

GENETIC EVALUATION OF BITTER GOURD (*Momordica charantia* L.) GENOTYPES FOR YIELD AND QUALITY TRAITS UNDER LOW HILL CONDITIONS OF HIMACHAL PRADESH

Thesis

by

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CERTIFICATE-I

This is to certify that the thesis titled “**GENETIC EVALUATION OF BITTER GOURD (*Momordica charantia* L.) GENOTYPES FOR YIELD AND QUALITY TRAITS UNDER LOW HILL CONDITIONS OF Himachal Pradesh**” submitted in partial fulfilment of the requirements for the award of degree of **MASTER OF SCIENCE (HORTICULTURE) VEGETABLE SCIENCE** in the discipline of **VEGETABLE SCIENCE** of Dr. Yashwant Singh Parmar University of Horticulture and Forestry, Nauni, Solan (HP) – 173230 is a bonafide research work carried out by **Mr. VARUN RANA (NH-2021-47-M)** son of Sh. Harmesh Lal under my supervision and that no part of this thesis has been submitted for any other degree or diploma.

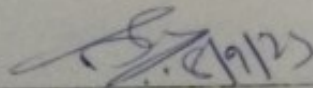
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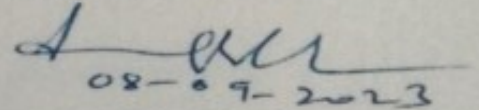
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CERTIFICATE - II

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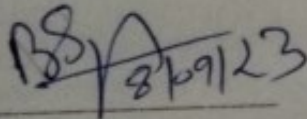


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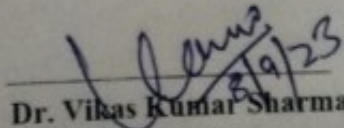

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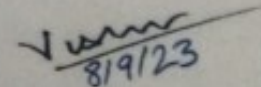
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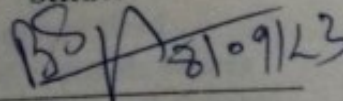
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This is to certify that all the mistakes and errors pointed out by external examiner have been incorporated in the thesis entitled “**Genetic evaluation of bitter gourd (*Momordica charantia* L.) genotype for yield and quality traits under low hill conditions of Himachal Pradesh**” submitted by **Mr. VARUN RANA (NH-2021-47-M)** son of Shri Harmesh Lal to Dr. Yashwant Singh Parmar University of Horticulture and Forestry, Nauni, Solan (HP) – 173 230 in partial fulfilment of the requirements for the award of degree of **MASTER OF SCIENCE (HORTICULTURE) VEGETABLE SCIENCE** in the discipline of **HORTICULTURAL SCIENCES**.

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When the heart speaks in seclusion...

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ABBREVIATIONS

%	:	Percentage
°C	:	Degree Celsius
CD	:	Critical Difference
cm	:	Centimeter
et al.	:	And co-worker/ and others
Fig	:	Figure
kg	:	Kilogram
ha	:	Hectare
i.e.	:	That is
m	:	Meter
RCBD:		Randomized Complete Block Design
mm	:	Milli Meter
/	:	Per
spp.	:	Species
mg	:	milligram
viz.	:	Videlicet (namely)
ANOVA	:	Analysis of Variance
CV	:	Coefficient of Variation
g	:	Gram
NHB	:	National Horticulture Board
SE	:	Standard Error
PCV	:	Phenotypic Coefficient of variation
GCV	:	Genotypic Coefficient of variation
MPKV	:	Mahatma Phule Krishi Vidyapeeth
=	:	Equal to
×	:	Multiplication

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The page features a light beige background with a central white rounded rectangle. In the four corners, there are decorative illustrations of leafy branches. The leaves are rendered in shades of brown and tan, with fine white speckles scattered across their surfaces, giving them a textured, natural appearance. The branches extend from the corners towards the center of the page.

INTRODUCTION

Chapter 1

INTRODUCTION

A well-balanced diet should include enough vegetables because they not only provide calories but also key protective nutrients like proteins, minerals, dietary fibres, micronutrients, and antioxidants. Diets high in vegetables are linked to general excellent health and lower the risk of heart attacks and strokes, among other cardiovascular disorders (He et al. 2006).

The bitter gourd (*Momordica charantia* L.), one of the most significant fruits and vegetables in the cucurbitaceae family, the bitter gourd (*Momordica charantia* L.) has a $2n=2x=22$ genetic makeup. The origin of this important crop is probably India, with a secondary centre of diversity in China (Grubben 1977). It is acclimatized to very different environments and can be grown in tropical and subtropical climates (Lim 1998).

According to Jeffrey (1990), the genus *Momordica* is a member of the subtribe Thladianthinae, tribe Jolififiae, and subfamily Cucurbitoideae of the Cucurbitaceae. In Asia and Africa, there are 45 species of *Momordica* that have been domesticated (Robinson and Decker-Walters 1997). Only six legitimate species of the genus *Momordica* exist in India and they fall into two categories: monoecious (*M. charantia* L. and *M. balsamina* L.) and dioecious (*M. dioica* Roxb., *M. sahyadrica* Joseph & Antony, *M. cochinchinensis* (Lour.) Spreng.) and *M. subangulata* Blume. Although *Momordica cymbalaria* Fenz. [*Luffa cymbalaria* = *M. tuberosa* (Roxb.) Cogn.] is not included in the genus (Joseph 2005).

Momordica charantia has distinct yellow male and female flowers, is monoecious in nature, extensively cross-pollinated, shows a wide range of fruit and vegetative features (Resmi and Sreelathakumary 2012). Bitter gourds can be boiled, curried, stuffed, sliced and fried. They can also be pickled, preserved and dehydrated. They also have a wealth of medicinal characteristics, including purgative, carminative and anti-diabetic ones. The fruit acts as an anthelmintic, stomachic, antibilious and laxative. In fact, it is a tonic fruit, used in rheumatism, gout and also for diabetes. A decoction of the root extract is helpful in abortion, hemorrhoids and also in biliaesness (Khulakpam et al. 2015).

It ranks 1st among vitamins with respect to vitamin C and minerals, particularly iron and phosphorus. The tender and immature fruit is a rich source of calcium (20 mg/100 g), phosphorus (55 mg/100 g), iron (1.8 mg/100 g), vitamin A (219 IU/100 g) and vitamin C (88 mg/100 g). The roots, vines, leaves, flowers and seeds of a bitter gourd are also used in medicinal preparations (Morton 1967). Although it is used extensively in folk medicine, it also has various culinary purposes, particularly in south, southeast and east Asia. It is also grown as an ornamental (Heiser 1979). The bitter flavored fruit of *Momordica charantia* have been more favoured for consumption in contrast to other cucurbitaceous vegetables (Marr et al. 2004). Cucurbitacins are mostly to blame for the bitterness of most cucurbits (Decker-Walters 1999). The cucurbitacin-like alkaloid momordicine and triterpene glycosides (momordicoside K and L) are the compounds which gives bitter gourd its bitter flavor (Jeffrey 1980; Okabe et al. 1982). These substances are the most bitter in the plant kingdom (Johns 1990) but lacks the oxygen function at C-11 which distinguishes "true" cucurbitacins (Neuwinger 1994). Rats wound healing and tissue regeneration are similarly accelerated by applying bitter gourd fruit powder to wound sites (Prasad et al. 2006). According to Omoregbe et al. (1996), *Escherichia coli*, *Pseudomonas*, *Salmonella*, *Streptobacillus* and *Streptococcus* are the main microorganisms on which the bitter gourd leaf extracts have most far-reaching effects. Furthermore, antiprotozoal efficacy against *Entamoeba histolytica* has been demonstrated by whole plant extracts. Fruit extracts from *M. charantia* L. have specifically shown activity against tuberculosis and the bacteria *Helicobacter pylori* that causes stomach ulcers (Hussain and Deeni 1991; Omoregbe et al. 1996 and Yesilada et al. 1999). Cucurbits are farmed on an average of 84863.93 thousand metric tonnes per hectare on an area of 2156.04 thousand hectares over the world (Anonymous 2020a). Karnataka, Maharashtra, Tamil Nadu and Kerala are the main farming states of this crop and is grown on an area of roughly 107 thousand hectares in India with an annual production of 1292 thousand metric tonnes and productivity of 12.07 tonnes per hectare (Anonymous 2020b). Whereas in Himachal Pradesh cucurbits are grown on an area of 2927.41 hectares with a production of 73361 metric tonnes (Anonymous 2020c).

The primary criterion for assessing a crop improvement is fruit production. Selection of desired types should be based on performance as well as other

determining characteristics. Information yielding and performance-related relationships and determination of traits is very important for effective use of available genetic stocks in a crop improvement program for bitter gourd. Similar to other quantitative traits, bitter gourd yield is greatly impacted by other yield-related characteristics. Yield and other qualities that contribute to yield should be taken into consideration while choosing desirable types. For the effective use of the genetic stock that is presently available in the bitter gourd crop development programme, knowledge of the relationships between yield and variables that contribute to yield is crucial. The number of primary branches per vine, the number of nodes per vine, the sex ratio, the number of fruits per vine and the average fruit weight are some of the variables that have a massive impact on bitter gourd yield. Heritability provides factual data for the genetic selection process by indicating how much phenotypic variability has a genetic basis. For any planned breeding effort intended to increase agricultural yield potential, it is essential to gather sufficient data on the level and nature of genetic diversity and its accompanying heritability. In order to choose the finest genotypes for rapid improvement in yield and associated features, as well as to pick the most suitable parents for the hybridization programme, genetic diversity in a crop plays a crucial role (Naseeruddin et al. 2011; Singh et al. 2014).

Therefore, the present investigations entitled “**Genetic evaluation of bitter gourd (*Momordica charantia* L.) genotypes for yield and quality traits under low hill conditions of Himachal Pradesh**” shall be carried out at Experimental Farm of RHRTS, Jachh with the following objectives:

- To study the performance and extent of genetic variability in the Bitter gourd genotypes under low hill conditions of Himachal Pradesh.
- To study the correlation and path coefficient analysis for different traits in various Bitter gourd genotypes.
- To identify the promising genotypes with desirable horticultural traits.
- To study the genetic divergence of different genotypes of Bitter gourd.

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***REVIEW
OF
LITERATURE***

Chapter-2

REVIEW OF LITERATURE

All programmes for crop development are built around genetic diversity. Vavilov (1951), who came to the conclusion that a large range of variability offers a better scope of selection, was the first to recognize the significance of genetic diversity. The performance, genetic variability, heritability, divergence, character association and path coefficient analysis of the bitter gourd will be studied in the current project. The following subheads provide a brief review of the pertinent literature on the many topics included in the present study:

2.1 Genetic variability

2.2 Heritability and genetic advance

2.3 Correlation coefficient

2.4 Path coefficient analysis

2.5 Genetic divergence

2.1 Genetic variability

Information on the maturity and scope of genetic diversity, as well as the degree of transmission of the traits is crucial for a successful crop improvement programme. In order to efficiently conduct selection, the population's variability can be divided into heritable and non-heritable components, namely the phenotypic and genotypic coefficients of variation, heritability and genetic progress. High heritability alone cannot lead to effective selection in segregating generations unless it is combined with information about a significant amount of genetic advancement (Johnson et al. 1955).

Studies on bitter gourd's genetic diversity, however, are scarce. In order to gain insight into the issues faced in genetic studies, work done in similar cucurbitaceous crops such as cucumber, musk melon, bottle gourd and ridge gourd, among others was included in the review of literature.

Yadav et al. (2008) significant variations were revealed by the variance

analysis for 17 plant characteristics. The longest vine ever measured was found in IC-85635A. Internodal length and the number of primary branches per vine were both noticeably higher in IC-85639. JMC-4 had the most nodes as was seen. Significantly decreased minimum and maximum fruit length, fruit breadth, yield per vine, yield per plot and yield/ha values were noted in MC-84. GY-I had the most fruits per vine whereas JMC-22 had the least amount of powdery mildew infestation.

For 15 characteristics, Banik et al. (2009) examined the genetic variation of 26 genotypes of snake gourd. Crop production per plant, node number to first female and male bloom and primary vine length are all significant variables to take into account because of the reported high levels of variability. Strong genetic gain and heritability were seen for fruit yield per plant, vine length and the number of first male flower nodes. These results suggest that character selections based on the pertinent characters will be quite successful.

Islam et al. (2009) analyzed 20 different genotypes of bitter gourd and found that there was significant genetic variation between genotypes for the number of fruit plants, yield plant and vine branches. In contrast to days until the first male and female flowering, which had a low genotypic co-efficient of variation (GCV), high genotypic co-efficient of variation (GCV) were found for branches vine, yield plant1 and quantity of fruit plant.

The bitter gourd's domestication, nutritional benefits and therapeutic characteristics were discussed by Behera et al. in 2010. (*Momordica charantia* L.). the bitter gourd's biological characteristics (taxonomy, morphology and reproductive biology), horticultural characteristics (climate and soil, culture, sex expression and modification, harvest, seed production and pests and diseases) and breeding characteristics (genetic variation and germplasm development, inheritance, character association, goals, cultivar development, breeding techniques and biotechnology).

Yadav et al. (2013) assessed the genetic diversity of 13 characteristics in 13

different genotypes of bitter gourd grown in Allahabad in 2007 and 2008. The trait yield per hectare had the widest range of variation followed by fruit weight, nodes per vine, days until the first appearance of female flowers, days until the first appearance of male flowers and fruit length. The trait yield per vine had the narrowest range of variation.

In a field study done at the Sher-e-Bangla Agricultural University's experimental field in Dhaka from April 2009 to September 2010, seventeen genotypes of bitter gourd (*Momordica charantia* L.) were examined by Khan et al. (2015). The study's goals included estimating genetic factors, character association and yield-contributing genotype variability and character association and genotype variability. For each character the genotypes showed a substantial lot of statistically significant variation.

In order to ascertain the various parameters of genetic variability and the nature of interrelationships among traits affecting yield in bitter gourd, 28 F1 crosses created from 8 x 8 diallel analysis excluding reciprocals were evaluated at Model Orchard, College of Horticulture, Rajendranagar, Hyderabad during 2011–12 by Rani et al. (2015). All of the analysed characters had extremely significant differences, according to the analysis of variance. For yield/vine, number of fruits/vines, average fruit weight, length of fruit, length of vine and number of laterals/vines. High heritability in conjunction with high genetic progress as a percentage of mean was observed. In contrast to the significant negative association with the sex ratio, days to the first female flower and node number. Yield per vine showed positive and significant genotypic associations with the number of fruits/vine, average fruit weight, vine length, number of laterals/vine and fruit length.

Singh et al. (2017) The current study examined twenty strains and was carried out at the Horticultural Research Centre of H. N. B University in Srinagar Garhwal, Uttarakhand (India) in the summer of 2014. This field study's major goal was to calculate the variance component phenotypic and genotypic coefficient,

heritability and genetic advance over mean for various growth, yield and quality indicators. Fruit production per vine indicated the greatest difference between PCV and GCV while the remaining attributes showed moderate to low PCV and GVC with very little difference between them. This demonstrated that environmental influences have a very small impact on these parameters.

Study conducted by Tiwari et al. (2018) over the course of two years at MES Vegetable Science N.D.U.A. on nine parental lines of bitter gourd, including NDBT-7, NDBT-9, NDBT-3, NDBT-2, Pusa Do Mausmi, NDBT-12, NDBT-1, K. Sona and NDBT-5 with the goal of determining genetic diversity and heritability in a restricted sense at Faizabad, Uttar Pradesh summers of 2011 and 2012. For all the characters, the analysis of variance due to genotype, parents, hybrids and parents vs. hybrids was almost highly significant, with the exception of the days to the first staminate flower opening and the node number to the first staminate and pistillate flower appearance due to parents vs. hybrids in both 2011 and 2012. Fruit output per plant and fruit quantity per plant showed high estimates of genotypic and phenotypic coefficients of variability in 2011 and 2012. 2011 saw merely an increase in the phenotypic coefficients of variability for fruit output per plant. Fruit yield per plant exhibited moderate variation. The remaining characters displayed a low coefficient of variation.

20 genotypes of bitter gourd (*Momordica charantia* L.) have been studied by Reddy and Singh (2019) for genetic diversity, heritability and correlation. According to the results of the experiment which used a randomised block design and three replications, Genotype Co-1 (1.61 kg) and Susi Long (1.55 kg) of bitter gourd shown high fruit yield per plant. According to analysis of variance, substantial differences were found for all quantitative and qualitative qualities, demonstrating that genotypes have a lot of variation.

In order to determine variability, heritability and genetic advancement, 40 genotypes of bitter gourd that were gathered from various agroclimatic zones of India were studied. Days to first male flower, days to first female flower, node

number of first male flower, node number of first female flower, sex ratio, vine length (m), number of primary branches per vine, days until first fruit harvest, length of fruit, fruit girth, average fruit weight, number of fruits per vine, number of seeds per fruit, TSS (Brix^o), ascorbic acid content (mg/100g) and fruit yield per plant (kg) were studied as quantitative and qualitative characters. In variability studies, among 40 genotypes MC 13 was identified as the best genotypes as it recorded higher yield per vine followed by MC 1, MC 20 and MC 14. Maximum phenotypic and genotypic coefficient of variation (PCV and GCV) was found for fruit yield per vine followed by the number of fruits per plant and sex ratio. (Singh & Kandasamy, 2020).

The fruit per vine-1 (91.36 percent and 49.11 percent), fruit circumference (91.12 percent and 26.74 percent) and number of seeds per fruit-1 were observed by Pradhan et al. (2021). Total green fruit output (89.35 percent and 44.67 percent), 89.85 percent and 38.21 percent Internodal length (87.82 percent), sex ratio (88.10 percent and 63.38 percent) and fruit length (87.82 percent and 46.43 percent). Consequently, direct the potential for selecting these traits in bitter gourd is great.

The investigation was carried out in the vegetable block at the College of Horticulture in Mysuru's Department of Vegetable Science. During kharif 2017, 40 genotypes of bitter gourd gathered from various sources were examined by Nithinkumar et al. (2022) in a randomised block design with two replications. For all of the studied features the analysis of variance revealed genotype differences that were statistically significant, showing a high degree of genotype variability. Fruit length, average fruit weight, fruit production per vine, fruit output per hectare, number of seeds per fruit and flesh thickness were among the 16 examined features for which higher heritability estimates and genetic advance over mean (GAM) estimations were found. This suggests that additive components are more prevalent for these qualities, therefore direct selection would be more effective in improving these traits.

2.2 Heritability and genetic advance

For a breeder, a character heritability in a broad sense is crucial since it shows whether and how much improvement through selection is achievable. The degree to which a character may be passed from parent to child is frequently determined by looking at the relationship between the parent and their descendants. But without a significant amount of genetic development, high heritability alone is insufficient to make effective selection in advanced generations (Burton 1952). Commonly, heritability ratio and selection differentials are used to predict the genetic advance.

Rajput et al. (1996) examined eleven characteristics in 21 distinct genotypes of bitter gourds and all of the traits exhibited higher heritability values, ranging from 83.4 to 97.9%. The number of seeds per fruit, fruit weight, fruit breadth, fruit length and yield per vine are attributes with very high heritability estimates. There was a genetic advance of between 0.631 and 224.8. The attributes of fruit weight, fruit number, fruit weight per vine and vine length were considerably improved.

In 40 genotypes of bitter gourd, Kutty and Dharamatti (2004) assessed 10 quantitative factors. The results distinctly show a great deal of variation in yield and its constituent parts at both the phenotypic and genotypic levels. Significant heritability was found along with strong genetic progress as a percent of mean for the number of fruits per vine, fruit weight and total fruit output per plant, demonstrating the effects of gene activity for such variables. The application of selection procedures may help to enhance the genotypes of bitter gourds. Of the 40 genotypes, BLG-1, DWD-2, NRN-1 and IC 44418 showed the greatest promise.

Ahmed and Mufti (2006) assessed fifteen different bitter gourd genotypes (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 and number of branches per vines, length of Preethi had the highest values for most yield-related traits, including the best fruit yield (2.89 kg), largest number of fruits per plant (16.00) and biggest fruit diameter (5.50 cm). The largest fruit length and fruit weight were found in BGR-1. With strong phenotypic and genotypic variability components

each characteristic was highly heritable.

High heritability and few genetic advance days to first female flowering was found in Islam et al. (2009)'s study of 20 bitter gourd genotypes, suggesting that no additive gene effects were involved in the expression of this trait and that selection for such a characteristic might not be beneficial. Indicating that this attribute was under additive gene control and that genetic augmentation for strait would be successful through selection, yield per plant and vine length both shown strong heritabilities and high genetic advancement.

Dey et al. (2009) investigated 38 genotypes of bitter gourd and discovered that traits like average fruit weight exhibited substantial genetic progress and heritability (g). Average flesh thickness (in cm), yield per plant (g) and node to first female flower all indicate that additive gene action predominates and that selection for these commercially important traits can effectively increase a crop.

Kumar et al. (2011) studied for fruit output per plant, the number of seeds per fruit and fruit diameter in bottle gourds, heritability was high. In 24 hybrids created by crossing 11 parents, the genetic advancement for fruit output per plant was high.

Husna et al. (2011) conducted a study for yield per plant and days of first male sowing in bottle gourd, substantial heritability and significant genetic advance were found, suggesting that this trait was under additive gene control and that genetic improvement for this trait would be successful through selection.

In 40 different bottle gourd genotypes, Emina et al. (2012) discovered that the heritability estimates were high (>90%) for plant height, fruit weight, length, circumference and number of seeds per plant, but lower (78.29%) for 100-seed mass.

The current study conducted by Singh et al. (2017) examined 20 strains and was carried out in the summer of 2014 at the Horticultural Research Centre, H. N. B University, Srinagar Garhwal, Uttarakhand. This field study was primarily concerned with estimating the variance component, phenotypic and genotypic coefficient, heritability and genetic advance over mean for various growth, yield and quality indicators. The majority of characteristics, with the exception of total soluble solids, exhibited high to moderate heritability and high to moderate genetic advance above mean. This demonstrated that these qualities are appropriate for direct selection and enhancement.

Talukder et al. (2018) conducted a field test with 20 genotypes of bitter gourd. (*Momordica charantia* L.) at the Sher-e-Bangla Agricultural University's experimental farm in Dhaka to examine the variation in genotypes for yield and traits that increase yield, estimate genetic parameters, the characters' relationships and their involvement to produce between April and September 2015. Characters like vine showed a high heritability (>60%) length, number of branches and nodes per vine, size and weight of the fruit output per plant as well as fruit per plant. Given the high heritability and with a substantial genetic progress in branches per cent of the mean observed Fruit output per plant, fruit weight, fruit weight per fruit and fruit length all suggested. These characters are capable of being chosen well. Fruit production per plant revealed the maximum favourable direct impact (0.88 with plants per branch).

At the Bihar Agricultural University's Vegetable Research Farm in Sabour (Bhagalpur), an experiment was carried out in 2017–18 to examine the genetic diversity that currently exists and to evaluate the relationships between sixteen yield-related variables and their contributing traits in twenty-eight genotypes of Bihar's bitter gourd. Chlorophyll content showed strong heritability and high genetic progress as a percentage of the mean; this indicates that this attribute was improved through simple selection. According to a correlation analysis, the amount of total chlorophyll, fruit weight and fruit length all significantly and favourably correlated with plant yield. (Kumari et al. 2018).

Nithinkumar et al. (2022) at the Department of Vegetable Science, College of Horticulture, Mysuru, the investigation was carried out in the vegetable block. In a randomised block design with two replications, forty bitter gourd genotypes gathered from various sources were assessed in kharif 2017. For all of the features under study, the analysis of variance indicated significant genotype differences, showing a high degree of genetic variability. Fruit length, average fruit weight, fruit production per vine, fruit yield per hectare, number of seeds per fruit and thickness of the flesh were among the 16 features that showed the highest genetic advance over mean (GAM) and higher GCV estimates. This shows that these features have a dominant additive component, therefore direct selection would be more effective in improving these traits.

