0.102) and titratable acidity (0.94) and highly negative correlation with total soluble solids (-0.378**) and total sugars (-0.210**).

It is evident from data that the node number to first pistillate flowers showed highly significant and positive correlation with number of fruits per plant (0.466**) followed by reducing sugar (0.350**) whereas it non-significant and positive with seeds weight per fruit (0.234) followed by average fruit weight (0.232), nodes per plant (0.168) and days to anthesis of first pistillate flowers (0.162), whereas the negative correlation with days to first fruit harvest (-0.436*) followed by total soluble solids (-0.242) and number of seeds per fruit (-0.234).

It is obvious from the data on days to anthesis of first staminate flowers showed highly significant and positive correlation with nodes per plant (0.400**) followed by number of seeds per fruit (0.308**) and reducing sugar (0.263**) whereas it is non significant and

positive correlation with total soluble solids (0.102) followed by vine length (0.99) and non-reducing sugar (0.93) and negative significant correlation with average fruit weight (-0.252) followed by number of fruit per plant (-0.209).

The data indicated on days to anthesis of first pistillate flowers showed highly significant and positive correlation with days to first fruit harvest (0.271**) followed by nodes per plant (0.317**), total sugars (0.211**) and total soluble solids (0.232**). However it is non significant and positive correlation with non-reducing sugar (0.179) followed by number of seeds per fruit (0.145) and highly negative significant correlation with ascorbic acid (-0.437**).

The data assembled towards days to first fruit harvest showed highly significant and positive correlation with total soluble solids (0.425**) whereas it is non significant and positive correlation with fruit length (0.302) followed by number of seeds per fruit (0.210*), number of branches per plant (0.158) and negative significant correlation with number of fruits per plant (-0.220) followed by average fruit weight (-0.218), vine length (-0.189) and non-reducing sugar (-0.151).

The data clearly revealed that the vine length positive non-significant correlation with fruit length (0.113) and negative significant correlation with titratable acidity (-0.477) followed by ascorbic acid (-0.427), reducing sugar (-0.394) and number of seeds per fruit (-0.352) and number of fruit per plant (-0.329).

It is lucid from the data showed on fruit length showed highly significant and positive correlation with total soluble solids (0.273**) followed by fruit diameter (0.245**) whereas it is non significant and positive correlation with non-reducing sugar (0.179) followed by reducing sugar (0.167), ascorbic acid (0.162) and total sugars (0.149) and negative significant correlation with number of branches of per plant (-0.142) followed by number of fruit per plant (-0.128) and seeds weight per fruit (-0.110).

It is explicit from the observed on nodes per plant showed highly significant and positive correlation with reducing sugar (0.480**) followed by number of seeds per fruit (0.419**) and average fruit weight (0.249**) whereas it is non significant and positive correlation with seeds weight per fruit (0.215) followed by number of fruits per plant

(0.121) and negative significant correlation with total soluble solids (-0.422**) followed by ascorbic acid (-0.302**) and titratable acidity (-0.174**).

It is apparent from the data recorded on number of branches per plant showed highly significant and positive correlation with fruit diameter (0.489**) followed by number of fruits per plant (0.350**), seeds weight per fruit (0.342**) and reducing sugar (0.313**). However, it is non significant and positive correlation with total soluble solids (0.191*) and average fruit weight (0.177) and negative significant correlation with titratable acidity (-0.240) and ascorbic acid (-0.152).

It is quite clear from the data observed on number of seeds per fruit showed highly significant and positive correlation with reducing sugar (0.412**) followed by fruit diameter (0.342**) and non-reducing sugar (0.264**). However, it is non significant and positive correlation with total sugars (0.227*) followed by average fruit weight (0.184*) and seeds weight per fruit (0.133) and negative significant correlation with titratable acidity (-0.118).

It is obvious from the data showed on fruit diameter showed highly significant and positive correlation with average fruit weight (0.308**) followed by non-reducing sugar (0.284), total sugars (0.244) and reducing sugar (0.237). However, it is non significant and positive correlation with number of fruits per plant (0.179*) followed by total soluble solids (0.134) and highly negative significant correlation with titratable acidity (-0.300**).

The data showed that the number of fruits per plant showed highly significant and positive correlation with average fruit weight (0.435**) followed by reducing sugar (0.424**), seeds weight per fruit (0.358**) and non-reducing sugar (0.309**). While it is non significant and positive correlation with total sugars (0.145*) and highly negative significant correlation with total soluble solids (-0.230*).

It is conspicuous from the data revealed that the seeds weight per fruit showed highly significant and positive correlation with reducing sugar (0.331**). Whereas, it is non significant and positive correlation with average fruit weight (0.204*) followed by non-

reducing sugar (0.106) and negative significant correlation with total sugars (-0.312) followed by ascorbic acid (-0.210*) and titratable acidity (-0.117).

The data indicated that the average fruit weight showed highly significant and positive correlation with ascorbic acid (0.183*). Whereas, it is non significant and positive correlation with reducing sugar (0.101) and negative significant correlation with total soluble solids (-0.632**) followed by titratable acidity (-0.566**) and total sugars (-0.262**).

The data observed that the ascorbic acid showed positive and non significant correlation with non-reducing sugar (0.168) followed by total sugars (0.142) and highly negative significant correlation with titratable acidity (-0.287**).

The data recorded on reducing sugar showed highly significant and positive correlation with non-reducing sugar (0.446**) followed by total sugars (0.394**).

It is evident from the data recorded on non-reducing sugar showed highly significant and positive correlation with total sugars (0.874**) followed by total soluble solids (0.323**).

The data recorded on total sugars showed highly significant and positive correlation with total soluble solids (0.458**).

The data observed on total soluble solids showed highly significant and positive correlation with titratable acidity (0.272**).

Path coefficients analysis

The path coefficients analysis was estimated at phenotypic and genotypic correlation to resolve the direct and indirect effect of twenty one characters on correlation with marketable fruit yield per plant.

Phenotypic path analysis

The direct and indirect effects of different characters on marketable fruit yield per plant at phenotypic levels had been presented in **Table-4.6**. The highest magnitude of positive direct effect on marketable fruit yield per plant was exerted by fruit length (0.485) followed by number of fruits plant (0.362), number of seeds per fruit (0.353), vine length (0.223), node number to first pistillate flowers (0.200), days to first fruit harvest (0.179)

and total sugars (0.148). While the higher magnitude of negative direct effect on marketable fruit yield per plant was exhibited by days to anthesis of first pistillate flowers (-0.363) followed by ascorbic acid (-0.218), number of branches per plant (-0.143), reducing sugar (-0.140) and non-reducing sugar (-0.101).

Considerable highly positive indirect effect on marketable fruit yield per plant was shown by fruit length (0.280) followed by reducing sugar (0.202), number of fruits per plant (0.196) and vine length (0.132) followed by node number to first staminate flowers (0.122) showed low positive indirect effect.

