

**VARIABILITY, CHARACTER ASSOCIATION AND
DIVERSITY ANALYSIS IN CHILLI
(*Capsicum annum* L.) GENOTYPES**

A Thesis

Submitted to

Uttar Banga Krishi Viswavidyalaya

In partial fulfillment of the requirements for the award of the Degree of

MASTER OF SCIENCE (HORTICULTURE)

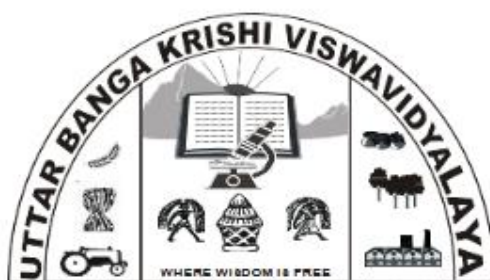
In

VEGETABLE SCIENCE

By

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(H-2021-031-M)



DEPARTMENT OF VEGETABLE AND SPICE CROPS

FACULTY OF HORTICULTURE

UTTAR BANGA KRISHI VISWAVIDYALAYA

PUNDIBARI-736165, COOCH BEHAR, WEST BENGAL

2023



*Dedicated to my
parents S.Raja Sekhar
& M.Vandana*

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CERTIFICATE - I

This is to certify that the work recorded in the thesis entitled, **Variability, character association and diversity analysis in chilli (*Capsicum annuum* L.) genotypes**, submitted by **SURA VENKATA VAISHNAVI (Reg. No. H- 2021-031-M)** in partial fulfillment of the requirements for the degree of **M.Sc. (Horticulture) in Vegetable Science** of the Uttar Banga Krishi Viswavidyalaya, Pundibari, is the faithful and bonafide research work carried out under my personal supervision and guidance. The results of the study reported in the thesis have not so far been submitted for any other degree or diploma. The assistance and help received from various sources during the course of investigation have been duly acknowledged.

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Certified that the thesis entitled, **Variability, character association and diversity analysis in chilli (*Capsicum annuum* L.) genotypes**, submitted by **SURA VENKATA VAISHNAVI (Reg. No. H-2021-031-M)** towards partial fulfillment of the requirements for the award of Master Degree from the Department of Vegetable Science under Uttar Banga Krishi Viswavidyalaya has been checked against plagiarism through **URKUND** Software on 16th August 2023 and that the similarity index has been achieved as **4 %** which is below the maximum tolerable range as per stipulation of this Viswavidyalaya. The thesis of **Ms. SURA VENKATA VAISHNAVI** may be accepted for the award of the Master Degree in Department of Vegetable and Spice Crops of Uttar Banga Krishi Viswavidyalaya.

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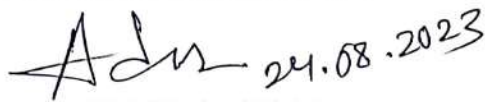
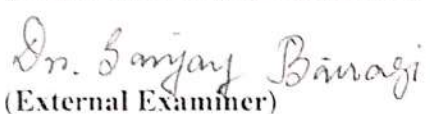
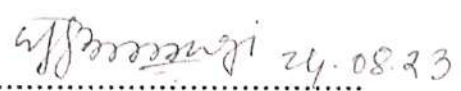
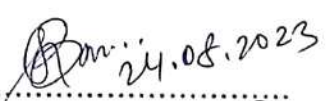
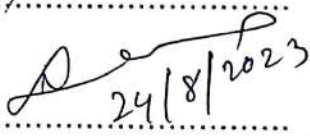
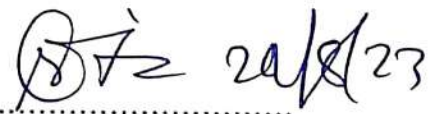
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**APPROVAL OF EXAMINERS FOR THE AWARD OF THE DEGREE OF
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We, the undersigned, having been satisfied with the performance of Ms. SURA VENKATA VAISHNAVI (Reg. No. H-2021-031-M), in the viva-voce examination of the thesis, conducted today, 24th August 2023, recommended that the thesis would be accepted for the award of the degree of Master of Science (Horticulture) in Vegetable Science.

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ABSTRACT

Title of Thesis	:	Variability, character association and diversity analysis in Chilli (<i>Capsicum annuum</i> L.) genotypes.
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An experiment was conducted at Instructional farm, Department of Vegetable and Spice Crops, Faculty of Horticulture, Uttar Banga Krishi Viswavidyalaya during winter season of 2021-22 for evaluation of 57 chilli genotypes for characterization, variability, diversity and association study in a simple randomized block design with 5 replications. A total 14 characters viz. growth, yield and morphological were studied and significant variation was observed among the genotypes collected across the country. This variation may be due to the effect of genotype, environment, or their interaction. Genotype UBC-62(7.32) followed by UBC-59(7.05) is the highest yielder/ha for that seasons, UBC-8 is superior to any other genotypes in fruit weight (8.32 gm) and UBC-48 in case of number of fruits per plant i.e., (86.00). Minimum days to flowering was recorded by UBC1(33.6 DAT) and first red ripe fruit maturity in UBC-9 (92 DAT). The characters that exhibited higher Phenotypic and Genotypic Co-efficient of variation values were fruit yield/plant (47.85 & 49.08) followed by yield/ha (47.77 & 49) and fruit weight (37.99 & 38.08) indicating that a greater amount of genetic variability was present for these characters which provide greater scope for selection. High heritability coupled with high genetic advances percent of mean was observed

for the same characters depicting that these traits were under the strong influence of additive gene action and hence simple selection based on phenotypic performance of these traits would be more effective. Yield per plant had highly significant positive correlation with fruit weight and fruits per plant; number of primary branches, plant height, seed test weight and seeds/fruit. Although fruit diameter, fruit wall thickness, days to flowering and days to first red ripe maturity had negative association with yield/ha. The maximum positive direct effect was observed by fruit weight & plant height. The first three PCs accounted for 70.17% of variation. The PC1 added highly 43.03% to the total variability with significant loading for plant height, number of primary branches, days to flowering, number of seeds per fruit, seed test weight, fruit weight, number of fruits per plant and fruit yield per plant. All the character under study showed considerable divergence and the genotypes were grouped into ten clusters. Cluster I contained the maximum (34) number of genotypes, whereas cluster VII, VIII, IX, X contained minimum (1) genotypes. Intra-cluster distance was maximum (429.28) in cluster V. Whereas, maximum average inter-cluster distance ((6100.48) was recorded between cluster II and cluster VII. A total of 19 immune, 1 resistant and 4 moderately resistant genotypes were identified during field and artificial screening against chilli veinal mottle virus disease.

Key words: Characterization, Variability, Diversity, Chilli veinal mottle virus.

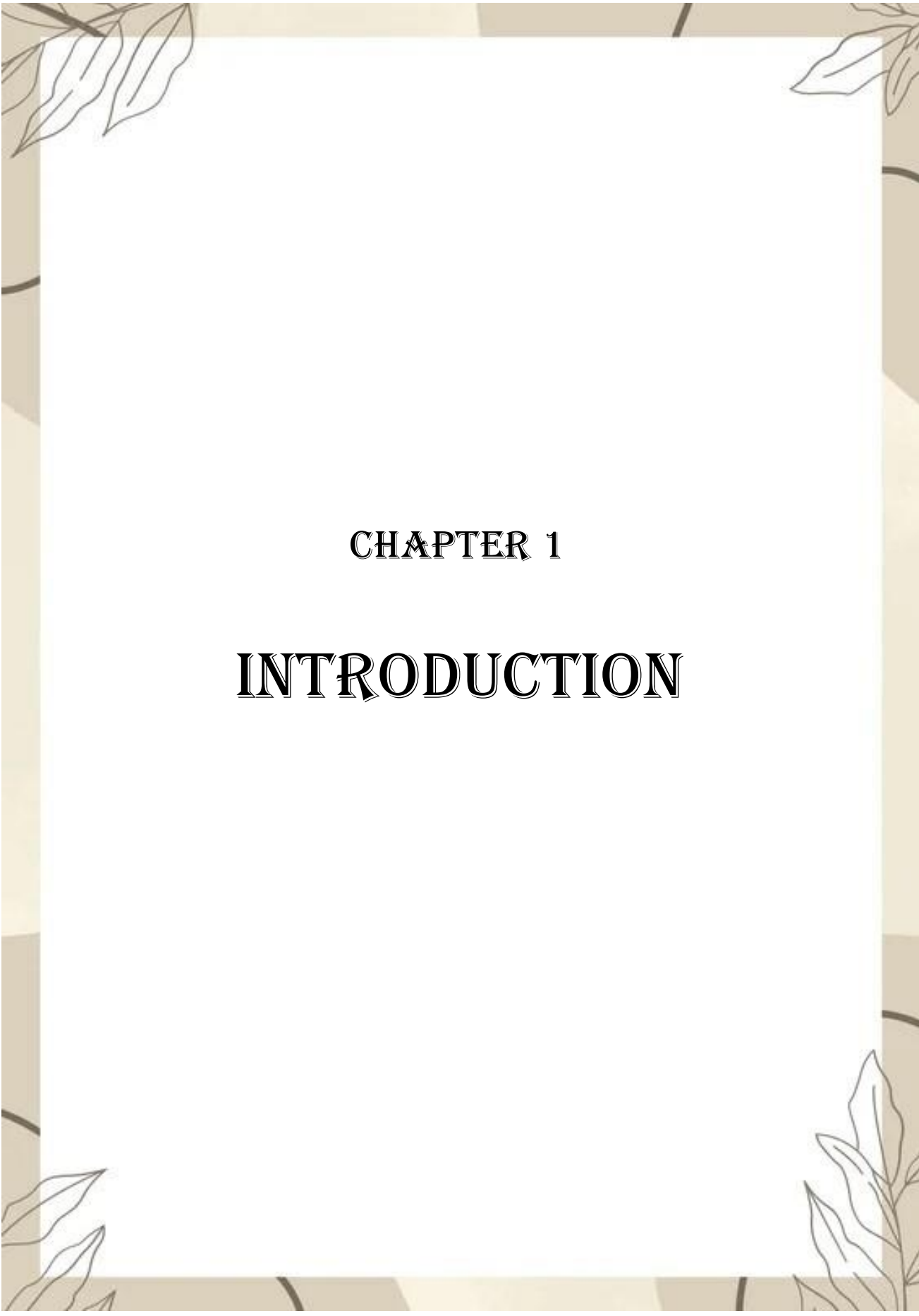


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CHAPTER 1

INTRODUCTION

Chilli (*Capsicum annuum*) is a member comes under Solanaceae family with chromosome no $2n=24$. It is one of the most important vegetable cum spice crop in India. Mexico is considered as the origin of chilli, Guatemala and Bulgaria are considered as secondary centres of origin (Salvador, 2002). Chilli was introduced into India by Portuguese in 17th century and was incorporated into national cuisines (Bosland and Vostava, 2000).

After Black pepper (*Piper nigrum*), chilli is the 2nd largest spice commodity in the international trade from India. Among the spices consumed per head in India, dry chilli has a major share. Ashoka *et al.*, (2013). India is the largest producer and exporter of spices in the world. Nearly 63 spices are grown in India according to Bureau of Indian standards (BIS). Chilli is closely related to 25 wild and 5 domesticated species namely *Capsicum annuum*, *Capsicum baccatum*, *Capsicum chinese*, *Capsicum frutescens* and *Capsicum pubescens*. (Bosland and Vostava (2000) Khan *et al.*, (2012) Jagtap *et al.*, (2012)). Among the five cultivated species *Capsicum annuum* is most cultivated species in India.