2.3 Correlation coefficient

Determine the elements of a complex character by using the correlation coefficient, which measures the relationship between two or more variables. The combination of a variety of variables and the surrounding environment results in yield, which has a complicated personality. Selection based on yield performance is typically ineffective for producing a high yielding genotype, whereas selection based on component traits may produce more effective outcomes.

Dey et al. (2005-2006) a total of 38 bitter gourd accessions were cultivated in a RBD with three replications from March to July 2004 at the Division of Vegetable Science, Indian Agricultural Research Institute, New Delhi. Data were statistically analysed and averaged. For all of the quantitative characteristics under study, the variability estimate showed that the phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV), but the difference between the PCV and GCV for ascorbic acid and total carotenoid content was insignificant, indicating that these quality traits are least influenced by the environment.

A total of fifteen different bitter gourd genotypes (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) were evaluated by Ahmed and Mufti for seven yield characteristics (length of vines, number of branches High genetic advancement was associated with high branch number per plant, average fruit length, average fruit diameter, fruit quantity and number of fruits per plant, strong genetic coefficient of variation and heritability estimates. Ahmed and Mufti (2006).

The number of fruits produced per plant, followed by fruit weight, was the most significant factor in the correlation between yield per plant and reproductive characteristics among the 31 bottle gourd genotypes studied by Husna et al. (2011).

Kumar et al. (2012) conducted an experiment was to identify desirable combiners in bottle gourds by examining correlation and Path coefficient effects. The experiment, which produced 24 hybrids by mating 11 parents (eight lines, C-29, C-37, C-74, C-78, C-4, C-55, C-34 and three testers C-12 (Azad Harit), C-21 (PSPL) and C-35), used eight lines for the experiment (KLG). The line x tester analysis was used to calculate the days to maturity, fruit production per plant, number of branches per plant, vine length (m), number of fruits per plant, number of seeds per fruit, fruit length (cm), fruit diameter (cm), number of days to germination and days to fruit setting.

Hanumegowda et al. (2012) performed a correlation co-efficient analysis on 30 ridge gourd genotypes and discovered that fruit yield per plant showed a positive and significant correlation with fruit length (0.795 and 0.784), fruit diameter (0.726 and 0.683), number of fruits per plant (0.889 and 0.862), average fruit weight (0.871 and 0.858), fruit yield per plot (0.821 and 0.807), fruit yield per hectare (0.821 and 0,807), number of fruits Selecting for these association qualities may boost plant yield because they point in the desired direction.

According to correlation analyses conducted by Mladenović et al. (2012) after they looked at 40 different bottle gourd genotypes, there is a positive

correlation between plant height and fruit length, seeds produced per plant and 100-seed mass, but a negative correlation with fruit weight.

The fruit yield per vine was found to have a positive and significant correlation with the number of branches per vine, vine length, node number of the first male flower, node number of the first female flower, length of edible fruits, number of fruits per vine, number of seeds per fruit and 100-seed mass at genotypic and phenotypic levels in 10 different bitter melon entries by Narayan et al. (2012).

Yadav et al. (2013) assessed the genetic diversity of 13 characteristics in 13 different genotypes of bitter melon grown in Allahabad in 2007 and 2008. The number of nodes per vine, internodal length, fruit breadth and number of fruits per vine all demonstrated a significant and positive connection with vine length. The number of primary branches per vine had a substantial negative association with internodal length and a significant positive correlation with fruit length.

Khan et al. (2015) a field experiment with 17 genotypes of bitter melon (*Momordica charantia* L.) was undertaken from April 2009 to September 2010 at the Sher-e-Bangla Agricultural University's experimental field in Dhaka. High genotypic co-efficient of variation (GCV) was found for branches per vine, yield per plant and number of fruits per plant when genetic characteristics were taken into account, however low GCV was found for days to first male and female flowering. It was discovered that the phenotypic co-efficient of variation outweighed the genotypic co-efficient of variation in each case. Branch per vine, fruit length, fruit weight and number of fruit plants showed the highest genotypic and phenotypic co-efficient of variance, indicating a wide range of genotype variability and providing better scope for selection.

Gupta et al. (2016) assessed 26 varieties of bitter melon, including check (Solan Hara) Analyze the interactions between the various components of the yield as well as any direct or indirect impacts on the overall yield of marketable fruit. The improvement of yield-attributing characters, which can also be superior as beaded curtains, must be taken into consideration when choosing for yield, even though the

correlation of various characters with yield is helpful for improvement and offers criteria for direct selection of component characters. Marketable fruits per vine (0.684), seeds per fruit (0.625) and average fruit weight (0.726) all showed a negative phenotypic association (0.591), while average fruit weight (0.726), marketable fruits per vine (0.547) and seeds per fruit (0.377) all had a positive phenotypic correlation. At the node when the first female flower appears, a genotypically favourable association between the total marketable fruit output per hectare was observed (0.338).

Maurya et al. (2019) the goal of the current study, which was conducted in summer 2017 at the Main Experiment Station of the Department of Vegetable Science, Narendra Deva University of Agriculture & Technology, Kumarganj, Faizabad (U.P.), was to increase yield by boosting the smallest yield components on an otherwise good cultivar. To observe their connections and direct and indirect effects on fruit yield, 30 genotypes of bitter gourd were evaluated for yield-contributing features. The majority of the time, the genotypic correlation coefficient was greater than the phenotypic correlation coefficient, showing that the environment's suppressive influence reduced the phenotypic correlation values, which in turn impacted the phenotypic manifestation of these traits. The number of fruits per plant, fruit yield per plant (kg), vine length (m), fruit length (cm), node number to anthesis of first staminate flower, average fruit weight (g), node number to anthesis of first pistillate flower, node number per vine and days of first fruit harvest were the phenotypic traits that showed the highest magnitude of coefficient of variation at both phenotypic and genotypic levels. The amount and nature of the phenotypic correlation coefficients between various traits were typically comparable to those of the corresponding genotypic correlation coefficient. At the phenotypic level with average fruit, a substantial and positive connection with yield per plant was established.

Yadagiri et al. (2017) during the 2012–2013 kharif season, a field experiment was carried out at the Rajmata Vijayaraje Scindia Krishi Vishwavidyalaya's Vegetable Research Farm in Indore (M.P.). To assess how well 20 genotypes of bitter gourd performed for several horticultural traits, the current

experiment was conducted. For all of the traits and genotypes, there was a significant amount of correlation. According to a correlation analysis, there was a significant positive correlation between the length of the vine, the number of branches per vine, the number of male and female flowers per vine, the number of fruits per vine, the length and weight of the fruits, the number of seeds per fruit and the number of seeds per fruit.

At the Vegetable Research Farm of the Bihar Agricultural University in Sabour (Bhagalpur) an experiment was carried out in 2017–18 to examine the genetic diversity that already existed and to evaluate the relationships between sixteen yield-related variables and its contributing traits in twenty-eight genotypes of bitter gourd. For the chlorophyll content, vine length and fruit weight, high GCV and PCV values were observed. chlorophyll content, TSS, ascorbic acid, the number of seeds per fruit, fruit weight, fruit length, fruit girth and the number of fruits per plant all had high heritability estimates. (Kumari et al. 2018).

Talukder et al. (2018) twenty genotypes of bitter gourd (*Momordica charantia* L.) were used in a field experiment at Sher-e-Bangla Agricultural University in Dhaka from April to September 2015 to examine genotype variability in yield and yield-contributing traits, estimate genetic parameters and examine associations between characters and their contributions to yield. According to genetic characteristics, fruit weight, yield per plant and fruit length showed high genotypic co-efficients of variation (GCV) whereas nodes per vine and days before the first male and female flowering showed low GCV. In every instance, it was discovered that the phenotypic co-efficient of variation was greater than the genotypic co-efficient of variation indicating a high degree of genetic diversity and providing a wider range of possibilities.

Alekar et al. (2019) evaluated the vine length following harvest, the number of primary branches per vine, the number of fruits per vine, the average fruit yield per vine, the average fruit weight, the average fruit length and the yield tonnes per hectare. According to correlation studies, fruit yield per hectare showed a strongly

favourable link with yield component features. When identifying high producing genotypes, variables including the quantity of female flowers per vine, the quantity of fruits per vine, the average fruit weight, crop duration, average fruit length and average fruit diameter should be highlighted.

Sowmya et al. (2019) assessed twenty four genotypes of bitter gourd during the summer of 2017–2018, at the College of Horticulture, Mudigere for yield-contributing features to observe their relationships and direct and indirect effects on fruit production. The study found that the genotypic correlation coefficient was greater than the corresponding phenotypic correlation coefficient, indicating that the genotype had less of an influence on how phenotypic expression was expressed. Fruit yield per plant significantly correlated positively with fruit length and weight. A strong positive direct relationship between fruit output per plant and vine length, node at which male flowers develop, number of fruits per vine, fruit weight and fruit length were found. These are significant characteristics to be taken into account for improving productivity.

Fruit length has significant levels of genotypic and phenotypic variation (78.19 and 78.29) which highlights the influence of the environment on the expression of these features. The characters with the highest heritability estimate included fruit yield/ha (quintal), fruit length (cm), fruit yield/plant (kg), fruit number/plant, fruit width (cm), seed germination percentage, node number to which initial female flowers develop and fruit specific gravity (cc). Fruit yield per plant (kg) showed a positive and very significant link with Fruit yield per hectare (0.999), whereas Fruit yield per plant had a positive but non-significant correlation with Fruit specific gravity (0.241) and TSS (0.087). Fruit yield per plant (kg) showed a positive and very significant link with fruit yield per ha (1.000), according to phenotypic correlation coefficient analysis. Fruit yield per plant also demonstrated a positive but non-significant association with specific gravity (0.210). Reddy and Singh, (2019).

During the months of March through July of 2022, a field experiment was

undertaken to ascertain the correlation coefficient and path analysis among 28 genotypes for the 18 features that make up fruit yield and its contributing factors. At the G. B. Pant University of Agriculture & Technology's Vegetable Research Centre, these genotypes were planted in a Randomised Block Design with three replications. The results showed that fruit weight (cm), fruit length (cm), fruit diameter (cm), total number of pickings (cm) and number of seeds per fruit showed the most significant and positive link at genotypic and phenotypic level. The path coefficient analysis revealed that the effect was significant at both the phenotypic and genotypic levels and that the character fruit weight (g) followed by pickings, fruit diameter (cm), days to first fruit harvest, main vine length (m), number of seeds per fruit, sex ratio, days to first female flower and node number at which the fruit was picked contributed positively directly to fruit yield per plant (kg). (Dhathri et al. 2022).

Nithinkumar et al. (2022) at the Department of Vegetable Science, College of Horticulture, Mysuru, the investigation was carried out in the vegetable block. In a randomised block design with two replications, forty bitter gourd genotypes gathered from various sources were assessed in kharif 2017. The correlation and path analysis findings showed a strong positive and significant relationship between fruit yield per vine and the characteristics of fruit length, fruit diameter, crop duration and average fruit weight. These characteristics also had a strong direct and indirect influence on fruit yield per vine. In order to increase fruit yield per vine, direct selection for these features would be more beneficial.

2.4 Path coefficient analysis

According to Sharma and Bhutani's (2001) analysis of the path coefficient in bitter gourd, the number of fruits per plant had the highest direct impact on production, followed by fruit length, fruit diameter and chlorophyll content. Internodal length, average fruit weight, fruit diameter and fruit length via the number of fruits per plant were the factors that had the next highest indirect effects on production after vine length.

Islam et al. (2009) study twenty bitter gourd genotypes for variability, correlation and path analysis. The highest direct contribution to yield per plant was found by path coefficient analysis to be the number of fruits per plant, followed by vine length. The following individuals were chosen for the 5 9 12 and 14 16 19 future breeding programme: G1 (Shaparan), G (Rampali Gaj), G (Nabil), G (Nandita), G (Eureca), G (Tia) and G (Maharaj).

Kumar et al. (2012) The goal of the current experiment was to identify desirable combiners in bottle gourds by examining correlation and Path coefficient effects. The experiment, which produced 24 hybrids by mating 11 parents (eight lines, C-29, C-37, C-74, C-78, C-4, C-55, C-34 and three testers, C-12 (Azad Harit), C-21 (PSPL) and C-35) used eight lines for the experiment (KLG). At the Horticultural Research Center of Sardar Vallabhbhai Patel University of Agriculture & Technology-Meerut, during Kharif 2008 and 2009, all the hybrids and their parents were cultivated in an RBD with three replications. To ascertain the direct and indirect effects on fruit yield per plant including days to germination, days to fruit setting, fruit length (cm), fruit diameter (cm), number of branches per plant, vine length (m), number of seeds per fruit, number of fruits per plant and days to maturity the path coefficient was analysed.

Khan et al. (2015) in a field study done at the Sher-e-Bangla Agricultural University experimental field in Dhaka from April 2009 to September 2010, seventeen genotypes of bitter gourd (*Momordica charantia* L.) were examined. According to path analysis, the average fruit weight, the quantity of fruits produced per plant, the number of days until male flowering and the length of the fruit all positively impacted fruit yield. In light of group distance and agronomic performance, inter-genotypic crossings between G2& G5, G2&G14, G14&G15, G2&G15, G10&G11, G10&G13, G11&G13, G5&G15 and G5&G14 would be a good option for a future hybridization programme.

In order to identify the interrelationships among the factors impacting bitter gourd yield 28 F1 crosses created from an 8 x 8 diallel analysis that excluded

reciprocals were tested in 2011–12 at the Model Orchard, College of Horticulture, Rajendranagar, Hyderabad. According to path analysis research, the most significant yield-attributing feature is the number of fruits/vine followed by average fruit weight. Therefore, while choosing genotypes to increase bitter gourd output, proper consideration should be paid to these features. Rani et al. (2015)

Mashiloa et al. (2016) to increase the effectiveness of selection in cultivar improvement knowledge of connections between yield and associated variables is essential. Path analyses were used in this work to identify the links between qualitative and quantitative features in bottle gourd landraces. When the fruit weight and the number of seeds per fruit were analysed a high direct path coefficient value (0.96) was found. The direct route coefficient value between the number of female flowers and the number of fruits per plant was positive (0.92) as well. Degree of warts and Number of seeds per fruit showed a rather high direct route coefficient value (0.47). This study showed that selection for greater fruit weight may enhance genetic gain in seed yield and fruit yield in the breeding of bottle gourds. The following landraces, including BG-06, BG07, BG-09, BG-11, BG-13, BG-24 and BG-67 were chosen for breeding based on the aforementioned analyses.

Yadagiri et al. (2017) At the Rajmata VijayarajeScindia Krishi Vishwavidyalaya's Vegetable Research Farm in Indore, a field experiment was conducted during the 2012–2013 kharif season (M.P.). The current experiment was carried out to evaluate the performance of 20 genotypes of bitter gourd for several horticultural parameters. By using route coefficient analysis the association was further separated into direct and indirect effects. It was discovered that yield was strongly correlated with crop duration, vine length, number of seeds per fruit and fruit length, suggesting that selection based on these traits would be more fruitful.

Thirty-one different genotypes of bitter gourds including two tick kinds (Pusa Vishes and Pusa Do Mausami) made up the experimental materials. At the Main Experiment Station (Vegetable Research Farm), Narendra Deva University of Agriculture and Technology, Kumarganj, Faizabad, India, the crop was planted

using a Randomised Block Design with three replications during the spring and summer of 2015. In imposing selection for the correlation of yield in bitter gourd, path analysis revealed that average fruit weight (g) and number of fruits per plant had the most direct effect on production at both the phenotypic and genotypic levels. Tyagi et al. (2018).

At the Bihar Agricultural University Vegetable Research Farm in Sabour (Bhagalpur) an experiment was carried out in 2017–18 to examine the genetic diversity that currently exists and to evaluate the relationships between sixteen yield-related variables and their contributing traits in twenty-eight genotypes of Bihar's bitter gourd. The correlation coefficient division into direct and indirect effects using path coefficient analysis was successful. It provides insight into the impact that each independent character has on the yield the dependent character. According to a path analysis ascorbic acid, the number of seeds per fruit, vine length, TSS, the weight of the fruit, the amount of chlorophyll, the node number at which the first female flower appears and the number of days until 50% flowering all had a favourable direct impact on fruit yield. Kumari et al. (2018).

Sowmya et al. (2019) path coefficients analysis can aid in determining the component characters on which selection can be based or yield improvement, as well as the mutual interaction between various plant traits. At the College of Horticulture, Mudigere, during the summer of 2017–18, 24 genotypes of bitter gourd were assessed for yield-contributing features to observe their relationships and direct and indirect effects on fruit production. Fruit yield per plant was found to have a strong positive direct relationship with vine length, the node at which male flowers develop, the quantity of fruits per vine, fruit weight and fruit length characteristics that must be taken into account in order to increase yield.

Maurya et al. (2019) the current study, "Study the correlation coefficient and path coefficient for the yield and yield component of bitter gourd (*Momordica charantia* L.), was conducted at Main Experiment Station, Department of Vegetable Science, Narendra Deva University of Agriculture & Technology, Kumarganj,

Faizabad (U.P.) during summer 2017. Its objectives included evaluating the genotypes that were available estimating the correlation coefficient and performing the path coefficient analysis for yield. The analysis of the path coefficient shows that the number of fruits per plant and fruit production/plant have a significant direct positive impact followed by the influence of vine length on fruit yield per plant.

Nithinkumar et al. (2022) the study was carried out in the vegetable block at the Department of Vegetable Science at the College of Horticulture in Mysuru. In kharif 2017 two replications of a randomised block design were used to assess forty bitter gourd genotypes that were gathered from various sources. Fruit length, fruit diameter, crop duration and average fruit weight were found to have a high positive and significant link with fruit production per vine as well as a high direct and indirect effect on fruit yield per vine according to the results of correlation and path analysis. For the purpose of increasing fruit yield per vine direct selection for these qualities would therefore be more beneficial.

The trials took place in the Rabi season of 2017–18 at the Vegetable Research Farm, College of Horticulture, Mojerla, SKLTSHU, Hyderabad (Telangana). For the evaluation of correlation and path co-efficient analysis of fruits yield and yield features in bitter gourd (*Momordica charantia* L.) 27 genotypes of the plant were examined. The number of primary branches per vine, days until the first and last fruit harvest, nodes at which the first and last male and female flowers appeared, average fruit weight, fruit fly infestation percentage and 100 seed weight all showed positive direct effects on fruit yield, according to a path coefficient analysis of various yield and yield contributing traits on fruit yield per plant. These characters play a significant role in recombination bred. Reddy et al. (2022).

2.5 Genetic divergence

Genetic divergence is the process by which two or more populations of an ancestral species accumulate separate genetic changes (mutations) over time. This process frequently results in reproductive isolation and continues mutation even after the populations have become reproductively isolated for a while because there

is no longer any genetic exchange.

Kutty and Dharmatti (2005) using Mahalanobis D₂ statistics, the genetic divergence among 40 genotypes of bitter gourd (*Momordica charantia* L.) from various ecogeographic origins was evaluated. Using D₂ values the overall genotypes were divided into 10 groups. The majority of the genotypes were divided into three clusters: I (16), II (11) and IV (4). The most divergent genotypes were those in cluster II, followed by those in clusters IV and I. Cluster VI and cluster IX had the greatest intercluster distance, which was followed by cluster VII and cluster IX. The traits that contributed the most to divergence were the number of leaves at 50% flowering and the productive length of the vine. In order to achieve superior heterotic effects. Bitter gourd crop modification could be tried with the genotypes of divergent clusters.

Devmore et al. (2007) the genetic diversity of fifteen genotypes of bitter gourd was investigated. There is no parallelism between diversity and regional divergence, as the genotypes were sorted into eight clusters regardless of geographic divergence. The greatest possible number of genotypes in cluster I (7). Days until the first female flower, nodal position for the first female flower, 100 seed weight, length, branches/vine, number of nodes/vine, number of fruits/vine, days until the first fruit harvest, weight of the fruit, length of the fruit, breadth of the fruit and fruit yield/vine were all important characteristics toward the maximum genetic divergence, according to the cluster mean. Cluster V and cluster VIII had the most genetic divergence (24.33), whereas cluster 1 had the lowest (9.50). However, it is not certain that geographic distribution and genetic divergence as calculated by D² statistics.

Islam et al. (2010) Moahalanobis D₂ and principal component analysis were used to examine the genetic divergence of 20 genotypes of bitter gourd. The study's genotypes can be divided into four groups. There were 10 genotypes in cluster I which had the most. Cluster IV has the fewest genotypes overall. The highest mean value for weight per fruit was achieved by Cluster II. Compared to intra cluster

distances inter cluster distances were much greater. Cluster I have the greatest intra-cluster distance, whereas cluster III has the smallest distance. The distance between clusters I and II was found to be the greatest whereas the distance between clusters II and IV was found to be the smallest. Cluster II had the highest weight per fruit intra cluster mean and five significant yield-contributing features. As a result more attention should be paid to the cluster when choosing genotypes to cross with the genotypes of cluster II in order to develop new recombinations with desirable features. The G1 (Shaparan), G5, (Rampali gaj), G9 (Nabil), G12 (Nandita), G14 (Eureca), G16 (Tia) and G19 (Maharaj) were chosen for the upcoming breeding scheme taking into account all the characters.

Kundu et al. (2012) Through the use of PCA, PCO, CVA, Cluster analysis (CLSA) and Mohalanobis D analysis, the genetic divergence among the 36 genotypes of bitter melon (*Momordica charantia* L.) was ascertained. 36 genotypes were classified into six dispersed clusters using multivariate analysis based on 22 features. Maximum genotypes are found in Cluster VI which is followed by Cluster I (with 6) and Cluster II (12). (6). There were 5, 4 and 3 genotypes in Clusters V, III and I respectively. The distances between the clusters were greater than those inside them. Cluster III and IV had the greatest inter-cluster distance (28.71), which was followed by Cluster I and Cluster IV (23.61). All six of the clusters' intra-cluster distances were rather low indicating that the genotypes within each cluster were near to one another. Cluster III had the highest intra-cluster distance (1.84), followed by cluster I (1.38). The genotypes within the same clusters were obtained from various locations while those obtained from the same location fall into separate clusters indicating that genetic divergence is not influenced by the location from where the genotypes were obtained. Through PCA, the genetic diversity of 36 genotypes was also evaluated. 60.04 percent of the overall variation was accounted for by the first three components. The factors that contributed most to the divergence were the number of primary branches per vine, fruit output per vine, days until green fruit maturity, seed weight per fruit mature seed width and days until the first male flower opened. The genotypes included in cluster III were significantly different from those of cluster IV whereas those belonging to clusters II and VI had the lowest levels of diversity.

Resmi and Sreelathakumary (2012) 33 genotypes of bitter gourd were used in a genetic divergence investigation for 20 characteristics. There is no correlation between geographic and genetic variety as these genotypes were sorted into five clusters regardless of geographic dispersion. The largest cluster Cluster-I had 11 genotypes. Clusters III and V both with 10 genotypes were next. Clusters II and IV each contained a single genotype. Clusters-II and IV scored better in terms of cluster means for the majority of the biometric features examined. Clusters III and IV showed the greatest inter-cluster distance followed by Clusters II and III and Clusters I and IV. Cluster I had the greatest intra-cluster distance.

Singh et al. (2013) In Uttar Pradesh, India, during the month of Zaid 2005, a study was carried out to assess the type and degree of genetic diversity in 30 genotypes of bitter gourd. The results showed a high level of genetic diversity. Using Tocher 2 methodology and Mahalanobis D statistics the genotypes were divided into 6 groups. The genotype clustering pattern demonstrated that genetic diversity was distinct from geographic diversity. The cluster with the most genotypes among the six was cluster V while cluster III was discovered to be monogenotypic. Individual fruit weight made the largest contribution to the divergence of the 12 quantitative features examined followed by days until the initial appearance of the female flower. In order to select parents for heterosis breeding genotypes were ranked based on intra-cluster mean performance for these traits which are important sources of genetic variability.