Node number to first staminate flowers (0.184), node number to first pistillate flowers (0.168), average fruit weight (0.157) and reducing sugar (0.153) via number fruits per plant towards marketable fruit yield per plant. Whereas, negative indirect effect on marketable fruit yield per plant were exhibited by vine length (0.124) via number of seeds per fruit, vine length (-0.119) via number of fruits per plant, nodes per plant (-0.115) via days to anthesis of first pistillate flowers. The estimates of the residual effect was high (0.7971) obtained in this phenotypic path analysis.

Genotypic path analysis

The direct and indirect effects of different characters on marketable fruit yield per plant at genotypic levels had been presented in **Table-4.7**. The highest magnitude of positive direct effect on marketable fruit yield per plant was exerted by nodes per plant (8.835) followed by total sugars (7.436), days to first fruit harvest (6.964), node number to first pistillate flowers (6.243), vine length (5.828), node number to first staminate flowers (4.560). While the higher magnitude of negative direct effect on marketable fruit yield per plant was exhibited by reducing sugar (-8.768) followed by average fruit weight (-4.064), days to anthesis of first staminate flowers (-3.200) and seeds weight per fruit (-2.179).

Considerable highest positive indirect effect on marketable fruit yield per plant was shown by fruit length (0.433) followed by number of fruits per plant (0.307), reducing sugar (0.301), node number to first pistillate flowers (0.264), node number to first

staminate flowers (0.251), fruit diameter (0.223), number of seeds per fruit (0.211) and vine length (0.189) followed by days to anthesis of first pistillate flowers (0.175), average fruit weight (0.164) and non-reducing sugar (0.106) showed low positive indirect effect. Reducing sugar (4.524) followed by number of seeds per fruit (3.908), days to anthesis of first staminate flowers (3.678), seeds weight per fruit (3.339) and days to anthesis of first pistillate flowers (2.870) via nodes per plant towards marketable fruit yield per plant. Whereas, negative indirect effect on marketable fruit yield per plant were exhibited by total soluble solids (-3.822) followed by ascorbic acid (-2.773) and titratable acidity (-1.619) via nodes per plant. The estimates of the residual effect was low (-1.5186) obtained in this genotypic path analysis.

Estimation of genetic divergence (D^2)

The Mahalanobis (D^2) statistics analysis was applied to the studies of the genetic divergence existing among 20 genotypes of bitter gourd (*Momordica charantia* L.) on the basis of twenty one characters. The pseudo F-test revealed that 5 clusters arrangement were most appropriate for grouping the 20 genotypes. Therefore, the 20 genotypes were expected to be grouped into 5 non-overlapping clusters. The distribution of 20 bitter gourd genotypes in a cluster is presented in **Table-4.8**. The maximum number of the genotypes was observed in cluster number I followed by cluster number II which contained 9 and 8 entries, respectively. The minimum number of cluster III, IV and V which had one entry from the each clusters, respectively, which compared to all genotypes.

Table-4.8.A: Clustering pattern of 20 genotypes of bitter gourd on the basis Mahalanobis (D^2) statistics (2018-19)

Cluster No.	No. of genotypes	Genotypes
I.	9	Narendra Barahmasi-1 (G_3), Pusa Hybrid-1 (G_5), Arka Harit (G_1), Narendra Barahmasi-2 (G_{14}), Ultima-1405 (G_{18}), UDIT-008 (G_{17}), US-475 (G_{12}), Sagar (G_6) and Amanshri (G_{10})
II.	8	Meghana-2 (G_{11}), Pusa Hybrid-2 (G_{13}), Pusa Vishesh (G_2), VRBT-23 (G_{16}), Kalyanpur Sona (G_4), Kalyanpur Barahmasi (G_7), Arka Sujat (G_9) and Kashi Urvasi (G_8)
III.	1	US-484 (G_{19})
IV.	1	MC-23 (G_{20})
V.	1	Selection-5 (G_{15})

Table-4.8.B. Clustering pattern of 20 genotypes of bitter gourd on the basis Mahalanobis (D^2) statistics (2019-20)

Cluster No.	No. of genotypes	Genotypes
I.	12	Kashi Urvasi (G_8), US-484 (G_{19}), Arka Sujat (G_9), Arka Harit (G_1), Pusa Hybrid-1 (G_5), Narendra Barahmasi-1 (G_3), Narendra Barahmasi-2 (G_{14}), UDIT-008 (G_{17}), Sagar (G_6), Ultima-1405 (G_{18}), US-475 (G_{12}) and Kalyanpur Sona (G_4)
II.	5	Pusa Vishesh (G_2), Meghana-2 (G_{11}), VRBT-23 (G_{16}), Kalyanpur Barahmasi (G_7) and Pusa Hybrid-2 (G_{13})
III.	1	MC-23 (G_{20})
IV.	1	Selection-5 (G_{15})
V.	1	Amanshri (G_{10})

Table-4.8.C: Clustering pattern of 20 genotypes of bitter gourd on the basis Mahalanobis (D^2) statistics (Pooled data)

Cluster No.	No. of genotypes	Genotypes
I.	9	Arka Harit (G_1), Narendra Barahmasi-1 (G_3), Pusa Hybrid-1 (G_5), Narendra Barahmasi-2 (G_{14}), Ultima-1405 (G_{18}), MC-23 (G_{20}), Kashi Urvasi (G_8), US-484 (G_{19}) and Arka Sujat (G_9)
II.	8	US-475 (G_{12}), UDIT-008 (G_{17}), Kalyanpur Sona (G_4), Kalyanpur Barahmasi (G_7), Meghana-2 (G_{11}), Pusa Hybrid-2 (G_{13}), Pusa Vishesh (G_2) and VRBT-23 (G_{16})
III.	1	Sagar (G_6)
IV.	1	Selection-5 (G_{15})
V.	1	Amanshri (G_{10})

The estimate of intra and inter cluster distance for 5 clusters are presented in Table-4.9.

The highest intra cluster distance observed in the cluster II and II (127.20) followed by cluster I and I (112.39). Whereas the lowest intra clusters distance showed by cluster III, IV and V, respectively (0.00) indicating genetic similarity of genotypes belonging to the respective clusters.

The highest inter cluster distance was found in cluster II and V (401.57) followed by cluster II and IV (295.76), cluster IV and V (276.66), cluster II and III (272.23), cluster I and V (231.71), cluster I and II (201.99), cluster I and IV (167.65), cluster III and V (164.50) and cluster I and III (161.99). The lowest inter cluster distance was found in cluster III and IV (155.11).