Chilli is an important spice which not only adds wonderful colour to Indian dishes but also have medicinal and nutritional properties. Due to its pungency, flavour, aroma, chilli is used in all Indian cuisines, it is an indispensable spice. Chilli fruits are a good source of vitamins C, A, and E. The crystalline acrid volatile alkaloid known as capsaicin, which is contained in the placenta of the fruit and has a variety of preventive and therapeutic benefits in both allopathic and ayurvedic medicine (Sumathy and Mathew 1984). Two major alkaloid compounds that produce the pungency, which are Capsaicin (N-[(4-hydroxy-3-methoxyphenyl) methyl]-8-methyl-E-6-nonenamide) and Dihydrocapsaicin (N-[(4-hydroxy-3-methoxyphenyl) methyl]-8-methyl-6-nonenamide)) which comprises over 90% of the total alkaloid present in the fruit (Usman *et al.*, 2014). Capsaicin is responsible for the pungency.

A part from rich source of vitamins, a small quantity of proteins, fats carbohydrates and minerals are identified (Hosamani, 1993). It is also a good source of oleoresin. Essential oil oleoresin that is used in pharmaceutical, food and beverage industries for the preparation of value-added products. The natural colour extracts of chilli are also finding their increased value in place of artificial colours in the food items, especially in the developed nations (Owens, 1992). Mostly Paprika varieties are rich in capsanthin and capsorubin that is used for

natural coloration agent in food processing industries. Chilli has diverse uses it can be used as vegetable, spice, condiment, medicine, ornamental plant, and culinary supplement.

Chilli is a tropical crop, widely grown throughout the world with an estimated global area coverage of 1.78 million hectares and production about 7.18 million tons (Gade *et al.*, 2020). India ranks first in production followed by China in the world with area under chilli cultivation in India is 316.47 thousand hectares and total production is 3633.99 thousand MT (Gade *et al.*, 2020). India is the world's largest producer, consumer, and exporter of chilli. India exports 557,168 tonnes with a net worth of 858,188.59 lakhs (Spice board of India 2021-22). Andhra Pradesh contributes 75% of Indian chillis export. Andhra Pradesh ranks 1st in chilli production, total production of Andhra Pradesh is 6,27,849 tons under 22,5000 hectares of cultivated area (Spice board of India 2022-2023). West Bengal ranks 6th in production i.e., 27,646 tons under 17,146 hectares of cultivated area (Spice Board of India, 2022-23).

Genetic improvement mainly depends upon the amount of genetic variability present in the population. Variability plays an important role in plant breeding because hybrids between lines of different origin generally possess greater heterosis than those closely related species (Singh 1983). Information regarding genetic variability provides an information to identify right genotypes that would help plant breeder in breeding programme. Germplasm serves as a valuable source of base population and provides scope for wide variability. It is essential to find out the relative magnitude of additive and non-additive genetic variances, heritability, and genetic gain regarding the characters of concern to the breeder.

Knowledge on the genetic architecture of genotypes is necessary to formulate efficient breeding methodology. The phases in the systematic breeding program involve creating genetic diversity, conducting genotype selection, and using those genotypes to develop promising cultivars. Improvement in yield and quality of any crop is achieved by selecting genotypes with desirable character combinations (Golakia and Maken, 1992). The variability available in a population divided into heritable and non-heritable components with the help of genetic parameters. Using suitable biometrical and genetical approaches, the percentage of genotypic variance and phenotypic variance may be estimated. Genotypic (GCV) and phenotypic (PCV) co-efficient of variation are higher than coefficient indicates the wider diversity. The degree of relationship between different characters is shown through genotypic, phenotypic, correlations. When two opposed desired characters impacting the principal character selected, it helps to base the selection technique on an essential balance. It also helps to improve different characters simultaneously (Falconer, 1981). D² statistics developed by

Mahalanobis (1936) provides a measure of magnitude for divergence between two genotypes under comparison. Grouping of genotypes based on D^2 analysis will be useful in selecting superior parental lines in further breeding programme.

The present study was undertaken to evaluate the genetic variability of different genotypes to estimate the scope for advance selection of diverse genotypes and selection of suitable parents for hybridization to improve yield attributing traits and to induce resistance against biotic stress (ChiVMV disease).

Viral diseases cause serious loss in chilli and become a major limitation in chilli production. Chilli is known to be infected by more than 45 viruses in the world and these mainly contribute to the lower yield and reduced fruit quality (Green and Kim 1991). More than 50 percent are mainly aphid transmitted. Out of several virus reported in India (Ramakrishna 1961, Green and Kim 1991, Joseph and Savithri, 1999). ChiVMV is the most important virus of *Capsicum annuum* and *Capsicum frutescens* in Asia and known to be occurring in Indonesia, Korea, Taiwan, Thailand Malaysia, India and Philippines (Green and Kim, 1991; Siriwong et al, 1995). Chilli veinal mottle virus was reported by Reddy *et al.*, (2001) from Karnataka, Tamil Nadu, and Andhra Pradesh states of India. ChiVMV belongs to the genus *Potyvirus* which comprised of more than 30% of known plant virus King *et al.*, (2011). Estimated yield loss due to chilli veinal mottle virus >30 percent in Asian countries (AVRDC). It causes significant losses in agricultural, horticultural, and ornamental crops Ward *et al.*, (1991).

ChiVMV is transmitted non persistently by aphids. Major symptoms are dark green vein banding, shoe string, leaf mottling results in heavy loss of yield Moury *et al.*, (2005). Due to broad host range of these virus, it is difficult to control genetic resistance in the host plant is the best way to combat these viruses Chaim *et al.*, (2001). Detection of Chilli veinal mottle virus and screening of genotypes against ChiVMV in relation to identify resistant genotypes and resistant genotypes are used in further breeding programmes.

Therefore, the investigation on genetic variability and character association among different chilli genotypes for various traits and identify the resistant genotypes against ChiVMV was done with the following objectives.

Objectives

- 1.Characterization, variability and character association study in Chilli genotypes
- 2.Assessment of diversity among genotypes
- 3.Molecular detection and screening of chilli genotypes against chilli veinal mottle virus.

CHAPTER 2

REVIEW
OF
LITERATURE

Any scientific experiment must first be set up after a comprehensive evaluation of the literature and analysis of prior work. It is crucial for identifying the issues, probable solutions, and developing a research hypothesis and an experimental plan. Hence, in the current study, a thorough assessment of the relevant literature related to the characterization and genetic variability, diversity analysis, principal component analysis of chilli has been stated.

Genetic variability

In crop improvement programme, a critical estimate of genetic variability is required before starting proper breeding programme. The observed variability in populations could be due to genetic and environmental factors. According to Johansen (1909), variation in segregating populations is due to both heritable and non-heritable factors, while variation within pure lines is mainly due to environmental influences. Later, Nilson-Ehle (1909) validated Johansen's work and demonstrated that continuous variation also confirms Mendelian Genetics. Charles and Smith (1939), Powers (1942) and Powers *et al.*, (1950) used the estimate of environmental variance in non-segregating populations to separate genetic variance from total variance. Studies on assessment of genetic variability in chilli for morphological and yield parameters have been performed by several workers in the past.

Bhagya lekshmi *et al.*, (1990) had studied genetic advance, heritability, and character association in (*Capsicum annum* L.) for the traits plant height, branches per plant, time between fruit set, maturity, fresh fruit weight, seeds/fruit and 100 seed weight all had moderate heritability estimates. Days to 50% flowering (0.829), fruits/plant (0.894), fruit length (0.827), fruit girth (0.890) all had high heritability. Suggested that improvement can be made through simple selection. Simple selection can lead to advancement.

Shirshat *et al.*, (2000) had studied genetic variability in 72 chilli genotypes. For all traits, the phenotypic coefficient of variance was greater than the genotypic coefficient of variation, showing that environment influence on these characters. Fruit attributes such as fruit length, fruit surface area, dry fruit weight, pericarp weight, number of seeds per fruit, weight of seeds per fruit, stalk length, ascorbic acid, and sugar content showed very narrow differences between genotypic and phenotypic coefficients of variation, indicating less sensitivity to environmental influences.

Munshi *et al.*, (2000) had studied 30 chilli germplasm lines for yield contributing features (*Capsicum annum* L). Except for fruit girth, this study found a significant level of genetic

variability for all the traits evaluated. The number of fruits produced per plant had the highest genotypic and phenotypic coefficients of variation (GCV and PCV). For fruit length, number of fruits per plant, yield per plant all had high estimates of genetic advance and broad sense heritability.

Manju and Sreelathakumary (2002) had studied 32 chilli (*Capsicum chinense* Jacq.) genotypes and for the traits like fruits per plant, yield per plant, seeds per fruit, and fruit weight had observed higher genotypic and phenotypic coefficients of variations.

Khurana *et al.*, (2003) had observed for the trait's fruits per plant, fruit yield, seeds per fruit all had higher heritability and high magnitude of genetic advance.

Verma *et al.*, (2004) had studied high heritability along with genetic advancement as a percentage of mean in traits such as number of fruits per plant, fruit length, and plant height.

Sarkar *et al.*, (2009) studied 49 chilli genotypes for 12 growth and fruit traits. There was significant variation among the genotypes. Highest genotypic coefficient variation and phenotypic coefficient variation were observed in plant height(cm) fruit yield (g)/plant, number of fruits per plant, fruit length (cm), placenta length (cm), fruit weight (g) and number of seeds per fruit.

Sharma *et al.*, (2010) studied 23 genotypes of bell pepper and reported significant differences in all characteristics. Based on mean performance, genotypes PRC-1, SSP, Kandaghat Se-1, and Ranichauri Sel-1 were performed good in terms of fruit yield per plant, average fruit weight, number of fruits per plant, and days to 50% flowering. Fruit yield per plant and ascorbic acid concentration had high phenotypic and genotypic coefficients of variation (PCV and GCV), indicating that these parameters had wide genetic variability and would respond better.

Data and Das (2013) studied 43 genotypes of chilli (*Capsicum annuum* L.) and reported a wide range of variability for all the traits evaluated. The number of fruits per plant (25.62%) had the highest GCV, followed by yield per hectare (22.34%). Plant spread (10.2 and 11.5%) GCV and PCV had moderate estimates.

Jogi *et al.*, (2015) evaluated 50 chilli genotypes for 11 different traits. All characters showed a high degree of variation. Maximum traits, had shown negligible difference between phenotypic and genotypic coefficients of variation.

Sahu *et al.*, (2016) studied 19 chilli genotypes for heritability, GCV, PCV study. For number of fruits per plant (47.18% and 52.69%), fruit yield per plot (34.45% and 39.30%), and fruit

yield per ha (33.19% and 38.08%) had the highest genotypic and phenotypic coefficients of variation. The phenotypic coefficients of variance were greater than the genotypic coefficients.

Pujar *et al.*, (2017) observed a high significant difference within the genotypes for all the characters studied. As observed that narrow gap between genotypic and phenotypic coefficients of variation, environmental influence on character expression was low. Except for green and dry fruit weight, the genotypic and phenotypic coefficients of variation were moderate to high.

Nagaraju *et al.*, (2018) studied 53 chilli genotypes. Highest variability was observed for maximum characters. For the traits red ripe fruit yield per plant (238.89 to 1028.45 g), number of fruits per plant (11.44 to 798.67), number of seeds per fruit (24.40 to 153.62). Minimum for the trait's primary branches per plant (2.20 to 5.33 cm) and 1000 seed weight (0.30 to 3.38 g). Characters with a wide range of variation provide great opportunity for selecting superior types.

Kumar *et al.*, (2020) studied 37 chilli genotypes maximum phenotypic variation was observed for the traits fruit yield per plant (g) (40.30), number of fruits per plant (37.96) and fruit yield per ha (37.93) and moderate to low was observed for remaining traits. For all the traits, the magnitude of the phenotypic coefficient of variability was greater than the magnitude of the genotypic coefficient of variability, indicating that environment has an influence on their genetic expression. Maximum amount of genotypic coefficient of variation was observed for the traits. Number of fruits per plant (36.83), Fruit yield per ha (34.57), Fruit yield per plant (g) 32.37 and minimum coefficient of genotypic variance was observed for Plant height (cm) 90 DAT, Primary branches, number of days to 50% flowering, fruit length (cm), fruit diameter. There is a better opportunity for improvement through selection due to higher magnitude of genotypic coefficient variation.