Singh et al. (2014). During the summers of 2011 and 2012, an experiment was conducted to examine yield and its eleven contributing variables using multivariate analysis based on cluster and principal component (PC) in 32 bitter gourd genotypes including two checks Pusa Do Mausami and Kalyanpur Sona. All 32 genotypes of bitter gourd were divided into 6 main clusters using the cluster analysis. Extreme genetic divergence between groups was estimated. The largest average inter-cluster distance (717.86) was discovered between cluster VI and cluster V (NDBT-12) (NDBT-76). Fruit length and weight made a proportionate 13% and 74% contribution to genetic difference respectively. Cluster V and cluster

II had the highest cluster mean values for fruits/plant, fruit weight (g) and fruit yield/plant (kg) respectively. The first six principal components (PC1, PC2, PC3, PC4, PC5 and PC6), which had proportionated contribution values of 23.88, 16.81, 13.28, 11.23, 9.38 and 8.61% respectively, were found to account for 83.19% of the total variances. The first PC has a positive correlation with the node number to first staminate anthesis and the number of days till first fruit harvest, but a negative correlation with fruit weight (g), fruits/plant and fruit yield/plant (kg). Cluster and PC analyses were used to identify promising diverse parents which were then chosen for a future hybridization programme.

Tyagi et al. (2017) The experiment was carried out in Eastern Uttar Pradesh throughout the spring and summer of 2015 to assess the nature and 2 degrees of genetic divergence among the 31 genotypes of bitter gourd. By using Tocher approach all bitter gourd genotypes were divided into six unique clusters based on D values. The cluster IV had the most genotypes (a total of 7) followed by the cluster V. The distances between the clusters were greater than those inside them. Cluster III and VI had the greatest inter-cluster distance (58.37) which indicates that the individuals in these two clusters have significantly different genetic make-ups from one another. Cluster I (18.42) was found to have the greatest intra-cluster distance, followed by cluster V. Most of the biometric traits were performed better by the clusters IV, III and II. In the study of 12 variables, vine length had the greatest effect on genetic divergence (34.41%) followed by fruit diameter and average fruit weight in bitter gourd. In order to select parents for heterosis breeding, genotypes were ranked based on intra-cluster mean performance for these traits, which are important sources of genetic variability.

Angadi and Mulge (2018) In order to assess the kind and extent of genetic divergence in 55 bitter gourd genotypes a study was carried out in Karnataka, India, during the 2013 kharif season. Wide genetic variety was found according to the results. Tocher approach was used to divide the genotypes into 10 groups based on Mahalanobis D₂ statistics. The genotype clustering pattern showed that the genetic diversity was separate from the geographical diversity. The most genotypes were

detected in cluster I out of the 10 clusters. Among the 19 quantitative characteristics examined fruit yield per vine had the largest contribution to the disparity at 35.01%. The ranking of genotypes based on intra cluster mean performance for these traits which are important genetic diversity contributors proved their value in deciding which parents to utilize for heterosis breeding.

The maximum mean values for vine length (m), node count per vine, primary branch count per plant and fruit length were found in cluster VI, according to Singh et al. (2019). Both clusters I and VI would offer a good chance for crop improvement through a hybrid breeding programme based on selective reasoning. The characteristics that most influenced genetic divergence and consequently had a significant impact on the development of sponge gourds were 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).

Bhattacharjee et al. (2019) under the undulating topography of Tripura, multivariate analysis was used to examine the genetic divergence among nine genotypes of bitter gourd (*Momordica charantia* L.) for fifteen significant yield-attributing factors and one qualitative feature. Using divergence analysis, the genotypes were logically divided into three clusters. The genotype distribution pattern showed no evidence of a connection between genetic distance and geographic dispersion. Cluster II and cluster III have a high intercluster distance which suggests that the genotypes from each cluster will be used in a hybridization procedure in order to evolve a favourable hybrid or segregate. The largest genetic difference among the traits was caused by vine length which was followed by primary branches per plant, internodal length, days until the first male flower and days until the first female bloom. A total of 100% of the variation was accounted for by five out of the 16 characters, who each had an eigenvalue greater than 1. Two genotypes, Malda local and Pusa Do Mousumi had distinct differences in their genotypic characteristics and the best combinations of all variables. According to D2 statistics principal component analysis and average values. These genotypes could be used as parents in a hybridization programme to create a high-yielding

bitter gourd variety.

Singh and Kandasamy (2020) 40 genotypes of bitter gourd were used in a study on genetic divergence. Six clusters were formed by applying the clustering algorithm to them. The cluster II had the most genotypes (19) followed by the cluster II which had 13 genotypes and the clusters III and IV which each had 3 genotypes. It was discovered that Cluster V and VI were mono-genotypic. They estimated the intra- and inter-cluster divergence. From 0.00 to 43.68 the intra-cluster divergence was measured. Cluster II (41.32) and Cluster I were the clusters with the highest intra-cluster divergence followed by Cluster IV (43.68) (38.85). The least intra-cluster divergence was found in Clusters V and VI which was 0.00. The largest inter-cluster divergence was discovered between clusters I and VI (88.84) whereas the smallest inter-cluster divergence was found between clusters II and IV (51.97). Fruit yield per vine in Cluster III was measured with the highest mean value (2.22) whereas in Cluster I, the lowest mean value was reported (0.71).

A study was carried out in Uttar Pradesh, India, during the 2019 kharif season to assess the kind and extent of genetic divergence in 15 genotypes of bitter gourd. The results showed a high level of genetic diversity. Using Torcher approach, the genotypes were divided into 4 clusters based on Mahalanobis D² statistics. The genotype clustering pattern demonstrated that genetic diversity was distinct from geographic diversity. Cluster I of the four clusters included the greatest number of genotypes while Cluster IV was discovered to be mono-genotypic. The biggest contribution to the divergence among the 14 quantitative features examined came from the number of fruits per plants, which was followed by fruit yield (q/ha). In order to select parents for heterosis breeding genotypes were ranked based on intra-cluster mean performance for these traits which are important sources of genetic variability. Chandrashekhar et al. (2020).

Ankitha et al. (2023) 33 genotypes of bitter gourds were used to analyse the genetic divergence for yield and yield characteristics across 17 variables. Characteristics like the number of days until the first male flower appears, the

number of days until the first female flower appears, the node of the first male flower and the node of the first female flower. For analyzing the genetic divergence among the genotypes, the following variables were used: number of male flowers per vine, number of female flowers per vine, days until first harvest, number of harvests, fruit length (cm), fruit girth (cm), individual fruit weight (g), vine length (cm), number of primary branches per vine, number of fruits per vine, sex ratio, number of seeds per fruit and yield of fruits per vine (g). Utilizing D 2 statistics five groups of genotypes were created. Ward strategy was used to generate a dendrogram. The largest of the five clusters with 14 genotypes, was cluster I. Since cluster III and cluster V have the greatest inter-cluster distance various parents for hybridization may be chosen from these two clusters.

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***MATERIAL
AND
METHODS***

CHAPTER-3

MATERIALS AND METHODS

The present investigation entitled “**Genetic evaluation of Bitter gourd (*Momordica charantia* L.) genotypes for yield and quality traits under low hill conditions of Himachal Pradesh.**” was carried out at RHR&TS, Jachh in summer season of the year 2022 at Vegetable Experimental Farm, Department of Vegetable Science. The details of experimental site, material used and methodology employed during study are discussed in this chapter. Experiment-I Field evaluation of Bitter gourd (*Momordica charantia* L.) genotypes. The experimental material comprised of 37 genotypes of Bitter gourd (*Momordica charantia* L.) were transplanted in Randomized Complete Block Design with three replications during the summer season of (April- Sept) 2022 to study the extent of genetic variation and their related components in the existing germplasm.

3.1 About Experimental Site:

The Experimental Research Farm of Regional Horticultural Research Station, Jachh Department of Vegetable Science, Himachal Pradesh is located on the Pathankot-Mandi National Highway (NH-22) at an altitude of 428 m above mean sea level, lying between 32°16'54.02" N latitude and 75°51'4.38" E longitude under sub-mountain and low hill sub-tropical agro-climatic zone of Himachal Pradesh, India.

3.1.1 Climate:

This region is characterized with mild winters and hot summers. More than 90% rainfall is received during July- August. Data recorded for mean monthly weather parameters during the present investigation have been presented in appendix 1.

3.1.2 Planting Material:

Present investigation comprised of 37 different genotypes of Bitter gourd (*Momordica charantia* L.) which are as follows:

Table 3.1.2 List of genotypes and their source of collection:

Sr. No.	GENOTYPE	Source
1	TCR-85 (IC- 68232)	NBPGR, New Delhi
2	TCR-125 (IC- 68272)	NBPGR, New Delhi
3	TCR-128 (IC- 68275)	NBPGR, New Delhi
4	TCR-147 (IC- 68294)	NBPGR, New Delhi
5	TCR-162 (IC- 68309)	NBPGR, New Delhi
6	TCR-163 (IC- 68310)	NBPGR, New Delhi
7	TCR-167 (IC- 68314)	NBPGR, New Delhi
8	TCR-188 (IC- 68335)	NBPGR, New Delhi
9	TCR-239 (IC- 85626)	NBPGR, New Delhi
10	TCR-242 (IC- 85628)	NBPGR, New Delhi
11	TCR-249 (IC- 85633)	NBPGR, New Delhi
12	TCR-250 (IC- 86634)	NBPGR, New Delhi
13	TCR-251 (IC- 85635)	NBPGR, New Delhi
14	TCR-252 (IC- 85638)	NBPGR, New Delhi
15	TCR-257 (IC- 113875)	NBPGR, New Delhi
16	TCR-344 (IC- 505640)	NBPGR, New Delhi
17	TCR-271 (IC- 85647)	NBPGR, New Delhi
18	TCR-276 A (IC- 85649 A)	NBPGR, New Delhi
19	TCR-289 (IC- 65972)	NBPGR, New Delhi
20	TCR-290 (IC- 66023)	NBPGR, New Delhi
21	TCR-298 (IC- 85650)	NBPGR, New Delhi
22	TCR-331 (IC-505638)	NBPGR, New Delhi
23	TCR-332 (IC- 505639)	NBPGR, New Delhi
24	TCR-333 (IC- 470535)	NBPGR, New Delhi
25	TCR-334 (IC- 505629)	NBPGR, New Delhi
26	TCR-336 (IC- 505637)	NBPGR, New Delhi
27	TCR-337 (IC- 113876)	NBPGR, New Delhi
28	TCR-345 (IC- 505623)	NBPGR, New Delhi
29	TCR-349 (IC- 505626)	NBPGR, New Delhi
30	TCR-356 (IC- 505621)	NBPGR, New Delhi
31	TCR-361 (IC- 470554)	NBPGR, New Delhi

32	TCR-362 (IC- 470555)	NBPGR, New Delhi
33	TCR-364 (IC- 505632)	NBPGR, New Delhi
34	TCR-369 (IC- 505635)	NBPGR, New Delhi
35	Hirkani	MPKV, Rahuri (Maharashtra)
36	Phule Green Gold	MPKV, Rahuri (Maharashtra)
37	Solan Hara (Check)	UHF, Nauni, Solan.

3.2 Experimental Design and layout:

Number of genotypes	:	37 (including check)
Plot Size	:	2.7 m × 1.8 m
Spacing	:	90 cm × 60 cm
Design	:	Randomized Complete Block Design
No. of Replications	:	3
Number of plants/plot	:	9
Check	:	Solan Hara
Date of transplanting	:	23 th May, 2022

3.3 Nursery raising, transplanting and cultural practices

The seeds of all the genotypes of Bitter gourd were sown at experimental farm under special care in 1.5 cm deep in the polytubes. 3 seeds per polybag were sown. Before sowing, the soils of seed beds were prepared to obtain good tilth to provide favourable conditions for vigorous growth of young seedlings. Weeds, stubbles and dried roots of previous crops were removed. The seeds are soak in water overnight for better germination.

3.3.1 Field preparation

The experimental field was ploughed thoroughly with the help of power tiller. Stones, pebbles and crop residues of previous crop were removed manually. The field was brought to the fine tilth and it was levelled for proper drainage of water. Well rotten farm yard manure was applied at the time of field preparation. After levelling, plots were made according to the layout plan.

3.3.2 Transplanting

After four weeks of seed sowing, transplanting was done. Nine plants were planted in each plot of size 2.7 m X 1.8 m. The seedlings were transplanted in the field on 23 May, 2022 at spacing of 90 cm X 60 cm. The transplanting was done in the morning hours and immediately irrigation was done for proper establishment of seedlings.

3.3.3 Cultural practices

Recommended Package of Practices (Anonymous 2020d) were followed during growth period of the crop. Besides the application of farmyard manure 100q/ha, chemical fertilizers were applied as per the recommended package of practices (200kg/ha Urea, 310kg/ha SSP and 90kg/ha MOP). The intercultural operations, irrigations and pest-control were carried out in accordance with the recommended schedule.

3.4 Observation recorded

Observations were recorded on various growth, yield and quality traits in order to study the magnitude of genetic variability and the level of genetic divergence in the material. Five competitive plants were selected at random and tagged for recording of biometrical parameters under study. Observations were recorded at appropriate developmental stages of the plant growth as per the description given below.

3.4.1 Days to first female flowering appearance

Number of days taken from the date of sowing to the date of first female flower appearance were recorded.

3.4.2 Node at which first female flower appear

The node number at which first flower female appears was counted.

3.4.3 Number of days to first picking

Number of days from sowing to first fruit harvest was counted and mean was taken out for that observation.

3.4.4 Average fruit weight (g)

After harvesting, the fresh fruit weight was weighed on a digital weighing balance and the average value was calculated in (g).

3.4.5 Fruit length (cm)

Fruit length of randomly selected five fruits was measured during harvesting from the base of calyx to the tip of fruit and was expressed in centimeter (cm).

3.4.6 Fruit diameter (cm)

Fruit diameter of randomly selected fruits was measured by using digital vernier caliper at the middle point of fruit. It was expressed in centimeters (cm).

3.4.7 Number of ridges per fruit

Number of ridges per fruit of randomly selected five fruits was measured manually in each replication and then averaged to obtain number of ridges pr fruit.

3.4.8 Number of seed per fruit

Total number of seeds from five randomly selected fruits in each replication were counted by cutting the fruit longitudinally and then averaged to obtained number of seed per fruit.

3.4.9 Length of leaf (cm)

Leaf length from five randomly selected leaves of each plant was measured in centimeters from the base of the leaf blade to the leaf tip leaving petiole and the average of five plants of the treatment was worked out.

3.4.10 Width of leaf (cm)

Leaves used for recording length were taken for measuring leaf breadth too. The leaf breadth was measured from the centre of leaf in horizontal axis and the average of the five plants was worked out.

3.4.11 Vine length (cm)

Vine length measured in centimeter in main vine and average data was recorded.

3.4.12 Number of fruits per plant

The number of fruits picked at each harvest was taken into consideration to work out mean number of fruits per plant.

3.4.13 Internodal distance per vine (cm)

Distance between two adjacent nodes at middle portion of vine was measured with the help of scale

3.4.14 Vitamin C (mg/100 g)

The vitamin C content in bitter gourd was estimated by using the method given by Ranganna (1986).

Reagents

1. 3% meta phosphoric acid (HPO₃): Prepared by dissolving the pellets of HPO₃ in glass distilled water.
2. Vitamin C standard: Weigh accurately 100 mg of l-vitamin C and make up to 100 ml with 3% HPO₃. Dilute 10 ml to 100 ml with 3% HPO₃ (1 ml = 0.1 mg of ascorbic acid).
3. Dye solution: Dissolved 50 mg of sodium salt of 2, 6-dichlorophenolindophenol in approximately 150 ml of hot glass distilled water containing 42 mg of sodium bicarbonate. Cool and diluted with glass distilled water to 200 ml.

Standardization of dye. Take 5 ml of standard vitamin C solution and add 5 ml of HPO₃. Fill a micro burette with the dye. Titrate with the dye solution to a pink colour which should persist for 15 seconds. Determined the dye factor, i.e., mg of vitamin C per ml of the dye, using the formula:

$$\text{Dye Factor} = \frac{0.5}{\text{Titre value}}$$

Preparation of sample: Take 10 ml sample of bitter gourd, blend with 3% HPO₃ and make up to 100 ml with HPO₃. Filter or centrifuge the sample before titration.

Procedure: Take an aliquot 10 ml of the HPO₃ extract of sample and titrate with the standard dye to a pink end- point which should persist for at least 15 seconds. Note the reading and calculation was made to determine the vitamin C content.

Calculate the vitamin C content of the sample from the following equation:

$$\text{Vitamin C (mg/100g)} = \frac{\text{Titre} \times \text{Dye factor} \times \text{Volume made up} \times 100}{\text{Aliquot of extract taken} \times \text{Weight of sample for estimation}}$$

3.4.15 Yield per plant (kg)

Total weight of fruits harvested from each selected vine was taken mean value were worked out in kilograms.

3.4.16 Yield per hectare (t)

Yield per hectare was calculated as follows:

$$\text{Yield per hectare} = \frac{\text{Yield per plant (kg)} \times 10000}{0.54 \times 1000}$$

0.54 = Spacing (Row to Row × Plant to Plant)

3.4.17 Fruit colour (light green, medium green, dark green and white)

The colour of each individual fruit was visually analysed for recording the fruit colour of the genotypes at the end of harvest. Based on visual observation light green, medium green, dark green and white fruits were obtained.

3.4.18 Incidence of insect-pest and disease (if any)

All the genotypes were carefully examined for the prevalence of diseases throughout the growing season i.e., from germination of seedlings till final harvesting of the plant under natural epiphytotic conditions.

STATISTICAL ANALYSIS

The analysis of variance will be carried out as per the procedure given by Panse and Sukhatme (1967). The various genetic parameters, viz., genotypic, phenotypic variance, genotypic and phenotypic coefficient of variation, heritability and genetic advance will be estimated for the various quantitative horticultural traits under study.

The correlation coefficient among all important quantitative character combinations at phenotypic and genotypic level will be estimated by employing the formula given by Al. Jibouri et al. (1958).

Path coefficient analysis suggested by Wright (1921) and Dewey and Lu (1957) will be carried out to know the direct and indirect effect of the morphological traits on the yield per plant.

ANOVA

Source of Variation	Degree of Freedom	Sum of square	Mean sum of Square	Expected mean of sum of Squares
Replication (r)	r-1	S _r	S _r /(r-1) =M _r	e ² +g2r
Genotypes (g)	g-1	S _g	S _g /(g-1) =M _g	e ² +r2g
Error (e)	(r-1) (g-1)	S _e	S _e /(r-1) (g-1)= M _e = V _e	e ²

Where,

r = number of replications

g =Number of genotypes

S_r = Sum of squares due to replications

S_g = Sum of squares due to genotypes

S_t = Sum of squares due to error

M_r = Mean sum of squares due to replications

M_g = Mean sum of squares due to genotypes

M_t = Mean sum of squares due to error

σ²r = Variance due to replications

σ²g = Variance due to entries

σ²e = Error variance

Tests were conducted for the replications and genotypes mean sum of squares against error mean sum of squares by 'F' test for (r-1), (r-1) (g-1) and (g-1), (r-1) (g-1) degree of freedom at P= 0.05. Comparison between calculated F-value and tabulated F-value were done. When significant F-test was found,

calculation of critical difference was done to find out the superiority of one genotype over the other.

The standard error and critical differences were calculated as follows:

$$SE (m) \pm = \pm \sqrt{\frac{Me}{r}}$$

$$SE (d) \pm = \pm \sqrt{\frac{2Me}{r}}$$

$$CD_{0.05} = SE (d) \times t_{0.05 (r-1) (g-1) df}$$

Where,

SE (m) \pm = Standard error of mean

SE (d) \pm = Standard error of difference

CD_{0.05} = Critical difference at 5% level of significance

Parameters of Variability:

Study on parameters of variability was calculated as per suggested by Burton and De Vane (1953) as follows:

Genotypic coefficient of variation

$$PCV (\%) = \frac{\sqrt{\text{Phenotypic variance}(Vp)}}{\text{General mean of population}(GM)}$$

Phenotypic coefficient of variation

$$GCV (\%) = \frac{\sqrt{\text{Genotypic variance}(Vg)}}{\text{General mean of population}(GM)} \times 100$$

Where,

$$Vg = \text{Genotypic variance } \frac{(Mg - Me)}{r}$$

$$V_{px} = \text{Phenotypic variance } (Vg + V_e)$$

3.5 Heritability:

Heritability in broad sense was studied as per the formula given by Burton and De Vane (1953) and Allard (1960).

$$\text{Heritability } (\%) = \frac{\text{Genotypic Variance}}{\text{Phenotypic Variance}} \times 100$$

3.6 Genetic Advance:

The expected genetic advance was worked out by selecting five per cent superior individuals as per the formula given by Allard (1960):

$$GA = H \times \sigma_p \times K$$

Where,

H=Heritability % in broad sense

σ_p = Phenotypic standard deviation

K = Selection differential at 5% selection index (K = 2.06)

3.7 Genetic Advance as percentage of mean/ Genetic Gain:

Genetic Advance as percentage of mean was calculated as per the formula given by Johnson et al. (1955):

$$\text{Genetic Advance as percentage of mean (\%)} = (GA / \mu) \times 100$$

GA= Genetic Advance

μ = General Mean of Population

For categorization of magnitude of different parameters, following limits were used (Warshamana 2005).

PCV and GCV

>30%	-	High
15 – 30%	-	Medium
<15%	-	Low

Heritability

>80%	-	High
50 – 80%	-	Medium
<50%	-	Low

Genetic gain

>50%	-	High
25-50%	-	Moderate
<25%	-	Low

3.8 Correlation Analysis Study:

The genotypic and phenotypic correlation was studied as per formula given by Al Jibouri et al. (1958) which is given below:

a) Genotypic correlation between characters x and y:

$$r_{xy}(g) = \frac{Cov_{xy}(g)}{\sqrt{V_x(g) \times V_y(g)}}$$

b) Phenotypic correlation between characters x and y:

$$r_{xy}(p) = \frac{Cov_{xy}(p)}{\sqrt{V_x(p) \times V_y(p)}}$$

Where,

$Cov_{xy}(g)$ = Genotypic co-variance between x and y characters

$Cov_{xy}(p)$ = Phenotypic co-variance between x and y characters

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

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

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

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

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

3.9 Path Coefficient Analysis

Path coefficient was studied as per the procedure suggested by Wright (1921) and was elaborated by Dewey and Lu (1957).

Yield components were included in the path coefficient analysis to reveal their direct and indirect effects upon yield. Residual factor was also included in the causal system which represents all other factor, which might affect yield.

For estimation of direct and indirect effects, following formula was used:

$$r_{iy} = r_{in}P_{iy} + \dots + P_{iy} \dots + r_{in}P_{ny}$$

Where,

r_{iy} = coefficient of correlation between causal factor X_i and dependent character Y .

r_{in} = coefficient of correlation among all possible combinations of causal factors.

P_{iy} = direct effect of character X_i upon the character Y .

Residual factor was worked out as follows:

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

Where,

$$R^2 = \sum_{t=1} P_{iy}^2 + 2 \sum_{i < j} P_{iy} P_{jy} r_{ij}$$

Which is the square of the multiple correlation coefficient (R) and is known as coefficient of determination.