Table-4.9.A: Average intra and inter clusters distance (D^2) values for five clusters in bitter gourd (2018-19)

Cluster No.	Cluster-I	Cluster-II	Cluster-III	Cluster-IV	Cluster-V
Cluster-I	459.04	1167.07	2334.50	815.15	1175.39
Cluster-II		501.06	902.42	1811.82	2936.68
Cluster-III			0.00	2591.15	4491.90
Cluster-IV				0.00	683.03
Cluster-V					0.00

Table-4.9.B: Average intra and inter clusters distance (D^2) values for five clusters in bitter gourd (2019-20)

Cluster No.	Cluster-I	Cluster-II	Cluster-III	Cluster-IV	Cluster-V
Cluster-I	459.94	818.39	979.69	736.87	990.40
Cluster-II		356.99	1870.73	1498.30	2010.83
Cluster-III			0.00	415.40	757.93
Cluster-IV				0.00	994.22
Cluster-V					0.00

Table-4.9.C: Average intra and inter clusters distance (D^2) values for five clusters in bitter gourd (Pooled data)

Cluster No.	Cluster-I	Cluster-II	Cluster-III	Cluster-IV	Cluster-V
Cluster-I	112.39	201.99	161.99	167.65	231.71
Cluster-II		127.20	272.23	295.76	401.57
Cluster-III			0.00	155.11	164.50
Cluster-IV				0.00	276.66
Cluster-V					0.00

Bold values shows intra clusters and normal values shows inter clusters

Table-4.10

A perusal of Table-4.10 showed that cluster means for different characters indicated considerable differences between the clusters.

The maximum cluster mean value for node number to first staminate flowers was found in cluster V (13.83) followed by cluster II (12.60) and cluster III (12.33). The lower cluster mean value for node number to first staminate flowers was recorded in cluster IV (11.67) and cluster I (11.57).

The highest cluster mean for node number to first pistillate flowers was observed in cluster III (15.33) followed by cluster V (14.33). The lowest cluster mean for node number to first pistillate flowers was recorded in cluster II (12.50) followed by cluster I (11.59), while cluster IV showed minimum mean value (7.83).

The highest cluster mean value for days to anthesis of first staminate flowers was observed in cluster III (51.44) followed by cluster I (39.23). The lowest clusters mean value for days to anthesis of first staminate flowers was recorded in cluster II (38.95) followed by cluster V (37.81) and cluster IV (36.33).

The highest cluster mean value for days to anthesis of first pistillate flowers was found in cluster IV (55.06) and cluster III (49.27). The lowest clusters mean value for days to anthesis of first pistillate flowers was recorded in cluster II (44.47) followed by cluster I (39.14) and cluster V (35.91).

The highest cluster mean value for days to first fruit harvest was observed in cluster IV (61.83) followed by cluster I (53.22) and cluster V (52.50). The lowest clusters mean value for days to first fruit harvest was recorded in cluster II (52.17) followed by cluster III (46.33).

The highest cluster mean value for vine length was observed in cluster IV (5.65) followed by cluster III (5.56) and cluster I (5.06). The lowest clusters mean value for vine length was recorded in cluster II (4.29) followed by cluster III (3.25).

The highest cluster mean value for fruit length was observed in cluster IV (24.40) followed by cluster III (22.90) and cluster V (20.24). The lowest clusters mean value for fruit length was recorded in cluster II (19.57) followed by cluster I (18.54).

The highest cluster mean value for nodes per plant was observed in cluster III (61.33) followed by cluster II (61.23) and cluster I (55.04). The lowest clusters mean

value for nodes per plant was recorded in cluster V (42.00) followed by cluster IV (40.83).

The highest cluster mean value for number of branches per plant was observed in cluster V (24.83) followed by cluster IV (19.83) and cluster II (19.42). The lowest clusters mean value for number of branches per plant was recorded in cluster I (16.31) followed by cluster III (15.50).

The highest cluster mean value for number of seeds per fruit was observed in cluster II (23.54) followed by cluster IV (22.00) and cluster V (21.17). The lowest clusters mean value for number of seeds per fruit was recorded in cluster I (20.72) followed by cluster III (20.50).

The highest cluster mean value for fruit diameter per fruit was observed in cluster V (7.75) followed by cluster IV (7.49) and cluster II (6.87). The lowest clusters mean value for fruit diameter was recorded in cluster III (5.90) followed by cluster I (5.82).

The highest cluster mean value for number of fruits per plant was observed in cluster V (18.50) followed by cluster II (15.31). The lowest clusters mean value for number of fruits per plant was recorded in cluster I (12.57) followed by cluster III (12.50) and cluster IV (12.17).

The highest cluster mean value for seeds weight per fruit was observed in cluster II (3.60) followed by cluster V (3.50) and cluster I (3.27). The lowest clusters mean value for seeds weight per fruit was recorded in cluster III (3.22) followed by cluster IV (2.54).

The highest cluster mean value for average fruit weight was observed in cluster II (107.00) followed by cluster I (67.59) and cluster III (63.83). The lowest clusters mean value for average fruit weight was recorded in cluster V (61.83) followed by cluster III (55.00).

The highest cluster mean value for ascorbic acid was observed in cluster V (95.50) followed by cluster II (86.75) and cluster I (86.41). The lowest clusters mean value for ascorbic acid was recorded in cluster III (86.33) followed by cluster IV (79.50).

The highest cluster mean value for reducing and non-reducing sugar was observed in cluster V (0.98, 0.73) followed by cluster III (0.94, 0.62) and cluster II (0.85, 0.52), respectively. The lowest clusters mean value for reducing and non-reducing sugar was recorded in cluster I (0.78, 0.47) followed by cluster IV (0.70, 0.45), respectively.

The highest cluster mean value for total sugars was observed in cluster V (1.72) followed by cluster III (1.61) and cluster II (1.41). The lowest clusters mean value for total sugars was recorded in cluster IV (1.40) followed by cluster I (1.34).

The highest cluster mean value for total soluble solids (T.S.S) was observed in cluster V (5.31) followed by cluster IV (5.23) and cluster III (4.54). The lowest clusters mean value for total soluble solids (T.S.S) was recorded in cluster I (3.60) followed by cluster II (2.98).

The highest cluster mean value for titratable acidity was observed in cluster IV (0.31) followed by cluster I (0.28) and cluster III (0.27). The lowest clusters mean value for titratable acidity was recorded in cluster V (0.22) followed by cluster II (0.18).

The highest cluster mean value for marketable fruit yield per plant was observed in cluster IV (3.55) followed by cluster III (3.10) and cluster II (2.87). The lowest clusters mean value for marketable fruit yield per plant was recorded in cluster V (2.80) followed by cluster I (2.75).

Table-4.10.A: Cluster mean for twenty one characters in bitter gourd (2018-19)

Characters Cluster No.	Node no. to I st staminate flowers	Node no. to I st pistillate flowers	Days to anthesis of I st staminate flowers	Days to anthesis of I st pistillate flowers	Days to I st fruit harvest	Vine length (m)	Fruit length (cm)
	1	2	3	4	5	6	7
Cluster-I	12.04	12.26	39.04	42.07	53.70	4.73	19.90
Cluster-II	13.21	13.29	39.80	42.82	53.13	4.57	19.20
Cluster-III	13.33	10.33	42.20	32.43	59.67	4.50	17.99
Cluster-IV	8.67	9.00	41.60	37.16	48.00	5.37	15.62
Cluster-V	11.33	7.67	36.17	54.74	62.00	5.72	24.35

Continued ...