Patel *et al.*, (2022) studied 30 different chilli genotypes. Genotypic coefficient variation and phenotypic coefficient of variation was observed in all the traits. The difference between GCV and PCV estimations was, however, extremely minor for all the traits studied, except for primary and secondary branches per plant, number of seeds per fruit, and 1000 seed weight. GCV estimates were shown to be higher (>20%) for fruits per plant, fruit length, dry fruit weight, dry fruit yield per plant, number of seeds per fruit. Greater estimates for yield-related economically important traits and difference between GCV values and PCV values

is very less indicated that the environment had little impact on trait expression.

Heritability and genetic advance

The genetic component of variation plays an important role in crop improvement, since it is the only component that is transmitted to the following generation. Hanson *et al.*, (1956) define heritability as the ratio of genotypic variation to total variance in a non-segregating population. Thus, heritability defines the proportion of phenotypic variance that is heritable due to heredity. Heritability varies depending on the populations studied. The heritability estimations serve as a helpful guidance for the breeder. Selection for the trait would be very simple due to less difference between genotype and phenotype due to the phenotype's comparatively reduced impact from environment. However, due to the masking impact of environment on the genotypic effect, selection for a low heritability feature may be extremely difficult or almost impossible (Singh, 1991).

Genetic advance

Improvement of genotypic value of selected plants over parental population is known as genetic advance. The estimates of heritability indicate the amount of progress estimated from selection. Factors like as selection intensity, heritability, and phenotypic variation all affect genetic advance. High genetic advance combined with high heritability indication of stronger additive gene activity (Panse, 1957).

Munshi and Behera (2000) studied heritability and genetic advancement for several yield contributing traits in 30 chilli genotypes (*Capsicum annuum*). For the traits fruit length, number of fruits per plant, and yield per plant reported higher genetic advance. Selection can significantly improve these traits.

Manju and Sreelathakumary (2002) reported that for the traits fruit weight, fruits per plant, yield per plant and seeds per fruit have higher heritability estimates together with higher genetic advance indicating that they may be successfully improved by selection.

Sharma *et al.*, (2010) reported high heritability estimates and higher genetic advance for the traits fruit weight, fruit yield per plant, fruit diameter, Number of days to first harvest and ascorbic acid content which indicates the importance of additive gene activity for the inheritance of specific traits.

Ullah *et al.*, (2011) observed that the parameters fruit yield per plant, fruits per plant, plant height, and days to 50% flowering had high heritability with high genetic advance in

percentage of mean. The main characters were number of fruits per plant, fruit length, and fruit diameter. These are the Major contributing traits to yield because these characteristics were significantly and positively associated with the total plant yield.

Kumar *et al.*, (2012) reported that traits like plant height 150 days after transplanting (DAT), number of fruits per plant, ascorbic acid, and fruit yield per plant have been observed higher genetic advance. For traits like days to first flowering and days to first harvest, genetic advance was low.

Datta and Das (2013) reported higher heritability coupled with high genetic advance for the traits number of primary branches per plant number of fruits per plant, yield per plant These traits may be consider for reliable selection. They may be governed by additive gene effect.

Pandit and Adhikary (2014) reported very high genetic advance as a percentage over mean in fruit yield per plant and moderately high genetic advance as a percentage over mean in number of days to 50 percent flowering, fruit length, number of fruits per plant, and number of seeds per fruit, indicating that these traits are most likely governed by additive gene action and thus rewarding in selection.

Janaki *et al.*, (2015) reported higher heritability together with high genetic advance as a percentage over mean for all the traits evaluated except days to 50% flowering. The traits with higher genetic advance governed by additive gene action

Patel *et al.*, (2016) studied nine diverse chilli genotypes and reported high heritability and genetic advance was observed for all the characters Except for the number of primary branches, fruit width, days to first harvest indicate that these traits are governed by additive gene activity.

Jogi *et al.*, (2017) studied for the traits number of fruits per plant at first picking (98.20%) and early yield (94.67%), plant spread(N-S) at 60 days (64.27%) and 120 day (65.47%) and (EW)at 60 days (60.56%). Reported higher estimates of heritability.

Kumar *et al.*, (2020) studied 37 chilli genotypes the traits fruit diameter and average dry fruit reported with higher heritability and moderate genetic gain. Remaining traits exhibit high heritability with moderate to low genetic advance. Through multiple crosses percent of mean can be improved.

Correlation

The expression of a character in a plant is the result of a series of interrelationships /interactions between characters, either directly or indirectly. Fruit yield is a main trait that is impacted by various other traits in crop. Selection for such traits may not always result in improvement unless the unfavorable links between such traits are altered favorably through hybridization. The correlation characters may be due to genetic linkage or pleiotropy (Harland, 1939). The mutual relationship between various traits are measured by correlation coefficient analysis. Positive correlation or negative correlation measured by correlation coefficients. There are three types of correlations: phenotypic, genotypic, and environmental. The observable correlation between two variables that includes both genotypic and environmental influences is known as phenotypic correlation. Genotypic correlation, on the other hand, is the intrinsic relationship between two variables that can be caused by pleiotropic gene activity, linkage, or both. Environmental correlation emerges only as a result of environmental factors. Correlation ranges between -1 and +1 for negative and positive correlation. If the correlation is 0, then they are said to have no correlation and they are completely due to random. A brief review related to the nature of character association in chilli studied by several researchers is provided below.

Mathew *et al.*, (2004) studied that genotypic correlation coefficients were higher than phenotypic correlation coefficients. Fruit width, fruit length, single fruit weight, seed number, and 1000 seed weight were all significant and positively correlated with yield. Number of days to first flowering were shown to be negatively correlated with the number of fruits per plant, fruit length, and fruit yield, whereas yield per plant was found to be highly significant and positively correlated with the number of fruits per plant, fruit length, fruit girth, and fruit weight.

Sharma *et al.*, (2007) reported that genotypic correlation coefficients were higher than phenotypic correlation coefficients for maximum traits. At both the genotypic and phenotypic correlation, fruit yield per plant had a strong positive correlation with average fruit weight and number of seeds per fruit. The number of fruits per plant correlated positively with plant height. At the genotypic level average fruit weight was negatively correlated with fruit length.

Patil *et al.*, (2009) evaluated 38 chilli genotypes (*Capsicum annuum L.*) for morphological and qualitative traits. The green fruit yield per plant had a highly significant and positive

correlation with the number of primary branches per plant, the number of fruits per plant, fruit length, fruit girth and the weight of the fruit.

Wilson and Philip (2009) evaluated that the genotypic correlation coefficient was higher than the phenotypic correlation coefficient. Yield per plant was significantly associated with number of fruits per plant, fruit length, fruit weight, 100 seed weight, plant height. It was negatively correlated to number of days to 50 percent flowering.

Datta and Jana (2010) evaluated that fruit yield per plant was positively correlated and significant with number of primary and secondary branches per plant, no of fruits per plant and fruit diameter.

Yadeta *et al.*, (2011) studied the association between yield and remaining traits of several *Capsicum* genotypes grown in Ethiopia. Some of the traits showed significant correlation at both the phenotypic and genotypic levels. Fruit yield per plant significant and positively correlated with fruit length ($r_p=0.537$), fruit weight ($r_p=0.616$), and canopy diameter ($r_p=0.647$). Genotypic correlation coefficients were positive and high for these traits.

Choudhary *et al.*, (2013) evaluated 35 genotypes chilli genotypes (10 parents and 25 F1 hybrids) for yield per plant and quality traits reported highly significant correlation.

Amit *et al.*, (2014) evaluated 23 chilli genotypes assessed correlation and genetic variability and reported that fruit yield per plant for both green and red was positively correlated and significant with number of fruits per plant and fruit length.

Bijalwan and Mishra (2014) studied correlation and path coefficient analyses in 16 chilli genotypes for 15 distinct qualitative and quantitative traits. Correlation coefficients at the genotypic and phenotypic levels revealed that fruit yield per plant was significant and positively correlated with number of fruits per plant, fruit weight, fruit length, number of branches and ascorbic acid content and but significant and negatively correlated with number of days to 50 percent flowering.

Ajith and Manju (2015) studied 76 genotypes of chilli and evaluated that fruit yield was positive correlated and significant with green fruit weight, fruit length, number of branches, number of fruits per plant, 100-seed weight, and capsaicin content.

Hasan *et al.*, (2016) studied 30 genotypes of chilli. In both phenotypic and genotypic correlation levels fruit length, fruit weight, 100 seed weight, and fruit per plant all shown a significant and positive association with yield per plant. Determine that genetic association

and selection indices between yield and major yield contributing traits.

Pujar *et al.*, (2017) reported a positive and very significant association between fruit set percentage and the number of fruits per plant and fruit set %. The strong correlation of these traits suggested that selection based on these traits will eventually enhance fruit yield and suggested that hybridization of genotypes having a combination of such characters is most effective for developing desirable high yielding segregants.

Janaki *et al.*, (2018) reported correlation studies on 71 genotypes of chilli (*Capsicum annum* L.) To determine the phenotypic and genotypic association of fruit yield per plant with plant height, plant spread, number of fruits per plant, and days to fruit maturity. Both genotypic and phenotypic correlation are significant and positively correlated indicating the importance of these traits in yield selection.

Rao *et al.*, (2020) reported correlation studies on 30 chilli genotypes. Fruit yield per plant was significant and positively correlated with number of fruits per plant, fruit diameter, fruit weight, dry fruit weight, seed content, ascorbic acid content, oleoresin content and capsanthin content. But number of flowers per axil, number of primary branches, fruit length was negatively correlated.

Chavan *et al.*, (2021) reported fruit weight per plant was positively and significantly correlated with fruit yield per plot, Total number of fruits per plant, number of primary branches, fruit length and average fruit weight, but a negatively correlated and significant association was found with number of days to 50% flowering.

Lata and Sharma (2022) studied 14 chilli genotypes. Correlation studies revealed that Marketable green fruits per plant, total green fruits per plant, marketable green fruits per plant percentage, and fruit girth all showed a positive significant correlation with marketable yield per plant, showing the importance of these qualities in yield selection.

Path Coefficient analysis

Wright (1923) developed path coefficient analysis, but Dewey and Lu (1959) were the first to apply it technically in plant breeding. The ratio of the standard deviation of the effect caused by a given cause to the total standard deviation of the effect is defined as path coefficient analysis. It is a technique used to improve the efficiency of selection programs by determining the relative contribution of component characters directly on the main characters and indirectly through other characters. The method of path coefficient had proved useful in

analyzing the correlation coefficients in this system of interrelated variables.

Nandadevi and Hosmani (2003) reported the path coefficient studies number of fruits per plant had maximum direct effect on fruit yield, pedicel length and pericarp thickness. Fruit weight with yield per plant has low negative direct effect.

Sarkar *et al.*, (2009) revealed that number of fruits per plant, fruit weight and test weight of seed had high direct and positive effect on fruit yield indicating their reliability as a selection criterion to improve the yield of chilli.

Krishna *et al.*, (2007) studied that green fruit yield per plant had highest direct positive effect on both early and late fruit yield. Therefore, selection criteria based on early and late fruit yield would be rewarding.

Patil *et al.*, (2009) investigated 38 genotypes of chilli (*Capsicum annuum* L.) for morphological and qualitative characteristics. Path coefficient study revealed that the number of fruits per plant, fruit weight, fruit length, and number of primary branches per plant all had a positive direct effect on green fruit yield per plant.

Datta and Jana (2010) reported that among the many traits, individual fruit weight, number of fruits per plant, primary and secondary branches per plant, and fruit diameter had the higher direct effect. As a result, the number of fruits, individual fruit weight, fruit diameter, primary and secondary branches per plant, should be given more priority during selection for higher yield in green chilli.

Ullah *et al.*, (2011) revealed that maximum contribution for number of fruits per plant to yield in path coefficient analysis, was followed by average fruit weight, number of days to first flowering and fruit length.