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***RESULTS
AND
DISCUSSION***

Chapter-4

RESULTS AND DISCUSSION

The current research entitled “**Genetic evaluation of Bitter gourd (*Momordica charantia* L.) genotypes for yield and quality traits under low hill conditions of Himachal Pradesh.**” was carried out at vegetable farm situated at Regional Horticultural Research and Training Station, Dr. YS Parmar University of Horticulture and Forestry, Jachh (Nurpur), District-Kangra, Himachal Pradesh in the year 2022 (Summer). The 36 selections of diverse genotypes of bitter gourd along with one check were investigated for conducting the current research. The results of the experiment so are mentioned under the headings:

4.1 Variability studies

4.1.1 Mean performance of genotypes

4.1.2 Parameters of variability

4.2 Heritability and genetic advance

4.3 Correlation studies

4.4 Path coefficient analysis

4.5 Genetic divergence

4.1 VARIABILITY STUDIES

4.1.1 Mean performance of genotypes

Significant genotypic variation was observed when the traits (Appendix-I) were examined, showing that the germplasm under examination included enough variance overall. The following explanations explain both the variability of parameters for the various horticultural qualities and the mean performance of 37 genotypes:

4.1.1.1 Days to first female flowering appearance:

Days to 1st female flower indicate the earliness of the genotype which give indication about the early fruiting. In the present investigation significant differences were observed among the genotypes with range of 53.33 to 65 days and

overall mean performance 57.79 days. The genotype TCR-349 (IC- 505626) has minimum days to first female flower which was statistically at par with TCR-361 (IC- 470554), TCR-239 (IC- 85626), TCR-289 (IC- 65972), TCR-362 (IC- 470555), TCR-276 A (IC- 85649 A), TCR-332 (IC- 505639), TCR-356 (IC- 505621), TCR-344 (IC- 505640), TCR-128 (IC- 68275), TCR-298 (IC- 85650), TCR-334 (IC- 505629), TCR-349 (IC- 505626), Phule Green Gold, TCR-251 (IC- 85635), TCR-85 (IC- 68232), TCR-85 (IC- 68232), Hirkani. The 1st female flower appears late in TCR-163 (IC- 68310) followed by TCR-257 (IC- 113875), TCR-242 (IC- 85628) and TCR-250 (IC- 86634). Wide range of variability for female flower appear also reported by Talukder et al. (2018) from 55.00 to 65.33 and Pradhan et al. (2021) from 45.27 to 59.70.

4.1.1.2 Node at which first female flower appear:

Node at 1st female flower give indication about the earliness of the genotype, lower the node which bear flower, earlier will be the genotype in fruit bearing and it is important for getting remunerative returns. Significant difference was observed among all the genotype with range from 11.33-15.99 with overall mean of 13.63. The genotype, TCR-188 (IC- 68335) produce 1st female flower at the lowest node (11.33), which was statistically at par with the nine genotype TCR-128 (IC- 68275) (11.65), TCR-345 (IC- 505623) (11.70), TCR-349 (IC- 505626) (11.75), TCR-362 (IC- 470555) (11.95), TCR-239 (IC- 85626) (12.10), TCR-85 (IC- 68232) (12.21), TCR-162 (IC- 68309) (12.34), TCR-289 (IC- 65972) (12.39). The 1st female flower appears very late in the genotype TCR-242 (IC- 85628) (15.99), followed by the genotype TCR-251 (IC- 85635) (15.29), TCR-290 (IC- 66023) (15.51), TCR-332 (IC- 505639) (15.69), TCR-333 (IC- 470535) (15.55) and TCR-337 (IC- 113876) (15.80). Wide range of with this trait was also reported by Singh and Kandasamy (2020) from 12.51 to 20.47 and Khan et al. (2015) from 63.00 to 71.00.

4.1.1.3 Number of days to first picking:

Days to first harvest is an important character in bitter gourd. Less days to 1st harvest is desirable in crop like bitter gourd. Days to 1st pickling ranges from 65.00- 76.00 days with overall mean of 69.69 days. Minimum days was recorded in the genotype TCR-349 (IC- 505626) (65.00 days) which was statistically at par with the genotype TCR-239 (IC- 85626) (65.67 days), TCR-361 (IC- 470554)

(66.33 days), TCR-362 (IC- 470555) (66.33 days), TCR-276 A (IC- 85649 A) (67.00 days), TCR-356 (IC- 505621) (67.00 days), TCR-128 (IC- 68275) (67.33 days), TCR-334 (IC- 505629) (67.33 days), TCR-289 (IC- 65972) (66.67 days), TCR-332 (IC- 505639) (67.67 days), Phule Green Gold (67.67 days). Maximum days to 1st pickling was observed in bitter gourd genotype TCR-163 (IC- 68310) (76.00 days) and TCR-242 (IC- 85628) (76.00 days) which were statistically at par with the genotype TCR-257 (IC- 113875) (75.33 days), TCR-250 (IC- 86634) (74.00 days) and TCR-331 (IC-505638) (73.33 days). Similar result was found in Nithinkumar et al. (2022) from 48.2 to 65.7, Chinthan et al. (2021) from 56.92 to 75.50 and Tyagi et al. (2018) from 53.33 to 76.00.

4.1.1.4 Average fruit weight (g):

Fruit weight is one of the most important and major yield contributing factor. Genotype under study manifest variability with respect to fruit weight ranging from 22.93g to 95.47g with overall mean performance 56.72g.

Maximum fruit weight of 95.47g was recorded in genotype TCR-362 (IC- 470555) which was statistically at par with TCR-364 (IC- 505632) (94.87g) and TCR-361 (IC- 470554) (92.90g). While TCR-242 (IC- 85628) (22.93g) was statistically at par with genotype TCR-336 (IC- 505637) (25.35g). The check variety, Solan Hara recorded fruit weight of 74.47g which was statistically at par with TCR-298 (IC- 85650) (70.16g), TCR-85 (IC- 68232) (74.91g), TCR-250 (IC- 86634) (75.93g), TCR-349 (IC- 505626) (79.25g) and Phule Green Gold (81.15g). Seven genotypes to recorded more fruit weight than the check variety. These results of average fruit weight are similar to finding by Chinthan et al. (2021) from 34.17 to 74.49g and Tyagi et al. (2018) from 42.43 to 129.46g.

Table: 4.1.1.1 Mean performance of various quantitative horticultural traits in different bitter gourd (*Momordica charantia* L.) genotypes:

Genotype	Days to first female flowering appearance	Node at which first flower appear	Number of days to first picking	Average fruit weight (g)
TCR-85 (IC- 68232)	56.33	13.43	68.67	50.90
TCR-125 (IC- 68272)	58.67	12.43	71.00	58.15
TCR-128 (IC- 68275)	55.33	11.65	67.33	58.10

TCR-147 (IC- 68294)	57.00	13.14	68.33	45.59
TCR-162 (IC- 68309)	59.33	12.34	71.33	45.49
TCR-163 (IC- 68310)	65.00	13.35	76.00	46.03
TCR-167 (IC- 68314)	56.33	12.21	68.00	74.91
TCR-188 (IC- 68335)	60.33	11.33	72.00	66.33
TCR-239 (IC- 85626)	54.00	12.10	65.67	63.35
TCR-242 (IC- 85628)	64.33	15.99	76.00	22.93
TCR-249 (IC- 85633)	58.00	12.93	70.00	45.51
TCR-250 (IC- 86634)	62.00	14.41	74.00	75.93
TCR-251 (IC- 85635)	56.00	15.29	68.00	46.00
TCR-252 (IC- 85638)	57.00	14.56	69.00	45.10
TCR-257 (IC- 113875)	64.33	14.18	75.33	33.93
TCR-344 (IC- 505640)	55.00	14.23	67.00	67.26
TCR-271 (IC- 85647)	56.67	14.13	68.67	51.71
TCR-276 A (IC- 85649 A)	55.00	14.41	67.00	35.70
TCR-289 (IC- 65972)	54.00	12.39	66.67	60.37
TCR-290 (IC- 66023)	59.67	15.51	71.67	42.92
TCR-298 (IC- 85650)	55.33	13.83	68.00	70.16
TCR-331 (IC-505638)	61.33	14.74	73.33	43.70
TCR-332 (IC- 505639)	55.00	15.69	67.67	45.66
TCR-333 (IC- 470535)	58.67	15.55	70.67	48.80
TCR-334 (IC- 505629)	55.33	12.86	67.33	40.47
TCR-336 (IC- 505637)	61.00	14.42	73.00	25.35
TCR-337 (IC- 113876)	59.33	15.80	71.33	55.23
TCR-345 (IC- 505623)	61.00	11.70	73.00	59.53
TCR-349 (IC- 505626)	53.33	11.75	65.00	79.25
TCR-356 (IC- 505621)	55.00	13.13	67.00	55.65
TCR-361 (IC- 470554)	53.67	13.78	66.33	92.90
TCR-362 (IC- 470555)	54.67	11.95	66.33	95.47
TCR-364 (IC- 505632)	57.67	14.80	69.67	94.87
TCR-369 (IC- 505635)	60.33	12.76	72.33	46.80
Hirkani	56.33	13.17	68.33	53.10
Phule Green Gold	55.67	14.14	67.67	81.15
Solan Hara (C)	60.33	14.25	70.00	74.47
Mean	57.79	13.63	69.69	56.72
CD(0.05)	3.17	1.06	2.95	5.92
SE (m) ±	1.12	0.38	1.04	2.10
Range	53.33- 65.00	11.33- 15.99	65.00- 76.00	22.93- 95.47
CV (%)	3.37	4.77	2.59	6.40

4.1.1.5 Fruit length (cm):

Fruit length is also important character for determining the fruit yield. The

genotype under study showed variation among them. It ranged from 8.07cm - 20.27cm being maximum in Phule Green Gold (20.27cm) which was statistically at par with six genotype including check variety *viz.*, Solan Hara (20.20 cm), TCR-349 (IC- 505626) (19.26 cm), Hirkani (18.22 cm), TCR-361 (IC- 470554) (17.83 cm), TCR-362 (IC- 470555) (17.53 cm) and TCR-289 (IC- 65972) (17.31cm). Minimum fruit length of 8.07cm recorded in TCR-276 A (IC- 85649 A) which was statistically different from other genotypes. Various scientist reported broad range of variability for fruit length in bitter gourd *viz.*, Chinthan et al. (2021) from 8.67 to 24.79, Singh et al. (2014) from 4.35 to 18.56 cm, Tyagi et al. (2018) from 8.10 to 20.80 cm and Thakur et al. (2018) from 9.68 to 19.27.

4.1.1.6 Fruit diameter (cm):

Fruit diameter is one of the major factor for yield determination as well as quality trait and consumer preference for fruit. The study of variance shows great variation for fruit diameter among the genotypes with overall mean performance 3.44 cm and data varies from 2.23 cm to 4.85 cm diameter of fruit. Maximum fruit diameter was recorded in genotype TCR-364 (IC- 505632) (4.85 cm) which was statistically at par with TCR-250 (IC- 86634) (4.79 cm). While minimum fruit diameter (2.23 cm) was observed in TCR-334 (IC- 505629). Solan Hara (standard check) recorded fruit diameter 3.60 cm which was statistically at par with most of the genotype. Similar results were also observed by Tyagi et al. (2018) with fruit diameter ranging from 2.36 to 4.06 cm and Singh et al. (2014) from 1.10 to 4.10 cm.

4.1.1.7 Number of ridges per fruit:

Number of ridges per fruit observed visually and counted. Significant difference were observed among genotypes TCR-361 (IC- 470554) had maximum number of ridges per fruit (9.40) which is statistically at par with genotypes TCR-364 (IC- 505632) (9.39) , TCR-298 (IC- 85650) (9.38), TCR-331 (IC-505638) (9.35), TCR-250 (IC- 86634) (9.29), TCR-249 (IC- 85633) (9.28), TCR-252 (IC- 85638) (9.28), TCR-251 (IC- 85635) (9.26), TCR-276 A (IC- 85649 A) (9.21), TCR-334 (IC- 505629) (9.19), TCR-333 (IC- 470535) (9.13), TCR-349 (IC- 505626) (8.72) with overall mean value of 8.65 and range 9.40-7.48. Minimum number of ridges were found in genotype TCR-242 (IC- 85628) (7.48) which was

statistically at par with the TCR-336 (IC- 505637) (8.07), TCR-345 (IC- 505623) (8.13), TCR-290 (IC- 66023) (8.17). Sixteen genotypes have a greater number of ridges per fruit than the check variety Solan Hara. Similar kinds of result were found by Gupta (2013) from 7.80 to 10.03.

4.1.1.8 Number of seeds per fruit:

The data recorded for number of seeds per fruit show significant variation among the genotypes. The observations taken showed that number of seeds per fruit varies from 13.80 - 41.43 with overall mean performance of 24.54. Maximum number of seeds per fruit were recorded in genotype TCR-362 (IC- 470555) (41.43) followed by TCR-364 (IC- 505632) (40.73). Minimum number of seeds per fruit were recorded in genotype TCR-242 (IC- 85628) (13.80) followed by TCR-336 (IC- 505637) (14.49). The check Solan Hara has 21.00 seeds per fruit which is statistically at par with genotype TCR-85 (IC- 68232), TCR-125 (IC- 68272), TCR-128 (IC- 68275), TCR-147 (IC- 68294), TCR-162 (IC- 68309), TCR-163 (IC- 68310), TCR-249 (IC- 85633), TCR-251 (IC- 85635), TCR-252 (IC- 85638), TCR-257 (IC- 113875), TCR-271 (IC- 85647), TCR-276 A (IC- 85649 A), TCR-290 (IC- 66023), TCR-331 (IC-505638), TCR-332 (IC- 505639), TCR-333 (IC- 470535), TCR-334 (IC- 505629), TCR-337 (IC- 113876), TCR-345 (IC- 505623), TCR-356 (IC- 505621), TCR-369 (IC- 505635) and Hirkani. Similar results were also reported by Kumari et al. (2018) from 17.58 to 30.02.

Table: 4.1.1.2 Mean performance of various quantitative horticultural traits in different bitter gourd (*Momordica charantia* L.) genotypes

Genotype	Fruit length (cm)	Fruit diameter (cm)	Number of ridges per fruit	Number of seed per fruit
TCR-85 (IC- 68232)	11.83	3.27	8.41	22.77
TCR-125 (IC- 68272)	13.87	3.47	8.42	26.07
TCR-128 (IC- 68275)	13.68	3.77	8.61	26.20
TCR-147 (IC- 68294)	12.53	3.66	8.57	19.93
TCR-162 (IC- 68309)	12.07	3.33	8.49	20.23
TCR-163 (IC- 68310)	12.53	3.52	8.58	20.50
TCR-167 (IC- 68314)	14.00	3.49	8.50	31.10
TCR-188 (IC- 68335)	12.33	3.83	8.61	29.10
TCR-239 (IC- 85626)	15.45	3.30	8.51	27.77

TCR-242 (IC- 85628)	9.93	2.62	7.48	13.80
TCR-249 (IC- 85633)	12.37	3.64	9.28	19.25
TCR-250 (IC- 86634)	15.63	4.79	9.29	32.17
TCR-251 (IC- 85635)	12.76	3.23	9.26	19.30
TCR-252 (IC- 85638)	11.01	3.29	9.28	18.18
TCR-257 (IC- 113875)	10.00	2.89	8.38	16.97
TCR-344 (IC- 505640)	14.72	2.90	8.31	29.30
TCR-271 (IC- 85647)	13.88	2.28	8.32	22.47
TCR-276 A (IC- 85649 A)	8.07	3.30	9.21	18.10
TCR-289 (IC- 65972)	17.31	3.37	8.33	27.60
TCR-290 (IC- 66023)	12.79	3.43	8.17	18.18
TCR-298 (IC- 85650)	12.81	3.62	9.38	30.83
TCR-331 (IC-505638)	10.90	3.40	9.35	19.50
TCR-332 (IC- 505639)	11.62	3.36	8.48	20.36
TCR-333 (IC- 470535)	14.24	3.27	9.13	20.23
TCR-334 (IC- 505629)	13.85	2.23	9.19	18.05
TCR-336 (IC- 505637)	9.24	3.32	8.07	14.49
TCR-337 (IC- 113876)	13.03	3.57	8.41	25.50
TCR-345 (IC- 505623)	13.33	3.61	8.13	26.43
TCR-349 (IC- 505626)	19.26	3.77	8.72	32.97
TCR-356 (IC- 505621)	13.94	3.63	8.23	24.03
TCR-361 (IC- 470554)	17.83	4.27	9.40	37.30
TCR-362 (IC- 470555)	17.53	4.30	8.34	41.43
TCR-364 (IC- 505632)	16.38	4.85	9.39	40.73
TCR-369 (IC- 505635)	16.87	2.48	8.24	19.93
Hirkani	18.22	2.67	8.38	22.73
Phule Green Gold	20.27	3.91	8.50	33.50
Solan Hara (C)	20.20	3.60	8.55	21.00
Mean	13.95	3.44	8.65	24.54
CD_(0.05)	3.12	0.50	0.72	6.04
SE (m) ±	1.10	0.18	0.25	2.14
Range	8.07-20.27	2.23-4.85	7.48-9.40	13.80-41.43
CV (%)	13.70	8.93	5.07	15.10

4.1.1.9 Length of leaf (cm):

The length of a leaf was measured in centimetres, from the tip of the leaf to its base. With a mean of 7.31cm amongst all bitter gourd genotypes, the range of leaf lengths ranged from 5.26 to 9.85 cm. The maximum leaf length was recorded in the bitter gourd genotype TCR-364 (IC- 505632) (9.85 cm) which was statistically at par with the genotypes TCR-362 (IC- 470555) (9.70 cm), Phule Green Gold (9.62 cm), TCR-344 (IC- 505640) (9.40 cm), TCR-239 (IC- 85626)

(9.37 cm), TCR-361 (IC- 470554) (9.33 cm), Solan Hara (9.33 cm), TCR-289 (IC- 65972) (9.27 cm), TCR-298 (IC- 85650) (9.27 cm), TCR-349 (IC- 505626) (8.68 cm) and TCR-250 (IC- 86634) (8.52 cm). Least leaf length was seen in genotype TCR-242 (IC- 85628) (5.26 cm).

4.1.1.10 Width of leaf (cm):

The examined genotypes of bitter gourd showed significant diversity in terms of leaf width, with values for the character ranging from 5.44 to 14.01 cm and a mean value of 9.90 cm. Maximum width of the leaf in the genotype of bitter gourd found in TCR-362 (IC- 470555) (14.01 cm) statistically at par with genotype TCR-289 (IC- 65972) (13.90 cm), Phule Green Gold (13.71 cm), TCR-239 (IC- 85626) (13.39 cm), TCR-364 (IC- 505632) (13.38 cm), TCR-349 (IC- 505626) (13.27), TCR-361 (IC- 470554) (13.05 cm), Solan Hara (12.81cm) and TCR-298 (IC- 85650) (12.86 cm). The least leaf width was observed in the genotype TCR-242 (IC- 85628) (5.44 cm) which was statistically at par with the genotypes TCR-336 (IC- 505637) (5.73 cm), TCR-334 (IC- 505629) (7.01 cm) and TCR-257 (IC- 113875) (7.12 cm).

4.1.1.11 Vine Length (cm):

Different genotypes differed significantly for vine length, according to a comparison of the genotypes. The population's total mean value ranged from 329.77 to 419.9cm. The genotype TCR-344 (IC- 505640) had the shortest vine length (329.77 cm), while genotypes TCR-289 (IC- 65972) had the longest vines (419.90 cm) with overall mean performance 373.08 cm. The check variety Solan Hara had vine length 403.13 cm which is statistically at par with genotypes TCR-337 (IC- 113876) (382.60 cm), TCR-163 (IC- 68310) (383.53 cm), TCR-249 (IC- 85633) (386.63 cm), TCR-336 (IC- 505637) (387.00 cm), TCR-147 (IC- 68294) (387.57 cm), TCR-298 (IC- 85650) (394.10), TCR-162 (IC- 68309) (395.43 cm), TCR-128 (IC- 68275) (398.83 cm), TCR-334 (IC- 505629) (401.50), TCR-239 (IC- 85626) (402.67 cm), TCR-276 A (IC- 85649 A) (411.50 cm), Phule Green Gold (414.00 cm), TCR-349 (IC- 505626) (415.63 cm) and TCR-289 (IC- 65972) (419.90 cm). Similar results on vine length were reported by Tyagi et al. (2018) from 1.60 to 3.60 m and Yadav et al. (2008) from 1.22 to 5.42 m.

4.1.1.12 Number of fruits per plant:

Number of fruits per plant were recorded with range 10.28 to 25.52 with the mean value 17.19. Maximum number of fruits per plant were observed in the genotype TCR-276 A (IC- 85649 A) (25.52) which was statistically at par with the genotypes TCR-334 (IC- 505629) (24.52), TCR-147 (IC- 68294) (22.29) and TCR-332 (IC- 505639) (21.72). Minimum number of fruits are observed in genotype TCR-364 (IC- 505632) (10.28). Twenty- two genotypes had a greater number of fruits than the check variety Solan Hara (15.62). Similar findings were reported by Singh et al. (2014) from 8.51 to 48.57, Thakur et al. (2018) from 6.55 to 21.75 and Yadav et al. (2008) from 6.00 to 25.33.

Table: 4.1.1.3 Mean performance of various quantitative horticultural traits in different bitter gourd (*Momordica charantia* L.) genotypes

Genotype	Length of leaf (cm)	Width of leaf (cm)	Vine Length (cm)	Number of fruits per plant
TCR-85 (IC- 68232)	6.97	9.29	339.13	15.00
TCR-125 (IC- 68272)	5.89	9.33	352.33	16.33
TCR-128 (IC- 68275)	5.83	9.70	398.83	18.03
TCR-147 (IC- 68294)	6.54	8.20	387.57	22.29
TCR-162 (IC- 68309)	6.46	8.16	395.43	20.84
TCR-163 (IC- 68310)	5.91	8.19	383.53	20.73
TCR-167 (IC- 68314)	6.51	11.18	368.70	13.82
TCR-188 (IC- 68335)	6.31	10.45	365.97	14.83
TCR-239 (IC- 85626)	9.37	13.39	402.67	17.50
TCR-242 (IC- 85628)	5.26	5.44	380.37	19.85
TCR-249 (IC- 85633)	6.08	8.26	386.63	22.10
TCR-250 (IC- 86634)	8.52	11.76	330.87	11.07
TCR-251 (IC- 85635)	6.52	8.20	376.80	20.03
TCR-252 (IC- 85638)	5.73	8.25	364.73	18.23
TCR-257 (IC- 113875)	6.01	7.12	330.53	15.13
TCR-344 (IC- 505640)	9.40	10.52	329.77	14.23
TCR-271 (IC- 85647)	6.53	9.13	376.30	19.35
TCR-276 A (IC- 85649 A)	6.20	7.38	411.50	25.52
TCR-289 (IC- 65972)	9.27	13.90	419.90	18.97
TCR-290 (IC- 66023)	7.43	8.52	338.93	15.71
TCR-298 (IC- 85650)	9.27	12.86	394.10	16.12

TCR-331 (IC-505638)	5.80	7.89	335.00	13.02
TCR-332 (IC- 505639)	7.22	8.30	361.03	21.72
TCR-333 (IC- 470535)	6.22	8.81	362.33	18.80
TCR-334 (IC- 505629)	6.03	7.01	401.50	24.52
TCR-336 (IC- 505637)	5.73	5.73	387.00	20.33
TCR-337 (IC- 113876)	8.01	10.13	382.60	19.17
TCR-345 (IC- 505623)	7.37	9.75	381.10	18.26
TCR-349 (IC- 505626)	8.68	13.27	415.63	15.15
TCR-356 (IC- 505621)	8.03	10.41	361.37	17.37
TCR-361 (IC- 470554)	9.33	13.05	374.63	12.09
TCR-362 (IC- 470555)	9.70	14.01	374.70	11.15
TCR-364 (IC- 505632)	9.85	13.38	344.40	10.29
TCR-369 (IC- 505635)	6.27	8.60	340.40	14.90
Hirkani	7.20	10.04	330.37	13.77
Phule Green Gold	9.62	13.71	414.00	14.21
Solan Hara (C)	9.33	12.81	403.13	15.62
Mean	7.31	9.90	373.08	17.19
CD_(0.05)	1.36	1.76	21.21	4.35
SE (m) ±	0.48	0.62	7.51	1.54
Range	5.26-9.85	5.44-14.01	329.77-419.90	10.29-25.52
CV (%)	11.43	10.92	3.49	15.53

4.1.1.13 Internodal distance per vine (cm):

Internodal distance per vine is important for fruit bearing. Internodal distance per vine was recorded. The genotypes showed significant differences for internodal distance indicating the variation for internodal length. Internodal distance varied from 7.48 - 11.39 cm with overall mean 9.41 cm. Maximum distance for internode was observed in the genotype TCR-364 (IC- 505632) (11.39 cm). Minimum internodal distance was recorded in the genotype TCR-249 (IC- 85633) (7.48 cm). The check variety Solan Hara had internodal distance (8.26 cm) which was statistically at par with genotypes TCR-249 (IC- 85633) (7.48 cm), TCR-147 (IC- 68294) (7.67 cm), TCR-239 (IC- 85626) (8.33 cm), Phule Green Gold (8.34 cm), TCR-331 (IC-505638) (8.35 cm), TCR-163 (IC- 68310) (8.42 cm), TCR-162 (IC- 68309) (8.43 cm), TCR-276 A (IC- 85649 A) (8.45 cm), TCR-85 (IC- 68232) (8.47 cm), TCR-349 (IC- 505626) (8.57 cm), TCR-333 (IC- 470535)

(8.67 cm), TCR-356 (IC- 505621) (8.71 cm), TCR-345 (IC- 505623) (8.80 cm), TCR-369 (IC- 505635) (8.96 cm), TCR-289 (IC- 65972) (8.99 cm), TCR-332 (IC- 505639) (9.02 cm), TCR-188 (IC- 68335) (9.06 cm), TCR-250 (IC- 86634) (9.18 cm), TCR-334 (IC- 505629) (9.27 cm) and TCR-242 (IC- 85628) (9.29 cm). Additionally, the variance in internodal length has been documented by Chinthan et al. (2021) from 5.66 to 9.10 cm, Thakur et al. (2018) from 7.75 to 10.16 and Yadav et al. (2008) from 4.50 to 10.00 cm.