Characters Cluster No.	Nodes/ plant	No. of branches/ plant	No. of seeds/ fruit	Fruit diameter (cm)	No. of fruits/ plant	Seeds weight/ Fruit (g)	Average fruit weight (g)
	8	9	10	11	12	13	14
Cluster-I	55.85	16.52	22.30	6.38	14.00	3.43	71.93
Cluster-II	62.71	19.21	22.42	6.40	14.71	3.49	100.54
Cluster-III	56.67	21.00	21.67	6.07	12.00	3.48	74.00
Cluster-IV	44.67	20.33	17.33	6.57	9.33	2.55	53.00
Cluster-V	40.33	20.67	22.33	7.59	12.67	2.54	64.00

Continued ...

Characters Cluster No.	Ascorbic acid (mg/100g)	Reducing sugar (%)	Non- reducing sugar (%)	Total sugars (%)	T.S.S. (°Brix)	Titratable acidity (%)	Marketable fruit yield /plant (kg)
	15	16	17	18	19	20	21
Cluster-I	87.96	0.84	0.59	1.52	3.95	0.26	2.82
Cluster-II	85.87	0.83	0.45	1.29	2.86	0.21	2.97
Cluster-III	89.00	0.82	0.30	1.12	3.70	0.24	2.76
Cluster-IV	87.67	0.55	0.41	1.46	3.77	0.23	1.61
Cluster-V	79.00	0.69	0.45	1.40	5.20	0.32	3.65

Table-4.10.B: Cluster mean for twenty one characters in bitter gourd (2019-20)

Characters Cluster No.	Node no. to I st staminate flowers	Node no. to I st pistillate flowers	Days to anthesis of I st staminate flowers	Days to anthesis of I st pistillate flowers	Days to I st fruit harvest	Vine length (m)	Fruit length (cm)
	1	2	3	4	5	6	7
Cluster-I	11.69	11.83	40.35	42.82	53.25	4.75	19.58
Cluster-II	13.00	13.40	38.20	41.62	47.47	4.51	19.22
Cluster-III	7.33	8.67	40.60	37.70	46.00	5.43	15.60
Cluster-IV	12.00	8.00	36.50	55.37	61.67	5.58	24.44
Cluster-V	13.67	14.33	38.35	36.12	52.00	3.26	20.25

Continued ...

Characters Cluster No.	Nodes/ plant	No. of branches/ plant	No. of seeds/ fruit	Fruit diameter (cm)	No. of fruits/ plant	Seeds weight/ Fruit (g)	Average fruit weight (g)
	8	9	10	11	12	13	14
Cluster-I	58.67	16.83	22.06	6.07	13.47	3.46	72.72
Cluster-II	56.33	18.80	22.27	6.72	15.60	3.47	118.93
Cluster-III	44.00	20.67	17.00	6.41	10.33	2.57	54.33
Cluster-IV	41.33	19.00	21.67	7.39	11.67	2.55	63.67
Cluster-V	41.67	24.67	21.00	7.83	18.33	3.50	62.00

Continued ...

Characters Cluster No.	Ascorbic acid (mg/100g)	Reducing sugar (%)	Non- reducing sugar (%)	Total sugars (%)	T.S.S. (°Brix)	Titrateable acidity (%)	Marketable fruit yield /plant (kg)
	15	16	17	18	19	20	21
Cluster-I	85.22	0.85	0.53	1.41	3.69	0.25	2.86
Cluster-II	89.27	0.82	0.46	1.32	2.58	0.18	2.96
Cluster-III	87.33	0.54	0.53	1.47	3.87	0.22	1.65
Cluster-IV	80.00	0.71	0.44	1.41	5.25	0.29	3.45
Cluster-V	95.33	0.99	0.73	1.72	5.33	0.22	2.81

Table-4.10.C: Cluster mean for twenty one characters in bitter gourd (Pooled data)

Characters Cluster No.	Node no. to I st staminate flowers	Node no. to I st pistillate flowers	Days to anthesis of I st staminate flowers	Days to anthesis of I st pistillate flowers	Days to I st fruit harvest	Vine length (m)	Fruit length (cm)
	1	2	3	4	5	6	7
Cluster-I	11.57	11.59	39.23	39.14	53.22	5.06	18.54
Cluster-II	12.60	12.50	38.95	44.47	52.17	4.29	19.57
Cluster-III	12.33	15.33	51.44	49.27	46.33	5.56	22.90
Cluster-IV	11.67	7.83	36.33	55.06	61.83	5.65	24.40
Cluster-V	13.83	14.33	37.81	35.97	52.50	3.25	20.24

Continued ...

Character No.	Nodes/ plant	No. of branches/ plant	No. of seeds/ fruit	Fruit diameter (cm)	No. of fruits/ plant	Seeds weight/ Fruit (g)	Average fruit weight (g)
	8	9	10	11	12	13	14
Cluster-I	55.04	16.31	20.72	5.82	12.57	3.27	67.59
Cluster-II	61.23	19.42	23.54	6.87	15.31	3.60	107.00
Cluster-III	61.33	15.50	20.50	5.90	12.50	3.22	55.00
Cluster-IV	40.83	19.83	22.00	7.49	12.17	2.54	63.83
Cluster-V	42.00	24.83	21.17	7.75	18.50	3.50	61.83

Continued ...

Character No.	Ascorbic acid (mg/100g)	Reducing sugar (%)	Non- reducing sugar (%)	Total sugars (%)	T.S.S. (°Brix)	Titratable acidity (%)	Marketable fruit yield /plant (kg)
	15	16	17	18	19	20	21
Cluster-I	86.41	0.78	0.47	1.34	3.60	0.28	2.75
Cluster-II	86.75	0.85	0.52	1.41	2.98	0.18	2.87
Cluster-III	86.33	0.94	0.62	1.61	4.54	0.27	3.10
Cluster-IV	79.50	0.70	0.45	1.40	5.23	0.31	3.55
Cluster-V	95.50	0.98	0.73	1.72	5.31	0.22	2.80

Table-4.11: Percent of contribution of different characters in total genetic divergence in bitter gourd

The analysis of contribution of characters towards total genetic divergence between twenty genotypes of bitter gourd had been given in the Table-4.11. The highest manifestation of contribution of genetic divergence was made by average fruit weight (28.95%) followed by total sugars (15.79%), total soluble solids (12.11%), days to anthesis of first pistillate flowers (9.47%) and titratable acidity (8.95%). The lower percent contribution was observed in number of branches per plant and reducing sugar (4.74%), nodes per plant and non-reducing sugar (4.21%), days to anthesis of first

staminate flowers (2.63%), days to first fruit harvest (1.05 %) and number of fruit per plant (0.53%). The genetic divergence were very low in manifestation genetically in the available genotypes of characters was node number to first staminate flowers was followed by node number to first pistillate flowers, vine length, fruit length, fruit diameter, seeds weight per fruit and marketable fruit yield per plant (0.00%).