Singh *et al.*, (2014) investigated the correlation and path analysis in 23 chilli genotypes for growth and yield contributing traits. The path coefficient analysis revealed the number of fruits per plant, fruit width, and average fruit weight as important yield components that may be used as selection criteria for crop improvement. The results revealed that due to higher positive effect on dry fruit yield, genotypes with the highest number of fruits per plant, fruit length, fruit girth, and fruit weight should be prioritized in the selection process.

Patel *et al.*, (2015) studied on path analysis revealed that traits such as the number of secondary branches per plant, the number of fruits per plant, and the average fruit weight all had a high and positive direct effect on green fruit yield.

Hasan *et al.*, (2016) revealed that the number of fruits per plant had the maximum positive direct effect on yield. Fruit weight, fruit length, and the number of main branches per plant also had a positive direct effect on yield. Using five characters, discriminating functions were used to generate selection indices. In comparison to other combinations of traits, the highest relative efficiency was found for fruit weight, number of fruits per plant and yield per plant.

Pujar *et al.*, (2017) revealed path-coefficient analysis and reported that in both genotypic and phenotypic levels fruit set percentage and fruit weight had positive direct effect on fruit yield and Majority of fruit related traits contributed to fruit yield mainly fruit girth and fruit weight.

Lata and Sharma (2022) studied 14 chilli genotypes. Coefficient path analysis revealed that number of green fruits per plant, average fruit weight, fruit length, primary branches per plant and days to first harvest had positive direct effect on green fruit yield per plant

Genetic divergence and grouping of genotypes

The magnitude of divergence between two groups under consideration is provided by D^2 statistic developed by Mahalanobis (1936). First time D^2 statistic was applied for the biological population by Nair and Mukharji (1960) to classify the natural and plantation teak tree types. Murthy and Pavate (1962) observed that D^2 analysis can be extended to the situations where overlapping species need to be discriminated and when the discrimination at sub species level is needed. D^2 statistics determined by measuring the forces of differentiation at the intra- and inter-cluster levels relative contribution of each component trait to the total divergence. Later in vegetable crops this technique was subsequently used

Smitha and Basavaraja (2006) studied 40 chilli genotypes and divided into eight different clusters. Cluster A has the maximum inter and intra cluster distance. For the traits number of fruits per plant, fruit yield, number of branches, fruit weight, and number of fruits, between cluster H and E also has maximum inter and intra cluster distance which confirms the existence of a significant amount of divergence in genotypes and thus selection of superior genotypes for traits would be useful in utilising the maximum heterosis in future breeding programmes. Genotypes present in distant clusters heterosis can be exploited.

Thul *et al.*, (2009) reported the degree of genetic divergence in 24 chilli genotypes, which were grouped into six major clusters. Cluster I had maximum no of genotypes, followed by Clusters II, III, and IV. The highest intra cluster divergence for cluster I was usually less than the lowest inter cluster divergence between the cluster II and cluster III, and the inter cluster

distance was highest for the cluster V, followed by cluster III, and lowest for cluster IV.

Kumari *et al.*, (2010) studied degree of genetic divergence in 94 paprika (*Capsicum annuum* L.) genotypes for 17 traits. Through Mahalanobis D^2 analysis cluster analysis was done. They classified the 94 chilli genotypes into 10 different cluster groups which indicates that the material studied has a high level of genetic diversity.

Hasan *et al.*, (2015) studied genetic diversity in 54 Chili (*Capsicum annuum* L.) genotypes through Mahalanobis's D^2 . Genotypes were divided into seven different clusters for 12 different quantitative traits. Highest divergence reported between cluster III and cluster VI, cluster I and cluster III, cluster III, and cluster VII due to high level of diversity these genotypes can be used in future breeding programmes.

Pujar *et al.*, (2017) reported genetic diversity in 63 chilli genotypes. 63 genotypes were grouped into 5 different cluster groups using the Mahalanobis D^2 statistics analysis. The 63 chilli genotypes considered in the study. It is desirable to select genotypes from the cluster that are having higher inter cluster distance genotypes and for the trait with higher fruit yield would be useful in utilising the maximum heterosis in future breeding programmes.

Nagaraju *et al.*, (2018) studied genetic divergence among 53 chilli genotypes using Mahalanobis D^2 analysis for 20 quantitative traits. 53 genotypes are grouped into 9 different clusters. Wider genetic divergence was observed between Cluster VIII (California Wonder) and IX (Bhut Jolokia). Selection of these genotypes as parents in future breeding programme were useful in development of heterotic hybrid.

Nahak *et al.*, (2018) studied genetic diversity of 16 chilli genotypes. Diversity was evaluated using Mahalanobis' D^2 statistics. The genotypes were classified into four different cluster groups by Clustering that is not hierarchical. Cluster I have the higher number of genotypes (7). Clusters III and IV each had only one genotype. Clusters II and III ((249.759), II and IV (239.433) had highest inter cluster distance.

Kumari *et al.*, (2018) studied genetic divergence among 16 chilli genotypes based on fruit yield and its characters they are divide into three cluster groups. In cluster-III maximum number of nine genotypes were seen, followed by 5 genotypes in cluster-I. The highest inter-cluster divergence (5.531) was noticed between clusters II and III, indicating the most effective use of heterosis on hybridization.

Sen *et al.*, (2021) reported cluster analysis between parental and hybrid chilli genotypes

under this study they were grouped into five cluster groups. The inter-cluster Distance values ranged between 40.404 and 127.530. The minimum inter-cluster distance was reported between clusters III and IV (40.404) and the maximum inter-cluster distance was reported between clusters II and V (127.53). Selection of genotypes from the clusters having maximum inter cluster distance are used in further breeding program. Heterosis can be exploit for genotypes present in distant clusters.

Principal component analysis

Principal components (PCs) with an eigenvalue greater than one were chosen (Jeffers, 1967) and the PCA was carried out using the standardized values of the PAST 3 program and the computer software Microsoft Excel. Principal Component Analysis (PCA) is a powerful method for determining the fewest number of components while explaining the most variability out of total variability (Morrison, 1982). PCA aids in genotype ranking based on PC score the scree plot was used to visually examine the components that contributed the major share in the total variance.

Pugalendhi *et al.*, (2020) studied principal component analysis for 32 morphological traits. Principal Component Analysis revealed that ten principal components with eigen values greater than one accounted for 98.69% of the total variability, with the plant growth habit, anthocyanin colouration at nodes, intensity of anthocyanin, fruit color at intermediate stage, mature stage, and fruit color exhibiting the highest variability, while the remaining traits exhibited low variability. Based on PCA and the most diverse genotypes were found as CC-CBE-005, CA-CBE-201, CA-CBE-202, CA-CBE-199, CC-CBE-004, CF-CBE-007, CC-CBE-001, and CC-CBE-002.

Singh *et al.*, (2020) studied principal component analysis in chilli. Only five out of the ten principal components had >0.5 eigenvalues and showed around 88.85% variability in the traits. PC1 accounted for the highest variability (36.93%) of overall variability, followed by PC2 (22.87%), PC3 (15.62%), PC4 (7.46%), and PC5 (5.97%). As a result of the principal component analysis, these chilli genotype accessions have a high level of genetic diversity.

Molecular detection and screening of chilli genotypes against ChiVMV

During a survey done in 1997 and 1998, a viral disease of chilli was found, causing dark green mottling and deformation symptoms on leaves (Prakash *et al.*, 2002). The disease was widely distributed in eastern UP, with a disease incidence ranging from 5 to 75%. Gorakhpur had the highest incidence rates of up to 50% and 75% in 1997 and 1998, respectively.

Krishna Reddy *et al.*, (2004) screened 25 chilli pepper genotypes for resistance to Chilli veinal mottle virus (ChiVMV) isolates. They were divided into five categories based on the disease intensity values. Three lines were found to be immune; two lines were found to be resistant, 10 lines were found to be susceptible to different isolates of chilli veinal mottle virus.

Moury *et al.*, (2005) studied Variability of pepper-infecting potyviruses Pepper veinal mottle virus (PVMV) and Chili veinal mottle virus (ChiVMV) have been researched extensively in Africa and Asia. The sequence diversity of coat protein (CP) genes revealed three clades that corresponded to three geographical locations, with no evidence of the ChiVMV/Asian group in western or central Africa. These clades had isolates from two virus species that were closely related.

Satyaprakash and Singh, easily transferred ChiVMV in (2006) to chilli and other herbaceous hosts by sap inoculation. The virus was also transmitted non-persistently by aphids such as *A. gossypii*, *A. craccivora*, and *Myzus persicae*, but no seed transmission was reported.

Tsai *et al.*, (2008) reported that twenty-four isolates of Chilli veinal mottle virus (ChiVMV) from various countries to identify their genetic relatedness. The viral genomic RNA 3' terminal sequences were determined. In the 3'UTR of all isolates, the inverted repeat sequence GUGGNNCCAC was present. Because of their high CP amino acid and nucleotide similarity (more than 948 and 895, respectively) with previously described ChiVMV isolates, all 24 isolates were ChiVMV. Furthermore, in the C terminal of the CP gene of ChiVMV and Pepper veinal mottle virus (PVMV), a conserved sequence of 204 amino acids with more than 90% similarity was identified.

Hussain *et al.*, (2008) reported that Chilli veinal mottle virus (ChiVMV) as one of the most prevalent chilli-infecting viruses detected in Pakistan's chilli growing areas, seeing a 44.7% relative incidence of the virus in the country between 2003 and 2004. As a result, most of the viral symptoms related with insect pest symptoms observed in the study confirmed the existence and frequency of ChiVMV.

Shah *et al.*, (2009) reported that Chili veinal mottle virus (ChiVMV) was identified as one of the most common chili-infecting viruses found in Pakistan. They also discovered a relative incidence of the virus in the nation between 2003 and 2004. Sindh (47.3%) and Punjab (46.9%) had the highest relative incidence, followed by NWFP (41.3%) and Balochistan (35.7%). Except for a few districts in Sindh and Punjab, they reported that no district was free from the viral infection. During surveys, they discovered *Datura metal* among the weed flora of chili pepper in Punjab province, as well as insect vectors, *Aphis gossypii*.

Banerjee *et al.*, (2014) reported ChiVMV infection on Naga chilli from Meghalaya, indicating that the virus's prole in chilli decrease in North East India. High prevalence of viral infection was observed from visual observations of symptoms, green vein banding, mottling, curling and a recent study of ChiVMV infection on Naga chilli from Meghalaya suggested that it might be associated with a chilli decline in the Northeast region.

Naresh *et al.*, (2016) screened 50 Capsicum genotypes against Chilli veinal mottle virus (ChiVMV) and Cucumber mosaic virus (CMV). Screening was done through artificial sap inoculation method. To develop the resistance in chilli against (ChiVMV and CMV). Resistance developed by crossing the parents in diallel fashion .17 genotypes were reported immune, one was highly resistant, five genotypes were resistant, and two genotypes were moderately resistant.

Sanabam *et al.*, (2018) reported that out of a total of 127 chilli samples taken from various groves in Manipur, 81 (63.78%) tested positive for ChiVMV. Interestingly, the infection rate of ChiVMV was found higher in the hilly groves (69.23% positive samples) than in the valley groves (60% positive samples). The current study was on the relationship of ChiVMV with various symptoms such as cupping of leaf lamina with mottling, vein banding, and puckering in different chilli landraces by thorough surveys and molecular indexing work.

Devi *et al.*, (2019) reported survey of Viral disease incidence in chilli in Andhra Pradesh, India. The maximum disease incidence for was found 45.05 percent in Narpali mandal of Anantapur District, while the lowest incidence was 6.66 percent in N.G Padu village in Prakasam. The district wise average incidence was assessed by visual assessment in field highest incidence was found in Anantapur (45.05%), followed by Kadapa (25. 55%), Kurnool (17.99%), and Guntur (14.15%) and Prakasam (11.24%).