4.1.1.14 Vitamin C (mg/100g):

Bitter gourd is a good source of vitamin C and high amount of vitamin C in bitter gourd is a desirable character. This character exhibited a range of 59.33 to 136.19 mg for different genotypes of the bitter gourd studied. The overall mean performance of different genotypes was 84.02 mg/100g. The maximum vitamin C was recorded in the genotype TCR-249 (IC- 85633) (136.19) which is statistically at par with genotypes TCR-276 A (IC- 85649 A) (135.01), TCR-147 (IC- 68294) (133.01), TCR-349 (IC- 505626) (131.23) and TCR-345 (IC- 505623) (127.43). The lowest vitamin C was observed in the genotype TCR-361 (IC- 470554) (59.33). Similar kind of findings for vitamin C content were also reported by Yadav et al. (2008) from 49.33 to 170.00 and Nithinkumar et al. (2022) from 81.29 to 122.4 mg/100g

4.1.1.15 Yield per plant (kg):

Yield per plant is one of most important and desirable character from farmer's point of view. The value of yield per plant exhibited a range of 0.45 - 1.20 kg for different genotypes of bitter gourd studied. The overall mean performance with respect to different genotypes was 0.91 kg. The highest yield per plot was exhibited by the genotype TCR-349 (IC- 505626) (1.20 kg) which was statistically at par with the genotypes TCR-289 (IC- 65972) (1.14 kg), Phule Green Gold (1.11 kg), TCR-239 (IC- 85626) (1.10 kg), TCR-298 (IC- 85650) (1.09 kg), Solan Hara (1.08 kg). Minimum yield per plot was observed in the genotype TCR-242 (IC- 85628) (0.45 kg) which was statistically at par with the genotypes TCR-257 (IC- 113875) (0.50 kg), TCR-336 (IC- 505637) (0.52 kg) and TCR-331 (IC-505638) (0.56 kg). Similar kind of observations were found by Chinthan et al. (2021) from 0.55 to 2.67 kg, Tyagi et al. (2018) from 0.85 to 2.61 kg and Thakur et al. (2018)

from 0.32 to 1.16 kg.

4.1.1.16 Yield per hectare (t):

Yield per hectare is one of the chief important parameter in any research programme. All the research programme aims towards to getting more yield. In the present study, genotypes showed significant variation for yield per plot which ranges from 7.98 - 21.23 ton with mean value 16.39 ton. Twenty-seven genotypes gave more yield per hectare than the population mean. The highest yield was recorded in the genotype TCR-349 (IC- 505626) (21.23 ton) which is statistically at par with various genotypes i.e. TCR-289 (IC- 65972) (20.18 ton), Phule Green Gold (20.78 ton), TCR-239 (IC- 85626) (20.26 ton), TCR-298 (IC- 85650) (20.18 ton) and Solan Hara (18.72 ton). The standard check Solan Hara observed total yield of 18.72 ton per hectare which was statistically same to the maximum genotypes. Similar observations were reported by Yadav et al. (2008) from 3.8 ton to 17.9 ton/ha and Nithinkumar et al. (2022) from 3.61 to 12.74 ton/ha.

Table: 4.1.1.4 Mean performance of various quantitative horticultural traits in different bitter gourd (*Momordica charantia* L.) genotypes:

Genotype	Internodal distance per vine (cm)	Vitamin C (mg/100g)	Yield per plant (kg)	Yield per hectare (t)
TCR-85 (IC- 68232)	10.22	65.37	0.73	11.49
TCR-125 (IC- 68272)	9.97	63.67	0.94	16.81
TCR-128 (IC- 68275)	9.82	73.89	1.04	18.37
TCR-147 (IC- 68294)	7.67	133.01	1.01	18.39
TCR-162 (IC- 68309)	8.43	68.97	0.94	17.24
TCR-163 (IC- 68310)	8.42	64.63	0.95	17.22
TCR-167 (IC- 68314)	8.47	67.00	1.00	18.45
TCR-188 (IC- 68335)	9.06	94.00	0.98	18.40
TCR-239 (IC- 85626)	8.33	63.22	1.10	20.26
TCR-242 (IC- 85628)	9.29	67.70	0.45	7.98
TCR-249 (IC- 85633)	7.48	136.19	1.00	18.15
TCR-250 (IC- 86634)	9.18	66.85	0.80	14.49
TCR-251 (IC- 85635)	10.17	71.17	0.91	16.72
TCR-252 (IC- 85638)	10.07	73.10	0.81	14.74
TCR-257 (IC- 113875)	9.92	73.87	0.50	9.15

TCR-344 (IC- 505640)	10.93	105.95	0.89	16.52
TCR-271 (IC- 85647)	10.34	106.10	1.00	18.41
TCR-276 A (IC- 85649 A)	8.45	135.01	0.90	16.65
TCR-289 (IC- 65972)	8.99	87.17	1.14	20.18
TCR-290 (IC- 66023)	11.08	81.04	0.67	12.40
TCR-298 (IC- 85650)	10.29	81.42	1.09	18.17
TCR-331 (IC-505638)	8.35	89.28	0.56	10.44
TCR-332 (IC- 505639)	9.02	71.43	0.99	18.27
TCR-333 (IC- 470535)	8.67	78.60	0.91	16.71
TCR-334 (IC- 505629)	9.27	65.83	0.99	18.12
TCR-336 (IC- 505637)	9.85	72.50	0.52	9.24
TCR-337 (IC- 113876)	11.32	63.83	1.02	18.22
TCR-345 (IC- 505623)	8.80	127.43	1.03	18.13
TCR-349 (IC- 505626)	8.57	131.23	1.20	21.23
TCR-356 (IC- 505621)	8.71	71.40	0.90	17.12
TCR-361 (IC- 470554)	10.97	59.33	1.02	18.32
TCR-362 (IC- 470555)	9.82	95.86	1.00	17.66
TCR-364 (IC- 505632)	11.39	95.48	0.94	17.56
TCR-369 (IC- 505635)	8.96	59.90	0.81	12.69
Hirkani	11.13	68.64	0.73	13.04
Phule Green Gold	8.34	92.60	1.11	20.78
Solan Hara (C)	8.26	86.00	1.08	18.72
Mean	9.41	84.02	0.91	16.39
CD_(0.05)	1.53	14.29	0.13	2.71
SE (m) ±	0.54	5.06	0.05	0.96
Range	7.48-11.39	59.33-136.19	0.45-1.20	7.98-21.23
CV (%)	9.94	10.43	8.56	10.12

4.1.1.17 Fruit colour (Light Green, Medium Green, Dark Green and White):

The fruit colour revealed significant variance across all genotypes under study. Fruit colour is a crucial characteristic that affects customer choices. The visual observations used to generate the data in (Table 4.1.1.5) indicated a variety of colour intensities that were classed as Green, Cream and White. Twelve genotypes had Light Green fruits, thirteen genotypes Medium Green fruits, five genotypes Dark Green fruits, whereas seven genotypes had White colour. Same type of finding observed by Dey et al. (2005) and Suma et al. (2023).

Table: 4.1.1.5 Observations with respect to various qualitative traits in different bitter gourd (*Momordica charantia* L.) genotypes:

Genotype	Fruit colour	Genotype	Fruit colour
TCR-85 (IC- 68232)	Medium Green	TCR-290 (IC- 66023)	Medium Green
TCR-125 (IC- 68272)	Light Green	TCR-298 (IC- 85650)	Light Green
TCR-128 (IC- 68275)	Medium Green	TCR-331 (IC-505638)	Medium Green
TCR-147 (IC- 68294)	Light Green	TCR-332 (IC- 505639)	Dark Green
TCR-162 (IC- 68309)	Medium Green	TCR-333 (IC- 470535)	Medium Green
TCR-163 (IC- 68310)	Medium Green	TCR-334 (IC- 505629)	White
TCR-85 (IC- 68232)	Light Green	TCR-336 (IC- 505637)	Dark Green
TCR-188 (IC- 68335)	Medium Green	TCR-337 (IC- 113876)	Light Green
TCR-239 (IC- 85626)	White	TCR-345 (IC- 505623)	White
TCR-242 (IC- 85628)	White	TCR-349 (IC- 505626)	Light Green
TCR-249 (IC- 85633)	White	TCR-356 (IC- 505621)	Light Green
TCR-250 (IC- 86634)	Light Green	TCR-361 (IC- 470554)	Light Green
TCR-251 (IC- 85635)	Medium Green	TCR-362 (IC- 470555)	Light Green
TCR-252 (IC- 85638)	White	TCR-364 (IC- 505632)	Medium Green
TCR-257 (IC- 113875)	Light Green	TCR-369 (IC- 505635)	White
TCR-344 (IC- 505640)	Light Green	Hirkani	Dark Green
TCR-271 (IC- 85647)	Medium Green	Phule Green Gold	Dark Green
TCR-276 A (IC- 85649 A)	Medium Green	Solan Hara (C)	Dark Green
TCR-289 (IC- 65972)	Medium Green		

4.1.1.18 Incidence of insect pest and disease (if any):

From the germination of seedlings to the plant's final harvest under natural epiphytotic settings, all the genotypes were thoroughly investigated for the frequency of illnesses. The crop experienced a bitter gourd fruit fly infestation during the growing season while the research was ongoing.

Five plants per plot were randomly selected. The fruit fly infestation was recorded at 70, 85 and 100 days after sowing. The fruit fly infestation was found between 0.00% to 27.08% for 70 days, 5.08% to 28.04% for 85 days and 3.70% to 24.44% and the overall mean percent of fruit infection was found between 4.79% to 21.54%.

At 70 days, the fruit fly infestation ranged from 0.00% to 27.08% with mean value of 11.83%. The most infested genotype was TCR-331 (IC-505638) (27.08%) and least infestation (0.00%) was recorded in the genotypes TCR-250 (IC- 86634), TCR-298 (IC- 85650), TCR-332 (IC- 505639), TCR-369 (IC- 505635), Hirkani, Phule Green Gold and Solan Hara.

At 85 days, fruit fly infestation ranged from 5.08% to 28.04%, with a mean of 17.93%. The most infested genotype was TCR-298 (IC- 85650) (28.04%) and less infestation was recorded in the genotypes TCR-349 (IC- 505626) (5.08%) which was statistically at par with genotypes TCR-250 (IC- 86634) (6.08%), TCR-239 (IC- 85626) (6.83%), Phule Green Gold (6.27%), Hirkani (7.72%), TCR-356 (IC- 505621) (8.19%), Solan Hara (9.03%), TCR-289 (IC- 65972) (9.11%), TCR-361 (IC- 470554) (9.82%), TCR-369 (IC- 505635) (10.01%) and TCR-290 (IC- 66023) (12.04%).

At 100 days, the fruit fly infestation ranged from 3.70% to 24.44% with mean 12.73%. The most infested genotype was TCR-298 (IC- 85650) (24.44%) and least infestation was recorded in the genotype TCR-252 (IC- 85638) (3.70%) which was statistically at par with genotypes TCR-271 (IC- 85647) (5.42%), TCR-331 (IC- 505638) (5.56%), TCR-337 (IC- 113876) (5.78%), TCR-364 (IC- 505632) (6.06%), TCR-349 (IC- 505626) (6.94%), Phule Green Gold (8.10%), TCR-242 (IC- 85628) (8.33%), TCR-344 (IC- 505640) (9.58%) and TCR-167 (IC- 68314) (10.00%).

Overall mean of fruit fly infestation during growing period ranged from 4.79% to 21.54%. The maximum infestation was recorded in genotype TCR-257 (IC- 113875) (21.54%) and least infestation was recorded in genotype Phule Green Gold (4.79%) which were statistically at par with the genotypes Hirkani (5.52%), Solan Hara (5.95%), TCR-349 (IC- 505626) (6.95%), TCR-369 (IC- 505635) (7.41%), TCR-356 (IC- 505621) (7.85%), TCR-250 (IC- 86634) (7.92%), TCR-289 (IC- 65972) (8.00%) and TCR-252 (IC- 85638) (11.61%). Our results are consistent with the findings of Panday et al (2012).

Table:4.1.1.6 Fruit fly infestation in different genotypes of (*Momordica charantia* L.) at RHR&TS, Jachh

Treatment (genotypes)	Fruit fly infestation			
	70 days after sowing	85 days after sowing	100 days after sowing	Mean
TCR-85 (IC- 68232)	7.57 (2.91)	24.52 (5.04)	9.72 (3.26)	13.94 (3.74)
TCR-125 (IC- 68272)	22.70 (4.84)	19.76 (4.53)	15.58 (3.93)	19.35 (4.43)
TCR-128 (IC- 68275)	6.53 (2.73)	19.63 (4.54)	16.67 (4.15)	14.28 (3.81)
TCR-147 (IC- 68294)	21.02 (4.67)	26.93 (5.28)	12.54 (3.57)	20.16 (4.50)
TCR-162 (IC- 68309)	10.01 (3.29)	26.85 (5.26)	19.44 (4.50)	18.77 (4.35)
TCR-163 (IC- 68310)	26.11 (5.18)	27.78 (5.34)	8.83 (3.13)	20.91 (4.55)
TCR-167 (IC- 68314)	12.50 (3.64)	23.33 (4.88)	10.00 (2.97)	15.28 (3.83)
TCR-188 (IC- 68335)	11.27 (3.46)	15.96 (4.07)	16.19 (4.13)	14.47 (3.89)
TCR-239 (IC- 85626)	12.22 (3.62)	6.83 (2.74)	17.66 (4.31)	12.24 (3.55)
TCR-242 (IC- 85628)	14.01 (3.85)	19.44 (4.47)	8.33 (2.78)	13.93 (3.70)
TCR-249 (IC- 85633)	22.70 (4.84)	24.52 (5.04)	9.72 (3.26)	18.98 (4.38)
TCR-250 (IC- 86634)	0.00 (1.00)	6.08 (2.58)	17.66 (4.31)	7.69 (2.55)
TCR-251 (IC- 85635)	11.50 (3.52)	27.78 (5.34)	17.66 (4.31)	18.98 (4.39)
TCR-252 (IC- 85638)	6.11 (2.66)	25.00 (5.05)	3.70 (1.83)	11.61 (3.18)
TCR-257 (IC- 113875)	25.87 (5.09)	19.30 (4.50)	19.44 (4.50)	21.54 (4.70)
TCR-344 (IC- 505640)	15.42 (4.04)	28.04 (5.37)	9.58 (2.93)	17.68 (4.12)
TCR-271 (IC- 85647)	7.57 (2.91)	21.80 (4.77)	5.42 (2.34)	11.60 (3.34)
TCR-276 A (IC- 85649 A)	21.02 (4.67)	17.86 (4.34)	12.97 (3.73)	17.28 (4.25)
TCR-289 (IC- 65972)	5.75 (2.59)	9.11 (3.17)	9.14 (3.18)	8.00 (2.98)
TCR-290 (IC- 66023)	9.03	12.04	19.44	13.50

	(3.14)	(3.24)	(4.50)	(3.63)
TCR-298 (IC- 85650)	0.00 (1.00)	15.59 (4.05)	24.44 (5.01)	13.35 (3.35)
TCR-331 (IC-505638)	27.08 (5.25)	27.86 (5.37)	5.56 (2.07)	20.17 (4.23)
TCR-332 (IC- 505639)	0.00 (1.00)	26.19 (5.20)	24.29 (5.01)	16.83 (3.74)
TCR-333 (IC- 470535)	18.06 (4.33)	25.00 (5.05)	19.44 (4.50)	20.83 (4.63)
TCR-334 (IC- 505629)	8.96 (3.14)	21.56 (4.67)	16.19 (4.13)	15.57 (3.98)
TCR-336 (IC- 505637)	12.22 (3.62)	16.39 (4.15)	16.67 (4.15)	15.09 (3.98)
TCR-337 (IC- 113876)	19.58 (4.51)	12.26 (3.63)	5.78 (2.39)	12.54 (3.51)
TCR-345 (IC- 505623)	17.24 (4.26)	19.76 (4.53)	12.17 (3.62)	16.39 (4.14)
TCR-349 (IC- 505626)	8.84 (3.13)	5.08 (2.46)	6.94 (2.81)	6.95 (2.80)
TCR-356 (IC- 505621)	6.53 (2.73)	8.19 (3.03)	8.83 (3.13)	7.85 (2.96)
TCR-361 (IC- 470554)	21.02 (4.67)	9.82 (3.28)	16.19 (4.13)	15.68 (4.03)
TCR-362 (IC- 470555)	16.46 (4.15)	16.39 (4.15)	10.82 (3.42)	14.56 (3.91)
TCR-364 (IC- 505632)	12.93 (3.67)	24.44 (5.01)	6.06 (2.13)	14.48 (3.60)
TCR-369 (IC- 505635)	0.00 (1.00)	10.01 (3.29)	12.22 (3.61)	7.41 (2.63)
Hirkani	0.00 (1.00)	7.72 (2.95)	8.83 (3.13)	5.52 (2.36)
Phule Green Gold	0.00 (1.00)	6.27 (2.70)	8.10 (3.01)	4.79 (2.23)
Solan Hara (C)	0.00 (1.00)	9.03 (3.14)	8.83 (3.13)	5.95 (2.42)
Mean	11.83 (3.30)	17.93 (4.21)	12.73 (3.54)	14.17 (3.68)
CD_{0.05}	4.95 (0.50)	8.19 (1.01)	8.04 (1.39)	6.39 (0.95)
Range maximum	27.08 (5.25)	28.04 (5.37)	24.44 (5.01)	4.79 (4.70)
Range minimum	0.00 (1.00)	5.08 (2.46)	3.07 (1.83)	21.54 (2.23)

* Values in the parenthesis are the square root transformed values.



Plate 1: Fruit fly infestation

4.1.2 PARAMETERS OF VARIABILITY

Genetic heterogeneity in the population is crucial for genetic improvement of any crop, and plant breeding studies use the germplasm of the crop that has been gathered from diverse sources as a base population to increase genetic variability in the target crop. The fundamental prerequisite for the enhancement of the numerous horticultural qualities of a crop is genetic variability. Therefore, understanding genetic variation in relation to yield and other crucial traits is essential for bolstering any breeding plan.

The variance seen for the variables under research in the current study, which involved 37 genotypes of bitter melon, was due to an interaction between the environment and the genotype. Only genotypic and phenotypic coefficients of variation were examined to gauge the magnitude of genotypic and phenotypic variability in the current experiment since environmental variation is the only source of variability that cannot be fixed. Following is a discussion of the findings regarding genotypic and phenotypic coefficients:

4.1.2.1 Coefficients of variability:

The perusal of data present in Table 4.2 made it abundantly evident that for all the qualities examined, the phenotypic coefficient of variation (PCV) was larger than the genotypic coefficient of variation (GCV), indicating that the environment contributed more to variance among the different genotypes. For all the examined traits there was a smaller difference between PCV and GCV levels. According to the coefficient of variability determined by Warshamana (2005), the characters under research are divided into three distinct groups: low (<15%), moderate (15–30%) and high (>30%).

High phenotypic coefficient of variation (PCV) was observed for average fruit weight (32.14%) and number of seeds per fruit (30.83%) and high genotypic coefficient of variation (GCV) was observed for average fruit weight (31.50%). Similar findings by Gupta (2013) for heritability.

However, moderate value (15-30%) of PCV was recorded in 8 traits *viz.*,

Fruit length (24.02%), fruit diameter (18.20%), length of leaf (22.47%), width of leaf (25.75%), number of fruits per plant (25.08%), vitamin C (28.70%), yield per plant (22.46%) and yield per hectare (21.11%). Same type of findings recorded by Dey et al. (2005) for vitamin C (19.87). Moderate value (15-30%) of GCV was recorded in 9 traits *viz.*, Fruit length (19.78%), fruit diameter (15.87%), number of seeds per fruit (26.88%), length of leaf (19.56%), width of leaf (23.33%), number of fruits per plant (19.69%), vitamin C (26.74%), yield per plant (19.75%) and yield per hectare (19.66%). Similar type of findings for heritability were recorded by Dey et al. (2005) and Islam et al. (2009).

Low magnitude (<15%) for PCV and GCV was observed in 6 traits *viz.*, days to first female flowering appearance (PCV- 6.12% and GCV- 5.11%), Node at which first female flower appear (PCV- 10.42% and GCV- 9.26%), number of days to first picking (PCV- 4.76% and GCV- 3.97%), number of ridges per fruit (PCV- 6.84% and GCV- 4.61%), vine length (PCV- 7.77% and GCV- 6.95%), (PCV- % and GCV- %), (PCV- % and GCV- %), Internodal distance per vine (PCV- 13.90% and GCV- 9.71%). Similar findings were observed by Khan et al. (2015).

4.2 HERITABILITY AND GENETIC ADVANCE:

4.2.1 Heritability:

Heritability must be estimated since genetic variability by itself cannot provide an approximation of the heritable variance. According to Burton and Vane (1953), a genetic coefficient of variability and heritability estimates would provide the clearest picture of the level of advancement anticipated from selection in a given population. Heritability is a measure of genetic diversity that identifies the degree of traits handed down from a parent to a child. When a characteristic has a high heritability, we can apply direct selection to improve it from a single parent; however, when it has a low heritability, we must first evaluate the offspring before making a selection based on the progeny's traits.

Heritability in the broad sense was categorised as high when it exceeded

80%, moderate when it fell between 50% and 80%, and low when it fell below 50%. Heritability in a wide sense was found to range from 45.32 to 96.03% in the current investigation. The character average fruit weight showed the highest heredity value (96.03%) followed by vitamin C (86.80%) and width of leaf (82.04%). Similar findings were recorded by Nithinkumar et al. (2022) and Singh et al. (2017) for vitamin C.

While the trait's moderate (50–80%) heritability was noted in vine length (79.89%), yield per hectare (79.04%), Node at which first female flower appear (79.03%), yield per plant (77.32%), number of seeds per fruit (76.02%), fruit diameter (75.96%), length of leaf (75.76%), Days to first female flowering appearance (69.73%), number of days to first picking (69.45%), fruit length (67.84%) and number of fruits per plant (61.65%). Similar findings were observed by Tyagi et al. (2018) for fruit yield/plant (72.67%), Nithinkumar et al. (2022) and Singh and Kandasamy (2020) for vine length (73.30% and 76.12%).