Table-4.11. A: Percent contribution of twenty one characters towards total genetic divergence in bitter gourd (2018-19)

S. No.	Source	Times ranked 1 st	Contribution Percent
		1	2
1.	Node no. to I st staminate flowers	0	0
2.	Node no. to I st pistillate flowers	0	0
3.	Days to anthesis of I st staminate flowers	1	0.53
4.	Days to anthesis of I st pistillate flowers	13	6.84
5.	Days to first fruit harvest	0	0
6.	Vine length (m)	0	0
7.	Fruit length (cm)	0	0
8.	Nodes per plant	3	1.58
9.	No. of branches per plant	1	0.53
10.	No. of seeds per fruit	0	0
11.	Fruit diameter (cm)	0	0
12.	No. of fruits per plant	0	0
13.	Seeds weight per fruit (g)	0	0
14.	Average fruit weight (g)	4	2.11
15.	Ascorbic acid (mg/100g)	0	0
16.	Reducing sugar (%)	8	4.21
17.	Non-reducing sugar (%)	24	12.63
18.	Total sugars (%)	46	24.21
19.	T.S.S. (°Brix)	8	4.21
20.	Titrateable acidity (%)	81	42.63
21.	Marketable fruit yield per plant (kg)	1	0.53

Table-4.11.B: Percent contribution of twenty one characters towards total genetic divergence in bitter gourd (2019-20)

S. No.	Source	Times ranked 1 st	Contribution Percent
		1	2
1.	Node no. to 1 st staminate flowers	0	0
2.	Node no. to 1 st pistillate flowers	0	0
3.	Days to anthesis of 1 st staminate flowers	1	0.53
4.	Days to anthesis of 1 st pistillate flowers	5	2.63
5.	Days to first fruit harvest	3	1.58
6.	Vine length (m)	1	0.53
7.	Fruit length (cm)	0	0
8.	Nodes per plant	11	5.79
9.	No. of branches per plant	9	4.74
10.	No. of seeds per fruit	2	1.05
11.	Fruit diameter (cm)	1	0.53
12.	No. of fruits per plant	1	0.53
13.	Seeds weight per fruit (g)	0	0
14.	Average fruit weight (g)	41	21.58
15.	Ascorbic acid (mg/100g)	0	0
16.	Reducing sugar (%)	13	6.84
17.	Non-reducing sugar (%)	15	7.89
18.	Total sugars (%)	36	18.95
19.	T.S.S. (^o Brix)	35	18.42
20.	Titrateable acidity (%)	15	7.89
21.	Marketable fruit yield per plant (kg)	1	0.53

Table-4.11.C: Percent contribution of twenty one characters towards total genetic divergence in bitter gourd (Pooled data)

S. No.	Source	Times ranked 1 st	Contribution Percent
		1	2
1.	Node no. to 1 st staminate flowers	0	0
2.	Node no. to 1 st pistillate flowers	0	0
3.	Days to anthesis of 1 st staminate flowers	5	2.63
4.	Days to anthesis of 1 st pistillate flowers	18	9.47
5.	Days to first fruit harvest	2	1.05
6.	Vine length (m)	0	0
7.	Fruit length (cm)	0	0
8.	Nodes per plant	8	4.21
9.	No. of branches per plant	9	4.74
10.	No. of seeds per fruit	3	1.58
11.	Fruit diameter (cm)	0	0
12.	No. of fruits per plant	1	0.53
13.	Seeds weight per fruit (g)	0	0
14.	Average fruit weight (g)	55	28.95
15.	Ascorbic acid (mg/100g)	2	1.05
16.	Reducing sugar (%)	9	4.74
17.	Non-reducing sugar (%)	8	4.21
18.	Total sugars (%)	30	15.79
19.	T.S.S. (⁰ Brix)	23	12.11
20.	Titrateable acidity (%)	17	8.95
21.	Marketable fruit yield per plant (kg)	0	0

DISCUSSION

Genetic variation is the basis of every crop improvement strategy and the performance of selection is determined by the nature and intensity of species diversity as in genetic material under the plant breeder's control. In other words, variation is important for selection. Thus, to a large degree breeding methods. The frequency of expansion in every crop is controlled by the quantity and type of genetic variation available in the crop. Variability is hereditary and fundamental in selection.

The selection programme mainly depends on the situation of the quantity of the heritable component of variability. Estimates of heritability give information on the transfer of the character through parental material to progeny. The estimations allow for the assessment of genetic and environmental factors in phenotypic variance, which helps in selection. The heritability appraisal is used to evaluate genetic progress under selection, allowing breeders to indicate genetic enhancement and show success for selections of various kinds and levels. **Johnson *et al.* (1955)** have suggested that estimates of heritability in combination with genetic advancement are far more valuable for selection than heredity alone.

Because of the problems explained by **Grafius (1964)**, the importance of character association can scarcely be overstated. While path analysis seems to be probably of the plant breeder's usage is restricted, it does provide knowledge into the complicated interaction between various characteristics of a biological feature and indicates whether the observed correlates with direct effect via other factors. As a result, path analysis examines the causes as well as the characters' respective relevance. Considering the above aspects, the present investigation was under taken with the following objectives:

1. To investigate the variability, heritability and genetic advance for the quantitative characters,
2. To estimate correlation among the important economic traits,
3. To find out the direct and indirect effects of yield components by path analysis
4. To evaluate the genetic divergence for yield and yield attributing traits.

Aim of any plant breeding programme is to develop high yielding varieties with better quality superior over existing one. The variability in selection of genotypes. The

knowledge of association between characters and both direct and indirect effect contributions towards expression of yield is additional help to plant breeder in deciding the selection criteria. A Germplasm collection provides the richest source of variability (**Frankel and Hawkes, 1975**).

In the present investigation, twenty genotypes of bitter gourd sowing wide spectrum of variation for various marketable fruit yield per plant were evaluated in the field for twenty one characters during 2018-19 and 2019-20, respectively. The experiment was conducted in Randomized Block Design and replicated thrice at the Horticulture Research Farm-I, Babasaheb Bhimrao Ambedkar University (A Central University), Vidya Vihar, Rae Bareli Road, Lucknow (U.P.), India. The observations were recorded on 15 physical characters and 6 chemical characters in field and laboratory conditions were considered *viz.*, Node number to first staminate flowers, node number to first pistillate flowers, days to anthesis of first staminate flowers, days to anthesis of first pistillate flowers, days to first fruit harvest, vine length (m), fruit length (cm), nodes per plant, number of branches per plant, number of seeds per plant, fruit diameter (cm), number of fruits per plant, seeds weight per fruit (g), average fruit weight (g), ascorbic acid (mg/100g), reducing sugar (%), non-reducing sugar (%), total sugars (%), total soluble solids (⁰Brix), titratable acidity (%) and marketable fruit yield per plant (kg).