Jiao *et al.*, (2020) identified ChiVMV-LZ from infected tobacco in Luzhou, Sichuan, China in (2020). Tobacco plants inoculated with ChiVMV-LZ displayed typical symptoms such as

yellow and round spots on the leaves, as well as twisted and folded leaf margin, green vein banding, shoe string as seen in naturally ChiVMV-infected tobacco in the field. ChiVMV-LZ's full-length genomic sequence has been determined to be 9742 nucleotides long. ChiVMV-LZ was most closely linked to ChiVMV-Yp8 isolated from pepper plants in Sichuan province while being distantly connected to ChiVMV-YN from tobacco in Yunnan region, showing a possible geographical difference of ChiVMV isolates. RT-RPA method was 10-fold more sensitive than conventional RT-PCR method.

Chorgasti *et al.*, (2020) studied 50 chilli genotypes screened against ChiVMV through both symptomatology and serology under protected conditions in glass house. Five genotypes were highly resistant, ten genotypes showed resistant, six were moderately resistant and remaining were susceptible.

Disease incidence was recorded high in Ramanagar (54.85%) and the least incidence of disease was observed in Chikkaballapura (26.85%). Host range studies was done under protected conditions in glass house. ChiVMV is transmitted mechanically through inoculation. Among 16 host plants tested, 7 plant species (*Nicotiana tabacum* cv. *Samsun*, *N. glutinosa*, *N. occidentalis*, *Datura metel*, *Physalis floridana*, *S. nigrum*, *Capsicum annum*) were infected with the Chilli veinal mottle virus diseases and the symptom could be seen 20-25 days after post inoculation. Total five aphids per plant showed highest per cent transmission (100%) Praful *et al.*, (2021).

Borah *et al.*, (2022) reported molecular indexing of samples from 30 chilli genotypes from different plantation orchards of Jorhat and Golaghat districts of Assam. By using reverse transcription (RT)-PCR targeting the coat protein (CP) region of ChiVMV genome revealed a higher disease incidence and wide prevalence of the virus. Total 96 chilli samples collected from different orchards of Jorhat and Golaghat districts, 41 chilli samples (42.70%) were found to be positive for ChiVMV from both regions. Present study, reported revealed that association of ChiVMV with diverse symptoms like mosaic/mottling, dark green vein banding, leaf puckering, leaf distortion, narrow leaf lamina, shoe-string of leaves and stunted growth in King chilli.

CHAPTER 3

**MATERIALS
AND
METHODS**

3.1. Experiment site**3.1.1 Study area**

The present research on Variability, character association and diversity analysis in chilli (*Capsicum annuum*) was conducted in Uttar banga Krishi Vishwavidyalaya, Pundibari, Cooch Behar, West Bengal, India during 2021-2023. The experiment site is in the Instructional farm which is a part of Department of vegetable and spice crops, Faculty of Horticulture.

3.1.2 Geographical location

In Terms of location this region come under Terai agroclimatic zone, the farm is located at 25°57'N to 27° latitude and 88°54'E to 89°54'E longitude with the height of 43 meters above mean sea level. This region is having hot sub humid to humid with maximum temperature (31.1°) C. The lowest temperature is (10.5°), mean annual rain fall (2000-3000mm), significant relative humidity and a long period of winter with high soil moisture retention.

3.1.3 Soil

Soil of the region is fine loamy to clay sandy to sandy loam. Soil is acidic in nature (4.2-6.2) with limited water holding capacity (100-150mm/mt). Generally, soil in this area lighter in texture with low percentage of base content and maximum amount of fully decomposed organic materials, Due to this reason soil is black to grey black in colour.

3.14 Weather

During the research year, maximum monthly temperatures ranged from 24°C to 32°C while minimum temperatures ranged from 11° to 21°C. Minimum monthly relative humidity is between 45% and 75%, while the maximum monthly relative humidity is between 71% and 90%. However, there was minimal rainfall (0-4 mm) throughout the first three months of the winter season (November to January) and the crop subsequently received considerable rainfall from February to March. In the month of April, and March there was a heavy rainfall.

Table 3.1 Average monthly temperatures, relative humidity, and rainfall during the crop growth season (2021–2022)

Year	Months	Temperature (°C)		Relative humidity (%)		Rainfall (mm)
		Maximum	Minimum	Maximum	Minimum	
2021	November	29.0	12.0	74.0	51.0	0.0
	December	27.0	12.0	81.0	58.0	1.0
2022	January	24.0	11.0	90.0	55.0	4.0
	February	24.0	11.0	82.0	51.0	47.0
	March	32.0	18.0	71.0	45.0	28.0
	April	29.0	21.0	89.0	75.0	565.0
	May	31.0	22.0	83.0	71.0	623

Gramin Krishi Mousum Sewa Kendra of Indian Meteorological Department, U.B.K.V.
Pundibari, Cooch Behar, West Bengal

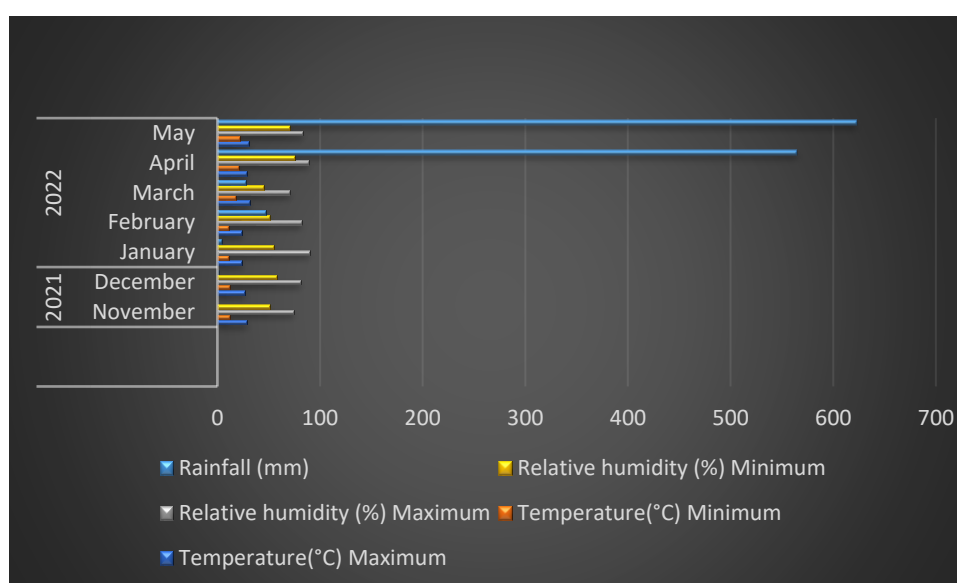


Fig 3.1 Temperatures, relative humidity, and rainfall during the period of field experiment

3.2 Experiment material

The experimental material comprised of 57 genotypes of chilli. Genotypes collected from different sources were used as research material. The accession numbers of different chilli genotypes with codes and sources are given in Table 3.2

Table 3.2 Genotypes used in the study

S.NO	Code	Genotypes	Source
1	UBC1	CHILLIVAR-1IET-2021	AICRP-VC-IIVR Varanasi
2	UBC2	CHILLIVAR-2IET-2021	AICRP-VC-IIVR Varanasi
3	UBC3	CHILLIVAR-3IET-2021	AICRP-VC-IIVR Varanasi
4	UBC4	CHILLIVAR-4IET-2021	AICRP-VC-IIVR Varanasi
5	UBC5	CHILLIVAR-5IET-2021	AICRP-VC-IIVR Varanasi
6	UBC6	CHILLIVAR-6IET-2021	AICRP-VC-IIVR Varanasi
7	UBC7	CHILLIVAR-7IET-2021	AICRP-VC-IIVR Varanasi
8	UBC8	CHILLIVAR-8IET-2021	AICRP-VC-IIVR Varanasi
9	UBC9	CHILLIVAR-9IET-2021	AICRP-VC-IIVR Varanasi
10	UBC10	CHILLIVAR-10IET-2021	AICRP-VC-IIVR Varanasi
11	UBC11	CHILLIVAR-11IET-2021	AICRP-VC-IIVR Varanasi
12	UBC12	CHILLIVAR-12IET-2021	AICRP-VC-IIVR Varanasi
13	UBC13	CHILLIVAR-13IET-2021	AICRP-VC-IIVR Varanasi
14	UBC14	CHILLIVAR-14IET-2021	AICRP-VC-IIVR Varanasi
15	UBC15	CHILLICVRRESIST2021/CHILLICVRES-1	AICRP-VC-IIVR Varanasi
16	UBC16	CHILLICVRRESIST2021/CHILLICVRES-2	AICRP-VC-IIVR Varanasi
17	UBC18	CHILLICVRRESIST2021/CHILLICVRES-3	AICRP-VC-IIVR Varanasi
18	UBC19	CHILLICVRRESIST2021/CHILLICVRES-4	AICRP-VC-IIVR Varanasi
19	UBC20	CHILLICVRRESIST2021/CHILLICVRES-5	AICRP-VC-IIVR Varanasi
20	UBC22	CHILLICVRRESIST2021/CHILLICVRES-7	AICRP-VC-IIVR Varanasi
21	UBC23	CHILLICVRRESIST2021/CHILLICVRES-8	AICRP-VC-IIVR Varanasi
22	UBC24	CHILLICVRRESIST2021/CHILLICVRES-9	AICRP-VC-IIVR Varanasi
23	UBC25	CHILLI-HPAVT-12021 CHILLIVAR-1	AICRP-VC-IIVR Varanasi
24	UBC26	CHILLI-HPAVT-12021 CHILLIVAR-2	AICRP-VC-IIVR Varanasi
25	UBC27	CHILLI-HPAVT-12021 CHILLIVAR-3	AICRP-VC-IIVR Varanasi
26	UBC28	CHILLI-HPAVT-12021 CHILLIVAR-4	AICRP-VC-IIVR Varanasi

27	UBC29	CHILLI-HPAVT-12021 CHILLIVAR-5	AICRP-VC-IIVR Varanasi
28	UBC30	CHILLI-HPAVT-12021 CHILLIVAR-6	AICRP-VC-IIVR Varanasi
29	UBC31	CHILLI-HPAVT-12021 CHILLIVAR-7	AICRP-VC-IIVR Varanasi
30	UBC32	CHILLI-HPAVT-12021 CHILLIVAR-8	AICRP-VC-IIVR Varanasi
31	UBC33	CHILLI-HPAVT-12021 CHILLIVAR-9	AICRP-VC-IIVR Varanasi
32	UBC34	CHILLI-HPAVT-12021 CHILLIVAR-10	AICRP-VC-IIVR Varanasi
33	UBC35	CHILLI-HPAVT-12021 CHILLIVAR-11	AICRP-VC-IIVR Varanasi
34	UBC37	CHILLI-HPAVT-12021 CHILLIVAR-12	AICRP-VC-IIVR Varanasi
35	UBC38	CHILLI-AVT-2-2019CHILLIVAR-1	AICRP-VC-IIVR Varanasi
36	UBC39	CHILLI-AVT-2-2019CHILLIVAR-2	AICRP-VC-IIVR Varanasi
37	UBC40	CHILLI-AVT-2-2019CHILLIVAR-4	AICRP-VC-IIVR Varanasi
38	UBC42	CHILLI-AVT-2-2019CHILLIVAR-6	AICRP-VC-IIVR Varanasi
39	UBC44	CHILLI-AVT-2-2019CHILLIVAR-9	AICRP-VC-IIVR Varanasi
40	UBC45	AP-1G4JAGANATH	Andhra Pradesh
41	UBC46	NW-2MITREMORO	Manipur
42	UBC47	CB-1	Cooch Behar
43	UBC48	LOCAL SOUTH BENGAL	South Bengal
44	UBC49	SUPER HELANCHA	Murshidabad
45	UBC50	ARKA HARITHA	IIHR-Bangalore
46	UBC51	ARKA KAYATHI	IIHR-Bangalore
47	UBC52	CHILLI-AVT-2 2018-CHILLIVAR-1	AICRP-VC- IIVR Varanasi
48	UBC53	CHILLI-AVT-1 2019-CHILLIVAR-4	AICRP-VC- IIVR Varanasi
49	UBC54	CHILLI-IET 2020-CHILLIVAR-12	AICRP-VC- IIVR Varanasi
50	UBC55	CHILLI-2018-HYB-AVT-5	AICRP-VC- IIVR Varanasi
51	UBC56	CHILLI-AVT-1 2019-CHILLIVAR-6	AICRP-VC- IIVR Varanasi
52	UBC57	CHILLI-IET 2020-CHILLIVAR-10	AICRP-VC- IIVR Varanasi
53	UBC58	CHILLI-AVT-1 -2019-CHILLIVAR-7	AICRP-VC- IIVR Varanasi
54	UBC59	CHILLI-IET2020-CHIVAR-8	AICRP-VC- IIVR Varanasi
55	UBC60	CHILLI-AVT-2-2018-CHILLIVAR-5	AICRP-VC- IIVR Varanasi
56	UBC61	CHILLI-AVT-2-2018-CHILLIVAR-3	AICRP-VC- IIVR Varanasi
57	UBC62	PUNDIBARI LOCAL	Pundibari