A low heritability value of (>50%) was observed for the traits *viz.*, number of ridges per fruit (45.32%) and internodal distance per vine (48.82%).

4.2.2 Genetic Advance (as per cent of mean):

Genetic advance expressed as a per cent of the mean is known as genetic gain. Genetic advance is influenced by the heritability of the trait being selected for, the genetic variation of the genotypes, and the level of selection. According to Johnson et al. (1955), traits with high heritability and high genetic advance would respond to selection more favourably than traits with high heritability but low genetic advance. High genetic progress and heritability indicate that attributes were mostly influenced by the additive gene effect, suggesting that selection could be useful for enhancing these features.

The genetic advance for the traits under research is divided into three categories: high (>50%), moderate (25–50%), and low (>25%). Genetic advance was computed as a percentage mean for yield and its components, which is shown in Fig. 4.2.

The genetic progress values in the current study ranged from 6.39 to 63.58% for all the characteristics. Maximum value for genetic advance was recorded in the horticultural trait *viz.*, average fruit weight (63.58%) followed by traits vitamin C (51.32%) and number of seeds per fruit (48.28%). Our results in concordance with those of Singh et al. (2017).

However, a low amount of genetic advance (25–50%) was found in the traits *viz.*, width of leaf (43.52%), yield per hectare (36.01%), yield per plant (35.78%), Length of leaf (35.07%), fruit length (33.56%) and number of fruits per plant (35.81%) and fruit diameter (28.48%). Our results in concordance with those of Tyagi et al. (2018) and Nithinkumar et al. (2022).

Whereas, low values (>25%) in terms of genetic advance were found for the traits *viz.*, node at which first female flower appear (16.96%), internodal distance per vine (13.98%), vine length (12.79%), days to first female flowering appearance (8.79%), number of days to first picking (6.81%) and number of ridges per fruit (6.39%). Similar findings were also reported by Tyagi et al. (2018) and Kumari et al. (2018).

Table: 4.2 The Estimates of phenotypic coefficients of variation, genetic advance, heritability (%), coefficients of variation, genetic gain and for various traits in bitter gourd:

Sr no.	Characters	Mean	Range	Coefficient of variation (%)		Heritability (%)	Genetic advance as % of mean
				Phenotypic	Genotypic		
1	Days to first female flowering appearance	57.79	53.33 – 65.00	6.12	5.11	69.73	8.79
2	Node at which first female flower appear	13.63	11.33 – 15.99	10.42	9.26	79.03	16.96
3	Number of days to first picking	69.69	65.00 – 76.00	4.76	3.97	69.45	6.81
4	Average fruit weight (g)	56.72	22.93 – 95.47	32.14	31.50	96.03	63.58
5	Fruit length (cm)	13.95	8.07 – 20.27	24.02	19.78	67.84	33.56
6	Fruit diameter (cm)	3.44	2.23 – 4.85	18.20	15.87	75.96	28.48
7	Number of ridges per fruit	8.65	7.48 – 9.40	6.84	4.61	45.32	6.39
8	Number of seed per fruit	24.54	13.80 – 41.43	30.43	26.88	76.02	48.28
9	Length of leaf (cm)	7.31	5.26 – 9.85	22.47	19.56	75.76	35.07
10	Width of leaf (cm)	9.90	5.44 – 14.01	25.75	23.33	82.04	43.52
11	Vine Length (cm)	373.08	329.77 – 419.90	7.77	6.95	79.89	12.79
12	Number of fruits per plant	17.19	10.28 – 25.52	25.08	19.69	61.65	31.85
13	Internodal distance per vine (cm)	9.41	7.48 -11.39	13.90	9.71	48.82	13.98
14	Vitamin C (mg/100g)	84.02	59.33 – 136.19	28.70	26.74	86.80	51.32
15	Yield per plant (kg)	0.91	0.45 – 1.20	22.46	19.75	77.32	35.78
16	Yield per hectare (t)	16.39	7.98 – 21.23	22.11	19.66	79.04	36.01

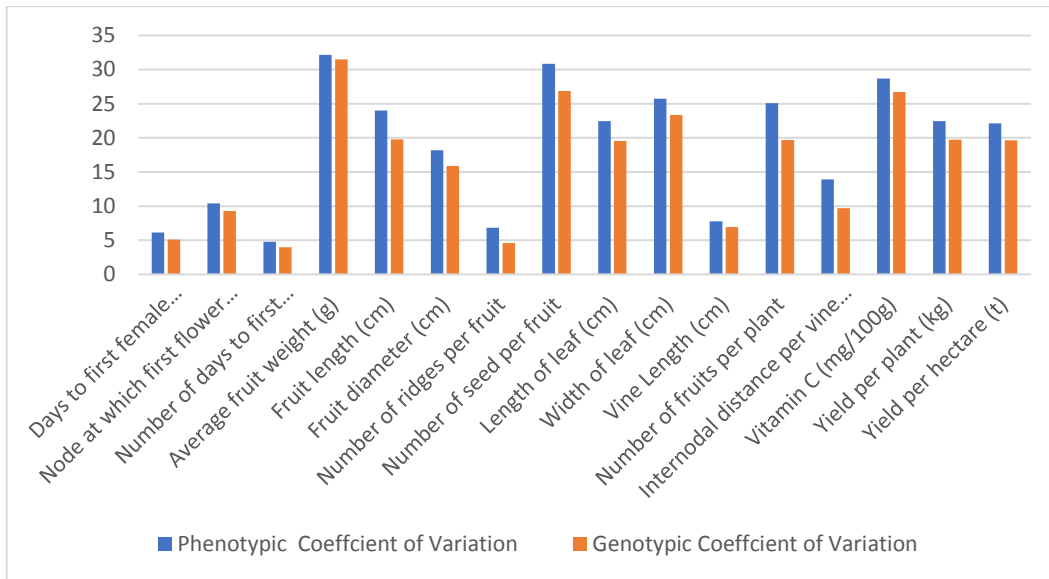


Fig 1: Graphical representation of phenotypic and genotypic coefficient of variation (%) for different traits in bitter gourd

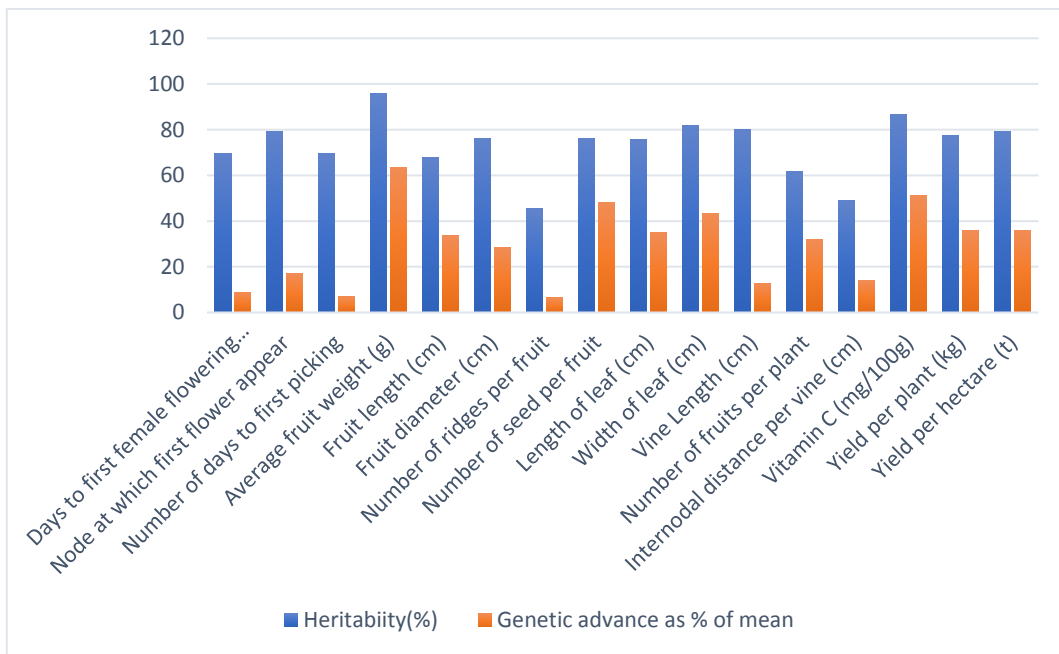


Fig 2: Graphical representation of heritability (%) and genetic advance (%) for different traits in bitter gourd.

4.3 CORRELATION STUDIES:

In any plant breeding programme that tries to improve the quality and yield attributes, character association is a key factor. Correlation establishes the connections between various characters, which enhances the effectiveness of selection. Additionally, understanding the degree of correlation between various crop characteristics improves the accuracy of genetic improvement. In the current study, correlation coefficient analysis was done for all conceivable combinations of 16 quantitative features in bitter gourd, both at the phenotypic and genotypic levels, respectively. Table 4.3 perusal revealed that for the majority of the features, the genotypic correlations were stronger in magnitude than the phenotypic correlations, indicating that the environment had less influence over the phenotype of the genotypes of bitter gourd under study. The several noteworthy relationships between distinct personalities have been covered below under pertinent headings:

4.3.1 Days to first female flowering appearance:

Days to first female flowering appearance showed negative and highly significant trait association with the average fruit weight (-0.479 and -0.358), number of seeds per fruit (-0.521 and -0.327), length of leaf (-0.518 and -0.392), width of leaf (-0.593 and -0.379), vine length (-0.316 and -0.372), yield per plant (-0.649 and -0.647) and yield per hectare (-0.599 and -0.616) at both phenotypic and genotypic levels. The character however, show significant negative and highly significant trait association with characters fruit length (-0.498), number of ridges per fruit (-0.308), internodal distance per vine (-0.222) and vitamin C (-0.196) at genotypic levels and fruit length (-0.215) and number of ridges per fruit (-0.203) at phenotypic levels. Days to first female flower appearance shows that early in the flowering, more is yield.

Whereas the days to first female flowering appearance observed positive and highly significant correlation with the characters node at which first flower appear (0.250 and 0.276) and number of days to first picking (0.998 and 0.970) at both phenotypic and genotypic levels. When the days of female flowering is early or late then the days to first fruit picking will also be early or late. Khan et al. (2015) finds similar for fruit length and Khan et al. (2018) for yield per plant and Kumari et al. (2018) had negative and significant correlation with number of seeds per fruit in bitter gourd.

4.3.2 Node at which first flower appear:

The character showed a significant and highly positive connection with number of days to first picking (0.294 and 0.280) and internodal distance per vine (0.326 and 0.338) at both phenotypic and genotypic levels.

While the character made a major and profoundly negative character association with average fruit weight (-0.345 and -0.280), number of seeds per fruit (-0.347 and -0.240), width of leaf (-0.400 and -0.277), vine length (-0.275 and -0.291), yield per plant (-0.436 and -0.463) and yield per hectare (-0.418 and -0.429). These character however, showed significant negative association with character both phenotypic and genotypic levels and fruit length (-0.367) vitamin C (-0.198) at genotypic level only. Similar results of negative and significant correlation with yield per plant were reported by Kumari et al. (2018)

4.3.3 Number of days to first picking:

Number of days to first picking observed negative and highly significant correlation with the character average fruit weight (-0.504 and -0.376), fruit length (-0.542 and -0.268), number of seeds per fruit (-0.513 and -0.316), length of leaf (-0.555 and -0.419), width of leaf (-0.627 and -0.389), vine length (-0.372 and -0.397), vitamin C (-0.255 and -0.192), yield per plant (-0.694 and -0.646) and yield per hectare (-0.652 and -0.629) at both phenotypic and genotypic levels and number of ridges per fruit (-0.305) at genotypic level only. Similar results were also reported by Kumari et al. (2018) where number of days to first picking had negative and significant correlation with number of seeds per fruit.

4.3.4 Average fruit weight (g):

Average fruit weight observed positive and highly significant correlation with the characters fruit length (0.785 and 0.720), fruit diameter (0.706 and 0.647), number of ridges per fruit (0.295 and 0.228), number of seeds per fruit (0.990 and 0.904), length of leaf (0.632 and 0.553), width of leaf (0.946 and 0.869), yield per plant (=0.700 and 0.567) and yield per hectare 0.652 and 0.629) at both phenotypic and genotypic levels. The character however, showed significant positive association with character number of ridges per fruit (0.228) at phenotypic level only.

Whereas the average fruit weight shows negative and highly significant trait

association with the Internodal distance per vine (-0.733 and -0.661) at both genotypic and phenotypic levels. Similar results were also reported by Khan et al. (2015) who observed positive and highly significant correlation with yield per plant.

4.3.5 Fruit length (cm):

The character showed a significant and highly positive connection with fruit diameter (0.270 and 0.322), number of seeds per fruit (0.646 and 0.625), length of leaf (0.594 and 0.432), width of leaf (0.866 and 0.706), yield per plant (0.647 and 0.339), yield per hectare (0.640 and 0.335) at both phenotypic and genotypic levels and vine length (genotypic=0.255) at genotypic level only.

While the character made a major and profoundly negative character association with number of fruits per plant (-0.494 and -0.593) at both phenotypic and genotypic levels. Kumari et al. (2018) reported same results for yield per plant.

4.3.6 Fruit diameter (cm):

Fruit diameter observed positive and highly significant correlation with the characters number of ridges per fruit (0.377 and 0.364), number of seeds per fruit (0.709 and 0.655), length of leaf (0.474 and 0.375), width of leaf (0.618 and 0.523), yield per plant (0.459 and 0.257) and yield per hectare (0.339) at both phenotypic and genotypic levels. The character however, showed significant positive association with character yield per hectare (0.233) at phenotypic level only.

Whereas the fruit diameter showed negative and highly significant trait association with the number of fruits per plant (-0.481 and -0.478) at both phenotypic and genotypic levels. Jatav et al. (2016) found same result for yield per hectare.

4.3.7 Number of ridges per fruit:

The character showed a significant and highly positive connection with yield per plant (0.373) and yield per hectare (0.327) at genotypic levels only. The character however, showed significant positive association with character number of seeds per fruit (215 and 212) at both phenotypic and genotypic levels. This indicates that increase in the number of ridges per fruit increases overall yield. Gupta (2013) finds same results.

4.3.8 Number of seeds per fruit:

Number of seeds per fruit observed positive and highly significant correlation with the characters length of leaf (0.589 and 0.480), width of leaf (0.935 and 0.778), yield per plant (0.705 and 0.468) and yield per hectare (0.615 and 0.415) at both phenotypic and genotypic levels and internodal distance per vine (0.245) at genotypic levels only. The character however, showed significant positive association with character internodal distance per vine (0.213) at phenotypic levels only. When the number of seeds per fruit increases the overall yield of the plant also increases.

Whereas the number of seeds per fruit showed negative and highly significant trait association with the number of fruits per plant (-0.715 and -0.639) at both phenotypic and genotypic levels. Nithinkumar et al. (2022) and Rani et al. (2015) observed that number of seeds/fruits had positive and significant correlation with yield per plant.

4.3.9 Length of leaf:

The character showed a significant and highly positive connection with width of leaf (0.676 and 0.620), yield per plant (0.457 and 0.360) and yield per hectare (0.443 and 0.343) at both phenotypic and genotypic levels. The character however, showed significant positive association with character vitamin C (0.212) at genotypic level only.

While the character made a major and profoundly negative character association with number of fruits per plant (-0.385 and -0.269) at both phenotypic and genotypic levels. Mladenović et al. (2012) find positive and highly significant correlation with leaf width in bottle gourd.

4.3.10 Width of leaf:

Width of leaf observed positive and highly significant correlation with the character yield per plant (0.788 and 0.556) at both phenotypic and genotypic levels while with vine length (0.257) and yield per hectare (0.711 0.515) at genotypic level only.

Whereas the width of leaf showed negative and highly significant trait association with the number of fruits per plant (-0.649 and -0.550) at both phenotypic and genotypic levels.

4.3.11 Vine length (cm):

The character showed a significant and highly positive connection with number of fruits per plant (0.475 and 0.571), vitamin C (0.307 and 0.273), yield per plant (0.587 and 0.603) and yield per hectare (0.593 and 0.602) at both phenotypic and genotypic levels.

While the character made a major and profoundly negative character association with the number of fruits per plant (-0.469 and -0.429) at both phenotypic and genotypic levels. Similar types of result showed by Jatav et al. (2016) and Tyagi et al. (2018a).

4.3.12 Number of fruits per plant:

Number of fruits per plant observed positive and significant correlation with the characters vitamin C (0.222) at genotypic level and yield per hectare (0.223) at phenotypic level only. Study suggested that as the number of fruits per plant increases, the yield per plant also increases.

Whereas the number of fruits per plant shows negative and highly significant trait association with the internodal distance per vine (0.343 and -0.404) at both phenotypic and genotypic levels. Dhathri et al. (2022) reported similar kind of result.

4.3.13 Internodal distance per vine (cm):

The character showed a significant and highly negative connection with vitamin C (-0.384 and -0.293) and yield per hectare (-0.206 and -0.307) at both phenotypic and genotypic levels and yield per plant (0.260) at phenotypic level only. This suggested that as the Internodal distance per vine increases the yield per plant and the yield per hectare decreases. Triveni et al. (2021) observed negative and highly significant correlation with yield per hectare.

4.3.14 Vitamin C (mg/100g):

Vitamin C showed negative and highly significant trait association with the yield per plant (0.300 and 0.268) and yield per hectare (0.327 and 0.229) at both phenotypic and genotypic levels indicating that as genotype's vitamin C content rises which yield per hectare also rises. Similar results also observed by Kumari et al. (2018) showed positive correlation with yield.

4.3.15 Yield per plant (kg):

The character showed a significant and highly positive connection with yield per hectare (0.989 and 0.973) at both phenotypic and genotypic levels indicating that as yield per plant character increases, the characteristic yield per hectare rises. Triveni et al (2021) found positive and highly significant correlation with yield per hectare.

4.3.16 Yield per hectare (t):

Yield per hectare observed positive and significant correlation with the characters average fruit weight (0.6333 and 0.514), fruit length (0.640 and 0.335), number of ridges per fruit (0.327 and 0.200), number of seeds per fruit (0.615 and 0.416), length of leaf (0.443 and 0.343), width of leaf (0.711 and 0.515), vine length (0.593 and 0.602), vitamin C (0.327 and 0.299), yield per plant (0.989 and 0.973) at both phenotypic and genotypic levels and fruit diameter (0.389) at genotypic level only. The character however, showed significant positive association with characters fruit diameter (0.233) and number of fruits per plant (0.223) at phenotypic level only.

Whereas the yield per hectare shows negative and highly significant trait association with the days to first female flowering appearance (-0.599 and -0.616), node at which first flower appear (-0.418 and -0.429), number of days to first picking (-0.649 and -0.632) and internodal distance per vine (-0.206 and -0.307) at both phenotypic and genotypic levels.

Table: 4.3 Genotypic and Phenotypic correlation coefficients between yield per plot and its component characters in bitter gourd (*Momordica charantia* L.):

		X 1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16
X1	G	1.000															
	P	1.000															
X2	G	0.250**	1.000														
	P	0.276**	1.000														
X3	G	0.998**	0.294**	1.000													
	P	0.970**	0.280**	1.000													
X4	G	-0.479**	-0.345**	-0.504**	1.000												
	P	-0.358**	-0.280**	-0.376**	1.000												
X5	G	-0.498**	-0.367**	-0.542**	0.785**	1.000											
	P	-0.215*	-0.173	-0.268**	0.720**	1.000											
X6	G	-0.116	-0.134	-0.11	0.706**	0.270**	1.000										
	P	-0.038	-0.047	-0.057	0.647**	0.322**	1.000										
X7	G	-0.308**	0.166	-0.305**	0.295**	-0.056	0.377**	1.000									
	P	-0.203*	0.089	-0.184	0.228*	0.102	0.364**	1.000									
X8	G	-0.521**	-0.400**	-0.513**	0.990**	0.646**	0.709**	0.215*	1.000								
	P	-0.327**	-0.277**	-0.316**	0.904**	0.625**	0.655**	0.212*	1.000								
X9	G	-0.518**	0.041	-0.555**	0.632**	0.594**	0.474**	0.149	0.589**	1.000							
	P	-0.392**	-0.034	-0.419**	0.553**	0.432**	0.375**	0.14	0.480**	1.000							
X10	G	-0.593**	-0.372**	-0.627**	0.946**	0.866**	0.618**	0.169	0.935**	0.676**	1.000						
	P	-0.379**	-0.288**	-0.389**	0.869**	0.706**	0.523**	0.164	0.778**	0.620**	1.000						
X11	G	-0.316**	-0.275**	-0.372**	0.085	0.255**	0.084	0.06	0.093	0.157	0.257**	1.000					
	P	-0.372**	-0.291**	-0.397**	0.012	-0.003	-0.037	-0.027	-0.053	0.106	0.149	1.000					
X12	G	0.098	0.182	0.079	-0.733**	-0.494**	-0.481**	0.003	-0.715**	-0.385**	-0.649**	0.475**	1.000				
	P	-0.141	-0.015	-0.128	-0.661**	-0.593**	-0.478**	-0.091	-0.639**	-0.269**	-0.550**	0.571**	1.000				
X13	G	-0.222*	0.326**	-0.137	0.168	-0.06	-0.048	-0.078	0.245**	0.176	0.081	-0.469**	-0.344**	1.000			
	P	0.039	0.338**	0.08	0.161	0.147	0.036	0.03	0.213*	0.088	0.082	-0.429**	-0.404**	1.000			
X14	G	-0.196*	-0.198*	-0.255**	0.089	-0.006	0.173	0.154	0.096	0.212*	0.084	0.307**	0.222*	-0.384**	1.000		
	P	-0.164	-0.162	-0.192*	0.082	-0.011	0.102	0.062	0.082	0.155	0.059	0.273**	0.171	-0.293**	1.000		
X15	G	-0.649**	-0.436**	-0.694**	0.700**	0.687**	0.459**	0.373**	0.705**	0.457**	0.778**	0.587**	-0.07	-0.121	0.300**	1.000	
	P	-0.647**	-0.463**	-0.646**	0.567**	0.339**	0.257**	0.169	0.468**	0.360**	0.556**	0.603**	0.183	-0.260**	0.268**	1.000	
X16	G	-0.599**	-0.418**	-0.652**	0.633**	0.640**	0.389**	0.327**	0.615**	0.443**	0.711**	0.593**	0.009	-0.206*	0.327**	0.989**	1.000
	P	-0.616**	-0.429**	-0.629**	0.514**	0.335**	0.233*	0.200*	0.416**	0.343**	0.515**	0.602**	0.223*	-0.307**	0.299**	0.973**	1.000

* Significant at 5% level of significance and ** significant at 1% level of significance

X1= Days to first female flowering appearance; X2= Node at which first flower appear; X3= Number of days to first picking; X4= Average fruit weight (g); X5= Fruit length (cm); X6= Fruit diameter (cm); X7= Number of ridges per fruit; X8= Number of seeds per fruit; X9= Length of leaf (cm); X10= Width of leaf (cm); X11= Vine Length (cm); X12= Number of fruits per plant; X13= Internodal distance per vine (cm); X14= Vitamin C (mg/100g); X15= Yield per plant (kg); X16=Yield per hectare (t).

4.4 Path Coefficient Analysis Studies:

The genotypic correlation coefficient of the character yield per hectare along with all of its components was partitioned into direct and indirect effects taking the character yield per plot as dependent variable. Path coefficient analysis studies were conducted in 37 genotypes of bitter melon, and the direct and indirect effects of various independent characters on the dependent character yield per plot have been tabulated in Table 4.4.

Wright (1921) was the first to introduce the path analysis concept, and Dewey and Lu (1957) employed it first. This technique proved to be highly useful in identifying various yield-contributing qualities and, as a result, proved advantageous for indirect selection.