The heritability in broad sense (**Hanson *et al.* 1963**) and genetic advance in percent of mean (**Johnson *et al.* 1955**) are computed to determine the characters' amplitude. The nature of association between different character is studies by using phenotypic and genotypic correlation coefficient (**Searle, 1961**), path analysis (**Dewey and Lu, 1959**) and genetic divergence (**Mahalanobis, 1928**).

In the genotype of bitter gourd in its diversification regions, there is a lot of genetic variation. Among the crop varieties of the bitter gourd, which is produced on a large scale has required the gathering of fundamental information on genetic as well as other morpho-physiological characteristics that aid in crop breeding and genetic modifications for increased production. With the objective in mind, twenty genotypes were collected from various institutes and analyzed for twenty-one characteristics. Considering phenotypic and genotypic coefficients of variation, heritability, genetic advance, correlation, path analysis and genetic divergence statistical parameters were

evaluated. The findings of this research have been examined under the following headings in relation to previously published studies on bitter gourd.

5.1 Analysis of variance

The analysis of variance for every character has been given in Table 4.1 and graphically illustrated in figure. The mean sum of square because of genotypes was high significantly of each the characters. That is to say, the genotype performances on these characteristics were statistically significant, showing that there is sufficiency of possibility for selection in the bitter gourd germplasm available.

5.2 Mean performance of genotype

In evaluating the genotypes in the data, the mean value of twenty genotypes for 21 characters has been given in Table 4.2 and graphically illustrated in figure. There is a lot of variation in genotypes' mean performance were observed for each characters under investigation. The comparison of mean performance of twenty genotypes of bitter gourd for twenty one characters using critical differences revealed variability in the genotypes utilised is quite great. The genotype Kalyanpur Barahmasi significantly out yielded (5.24 kg). While, in case of Kashi Urvasi (4.30 kg), Arka Harit (3.70 kg), Selection-5 (3.55 kg) and Pusa hybrid-1 (3.39 kg) were found significantly superior for marketable fruit yield per plant. Other characters revealed considerably higher mean performance for these genotypes. This result corroborative the findings of *Devi et al. (2013)*, *Talukder et al. (2018)*, *Tiwari et al. (2021)*, *Sureja et al. (2010)*, *Yadagiri et al. (2017)*, *Kumar et al. (2018)*, *Gupta et al. (2016)*, *Yadav et al. (2013)*, *Kumar et al. (2011)*, *Pathak et al. (2014)*, *Alekar et al. (2019)*, *Kumar et al. (2018)*, *Pradhan et al. (2021)* and *Kumari et al. (2015)*.

5.3 Coefficient of variation:

When genetic variance individually does not provide a verdict on which traits exhibit the greatest amount of variation, the evaluation of genotypic coefficient of variation is vital for breeders. As a result, phenotypical and genotypical coefficients of variation may be used to make reliable relative comparisons. For every characteristic studied, the phenotypical coefficient variations were also more than the genotypical coefficient of variation, indicating that the environment had a significant role in the manifestation of the characteristics.

The maximum level of genotypic and phenotypic coefficient of variation was observed for marketable fruit yield per plant followed by average fruit weight, number of branches per plant, titratable acidity, total soluble solids, fruit diameter, non-reducing sugar and number of fruits per plant. Similar results also have been reported by **Devi *et al.* (2013)**, **Talukder *et al.* (2018)**, **Tiwari *et al.* (2021)**, **Sureja *et al.* (2010)**, **Yadagiri *et al.* (2017)**, **Kumar *et al.* (2018)**, **Gupta *et al.* (2016)**, **Yadav *et al.* (2013)**, **Kumar *et al.* (2011)**, **Pathak *et al.* (2014)**, **Alekar *et al.* (2019)**, **Kumar *et al.* (2018)**, **Pradhan *et al.* (2021)** and **Kumari *et al.* (2015)**. For node number to first staminate flowers, seeds weight per fruit, numbers of seeds per fruit, fruit length and vine length moderate phenotypic coefficient variation and genotypic coefficient variation were reported. This result corroborated the findings of **Devi *et al.* (2013)**, **Talukder *et al.* (2018)**, **Tiwari *et al.* (2021)**, **Sureja *et al.* (2010)**, **Yadagiri *et al.* (2017)**, **Kumar *et al.* (2018)**, **Gupta *et al.* (2016)**, **Yadav *et al.* (2013)**, **Kumar *et al.* (2011)**, **Pathak *et al.* (2014)**, **Alekar *et al.* (2019)**, **Kumar *et al.* (2018)**, **Pradhan *et al.* (2021)** and **Kumari *et al.* (2015)**.

Total sugars, days to first fruit harvest, days to anthesis of first staminate flowers and ascorbic acid had lower genotypic as well as phenotypic coefficients of variation. For these characteristics, low phenotypic coefficient variation and genotypic coefficient variation showed that the genotypes used in this study were comparable.

5.4 Heritability and genetic advance:

Heritability is an important trait for the plant breeder in crop improvement because it implies the potential and degree of improvement through selection. Since it assesses the interaction among better parents and progeny, it is widely used in comparing the extent to which a characteristic may be conveyed through parents to progenies during the selection process. High heritability, even then, isn't able to attain adept selection in promoted generations. However, it's coupled with a significant quantity of genetic advance in per cent of mean (**Burton, 1952**). With estimates suggesting a high level of heritability and genetic advancement, there is a lot to improve in future generations.

The results on heritability in broad sense and genetic advance in per cent of mean of presently being investigated has been given in Table 4.3 and graphically

illustrated in figure. The heritability assess for each character ranged from 41.5 per cent (seeds weight per fruit) to 98.6 per cent (average fruit weight). High heritability was recorded for almost each characters except for average fruit weight followed by total soluble solids, total sugars, days to anthesis of first pistillate flowers, nodes per plant, non-reducing sugar, marketable fruit yield per plant, number of branches per plant, vine length, days to first fruit harvest, number of fruits per plant, fruit diameter. High heritability coupled with high genetic advance in per cent of mean were recorded for average fruit weight followed by titratable acidity, number of branches per plant, total soluble solids, marketable fruit yield per plant, non-reducing sugar, fruit diameter and number of fruits per plant showing that environmental factors having minor impact on these characteristics As a result, improvement requires a low level of selection intensity. Similar findings were reported by **Devi *et al.* (2013), Talukder *et al.* (2018), Tiwari *et al.* (2021), Sureja *et al.* (2010), Yadagiri *et al.* (2017), Kumar *et al.* (2018), Gupta *et al.* (2016), Yadav *et al.* (2013), Kumar *et al.* (2011), Pathak *et al.* (2014), Alekar *et al.* (2019), Kumar *et al.* (2018), Pradhan *et al.* (2021) and Kumari *et al.* (2015).**

5.5 Correlation coefficient:

For successful selection in future generations, it is important to perceive the nature and extent of the relationship involving the yield character and the important aspects of the characteristics. The natures of the population under investigation, as well as the degree of the correlation coefficient are frequently impacted by the progenies on which the observation data is based.