Table 3.3 Details of the experiment

Crop	Chilli
Year of study	2021-2023
Season	Rabi (October-April)
Experiment Design	Simple randomized block design
No of treatments	57 genotypes
Replications	5
Spacing	60cmx45cm
Plot size	3mx2.5m
No of plants per plot	27
Location	Instruction farm, Faculty of Horticulture, Pundibari

3.3 Cultural practices

3.3.1 Nursery raising

Seeds are sown in a raised nurse bed of 10mx1mx15cm were prepared. Soil is incorporated with 10kg of well decomposed farm yard manure. Seeds are sown in between the rows after the sowing seeds are covered with a thin layer of soil. Light irrigation was given immediately after sowing. Irrigation should be given regularly. Plant protection measures was carried out. During November 2021 field were prepared.

3.3.2 Preparation of experimental field

3.3.2.1 Layout of the experiment

The experiment was laid out in simple randomized block design (RBD) with 5 replications and 57 genotypes, each genotype is considered as one treatment. Plots were prepared with a plot size 3x2.5m followed by 60x45 cm spacing.

3.3.2.2 Land preparation

The soil was ploughed 3-4 times and harrowed to fine tilth. Field was incorporated with 25t of well decomposed farm yard manure as basal application. During entire crop period standard cultural practices were followed.

3.3.2.3 Planting

Field is divided into rows. Each row was covered with Silver metallic plastic mulch. One month old seedlings were transplanted at the spacing of 60x45cm. Immediately after transplanting irrigation was given.

3.3.2.4 Manures and fertilizers

Plants were nourished with recommended dose of N, P, and K at 150:75:75kg/ha. N is applied in the form of urea is applied in the form of, single super phosphate is applied in the form of muriate of potash. Based on fertilizer recommendation full dose of P and K (Single super phosphate and muriate of potash and 1/3rd of N(Urea) applied at the time of planting and remaining 2/3rd nitrogen was applied in split doses at 45 and 60 days after transplanting.

3.2.2.5 Weeding and Irrigation

Immediately after transplanting irrigation was given. Irrigation was given at 6-8 days interval depending on soil moisture. By periodical weeding plot was kept free from weeds.

3.4 Observations recorded

3.4.1 Collection of data

The following observations were recorded on five randomly selected plants each genotype. Both quantitative and qualitative characters were recorded on the 5 randomly selected plants.

3.4.1 Morphological characters

Morphological characterization was done, according to the description for different characters provided by the *Capsicum* descriptor of IPGRI, Rome and AVRDC, Taiwan, CATIE Costa Rica (1995).

3.4.1.1 Growth habit

Observed when 50% of plants bear fruits and classified into Prostrate, Intermediate and Erect.

3.4.1.2 Branching habit

Recorded when 50% of plants bear fruits and classified into Sparse, Intermediate and Dense.

3.4.1.3 Stem shape

Recorded at plant maturity stage and classified into Cylindrical, Angled and Flattened.

3.4.1.4 Stem pubescence

Recorded on mature plants, excluding first two nodes below the shoot and classified into Sparse, Intermediate and Dense

3.4.1.5 Stem colour

Recorded on young plants before transplanting and classified into Green, Green with purple stripes and Purple

3.4.1.6 Leaf colour

Recorded when in 50% of the plants the first fruit begun to ripen. Classified into Yellow, Light green, Dark green, Light purple, and Purple

3.4.1.7 Leaf shape

Recorded when in 50% of the plants the first fruit begun to ripen and classified into Deltoid, Ovate and Lanceolate

3.4.1.8 Leaf shape

Observed on the youngest mature leaves and classified into Sparse, Intermediate and Dense

3.4.1.9 Corolla colour

Recorded at full bloom stage and classified into White, Light-yellow, Yellow, Yellow green, Purple with white base, White with purple base and Purple

3.4.1.10 Corolla shape

Recorded at full bloom stage and classified into Rotate and Campanulate

3.4.1.11 Anther colour

Recorded immediately after blooming before anthesis and classified into White, Yellow, Pale blue, Blue and Purple

3.4.1.12 Filament colour

Recorded immediately at anthesis and classified into White, Yellow, Green, Blue, Light purple and Purple

3.4.1.13 Stigma exsertion

Recorded at full anthesis stage and classified into Inserted, same level and Exserted

3.4.1.14 Fruit colour at intermediate stage

Recorded on fruits just before ripening stage and classified into White, yellow, green, orange and purple

3.4.1.15 Fruit colour at mature stage

Fruit colour was recorded at near maturity stage and classified into Orange-yellow, Orange, light Red, red, Dark red and Purple

3.4.1.16 Fruit shape

Fruit colour was recorded at near maturity stage and classified into Elongate, almost round, Triangular and Campanulate

3.4.2 Quantitative characters

3.4.2.1 Plant height

Height of plant was expressed in centimetre. Height of plant was measured from ground level to the tip of top most leaf. Plant height was recorded at 90 days after transplanting

3.4.2.2 Number of primary branches

The branches arising from main stem above the ground level is recorded from five plants in each genotype. No branches were recorded at 90 days after transplanting and expressed in numbers

3.4.3 Earliness parameter

3.4.3.1 Days to First flowering

Recorded as number of days taken from transplanting to first flower opening in each genotype was recorded

3.4.4 Yield parameters

3.4.4.1 Number of fruits

Recorded as number of fruits from each genotype of the five tagged plants. Total the all fruits from each picking and average of five tagged plants were worked out

3.4.4.2 Fruit length (cm)

Recorded in cm. Length of five matured fruits which are randomly selected. Individual length of each fruit is taken from base of calyx to tip of the fruit.

3.4.4.3 Fruit diameter (cm)

Recorded in cm. Diameter of five matured fruits which are randomly selected. Individual diameter of each fruit is taken from the middle of the fruit

3.4.4.4 Fruit wall thickness (mm)

Recorded in mm. Diameter of five matured fruits which are randomly selected. Measured at a point of maximum width to one decimal point

3.4.4.5 Days to first red ripe

Days to first red ripe was recorded from number of days from transplanting to first red ripe stage in each genotype was recorded

3.4.4.6 Fruit weight (gm)

Recorded in gm. Average weight of five matured green fruits were recorded

3.4.4.7 Fruit yield per plant (gm)

Recorded in gm. Fruit weight per plant from all pickings from each plant and Total yield is recorded in grams by adding the yields of all the harvest from all the pickings

3.4.4.8 Fruit yield (t/ha)

Recorded in ton per hectare based on fruit yield per plot

3.4.4.9 Number of seeds per fruit

Seeds were extracted, washed and sundried at room temperature. Number of seeds was counted from five randomly selected fruits from each genotype. No of seeds were recorded as number

3.4.4.10 Seed weight (g/1000seeds)

Seeds which were used for recording seed no are used to work out test weight .1000 seeds taken from each sample to record test weight

3.5 Stastical analysis

3.5.1 Analysis of variance (ANOVA)

Analysis of variance was carried as per the procedure described by Panse and Sukatme (1961) using the mean values of five replications in each genotype were, analysed using MS Excel, OPSTAT, R studio (4.2.2).

The model of analysis of variance was as follows

Source	d.f	SS	MSS	Calculated F value
Replication	r-1	RSS	RSS/(r-1)	TMSS/EMSS
Treatment	t-1	TSS	TSS/(t-1)	
Error	(r-1) (t-1)	ESS	ESS/(r-1) (t-1)	
Total	(rt-1)			

Where,

t = Number of treatments

r = Number of replications

d.f = Degrees of freedom

SS= Sum of square

MSS= mean sum of square

The standard error was calculated by the formula given below,

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

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

$$\text{CD}_{0.05} = \text{S.E. (d)} \times t_{(0.05)} \text{ at } (r-1) (g-1) \text{ df}$$

Where,

SEm ($\pm$) = Standard error of mean

SE (d) $\pm$ = Standard error of difference

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

Statistical level of significance of variation due to genotypes were tested by comparing error mean sum of square calculated value to Table F value at 5 percent and 1 percent level of probability

3.5.2 Estimation of genetic parameters

3.5.2.1 Genotypic and phenotypic coefficient of variation

Genotypic and phenotypic coefficients of variation were estimated according to the method given by Burton and Devane (1953)

Genotypic Co-efficient of Variation (GCV)

$$\text{GCV (\%)} = \frac{\sqrt{\text{Genotypic variance (Vg)}}}{\text{Grand mean}(\bar{x}) \text{ of the population}} \times 100$$

Phenotypic coefficient of variation (PCV)

$$\text{PCV (\%)} = \frac{\sqrt{\text{Phenotypic variance (Vp)}}}{\text{Grand mean}(\bar{x}) \text{ of the population}} \times 100$$

PCV and GCV were categorized as per Robinson et al. (1949)

0-10%	Low
10-20%	Moderate
20% and above	High

3.5.2.2 Heritability (h²)

Broad sense heritability was estimated as the ratio of genotypic variance to the phenotypic variance and heritability was expressed in percentage (Falconer, 1981).

$$\text{Heritability} = \frac{\text{GV}}{\text{PV}} \times 100$$

Where,

GV= Genotypic variance

PV= Phenotypic variance

Heritability percentage was categorized as per Robinson (1966).

0-30%	Low
30-60%	Moderate
60% and above	High

3.5.2.4 Genetic advance (GA)

As per the formula given by Johnson *et al.*, (1995). Genetic Advance was estimated

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

Where,

h^2 =Heritability in broad sense

sp= Phenotypic standard deviation

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

3.5.2.5 Genetic advance as percentage over mean

Genetic advance as percentage over mean Genetic advance over per cent of mean was calculated by using the formula given by Johnson *et al.* (1955).

GA

$$\text{Genetic advance as percentage over mean} = \frac{\text{GA}}{\bar{X}} \times 100$$

Where

GA = Genetic advance

X = General mean

Genetic advance as percent over mean was given by Johnson *et al.*, (1955) as given below

0-10%	Low
11-20%	Moderate
21% above	High

3.5.3 Genotypic and phenotypic correlation

The correlation coefficients were estimated by using the formula given by (Al-Jibouri *et al.*,1958). Correlation coefficients were estimated in all possible character combinations at genotypic(r_g)and phenotypic level(r_p)

$$\text{Phenotypic correlation} = r_{xy}(p) = \frac{\text{Cov}_{xy}(p)}{\sqrt{V_x \times (p) \times V_y(p)}}$$

$$\text{Genotypic correlation} = r_{xy}(g) = \frac{\text{Cov}_{xy}(g)}{\sqrt{V_x \times (g) \times V_y(g)}}$$

Where

$\text{Cov}_{xy}(p)$ = Phenotypic coefficient of variance between x and y

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

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

$\text{Cov}_{xy}(g)$ = Genotypic coefficient of variance between x and y

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

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

Test of significance of correlation was tested by comparing the 'r' value with obtained value

3.5.4 Path coefficient analysis

The Dewey and Lu (1959) approach was used to calculate coefficient analysis. The direct and indirect impacts of the morphological features on plant yield were determined using the genotypic and phenotypic correlation coefficients. For evaluating various direct and indirect effects, the simultaneous equations below were formed and solved.

$$r1_y = a + r_{12}b + r_{13}c + \dots + r_{1i}i$$

$$r2_y = a + r_{21}a + b + r_{23}c + \dots + r_{2i}i$$

$$r3_y = r_{31}a + r_{32}b + c + \dots + r_{3i}i$$

$$r1_y = r_{11}a + r_{12}b + r_{13}c + \dots + I$$

where

i = Direct effect of character 'a' to 'I' and the dependent characters on y.