Together, path coefficient analysis and correlation studies produce highly useful results that demonstrate their value in further enhancing crops. If a certain attribute has a stronger direct impact on the correlation between yield and that trait, then that trait is particularly essential, and the selection of that trait can directly boost yield. In contrast, if the relationship between yield and a character is mostly the result of that character's indirect influence through another trait, then indirect selection through that feature is more efficient at improving yield than direct selection. The trait yield per hectare and its components' genotypic correlation coefficients were split into two categories: direct influence and indirect effect.

4.4.1 Days to first female flowering appearance:

The character days to first female flowering appearance showed negative direct effect (-1.3718) and negative genotypic correlation (-0.599) with the dependent trait yield per hectare which suggested that the selection directly through the trait days to first female flowering appearance is effective in increasing the values of the dependent trait.

However, the negative indirect effects were showed by the characters *viz.*, yield per plant (-0.7938) followed by number of seeds per fruit (-0.5311), length of leaf (-0.1655), fruit length (-0.1403), number of ridges per fruit (-0.0398) and vitamin C (-0.0046).

Highest positive indirect effects were showed by the characters number of days to

first picking (1.6821) followed by average fruit weight (0.4662), width of leaf (0.1461), internodal distance per vine (0.0669), vine length (0.0408), fruit diameter (0.0352), node at which first flower appear (0.0090) and number of fruits per plant (0.0013). Similar finding had been reported by Khan et al. (2018) and Triveni et al. (2021) for yield per hectare.

4.4.2 Node at which first flower appear:

The character node at which first flower appear showed positive direct effect (0.0360) and negative genotypic correlation (-0.418) with the dependent trait yield per hectare which suggested that the selection indirectly through the trait node at which first flower appear is effective in increasing the values of the dependent trait. Highest positive indirect effects were shown by the characters number of days to first picking (0.4956), average fruit weight (0.3355), width of leaf (0.0917), fruit diameter (0.04062), vine length (0.0355), number of ridges per fruit (0.02146), length of leaf (0.0130) and number of fruits per plant (0.0023).

However, the negative indirect effects were shown by the characters *viz.*, Vitamin C (-0.0046), internodal distance per vine (-0.0982), fruit length (-0.10342), days to first female flowering appearance (-0.3425) and number of seeds per fruit (-0.4077) and yield per plant (-0.5334). These outcomes corroborated those found by Jatav et al. (2016).

4.4.3 Number of days to first picking:

The character number of days to first picking showed positive direct effect (1.6853) and negative genotypic correlation (-0.652) with the dependent trait yield per hectare which suggested that the selection indirectly through the trait node at which first flower appear is effective in increasing the values of the dependent trait. Positive indirect effect was observed through the independent characters like average fruit weight (0.4904), width of leaf (0.1545), vine length (0.0480), internodal distance per vine (0.0412), fruit diameter (0.0332), node at which first flower appear (0.0106) and number of fruits per plant (0.0010).

However, the negative indirect effects were showed by the characters Vitamin C (-0.0060), number of ridges per fruit (-0.0394), fruit length (-0.1527), length of leaf (-0.1775), number of seeds per fruit (-0.5225), yield per plant (-0.8491) and days to first female flowering appearance (-1.3692). These outcomes match those attained

by Jatav et al. (2016).

4.4.4 Average fruit weight:

The character average fruit weight showed negative direct effect (-0.9731) and positive genotypic correlation (0.633) with the dependent trait yield per hectare which suggested that the selection indirectly through the trait average fruit weight is ineffective in increasing the values of the dependent trait.

Positive indirect effect was observed through the independent characters like number of seeds per fruit (1.0091), yield per plant (0.8561), days to first female flowering appearance (0.6573), fruit length (0.2212), length of leaf (0.2019), number of ridges per fruit (0.0382) and vitamin C (0.0021).

However, the negative indirect effects were showed by the characters number of fruits per plant (-0.0094), vine length (-0.0109), node at which first flower appear (-0.0124), internodal distance per vine (-0.0506), fruit diameter (-0.2135), width of leaf (-0.2334) and number of days to first picking (-0.8493). Similar results were also reported by Khan et al. (2018) and Islam et al. (2009).

4.4.5 Fruit length

The character fruit length showed positive direct effect (0.2818) and positive genotypic correlation (0.640) with the dependent trait yield per hectare which suggested that the selection directly through the trait fruit length is effective in increasing the values of the dependent trait.

Positive indirect effect was observed through the independent characters like yield per plant (0.8407), days to first female flowering appearance (0.6830), number of seeds per fruit (0.6580), length of leaf (0.1900) and internodal distance per vine (0.0181).

However, the negative indirect effects were shown by the characters vitamin C (-0.0001), number of fruits per plant (-0.0064), number of ridges per fruit (-0.0073), node at which first flower appear (-0.0132), vine length (-0.0329), fruit diameter (-0.0815), width of leaf (-0.2134), average fruit weight (-0.7638) and number of days to first picking (-0.9132). Similar results were recorded by Khan et al. (2015) and Khan et al. (2018).

4.4.6 Fruit diameter:

The character fruit diameter showed negative direct effect (-0.3023) and positive genotypic correlation (0.389) with the dependent trait yield per hectare which suggested that the selection indirectly through the trait fruit diameter is ineffective in increasing the values of the dependent trait.

Positive indirect effect was observed through the independent characters like number of seeds per fruit (0.7223), yield per plant (0.5619), days to first female flowering appearance (0.1595), length of leaf (0.1514), fruit length (0.0760), number of ridges per fruit (0.0487), internodal distance per vine (0.0145) and vitamin C (0.0041).

However, the negative indirect effects were showed by the characters node at which first flower appear (-0.0048), number of fruits per plant (-0.0062), vine length (-0.0108), width of leaf (-0.1523), number of days to first picking (-0.1853) and average fruit weight (-0.6872). The outcomes were consistent with what was discovered by Tyagi et al (2018b) in bitter gourd.

4.4.7 Number of ridges per fruit:

The character number of ridges per fruit showed positive direct effect (0.1292) and positive genotypic correlation (0.327) with the dependent trait yield per hectare which suggested that the selection directly through the trait number of ridges per fruit is effective in increasing the values of the dependent trait.

Positive indirect effect was observed through the independent characters like yield per plant (0.4560), days to first female flowering appearance (0.4222), number of seeds per fruit (0.2194), length of leaf (0.0477), internodal distance per vine (0.0236), node at which first flower appear (0.0060), vitamin C (0.0036) and number of fruits per plant (0.00004).

However, the negative indirect effects were showed by the characters vine length (-0.0077), fruit length (-0.0158), width of leaf (-0.0417), fruit diameter (-0.1140), average fruit weight (-0.2875) and number of days to first picking (-0.5144).

4.4.8 Number of seeds per fruit:

The character number of seeds per fruit showed positive direct effect (1.0193) and positive genotypic correlation (0.615) with the dependent trait yield

per hectare which suggested that the selection directly through the trait number of seeds per fruit is effective in increasing the values of the dependent trait.

Positive indirect effect was observed through the independent characters like yield per plant (0.8619), days to first female flowering appearance (0.7148), length of leaf (0.1882), fruit length (0.1819), number of ridges per fruit (0.0278) and vitamin C (0.0023)

However, the negative indirect effects were showed by the characters number of fruits per plant (-0.0092), vine length (-0.0119), node at which first flower appear (-0.0144), internodal distance per vine (-0.0740), fruit diameter (-0.2142), width of leaf (-0.2305), number of days to first picking (-0.8638) and average fruit weight (-0.9634). These outcomes match those attained by Jatav et al. (2016) and Rani et al. (2015).

4.4.9 Length of leaf:

The character length of leaf showed positive direct effect (0.3196) and positive genotypic correlation (0.443) with the dependent trait yield per hectare which suggested that the selection directly through the trait length of leaf was effective in increasing the values of the dependent trait.

Positive indirect effect was observed through the independent characters like days to first female flowering appearance (0.7104), number of seeds per fruit (0.6003), yield per plant (0.5587), fruit length (0.1675), number of ridges per fruit (0.0193), vitamin C (0.0050) and node at which first flower appear (0.0015)

However, the negative indirect effects were shown by the characters number of fruits per plant (-0.0050), vine length (-0.0203), internodal distance per vine (-0.0531), fruit diameter (-0.1432), width of leaf (-0.1667), average fruit weight (-0.6147) and number of days to first picking (-0.9357).

4.4.10 Width of leaf:

The character width of leaf showed negative direct effect (-0.2466) and positive genotypic correlation (0.711) with the dependent trait yield per hectare which suggested that the selection indirectly through the trait width of leaf was ineffective in increasing the values of the dependent trait.

Positive indirect effect was observed through the independent characters like

number of seeds per fruit (0.9527), yield per plant (0.951), days to first female flowering appearance (0.8130), fruit length (0.2439), length of leaf (0.2161), number of ridges per fruit (0.0218) and vitamin C (0.0020).

However, the negative indirect effects were shown by the characters number of fruits per plant (-0.0084), node at which first flower appear (-0.0134), internodal distance per vine (-0.0244), vine length (-0.0331), fruit diameter (-0.1868), average fruit weight (-0.9209) and number of days to first picking (-1.0565).

4.4.11 Vine length:

The character vine length showed negative direct effect (-0.1289) and positive genotypic correlation (0.593) with the dependent trait yield per hectare which suggested that the selection indirectly through the trait vine length is effective in increasing the values of the dependent trait.

Positive indirect effect was observed through the independent characters yield per plant (0.7177), days to first female flowering appearance (0.4338), internodal distance per vine (0.1413), number of seeds per fruit (0.0944), fruit length (0.0719), length of leaf (0.0503), number of ridges per fruit (0.0077), vitamin C (0.0072) and number of fruits per plant (0.0061).

However, the negative indirect effects were shown by the characters node at which first flower appear (-0.0099), fruit diameter (-0.0254), width of leaf (-0.0633), average fruit weight (-0.0826) and number of days to first picking (-0.6269). Similar findings were also observed by Khan et al. (2015)

4.4.12 Number of fruits per plant:

The character number of fruits per plant showed positive direct effect (0.0129) and positive genotypic correlation (0.009) with the dependent trait yield per hectare which suggested that the selection directly through the trait number of fruits per plant effective in increasing the values of the dependent trait.

Positive indirect effect was observed through the independent characters average fruit weight (0.7135), width of leaf (0.1599), fruit diameter (0.1454), number of days to first picking (0.1340), internodal distance per vine (0.1036), node at which first flower appear (0.0066), vitamin C (0.0052) and number of ridges per fruit (0.0005).

However, the negative indirect effects were shown by the characters vine length (-0.0613), yield per plant (-0.0862), length of leaf (-0.1232), days to first female flowering appearance (-0.1340), fruit length (-0.1392), number of seeds per fruit (-0.7291). Similar findings were observed by Khan et al. (2015) and Dhathri et al (2022).

4.4.13 Internodal distance per vine

The character internodal distance per vine showed negative direct effect (-0.30136) and negative genotypic correlation (-0.206) with the dependent trait yield per hectare which suggested that the selection directly through the trait internodal distance per vine is effective in increasing the values of the dependent trait.

Positive indirect effect was observed through the independent characters days to first female flowering appearance (0.3047), number of seeds per fruit (0.2502), vine length (0.0604), length of leaf (0.0563), fruit diameter (0.0145) and node at which first flower appear (0.0117).

However, negative indirect effect was observed through the independent vitamin C (-0.0090), number of fruits per plant (-0.0044), number of ridges per fruit (-0.0101), fruit length (-0.0169), width of leaf (-0.0200), yield per plant (-0.1484), number of days to first picking (-0.1635) and number of days to first picking (-0.2304). Dhathri et al (2022) reported same kind of path in bitter gourd.

4.4.14 Vitamin C (mg/100g):

The character number of fruits per plant showed positive direct effect (0.0235) and positive genotypic correlation (0.206) with the dependent trait yield per hectare which suggested that the selection directly through the trait number of fruits per plant is effective in increasing the values of the dependent trait.

Positive indirect effect was observed through the independent characters yield per plant (0.3672), days to first female flowering appearance (0.2692), internodal distance per vine (0.1158), number of seeds per fruit (0.0982), length of leaf (0.0678), number of ridges per fruit (0.0199) and number of fruits per plant (0.0029).

However, negative indirect effect was observed through the independent traits *viz.*, fruit length (-0.0016), node at which first flower appear (-0.0071), width of leaf (-0.0208), vine length (-0.0395), fruit diameter (-0.0523), average fruit weight (-

0.0863) and number of days to first picking (-0.4300).

4.4.15 Yield per plant:

The character yield per plant showed positive direct effect (1.2229) and positive genotypic correlation (0.989) with the dependent trait yield per hectare which suggested that the selection directly through the trait yield per plant is effective in increasing the values of the dependent trait.

Positive indirect effect was observed through the independent characters days to first female flowering appearance (0.8905), number of seeds per fruit (0.7184), fruit length (0.1937), length of leaf (0.1460), number of ridges per fruit (0.0482), internodal distance per vine (0.0366) and vitamin C (0.0071).

However, negative indirect effect was observed through the independent traits *i.e.* number of fruits per plant (-0.0009), node at which first flower appear (-0.0157), vine length (-0.0757), fruit diameter (-0.1389), width of leaf (-0.1918), average fruit weight (-0.6813) and number of days to first picking (-1.1701). These outcomes match those attained by Jatav et al. (2016).

Table:4.4 Genotypic path coefficient analysis for direct and indirect effects of component characters on yield of bitter gourd (*Momordica charantia* L.) 37 genotypes

	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16
X1	-1.3718	0.0090	1.6821	0.4662	-0.1403	0.0352	-0.0398	-0.5311	-0.1655	0.1461	0.0408	0.0013	0.0669	-0.0046	-0.7938	-0.599**
X2	-0.3425	0.0360	0.4956	0.3355	-0.1034	0.0406	0.0215	-0.4077	0.0130	0.0917	0.0355	0.0023	-0.0982	-0.0047	-0.5334	-0.418**
X3	-1.3692	0.0106	1.6853	0.4904	-0.1527	0.0332	-0.0394	-0.5225	-0.1775	0.1546	0.0480	0.0010	0.0412	-0.0060	-0.8491	-0.652**
X4	0.6573	-0.0124	-0.8494	-0.9731	0.2212	-0.2135	0.0382	1.0091	0.2019	-0.2334	-0.0109	-0.0094	-0.0506	0.0021	0.8561	0.633**
X5	0.6830	-0.0132	-0.9132	-0.7638	0.2818	-0.0815	-0.0073	0.6580	0.1900	-0.2134	-0.0329	-0.0064	0.0181	-0.0001	0.8407	0.640**
X6	0.1595	-0.0048	-0.1853	-0.6872	0.0760	-0.3023	0.0487	0.7223	0.1514	-0.1523	-0.0108	-0.0062	0.0145	0.0041	0.5619	0.389**
X7	0.4222	0.0060	-0.5144	-0.2875	-0.0158	-0.1140	0.1292	0.2194	0.0477	-0.0417	-0.0077	0.0000	0.0236	0.0036	0.4560	0.327**
X8	0.7148	-0.0144	-0.8638	-0.9634	0.1819	-0.2142	0.0278	1.0193	0.1882	-0.2305	-0.0119	-0.0092	-0.0740	0.0023	0.8619	0.615**
X9	0.7104	0.0015	-0.9357	-0.6148	0.1675	-0.1432	0.0193	0.6003	0.3196	-0.1667	-0.0203	-0.0050	-0.0531	0.0050	0.5587	0.443**
X10	0.8130	-0.0134	-1.0565	-0.9209	0.2439	-0.1868	0.0218	0.9527	0.2161	-0.2466	-0.0331	-0.0084	-0.0244	0.0020	0.9513	0.711**
X11	0.4338	-0.0099	-0.6269	-0.0826	0.0719	-0.0254	0.0077	0.0944	0.0503	-0.0633	-0.1289	0.0061	0.1413	0.0072	0.7177	0.593**
X12	-0.1340	0.0066	0.1340	0.7135	-0.1392	0.1454	0.0005	-0.7291	-0.1232	0.1599	-0.0613	0.0129	0.1036	0.0052	-0.0862	0.009
X13	0.3047	0.0117	-0.2304	-0.1635	-0.0169	0.0145	-0.0101	0.2502	0.0563	-0.0200	0.0604	-0.0044	-0.3014	-0.0090	-0.1484	-0.206*
X14	0.2692	-0.0071	-0.4300	-0.0863	-0.0016	-0.0523	0.0199	0.0982	0.0678	-0.0208	-0.0395	0.0029	0.1158	0.0235	0.3672	0.327**
X15	0.8905	-0.0157	-1.1701	-0.6813	0.1937	-0.1389	0.0482	0.7184	0.1460	-0.1918	-0.0757	-0.0009	0.0366	0.0071	1.2229	0.989**

Residual are 0.00702 * Significant at 5% level of significance and ** significant at 1% level of significance

X1= Days to first female flowering appearance; X2= Node at which first flower appear; X3= Number of days to first picking; X4= Average fruit weight (g); X5= Fruit length (cm); X6= Fruit diameter (cm); X7= Number of ridges per fruit; X8= Number of seeds per fruit; X9= Length of leaf (cm); X10= Width of leaf (cm); X11= Vine Length (cm); X12= Number of fruits per plant; X13= Internodal distance per vine (cm); X14= Vitamin C (mg/100g); X15= Yield per plant (kg); X16= Genotypic correlation with yield per hectare (t).

4.5 Genetic divergence:

Based on the effectiveness of particular features, Table 4.5 describes the pattern of clustering for 37 different genotypes of bitter gourd. All genotypes had been grouped into six clusters. The cluster III (9) has the highest number of genotypes grouped and the other five clusters contained rest 28 genotypes. Similarly, 33 diverse genotypes of bitter gourd were grouped into five clusters by Ankitha et al. (2023). Angadi and Mulge (2018) also placed 55 genotypes into ten clusters while; Khan et al. (2015) grouped 17 genotypes of bitter gourd into four clusters. Chandrashekhar et al. (2020) grouped 15 genotypes of bitter gourd in four clusters. The genotypes from one source of origin grouped with those from the other. The lack of a correlation between regional dispersion and genetic diversity was demonstrated by this. Angadi and Mulge (2018) and Singh et al. (2013) also found the similar trend.

Table:4.5 Bitter gourd 37 genotypes clustering pattern on the basis of genetic divergence

Number of Cluster	No. of Genotypes	Which Genotypes
I	4	TCR-85 (IC- 68232), 20, TCR-369 (IC- 505635), Hirkani
II	8	TCR-125 (IC- 68272), TCR-128 (IC- 68275), TCR-162 (IC- 68309), TCR-163 (IC- 68310), TCR-167 (IC- 68314), TCR-188 (IC- 68335), TCR-345 (IC- 505623), TCR-356 (IC- 505621)
III	9	TCR-147 (IC- 68294), TCR-249 (IC- 85633), TCR-251 (IC- 85635), TCR-252 (IC- 85638), TCR-271 (IC- 85647), TCR-276 A (IC- 85649 A), TCR-332 (IC- 505639), TCR-333 (IC- 470535), TCR-334 (IC- 505629)
IV	6	TCR-239 (IC- 85626), TCR-289 (IC- 65972), TCR-349 (IC- 505626), TCR-362 (IC- 470555), Phule Green Gold, Solan Hara
V	4	TCR-242 (IC- 85628), TCR-257 (IC- 113875), TCR-331 (IC-505638), TCR-336 (IC- 505637)
VI	6	TCR-250 (IC- 86634), TCR-344 (IC- 505640), TCR-298 (IC- 85650), TCR-337 (IC- 113876), TCR-361 (IC- 470554), TCR-364 (IC- 505632)

Community constellation of bitter gourd genotypes was also observed by genetic divergence by Khan et al (2015). Similarly, 33 diverse genotypes of bitter gourd

were grouped into five clusters by Ankitha et al. (2023). Fifteen diverse genotypes of bitter gourd were grouped into four different clusters by Chandrashekhar et al. (2020). Singh and Kandasamy (2020) grouped 40 genotypes of bitter gourd into six clusters. Angadi and Mulge (2018) studied 55 genotypes of bitter gourd for 19 quantitative characters and grouped them into ten clusters using Mahalanobis D^2 statistics.

Table: 4.5.1 Clustering pattern of 37 genotypes of bitter gourd based on genetic divergence

Cluster	I	II	III	IV	V	VI
I	6.82					
II	8.33	5.82				
III	10.11	7.29	7.63			
IV	8.60	7.43	6.73	6.44		
V	6.29	6.43	9.11	7.68	5.81	
VI	6.40	7.22	8.79	8.16	7.16	6.15

Average values for inter-cluster and intra-cluster divergence (D^2) are presented in Table 4.5.1. The diagonal figures in the table showed the distances of the intra-cluster. The distance for the intra-cluster was the highest in cluster III (7.63) and the lowest in cluster V (5.81). The highest inter-cluster distance was reported between cluster III and cluster I (10.11); while the lowest (6.29) was observed among cluster V and cluster I. Similarly, maximum inter-cluster distance was observed by Khan et al. (2015) and Ankitha et al. (2023).

The cluster values of different genotypes of bitter gourd are listed in Table 4.5.2 for different horticultural traits. The minimum number of days to first female flowering appearance was recorded in the cluster III (53.33) followed by cluster II (55.78), cluster VI (57.10), cluster IV (57.53), cluster I (59.00) and cluster V (59.10). The minimum node at which first flower appear was recorded in the cluster III (11.75) followed by cluster II (13.06), cluster VI (13.24), cluster IV (13.26), cluster I (13.67) and cluster V (14.58). The minimum number of days to first picking was recorded in the cluster III (65.00) followed by cluster II (67.56), cluster VI (69.05), cluster IV (69.40), cluster I (70.96) and cluster V (71.03). The maximum average

fruit weight was recorded in the cluster VI (81.80) followed by cluster III (79.25), cluster II (67.93), cluster I (48.41), cluster IV (47.61) and cluster V (42.11). The maximum fruit length was found in the cluster III (19.26), cluster II (16.62), cluster VI (15.49), cluster I (13.55), cluster IV (12.04), cluster V (12.03). The highest fruit diameter was found in the cluster VI (4.06) followed by cluster III (3.77), cluster II (3.60), cluster IV (3.30), cluster V (3.17) and cluster I (3.16). The highest number of ridges per fruit was recorded in the cluster VI (8.83) followed by cluster III (8.72), cluster IV (8.70), cluster II (8.65), cluster V (8.64) and cluster I (8.45). The maximum number of seeds per fruit was reported in the cluster VI (34.45) followed by cluster III (32.97), cluster II (30.76), cluster I (21.27), cluster V (19.06) and cluster IV (18.30). The maximum length of leaf was reported in the cluster II (8.78) followed by cluster II (8.68), cluster VI (8.52), cluster I (6.70), cluster IV (6.54) and cluster V (6.31). The maximum width of leaf was found in the cluster III (13.27) followed by cluster II (12.73), cluster VI (12.05), cluster I (8.90), cluster IV (8.54) and cluster V (7.82). The maximum vine length was observed in the cluster III (415.63) followed by cluster II (405.44), cluster IV (388.62), cluster V (379.53), cluster VI (355.58) and cluster I (341.01). The highest number of fruits per plant was found in the cluster IV (21.50) followed by cluster V (20.42), cluster II (16.74), cluster I (15.15), cluster III (15.15) and cluster VI (12.50). The minimum Internodal distance per vine was recorded in the cluster IV (8.55) followed by cluster III (8.57), cluster II (9.00), cluster V (9.45), cluster I (9.79) and cluster VI (9.97). The maximum vitamin C was reported in the cluster III (131.23) followed by cluster IV (127.55), cluster VI (83.50), cluster II (80.72), cluster I (71.65) and cluster V (69.78). The highest yield per plant was found in the cluster III (1.20) followed by cluster II (1.09), cluster IV (0.99), cluster VI (0.97), cluster V (0.85) and cluster I (0.72). The maximum yield per hectare was found in the cluster III (21.23) followed by cluster II (19.41), cluster IV (17.95), cluster VI (17.34), cluster V (15.45) and cluster I (12.89). Similar results were also reported by Ankitha et al. (2023), Chandrashekhar et al. (2020), Singh et al. (2013), Singh et al. (2014) and Kutty and Dharmatti (2005).