Correlations coefficient are responsible for gene linkage and pleiotropy between pairs of character. As a result, selecting one characteristic has an impact on the other traits that are connected and pleiotropically changed. Correlation studies have been given a lot of emphasis in the crop improvement field since they help with successful selection.

In the current investigation, correlation among twenty one characters were worked out in all possible combinations on genotypic as well as phenotypic levels has been given in Table 4.4 and 4.5, respectively. Overall, the amplitude of genotypic greater than phenotypic correlation coefficients proportional values. It apparent a significant genetic link between characteristics and phenotypic manifestation, which

has been reduced by environmental factors. This result with conformity of the findings of **Devi *et al.* (2013)**, **Talukder *et al.* (2018)**, **Tiwari *et al.* (2021)**, **Sureja *et al.* (2010)**, **Yadagiri *et al.* (2017)**, **Kumar *et al.* (2018)**, **Gupta *et al.* (2016)**, **Yadav *et al.* (2013)**, **Kumar *et al.* (2011)**, **Pathak *et al.* (2014)**, **Alekar *et al.* (2019)**, **Kumar *et al.* (2018)**, **Pradhan *et al.* (2021)** and **Kumari *et al.* (2015)** also reported higher magnitudes of genotypic correlation than the compatible phenotypic correlation among yield and yield attributing traits components.

The most important characters *viz.*, marketable fruit yield per plant having exhibited high significantly and positive phenotypic correlation with fruit length, reducing sugar, number of fruits per plant. Most important positive correlation and significant association was estimated between number of seeds per fruit followed by node number first pistillate flowers, days to anthesis of first staminate flowers, fruit diameter and seed weight per fruit was also found to have significant and positive correlation. While, it showed negative significant correlation with ascorbic acid followed by days to anthesis of first pistillate flowers and total soluble solids. This showed that traits having significant positive correlation with marketable fruit yield per plant also having significantly and positive correlation such as some other characters as well. The accessible literature has also observed in positive correlation among marketable fruit yield per plant and among them in bitter gourd. Similar association of traits in bitter gourd had also been reported by **Devi *et al.* (2013)**, **Talukder *et al.* (2018)**, **Tiwari *et al.* (2021)**, **Sureja *et al.* (2010)**, **Yadagiri *et al.* (2017)**, **Kumar *et al.* (2018)**, **Gupta *et al.* (2016)**, **Yadav *et al.* (2013)**, **Kumar *et al.* (2011)**, **Pathak *et al.* (2014)**, **Alekar *et al.* (2019)**, **Kumar *et al.* (2018)**, **Pradhan *et al.* (2021)** and **Kumari *et al.* (2015)**.

5.6 Path analysis:

Path analysis is a standard partial regression coefficient that divides the coefficient of correlation into direct and indirect effects of a set of independent factors on the dependent variable. The study proposed a method for distinguishing between the direct and indirect effects of various characteristics on marketable fruit yield per plant at the genotypic as well as phenotypic levels has been given in Table 4.6 and 4.7, respectively.

The higher magnitude of positive direct effect on marketable fruit yield per plant was exerted by fruit length, number of fruits plant, number of seeds per fruit, vine length, node number to first pistillate flowers, days to first fruit harvest and total sugars. The higher magnitude of negative direct effect on marketable fruit yield per plant was exhibited by days to anthesis of first pistillate flowers, ascorbic acid, number of branches per plant, reducing sugar and non-reducing sugar.

Considerable highly positive indirect effect on marketable fruit yield per plant was shown by fruit length, reducing sugar, number of fruits per plant and vine length followed by node number to first staminate flowers showed low positive indirect effect. As a result, these characters should be considered during the selection procedure. This finding is quite different from the disquisition of **Devi *et al.* (2013)**, **Talukder *et al.* (2018)**, **Tiwari *et al.* (2021)**, **Sureja *et al.* (2010)**, **Yadagiri *et al.* (2017)**, **Kumar *et al.* (2018)**, **Gupta *et al.* (2016)**, **Yadav *et al.* (2013)**, **Kumar *et al.* (2011)**, **Pathak *et al.* (2014)**, **Alekar *et al.* (2019)**, **Kumar *et al.* (2018)**, **Pradhan *et al.* (2021)** and **Kumari *et al.* (2015)**.

5.7 Genetic divergence:

The result of D^2 analysis are presented in Table 4.8, 4.9 4.10 and 4.11, respectively. The studies of genetic divergence between twenty genotypes of bitter gourd were carried out by Mahalanobis D^2 statistics'. In present investigation twenty genotypes of bitter gourd were clusters in five distinctive do not overlap clusters. This suggested that the genotypes had a lot of variations. The genotypes of diverse origins were commonly found in the major groups in the described genetic divergence investigation. However, genotypes from the same country or area were discovered to be clustered in concert in common clusters. It was common to see genotypes from various origins or from the identical geographical region grouped at one time in the same cluster. This implies that genetic and geographic diversity are not related. Grouping of genotypes into V cluster indicated presence of considerable diversity among the different traits in the available germplasm. Cluster number I followed by cluster number II which contained 9 and 8 entries, respectively. The minimum number of cluster III, IV and V which had one entry from the three clusters, respectively, which compared to all genotypes. The appraise of intra clusters and inter clusters distance recognized by D^2 values has been presented in Table-4.9. The intra cluster D^2 values varied from 0.00 (cluster III, VI and V) to 127.20 (cluster II). The

highest number of inter cluster distance was observed between clusters II to V (401.57), which suggested that members of these two clusters were genetically very diverse to each other. The inter-cluster values between cluster II and V (401.57) followed by cluster II and IV (295.76), cluster IV and V (276.66), cluster II and III (272.23), cluster I and V (231.71), cluster I and II (201.99), cluster I and IV (167.65), cluster III and V (164.50) and cluster I and III (161.99) were very high. The minimum inter-cluster D^2 values were recorded in case of cluster III and IV (155.11), respectively. The maximum inter clusters distance showed spacious genetic divergence among the genotypes of those clusters. While, lowest inter clusters values amongst the clusters indicated these clusters of genotypes were not much genetically diverse from each other. Further the crossing between lines of distant clusters may give rise desirable segregates. This result corroborates the findings of **Dey *et al.* (2007)**, **Remsi and Sreelathakumary (2012)**, **Shalini *et al.* (2000)**, **Khan (2006)**, **Angadi *et al.* (2018)**, **Gupta *et al.* (2016)**, **Singh *et al.* (2020)**, **Ghosh *et al.* (2015)** and **Singh *et al.* (2019)**.