Where, $r1_y$ to 11_y = Co-efficient of correlation between casual factors 1 to I with the dependent character on y.

r_{12} to r_{11} = Co-efficient of correlation among the casual factors a, b, c

Residual effect (R) was computed by using the following formula

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

3.5.5 Genetic Divergence

Mahalanobis's D^2 analysis (1936) was used to estimate genetic divergence between the genotypes in population

D^2 analysis was estimated by using the following formula

The D^2 value between i^{th} and j^{th} genotypes for p characters was calculated as

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

Y_{it} = Uncorrected mean value of i^{th} genotype for t^{th} character

Y_{jt} = Uncorrected mean value of j^{th} genotype for t^{th} character

D^2_{ij} = D^2 value between i^{th} and j^{th}

Transformation of standardized uncorrelated values from correlated variables was done before working out of the D^2 values. The sum of squares of the difference between the pair of corresponding uncorrelated (Y_s) values of any two genotypes is obtained as D^2 values

A total of

$$\frac{n(n-1)}{2} D^2 \text{ values were calculated}$$

Where, n = Number of genotypes.

3.5.5.1 Clustering of genotypes

Using Tocher method described by Rao (1952). Genotypes were grouped into cluster based on D^2 values

3.5.5.2 Intra and Inter cluster distances

The intra and inter clustering distances were calculated by the formula given by Singh and Chaudhary (1979).

$$\text{Square of inter cluster distance} = \frac{SD_{ij}^2}{n_{ij}}$$

Where,

D_{ij}^2 = Sum of distance between all possible combinations (n_{ij}) of the two clusters.

n_i = Number of genotypes in cluster 'i'

n_j = Number of genotypes in cluster 'j'

$$\text{Square of intra cluster distance} = \frac{SD_i^2}{N}$$

D_i^2 = Sum of D^2 values between all possible combinations of the genotypes included in cluster.

n = Number of genotypes in cluster

3.5.6 Principal component analysis

Principal components (PCs) with an eigenvalue greater than one were chosen (Jeffers.,1967) and the PCA was carried out using the standardized values of the PAST 3 program and the computer software Microsoft Excel. Principal Component Analysis (PCA) is a powerful method for determining the fewest number of components while explaining the most variability out of total variability (Morrison., 1982). PCA aids in genotype ranking based on PC score the scree plot was used to visually examine the components that contributed the major share in the total variance

Plate 1 Glimpses of field activities



Field preparation



Mulching



Transplanting



Transplanting in main field



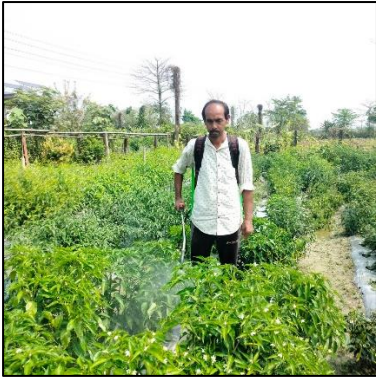
Irrigation



Fertilizer application



Plate 1 Glimpses of field activities



Spraying of All 19:19:19 (N:P: K)



Weeding



Plant height measurement



Seed extraction



Harvesting



3.6 Location and duration of experiment II

Screening of Chilli genotypes (including AICRP lines, released varieties and local cultivars) against chilli veinal mottle virus disease. Screening was conducted in both field level near Instruction farm and in green house of vegetable nursery near Department of vegetable and spice crops, Faculty of Horticulture, U.B.K.V, Pundibari. During the period from August, 2022 to January 2023.

A total of 39 chilli genotypes are collected. Including AICRP lines, local varieties

Table 3.4 List of genotypes used in the screening

S. No	Name of the genotypes	Source
1	CHILLI VAR-1IET-2021	AICRP-VC IIVR Varanasi
2	CHILLI VAR-3IET-2021	AICRP-VC IIVR Varanasi
3	CHILLI VAR-4IET-2021	AICRP-VC IIVR Varanasi
4	CHILLI VAR-6IET-2021	AICRP-VC IIVR Varanasi
5	CHILLI VAR-7IET-2021	AICRP-VC IIVR Varanasi
6	CHILLI VAR-9IET-2021	AICRP-VC IIVR Varanasi
7	CHILLI VAR-10IET-2021	AICRP-VC IIVR Varanasi
8	CHILLI VAR-11IET-2021	AICRP-VC IIVR Varanasi
9	CHILLI LCVRRRESIST2021/CHILLICVRES-1	AICRP-VC IIVR Varanasi
10	CHILLI LCVRRRESIST2021/CHILLICVRES-2	AICRP-VC IIVR Varanasi
11	CHILLI LCVRRRESIST2021/CHILLICVRES-4	AICRP-VC IIVR Varanasi
12	CHILLI LCVRRRESIST2021/CHILLICVRES-7	AICRP-VC IIVR Varanasi
13	CHILLI LCVRRRESIST2021/CHILLICVRES-8	AICRP-VC IIVR Varanasi
14	CHILLI LCVRRRESIST2021/CHILLICVRES-9	AICRP-VC IIVR Varanasi
15	CHILLI-HPAVT 1-2021-CHILLIVAR-1	AICRP-VC IIVR Varanasi
16	CHILLI-HPAVT -1-2021-CHILLIVAR-2	AICRP-VC IIVR Varanasi
17	CHILLI-HPAVT -1-2021-CHILLIVAR-3	AICRP-VC IIVR Varanasi
18	CHILLI-HPAVT -1-2021-CHILLIVAR-4	AICRP-VC IIVR Varanasi
19	CHILLI-HPAVT -1-2021-CHILLIVAR-5	AICRP-VC IIVR Varanasi
20	CHILLI-HPAVT- 1-2021-CHILLIVAR-6	AICRP-VC IIVR Varanasi
21	CHILLI-HPAVT- 1-2021-CHILLIVAR-7	AICRP-VC IIVR Varanasi
22	CHILLI-HPAVT -1-2021-CHILLIVAR-8	AICRP-VC IIVR Varanasi

23	CHILLI-HPAVT -1-2021-CHILLIVAR-9	AICRP-VC IIVR Varanasi
24	CHILLI-HPAVT -1-2021-CHILLIVAR-10	AICRP-VC IIVR Varanasi
25	CHILLI-HPAVT -1-2021-CHILLIVAR-11	AICRP-VC IIVR Varanasi
26	CHILLI-HPAVT -1-2021-CHILLIVAR-12	AICRP-VC IIVR Varanasi
27	CHILLI-AVT-2-2019-CHILLIVAR-1	AICRP-VC IIVR Varanasi
28	CHILLI-AVT-2-2019-CHILLIVAR-2	AICRP-VC IIVR Varanasi
29	CHILLI-AVT-2-2019-CHILLIVAR-4	AICRP-VC IIVR Varanasi
30	CHILLI-AVT-2-2019-CHILLIVAR-6	AICRP-VC IIVR Varanasi
31	AP-1-G4-JAGANATH	Andhra Pradesh
32	NW-2 MITREMORO	Manipur
33	CB-1	Cooch Behar
34	ARKA HARITHA	IIHR-Bangalore
35	CHILLI-AVT-2-2018-CHILLI-VAR-1	AICRP-VC IIVR Varanasi
36	CHILLI-IET-2020-CHILLI-VAR-12	AICRP-VC IIVR Varanasi
37	CHILLI-IET-2020-CHILLI-VAR8	AICRP-VC IIVR Varanasi
38	CHILLI-AVT-2-2018-CHILLI-VAR-5	AICRP-VC IIVR Varanasi
39	PUNDIBARI LOCAL	Pundibari

3.6.1 Nursery

The collected seeds were germinated during the third and fourth week of August. Plastic trays of 50 cells are used for sowing. Trays are filled with vermicompost and cocopeat in 40:60 ratio. In the month of September all the germinated seedlings have attained 4 leaf stage. These seedlings were used for Artificial sap mediated mechanical inoculation maintained in a closed room. A diseased plant with ChiVMV is used as the source plant for mechanical inoculation. Healthy plant was maintained in other growth chamber to avoid cross contamination.

3.7 Artificial sap inoculation method

Method given by (Sanabam. R *et al.*, (2018)) was followed.

1. Select an infected chilli plant (ChiVMV)
2. Sample was bought in icepack. RNA degrades fastly environment we must maintain in chilled conditions

3. Inoculum were prepared by crushing infected leaves in Phosphate buffer (0.2M, pH-7.4). Buffer should be in chilled condition
4. Before application of sap charcoal powder is applied on the leaves. It will create gentle injury on leaves
5. Apply the sap on healthy seedlings by rubbing
6. To eliminate the residues of celite, the inoculated leaves were rinsed with a jet of water with the help of a sprayer
7. After 2-3minutes sap was applied again this process should be repeated 2-3times
8. Symptoms were recorded 2-28 days of post inoculation

3.7.1 Scoring of disease Symptoms for ChiVMV:

Symptoms for ChiVMV (*Poty virus*) infection were evaluated according to Disease incidence percentage given by Reddy *et al.*, (2001) For each genotype at least 10 plants were scored. Observations were recorded for the field samples and mechanically inoculated samples at 2-28 days after post inoculation during infection development in chilli plants.

Table 3. 5 Scoring table (Reddy *et al.*, 2001)

Disease incidence percentage	Disease resistance
0	Immune
1-10	Highly Resistance
11-25	Resistant
26-40	Moderately resistant
41-60	Susceptible
>60%	Susceptible

3.7.2 Percent Disease Index (PDI)

The disease incidence observations were taken at weekly intervals for field evaluation. For mechanical inoculation observations were taken from 2-28 days after post inoculation. The per cent of disease incidence was calculated by the formula

$$\text{Per cent disease incidence (PDI)} = \frac{\text{Number of infected plants}}{\text{Total number of plants}} \times 100$$

3.8 Laboratory study

The experiments related to third objective of the present research were carried out in the ICAR- Niche Area of Excellence (NAE) Laboratory of Department of Biochemistry, UBKV which are summarized below.

3.8.1 Chemicals and reagents

All the chemicals, reagents (AR grade/MB grade) and kits used in the experiments were described in the table 3.6. The reagents were procured from Sigma Aldrich Inc, USA; HI Media Laboratories Pvt. Ltd, Mumbai, India, Merck Specialities Pvt. Ltd, Mumbai, India, Thermo fisher Scientific, India, Promega, India, Genetix, India and SRL Pvt. Ltd, Mumbai, India. Double distilled water and Milli-Q water which were used in the laboratory works as per requirement.

3.8.2 Instruments

The major instruments used in the present study along with their make and model have been enlisted in table 3.6

Table 3.6 List of instruments used and their model and make

S.NO	Name of the instrument	Model	Make
1	Table Top centrifuge	Centrifuge 5424	Eppendorf, Germani
2	Weighing balance	ME203E	Mettle Toledo, Switzer land
3	PCR/thermal cycler	Veriti	Applied biosystem, USA
4	Gel casting and running system	-	Atto, Japan, Biorad
5	Nano drop	Multi sky-high Micro-plate Spectrophotometer	Thermo fisher scientific, USA
6	Real time PCR	Quant studio 3 system 96 well,0.2ml	Applied biosystem, USA
7	Ice flake machine	Local	BR Biochem Life Sci, India
8	pH meter	pH 700	Eutech, Singapore
9	Chemi doc system	I Bright 750	Invitrogen USA
10	Dry bath	BBM-CP	Labins, India

3.9 PCR based screening of chilli genotypes

The chilli genotypes were screened for the presence of potyvirus using the specific primers designed for ChiVMV. The following activities associated with the objective have been presented in the following procedure

3.9.1 RNA Isolation: Total RNA is isolated using standard Tri-reagent method/Trizol method

Protocol:

Grind 50-100 mg tissue in liquid nitrogen and add 1ml TRIZOL (TRI) reagent and homogenise the tissue.