Table:4.5.2 Cluster means for various traits among 37 genotypes of bitter gourd

Traits	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Days to first female flowering appearance	59.00	55.78	53.33	57.53	59.10	57.10
Node at which first flower appear	13.67	13.06	11.75	13.26	14.58	13.24
Number of days to first picking	70.96	67.56	65.00	69.40	71.03	69.05
Average fruit weight (g)	48.14	67.93	79.25	47.61	42.11	81.10
Fruit length (cm)	13.55	16.62	19.26	12.04	12.03	15.49
Fruit diameter (cm)	3.16	3.60	3.77	3.30	3.17	4.06
Number of ridges per fruit	8.45	8.65	8.72	8.70	8.64	8.83
Number of seed per fruit	21.27	30.76	32.97	18.30	19.06	34.45
Length of leaf (cm)	6.70	8.78	8.68	6.54	6.31	8.52
Width of leaf (cm)	8.90	12.73	13.27	8.54	7.82	12.05
Vine Length (cm)	341.01	405.44	415.63	388.62	379.53	355.58
Number of fruits per plant	15.15	16.74	15.15	21.50	20.42	12.50
Internodal distance per vine (cm)	9.79	9.00	8.57	8.55	9.45	9.97
Vitamin C (mg/100g)	71.65	80.72	131.23	127.55	69.78	83.50
Yield per plant (kg)	0.72	1.09	1.20	0.99	0.85	0.97
Yield per hectare (t)	12.89	19.41	21.23	17.95	15.45	17.34



Plate 2(a): Variability in Bitter melon (*Momordica charantia* L.) Genotypes



Hirkani



TCR-332 (IC- 505639)



Phule Green Gold



TCR-356 (IC- 505621)



TCR-349 (IC- 505626)



TCR-162 (IC- 68309)



TCR-298 (IC- 85650)



TCR-163 (IC- 68310)



TCR-362 (IC- 470555)



TCR-250 (IC- 86634)



TCR-336 (IC- 505637)



TCR-257 (IC- 113875)



TCR-128 (IC- 68275)



TCR-290 (IC- 66023)



TCR-252 (IC- 85638)



Solan Hara

Plate 2(b): Variability in Bitter gourd (*Momordica charantia* L.) Genotypes

The page features decorative illustrations of leaves in the corners. The top-left and bottom-right corners show light brown leaves with dark brown veins. The top-right and bottom-left corners show darker brown leaves with white speckles and dark brown veins. The central text is in a bold, italicized, brown font.

***SUMMARY
AND
CONCLUSION***

Chapter-5

SUMMARY AND CONCLUSION

The current research entitled “**Genetic evaluation of Bitter gourd (*Momordica charantia* L.) genotypes for yield and quality traits under low hill conditions of Himachal Pradesh.**” was conducted at the RHR&TS, Jachh, Kangra, Dr. Y.S Parmar University of Horticulture and Forestry, Nauni, Solan, Himachal Pradesh during 2022. During the course of studies, 37 different bitter gourd genotypes consisting of 36 lines along with one check were assessed.

The traits investigated during germplasm assessment were days to first female flowering appearance, node at which first female flower appear, number of days to first picking, average fruit weight, fruit length, fruit diameter, number of ridges per fruit, number of seeds per fruit, length of leaf, width of leaf, vine length, number of fruits per plant, internodal distance per vine, vitamin C, yield per plant and yield per hectare.

MEAN PERFORMANCE

All horticultural and quality traits have enough genetic variability, according to the analysis of variance. The genotype TCR-349 (IC- 505626) (55.33) observed minimum days to first female flowering appearance followed by TCR-361 (IC- 470554) (53.67), TCR-239 (IC- 85626) (54.00), TCR-289 (IC- 65972) (54.00) and TCR-362 (IC- 470555) (54.67).

The genotype TCR-188 (IC- 68335) (11.33) has lowest number node at which first female flower appear followed by TCR-128 (IC- 68275) (11.65), TCR-345 (IC- 505623) (11.70), TCR-349 (IC- 505626) (11.75), TCR-362 (IC- 470555) (11.95) and TCR-239 (IC- 85626) (12.10). TCR-349 (IC- 505626) (65.00 days) genotype has minimum number of days to first picking followed by TCR-239 (IC- 85626) (65.67 days), TCR-361 (IC- 470554) (66.33 days), TCR-362 (IC- 470555) (66.33 days) and TCR-276 A (IC- 85649 A) (67.00 days).

Whereas the genotype TCR-362 (IC- 470555) (95.47g) has maximum average fruit weight followed by TCR-364 (IC- 505632) (94.87g), TCR-361 (IC- 470554) (92.90g), Phule Green Gold (81.15g) and TCR-349 (IC- 505626) (79.25g).

The genotype Phule Green Gold (20.27cm) has maximum fruit length followed by Solan Hara (20.20 cm), TCR-349 (IC- 505626) (19.26 cm), Hirkani (18.22 cm), TCR-361 (IC- 470554) (17.83 cm) and the genotype TCR-364 (IC- 505632) (4.85 cm) has maximum fruit width followed by TCR-250 (IC- 86634) (4.79 cm), TCR-362 (IC- 470555) (4.30cm), TCR-361 (IC- 470554) (4.27cm) and Phule Green Gold (3.91cm).

The highest number of ridges per fruit in the genotype TCR-361 (IC- 470554) (9.40) followed by TCR-364 (IC- 505632) (9.39), TCR-298 (IC- 85650) (9.38), TCR-331 (IC-505638) (9.35), TCR-250 (IC- 86634) (9.29) and maximum number of seeds per fruit in the genotype TCR-362 (IC- 470555) (41.43) followed by TCR-364 (IC- 505632) (40.73), TCR-361 (IC- 470554) (37.30), Phule Green Gold (33.50) and TCR-349 (IC- 505626) (32.97).

TCR-364 (IC- 505632) (9.85 cm) has maximum length of leaf followed by TCR-362 (IC- 470555) (9.70 cm), Phule Green Gold (9.62 cm), TCR-344 (IC- 505640) (9.40 cm), TCR-239 (IC- 85626) (9.37 cm) and TCR-362 (IC- 470555) (14.01 cm) has maximum width of leaf followed by TCR-289 (IC- 65972) (13.90 cm), Phule Green Gold (13.71 cm), TCR-239 (IC- 85626) (13.39 cm) and TCR-364 (IC- 505632) (13.38 cm).

The genotype TCR-289 (IC- 65972) (419.90 cm) has longest vine length followed by TCR-337 (IC- 113876) (382.60 cm), TCR-163 (IC- 68310) (383.53 cm), TCR-249 (IC- 85633) (386.63 cm) and TCR-336 (IC- 505637) (387.00 cm) and the genotype TCR-276 A (IC- 85649 A) (25.52) has maximum number of fruits per plant followed by TCR-334 (IC- 505629) (24.52), TCR-147 (IC- 68294) (22.29), TCR-332 (IC- 505639) (21.72) and TCR-162 (IC- 68309) (20.84).

The minimum internodal distance per vine in the genotype TCR-249 (IC- 85633) (7.48 cm) followed by TCR-249 (IC- 85633) (7.48 cm), TCR-147 (IC- 68294) (7.67 cm), Solan Hara (8.26 cm), TCR-239 (IC- 85626) (8.33 cm) and the maximum vitamin C content in the genotype TCR-249 (IC- 85633) (136.19) followed by TCR-276 A (IC- 85649 A) (135.01), TCR-147 (IC- 68294) (133.01), TCR-349 (IC- 505626) (131.23) and TCR-345 (IC- 505623) (127.43).

The yield per plant highest in the genotype TCR-349 (IC- 505626) (1.20 kg) followed by TCR-289 (IC- 65972) (1.14 kg), Phule Green Gold (1.11 kg), TCR-239 (IC- 85626) (1.10 kg), TCR-298 (IC- 85650) (1.09 kg) and highest yield per hectare in the genotype TCR-349 (IC- 505626) (21.23 ton), Phule Green Gold

(20.78 ton), TCR-239 (IC- 85626) (20.26 ton), TCR-289 (IC- 65972) (20.18 ton) and Solan Hara (18.72 ton).

The least incidence of bitter gourd fruit fly has been recorded in the genotype Phule Green Gold (4.79%), Hirkani (5.52%), Solan Hara TCR-250 (5.95%), TCR-250 (IC- 86634) (7.69%) and TCR-369 (IC- 505635) (7.41%).

High magnitude of phenotypic coefficients of variation were seen in traits average fruit weight (32.14%) and number of seeds per fruit (30.83%). High magnitude of genotypic coefficients of variation were seen in trait average fruit weight (31.50%). Most of the traits showed a slight difference between the phenotypic coefficient of variation and the genotypic coefficient of variation, suggesting that environmental factors had minimal influence.

VARIABILITY OF PARAMETERS

For the character, the highest heritability value and highest genetic advance as per cent mean were noted in average fruit weight (96.03% and 63.58%) and vitamin C (86.80% and 51.32%) depict that most likely the heritability for these traits is due to additive gene effects. Therefore, phenotypic selection for these features can lead to improvement. A high heritability and a moderate rate of genetic advance as % mean was observed in width of leaf (82.04% 43.52%) which may be contribution of additive and non-additive gene effects.

Table: 5.1 Top five promising genotypes for different characters studied in bitter gourd (*Momordica charantia* L.)

Parameters	Genotypes
Days to first female flowering appearance	TCR-349 (IC- 505626), TCR-361 (IC- 470554), TCR-239 (IC- 85626), TCR-289 (IC- 65972), TCR-362 (IC- 470555)
Node at which first flower appear	TCR-188 (IC- 68335), TCR-128 (IC- 68275), TCR-345 (IC- 505623), TCR-349 (IC- 505626), TCR-362 (IC- 470555), TCR-239 (IC- 85626)
Number of days to first picking	TCR-349 (IC- 505626), TCR-239 (IC- 85626), TCR-361 (IC- 470554), TCR-362 (IC- 470555), TCR-276 A (IC- 85649 A)
Average fruit weight (g)	TCR-362 (IC- 470555), TCR-364 (IC- 505632), TCR-361 (IC- 470554), Phule Green Gold, TCR-349 (IC- 505626)
Fruit length (cm)	Phule Green Gold, Solan Hara, TCR-349 (IC- 505626), Hirkani, TCR-361 (IC- 470554)
Fruit diameter (cm)	TCR-364 (IC- 505632), TCR-250 (IC- 86634), TCR-362 (IC- 470555), TCR-361 (IC- 470554), Phule Green Gold
Number of ridges per fruit	TCR-361 (IC- 470554), TCR-364 (IC- 505632), TCR-298 (IC- 85650), TCR-331 (IC-505638) and TCR-250 (IC- 86634)
Number of seeds per fruit	TCR-362 (IC- 470555), TCR-364 (IC- 505632), TCR-361 (IC- 470554), Phule Green Gold, TCR-349 (IC- 505626)
Length of leaf (cm)	TCR-364 (IC- 505632), TCR-362 (IC- 470555), Phule Green Gold, TCR-344 (IC- 505640), TCR-239 (IC- 85626)
Width of leaf (cm)	TCR-362 (IC- 470555), TCR-289 (IC- 65972), Phule Green Gol, TCR-239 (IC- 85626), TCR-364 (IC- 505632)

TABLE 5.1 (Continued....) Top five promising genotypes for different characters studied in bitter gourd (*Momordica charantia* L.)

Vine Length (cm)	TCR-289 (IC- 65972), TCR-337 (IC- 113876), TCR-163 (IC- 68310), TCR-249 (IC- 85633) and TCR-336 (IC- 505637)
Number of fruits per plant	TCR-276 A (IC- 85649 A), TCR-334 (IC- 505629), TCR-147 (IC- 68294), TCR-332 (IC- 505639), TCR-162 (IC- 68309)
Internodal distance per vine (cm)	TCR-249 (IC- 85633), TCR-249 (IC- 85633), TCR-147 (IC- 68294), Solan Hara, TCR-239 (IC- 85626)
Vitamin C (mg/100g)	TCR-249 (IC- 85633), TCR-276 A (IC- 85649 A), TCR-147 (IC- 68294), TCR-349 (IC- 505626), TCR-345 (IC- 505623)
Yield per plant (kg)	TCR-349 (IC- 505626), TCR-289 (IC- 65972), Phule Green Gold, TCR-239 (IC- 85626), TCR-298 (IC- 85650)
Yield per hectare (t)	TCR-349 (IC- 505626), Phule Green Gold, TCR-239 (IC- 85626), TCR-289 (IC- 65972), Solan Hara
Incidence of insect pest and disease (Bitter gourd fruit fly)	Phule Green Gold, Hirkani, Solan Hara, TCR-349 (IC- 505626), TCR-369 (IC- 505635)

CORRELATION STUDIES

Yield per hectare had significant and positive correlation at both genotypic and phenotypic levels with yield per plant (0.989 and 0.973), width of leaf (711 and 515), average fruit weight (0.633 and 0.514), number of seeds per fruit (0.615 and 0.416), fruit length (0.640 and 0.335), vine length (0.593 and 0.602), length of leaf (0.443 and 0.343), fruit diameter (0.389 and 0.233), number of ridges per fruit (0.327 and 0.200) and vitamin C (0.327 and 0.299). Selection of individuals based on these attributes can increase production per hectare because there is a strong genetic association between these particular characteristics and yield per hectare.

PATH COEFFICIENT ANALYSIS

The genotypic path coefficient study showed that the greatest positive direct effect on yield per hectare was seen by yield per plant (1.2229), number of seeds per fruit (1.0913), leaf length (0.3196), fruit length (0.2818), number of ridges per fruit (0.1292) and vitamin C (0.0235).

GENETIC DIVERGENCE

In the present study, a total of 37 bitter gourd genotypes were divided into six clusters, with cluster III containing the greatest number of genotypes. The six clusters demonstrated that genetic variation was unrelated to geographic variety. While cluster V had the smallest intra-cluster distance, cluster III had the highest intra-cluster distance.

The maximum inter-cluster distance was observed between cluster III and cluster I. Whereas, the minimum inter-cluster distance between cluster V with cluster I demonstrates how these genotypes can be crossed and utilized to segregate generations in this crop in order to produce the best recombinants or transgressive segregants. Furthermore, based on cluster mean cluster II was better for length of leaf and yield per plant. While cluster III was found better for days to first female flowering appearance, node at which first female flower appear, number of days to first picking, fruit length, width of leaf, vine length, vitamin C, yield per hectare and cluster IV was observed good for number of fruits per plant and internodal distance per vine, although cluster VI was found better for average fruit weight, fruit diameter, number of ridges per fruit and number of seeds per fruit.

CONCLUSION

- High magnitude of genotypic and phenotypic coefficients of variation were observed in traits like average fruit weight and number of seeds per fruit.
- The horticultural traits, specifically the average fruit weight, exhibited considerable variability along with high heritability and genetic advance. Moreover, the vitamin C content demonstrated both high heritability and genetic advance.
- Positive and significant correlation coefficients were observed between yield per hectare and various traits at both genotypic and phenotypic levels. These traits included average fruit weight, fruit length, fruit diameter, number of ridges per fruit, number of seeds per fruit, leaf length, width of leaf, vine length, vitamin C content, yield per plant and the number of fruits per plant at the phenotypic level.
- Based on the path coefficient analysis at the genotypic level, it was found that the most significant positive direct effect on yield per hectare was exerted by yield per plant. This was followed by the number of seeds per fruit, leaf length, fruit length, number of ridges per fruit and vitamin C content.
- In terms of overall performance, the genotypes TCR-349 (IC-505626), Hirkani, TCR-239 (IC-85626) and TCR-289 (IC-65972) were identified as superior due to their higher yield per hectare and significantly superior performance in other important traits.
- Cluster III exhibited the highest intra-cluster distance indicating significant dissimilarity within the cluster. Conversely, cluster V had the minimum intra-cluster distance suggesting a higher degree of similarity within that cluster. The largest inter-cluster distance was observed between cluster III and cluster I, reflecting substantial dissimilarity between these clusters. In contrast, the minimum inter-cluster distance was observed between cluster V and cluster I indicating a relatively lower dissimilarity between these clusters.

The page features decorative illustrations of brown leaves with white speckles in the corners. The top-left and bottom-right corners have partial leaf clusters, while the top-right and bottom-left corners have more complete clusters. The central text is set against a white background with rounded corners.

LITERATURE CITED

LITERATURE CITED

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The page features decorative illustrations of leaves in the corners. The top-left and bottom-right corners have light brown leaves, while the top-right and bottom-left corners have darker brown leaves with white speckles. The central text is in a bold, italicized, brown font.

APPENDICES

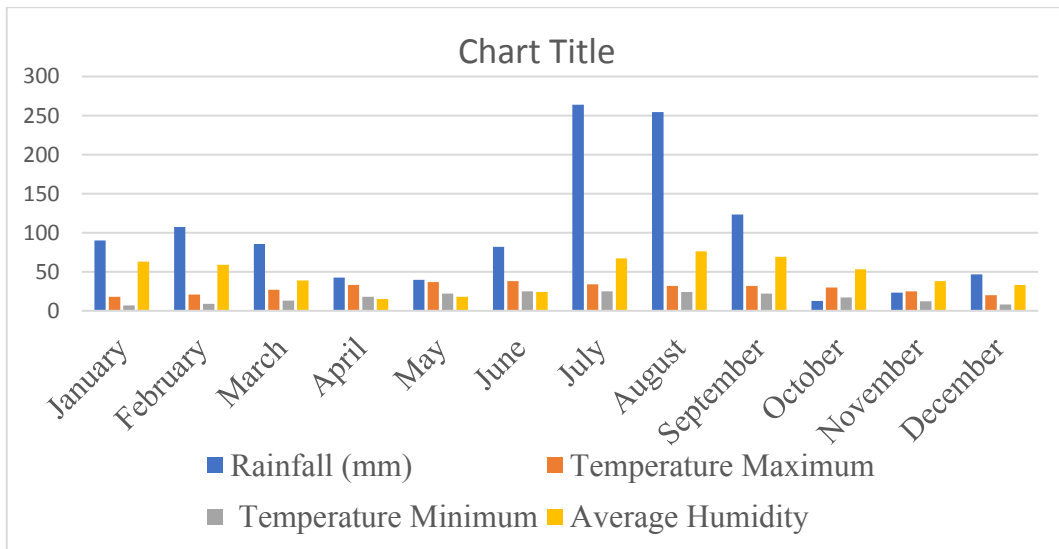
APPENDIX-I

Analysis of variance for various horticultural traits in bitter gourd.

Characters	Mean sum of squares		
	Replication	Genotype	Error
	2 (Degree of freedom)	36 (Degree of freedom)	72 (Degree of freedom)
Days to first female flowering appearance	1.523	29.914	3.782
Node at which first flower appear	0.786	5.201	0.423
Number of days to first picking	3.000	26.287	3.361
Average fruit weight (g)	3.273	970.680	13.194
Fruit length (cm)	0.651	26.426	3.606
Fruit diameter (cm)	0.087	0.988	0.094
Number of ridges per fruit	0.553	0.668	0.192
Number of seed per fruit	0.016	144.287	13.725
Length of leaf (cm)	0.315	6.945	0.669
Width of leaf (cm)	0.164	17.152	1.167
Vine Length (cm)	31.174	2183.103	169.041
Number of fruits per plant	0.382	41.501	7.127
Internodal distance per vine (cm)	0.433	3.377	0.875
Vitamin C (mg/100g)	8.093	1590.748	76.731
Yield per plant (kg)	0.007	0.107	0.010
Yield per hectare (t)	4.049	33.902	2.754

WEATHER DATA

Months	Rainfall (mm)	Temperature		Average Humidity
		Maximum	Minimum	
January	89.9	18	7	63
February	107.2	21	9	59
March	85.7	27	13	39
April	42.5	33	18	15
May	39.8	37	22	18
June	81.8	38	25	24
July	264.1	34	25	67
August	254.6	32	24	76
September	123.2	32	22	69
October	12.6	30	17	53
November	23.3	25	12	38
December	46.6	20	8	33



Source: <https://www.worldweatheronline.com/kangra-weather-averages/himachal-pradesh/in.aspx>.

The page features decorative illustrations of brown leaves with white speckles in the corners. The top-left and bottom-right corners have partial leaf branches, while the bottom-left corner has a more complete branch with several leaves. The central text is set against a white background with rounded corners.

ABSTRACT

**Department of Vegetable Science
College of Horticulture and Forestry, Neri
Dr. Yashwant Singh Parmar University of Horticulture and Forestry
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Title of Thesis : **“Genetic evaluation of bitter gourd (*Momordica charantia* L.) genotypes for yield and quality traits under low hill conditions of Himachal Pradesh.”**

Name of student : Varun Rana
Admission number : NH-2021-47-M
Major advisor : Dr. Dharminder Kumar
Major field : Vegetable Science
Minor field : i. Genetics and Plant Breeding
ii. Entomology

Date of Thesis submission :
No. of pages in thesis : 106 + ii
No. of words in Abstract : 366

Abstract

The present investigation entitled **“Genetic evaluation of bitter gourd (*Momordica charantia* L.) genotypes for yield and quality traits under low hill conditions of Himachal Pradesh”** was conducted at the experimental farm of RHR&TS, Jachh, Kangra, Dr. YS Parmar University of Horticulture and Forestry, Nauni, Solan, Himachal Pradesh during the summer season 2022-2023. Thirty-seven diverse genotypes of bitter gourd lines along with a check Solan Hara were evaluated in Randomized Complete Block Design with three replications to estimate the extent of genetic variability, heritability, correlation and path coefficient analysis for yield and other horticultural traits along with the estimation of genetic divergence among the genotypes. Significant variations were observed among all the genotypes for all the studied characteristics, as indicated by the analysis of variance. Based on overall performance, TCR-349 (IC- 505626), Hirkani, TCR-239 (IC- 85626) and TCR-289 (IC- 65972) were found superior for yield per hectare and other important horticultural traits. The prospect of incorporating them into future breeding programs is encouraging, given their potential as valuable parents. The estimates of PCV and GCV were high for traits like average fruit weight and number of seeds per fruit. High heritability estimates were recorded for the traits like average fruit weight, width of leaf and vitamin C content. The correlation studies revealed that yield per hectare had positive and significant correlation with average fruit weight, fruit length, fruit diameter, number of ridges per fruit, number of seeds per fruit, leaf length, width of leaf, vine length, vitamin C content, yield per plant both at genotypic and phenotypic level and the number of fruits per plant at the phenotypic level. The path coefficient analysis revealed the most significant positive direct effect on yield per hectare was exerted by yield per plant. This was followed by the number of seeds per fruit, leaf length, fruit length, number of ridges per fruit and vitamin C content. Under genetic divergence studies, 37 genotypes were grouped into six clusters and the highest intra-cluster distance was in cluster III while, the minimum intra-cluster distance was present in cluster V. The maximum inter-cluster distance was observed between cluster III and cluster I. Whereas, the minimum inter-cluster distance between cluster V with cluster I.

**Signature of Major Advisor
Dr. Dharminder Kumar
Dated:**

**Signature of the Student
Varun Rana
Dated:**

Countersigned

**Professor and Head
Department of Vegetable Science
College of Horticulture and Forestry, Neri Hamirpur**

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Academic Qualification:

Examination Passed	Month and Year	School	University/ Board	Percentage (%) or OGPA	Division
Matriculation	2015	HP BOSE	84.2%	First	2015
10+2	2017	HP BOSE	85.4%	First	2017
Graduation	2021	Dr. YS Parmar University of Horticulture and Forestry, Nauni, Solan, (H.P.)	78.90%	First	2021

Whether sponsored by some state/Central Govt./Univ./SAARC : No

Scholarship/ Stipend/ Fellowship, any other financial assistance received during the study period : University Stipend

Place: Neri, Hamirpur
Date:

(Varun Rana)