The analysis of contribution of characters towards genetic divergence between twenty genotypes of bitter gourd had been given in Table-4.11. The highest manifestation of contribution of genetic divergence was made by average fruit weight followed by total sugars, total soluble solids, days to anthesis of first pistillate flowers, titratable acidity. The genetic divergence were moderate in manifestation genetically in the available genotypes of characters was number of branches per plant and reducing sugar, nodes per plant and non-reducing sugar, days to anthesis of first staminate flowers, days to first fruit harvest and number of fruit per plant were low in manifestation of the genetic divergence in the germplasm that is provided. The genetic divergence were very low in manifestation genetically in the available genotypes of characters was node number to first staminate flowers was followed by node number to first pistillate flowers, vine length, fruit length, fruit diameter, seeds weight per fruit, marketable fruit yield per plant. The contributions of these characters for total genetic divergence were quite similar to the reports of **Dey *et al.* (2007)**, **Remsi and Sreelathakumary (2012)**, **Shalini *et al.* (2000)**, **Khan (2006)**, **Angadi *et al.* (2018)**, **Gupta *et al.* (2016)**, **Singh *et al.* (2020)**, **Ghosh *et al.* (2015)** and **Singh *et al.* (2019)**.

SUMMARY AND CONCLUSION

The present investigation entitled “**Studies on genetic variability, heritability, correlation and path analysis in bitter gourd (*Momordica charantia* L.)**” was undertaken with the objectives:

1. To investigate the variability, heritability and genetic advance for the quantitative characters,
2. To estimate correlation among the important economic traits,
3. To find out the direct and indirect effects of yield components by path analysis and
4. To evaluate the genetic divergence for yield and yield attributing traits.

In the present study, 20 genotypes of bitter gourd sowing wide spectrum of variation for various marketable fruit yield per plant were evaluated in the field for twenty one characters during 2018-19 and 2019-20, respectively. The experiment was conducted in Randomized Block Design and replicated thrice at the Horticulture Research Farm-I, Babasaheb Bhimrao Ambedkar University (A Central University), Vidya Vihar, Rae Bareli Road, Lucknow, (U.P.), India. The observations were recorded on 15 physical characters and 6 chemical characters in field as well as laboratory conditions were considered *viz.*, Node number to first staminate flowers, node number to first pistillate flowers, days to anthesis of first staminate flowers, days to anthesis of first pistillate flowers, days to first fruit harvest, vine length (m), fruit length (cm), nodes per plant, number of branches per plant, number of seeds per plant, fruit diameter (cm), number of fruits per plant, seeds weight per fruit (g), average fruit weight (g), ascorbic acid (mg/100g), reducing sugar (%), non-reducing sugar (%), total sugars (%), total soluble solids (⁰Brix), titratable acidity (%) and marketable fruit yield per plant (kg). Row-to-row and plant-to-plant distances were maintained as 2.5 m × 0.5 m. Each entry was grown in the plot size of and 3.0 m x 2.0 m. The observations were recorded on twenty one quantitative and qualitative traits. The mean data were subjected to the various statistical and biometrical analyses. The salient findings of the study are summarized below:

1. The analysis of variance (mean sum of square) due to genotypes was highly significant for all the characters. In other words, the performances of the genotypes with respect to the characters were statistically different, suggesting

that there exists ample scope for selection in the available germplasm of bitter gourd.

2. Based on mean performance only one genotype Kalyanpur Barahmasi. Kashi Urvasi followed by Arka Harit, Selection-5 and Pusa hybrid-1 were found significantly superior for marketable fruit yield per plant. These genotypes also showed significantly high mean performance for some other characters.
3. The estimates of phenotypic coefficients of variation (PCV) were higher than genotypic coefficients of variation (GCV) for all the traits. High magnitudes of variability were observed in case of marketable fruit yield per plant followed by average fruit weight, number of branches per plant, acidity, total soluble solids, fruit diameter, non-reducing sugar and number of fruits per plant.
4. High heritability coupled with high genetic advance in per cent of mean were observed for average fruit weight followed by total soluble solids, total sugars, days to anthesis of first pistillate flowers, nodes per plant, non-reducing sugar, marketable fruit yield per plant, number of branches per plant, vine length, days to first fruit harvest, number of fruits per plant, fruit diameter indicating scope of high selection response.
5. In general, genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients, suggesting a strong inherent relationship in different pairs of the traits. Marketable fruit yield per plant had exhibited highly significant and positive phenotypic correlation with fruit length, reducing sugar, number of fruits per plant showed significant and positive correlation with marketable fruit yield per plant. While, it showed negative significant correlation with ascorbic acid followed by days to anthesis of first pistillate flowers and total soluble solids and selection for traits with positive correlation. Would be effective for yield improvement in bitter gourd.
6. Path coefficient analysis revealed that marketable fruit yield per plant was exerted by fruit length, number of fruits plant, number of seeds per fruit, vine length, node number to first pistillate flowers, days to first fruit harvest and total sugars exhibited considerable positive direct effect on marketable fruit yield per plant. while negative direct contribution towards marketable fruit yield per plant were pronounced by days to anthesis of first pistillate flowers, ascorbic acid,

number of branches per plant, reducing sugar and non-reducing sugar both at phenotypic and genotypic levels.

7. Mahalanobis D^2 statistic distributed all the twenty genotypes into five diverse clusters.
8. Grouping of genotypes into V cluster indicated presence of considerable diversity among the different traits in the available germplasm. Cluster number I followed by cluster number II which contained 9 and 8 entries, respectively. The minimum number of cluster III, IV and V which had one entry from the three clusters, respectively, which compared to all genotypes.
9. The inter-cluster values between cluster II and V (401.57) followed by cluster II and IV (295.76), cluster IV and V (276.66), cluster II and III (272.23), cluster I and V (231.71), cluster I and II (201.99), cluster I and IV (167.65), cluster III and V (164.50) and cluster I and III (161.99) were very high. The minimum inter-cluster D^2 values were recorded in case of cluster III and IV (155.11). Whereas the lowest intra clusters distance showed by cluster III, IV and V, respectively (0.00) indicating genetic similarity of genotypes belonging to the respective clusters.
10. The quantitative traits which contributed maximum towards the genetic distance among the genotypes were of the average fruit weight followed by total sugars, total soluble solids, days to anthesis of first pistillate flowers, acidity. The genetic divergence were very low in manifestation genetically in the available genotypes of characters was node number to first staminate flowers was followed by node number to first pistillate flowers, vine length, fruit length, fruit diameter, seeds weight per fruit, marketable fruit yield per plant. The contribution of these traits for total genetic divergence.

Conclusion:

In the present study, maximum number of genotypes. Hence, it is concluded that there was a wide range of variation among the genotypes for all characters indicating that considerable scope existed for the improvement of bitter gourd through selections. Genetic parameters in association with correlation study indicated that for selection of superior genotypes. Out of twenty genotypes, five best high yielding genotypes Kalyanpur Barahmasi followed by Kashi Urvasi, Arka Harit, Selection-5 and Pusa hybrid-1 were found superior for marketable fruit yield per plant and these genotypes may be recommended for large scale cultivation among the farmers after proper testing in multilocational trials and these superior genotypes further can be used as donors in breeding programme.

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