Transfer the sample into 2.0ml vials (Eppendorf tube).



Add 200µl chloroform per ml TRI reagent used. Securely cap the tubes and vigorously shake the tubes for 15 seconds.



Incubate at RT (Room temperature) for 10 minutes.



Centrifuge the tubes at a maximum 12,000 rpm for 15 minutes



Following separation, a lower red phase, an interphase and a clear to light pink upper aqueous phases are visible. The RNA is exclusively in the aqueous upper phase.



Transfer the aqueous phase to a fresh 1.5ml vial (Eppendorf tube).



Add 500µl of chilled isopropyl alcohol / isopropanol for every 1ml Tri extract. Incubate at RT for 10 minutes and centrifuge at a maximum 12000 rpm for 10 min



A white colour pellet of RNA forms at the bottom of the tube.



Remove the supernatant and wash the RNA pellet with 70% ethanol prepared in DEPC treated water with the pipette man



Centrifuge at 7500 rpm for 5 min at. Discard the supernatant



Air dry the RNA pellet for 5-10 min. Do not over dry, dissolve the RNA pellet in appropriate volume of RNase-free water (55-60°C) in dry bath for 10 minutes

3.9.2 RNA purity check

The quality of RNA was checked by using a Nano drop. 2 µl of RNA placed in µdrop plate and inserted in Nano drop. Among different nucleic acids we must adjust RNA. absorbance is recorded at 260/280 nm wavelength. Purity of RNA lies in between 1.85 – 2.0. Samples which are near 2 were taken to prepare working samples. Later we prepared CDNA

3.9.3 CDNA Protocol

- 1) Take 5µg of RNA (volume varies based on concentration) and make it up to 9µl with RNase free water/ DEPC treated water in a 0.2ml tube (PCR tubes).
- 2) Add 1µl (10mM) oligo (dT) to the mixture.
- 3) Keep the tubes in thermal cycler or dry bath at 70°C for 5min.
- 4) Take out the samples and keep on ice for 5 min. Then proceed for cDNA synthesis
- 5) Take 2µl of RT-buffer (10X) with MgCl₂ (25mM) already present in the buffer into each oligo (dt) treated tube.
- 6) Add 1 µl (200U/ µl) of RT-enzyme (source: M-MLV) to it.
- 7) Now add 1 µl (0.1M) dNTP mix into each tube
- 8) Finally make up the volume to 20 µl by DEPC treated water.
- 9) Now keep the tubes in thermal cycler with the following temperature cycle for the synthesis of first strand cDNA synthesis.

Table 3.7 CDNA

Step	Temperature	Time
Oligo (dt) treatment	70°	5 min
CDNA synthesis		
Annealing of primer	25°	5min
Extension of CDNA strand	42°	60min
Enzyme deactivation	70°	15min

3.9.4 Confirmation of potyvirus infection by PCR reaction

For confirmation of the presence of ChiVMV, at first the ChiVMV specific primers were used. After initial confirmation, primers as enlisted in Table were used for further confirmation.

For PCR analysis the following reagents were used:

Go green taq master mix (Promega brand)

1) dNTPS-2 µl

2) Taq polymerase-1 µl

3) PCR Buffer (with 15mM MgCl₂)- 2 µl

Genomic DNA / Viral DNA	1 µl
Forward primer	1 µl
Reverse primer	1 µl
Nuclease free Water	2 µl
Go Taq green master mix	5 µl
Total	10 µl

The PCR amplification was carried out in a thermal cycler (Veriti, Applied Biosystems, USA)

Table 3.8 List of primers used in the study

Primer name	Sequence	Reference
CVMV1037Pol(F)	AGCATGGAGAGAGCGACA TTAGTC	Tsai W. S. <i>et al.</i> , (2008)
Oligo dt(R)	GCGGGATCCTTTTTTTTTT TTTTTTTTTT	Tsai W. S. <i>et al.</i> , (2008)
Pat-F	AACCTGAGCGTATAGTTTC A	Tsai W. S. <i>et al.</i> , (2008)
Pat-R	TACGCTTCAGCAAGATTG CT	Tsai W. S. <i>et al.</i> , (2008)
Chi-1F	TACGCTTCAGCAAGATTG CT	Jiao.Y. <i>et al.</i> , (2020)
Chi-1R	CTGGTGAWCCATCATCATA AG	Jiao.Y. <i>et al.</i> , (2020)
Chi-5F	CARGCATACTTTGTTAAAG AC	Jiao.Y. <i>et al.</i> , (2020)
Chi-5R	TCYACBACTGTTGATGGTT GTC	Jiao.Y. <i>et al.</i> , (2020)
Chi-6F	GCTGATGGRACAATAGTC AAG	Jiao.Y. <i>et al.</i> , (2020)
Chi-6R	CATRAAYCATAACAATAGT CTTTG	Jiao.Y. <i>et al.</i> , (2020)

During this experiment the PCR protocol followed was as follows

- Denaturation: 94°C for 1 minute.
- Annealing: 50-60°C for 30 seconds (35 cycles).
- Extension: 72°C for 1 minute.
- Final extension: 72°C for 10 minutes.
- Infinite Storage: 4°C.

3.9.5 Amplification and extraction of pure RNA fragment

After the extraction of RNA from plant sample the virus specific primers were used to amplify the desirable viral gene. The PCR the protocol and reagents are same as mentioned above. The primers were specific and targeting the coat protein (CP) region of ChiVMV for the experiment. After completion of the PCR the PCR product was separated by agarose gel electrophoresis of the sample in the 0.8% agarose gel. After the electrophoresis is completed, the desirable band was visualized under gel documentation unit

3.10 Protocol for Gel Electrophoresis

Gel electrophoresis is conducted to check if our desired band of DNA is present or not in our sample. it is explained step by step below

- 0.8% agarose gel was prepared by mixing 400mg of agarose in 50ml of TAE buffer
- The solution was heated in microwave oven for 1.30 minutes till it is transparent and without any granules.
- The solution was cooled a bit and added 4µl of EtBr (Ethidium bromide) and mixed gently.
- The solution was poured into the gel cassette gently and comb should be inserted.
- It was kept for solidifying for some time.
- The gel was then kept in running buffer present in gel unit.
- In the 1st well adjacent to the remaining wells the DNA ladder (1kb plus purple DNA ladder) was loaded in the 1st well.
- Then the samples completed PCR were loaded in the remaining wells.
- The gel was run at 65V for about 40 minutes.
- The run was halted after the band reached the half way in the gel.
- Picture of gel was taken in Chemi-doc machine.

Plate 2 Glimpses of mechanical inoculation



Filling of portrays



Irrigation



2 leaf stage



4 leaf stage



Infected plant (ChiVMV)



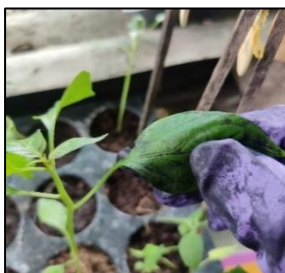
Buffer



Crushing the sample



Sap preparation



Appliction of
charcoal powder



Sap application



Spraying with water

Plate 3 Glimpses of Lab Work



1. Infected ChiVMV sample



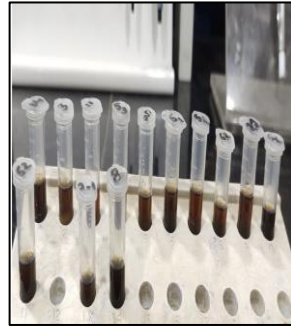
2. Crushing of sample



3. Trizol



4. Chloroform



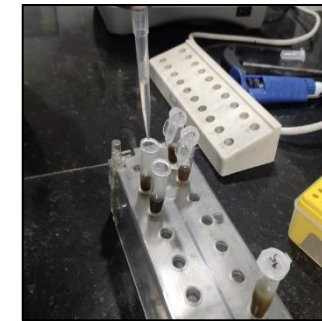
5. Room temperature for 10 min



6. Centrifuge



7. Phase separation



8. Iso P



9. Centrifuge



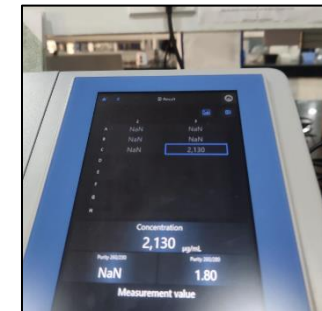
10. Ethanol wash pellet



11. Centrifuge



12. Dry bath



13. Nano drop

Plate 3 Glimpses of lab work



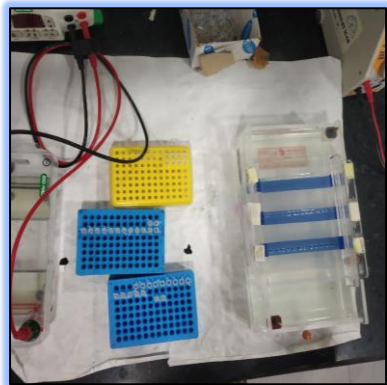
Sample preparation for C DNA



Sample preparation for PCR



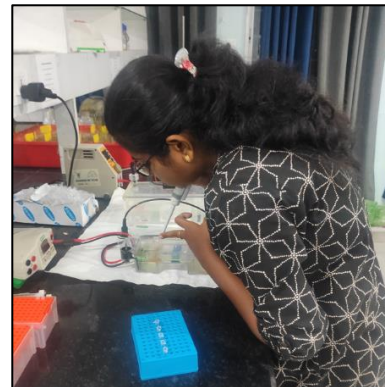
PCR machine with sample for amplification



Gel unit



1 kb plus ladder



Loading of PCR product



Gel documentation

CHAPTER 4

**RESULTS
AND
DISCUSSION**

The present study entitled Variability character association and diversity analysis in *Capsicum annuum*. L genotypes was carried out during Rabi 2021-2022 with 57 genotypes of chilli for 16 morphological traits and 13 quantitative traits. Screening of chilli genotypes against ChiVMV was carried out during August 2022-Jan 2023 with 39 genotypes. After completion of field and laboratory work, recorded data was subjected to stastical analysis. With a view to study the genetic variability in chilli the results of the experiment variability, correlation, path coefficient analysis, diversity analysis, principal component has been operated. Screening of chilli genotypes against ChiVMV for resistance have been designed both field and mechanical sap inoculation method and immune genotypes were been identified Results are presented under the following subheadings

4.1 Morphological characters of chilli genotypes

4.2 Mean performance of genotypes

4.3 Coefficient of variability

4.4 Heritability and genetic advance

4.5 Character association analysis

4.6 Path coefficient analysis

4.7 Principal component analysis

4.8 Genetic divergent analysis

4.9 Screening of genotypes

4.1Morphological characters of chilli genotypes

Morphological characters like Stem colour, Stem shape, Stem pubescence, Growth Habit, Branching Habit Leaf colour, Leaf shape, Leaf Pubescence, Corolla colour, Corolla shape, Anther colour, Filament colour, Stigma exertion, Fruit colour at intermediate stage, Fruit colour at mature stage, Fruit shape for all 54 genotypes were presented in table 4.1,4.2

Table 4.1 Morphological parameters for growth

Code	Stem colour	Stem shape	Stem pubescence	Leaf colour	Leaf shape	Leaf pubescence	Growth Habit	Branching Habit
UBC1	Green	Cylindrical	Sparse	Dark green	Ovate	Sparse	Prostrate	Intermediate
UBC2	Green with purple stripes	Cylindrical	Sparse	Dark green	Lanceolate	Sparse	Prostrate	Sparse
UBC3	Green	Cylindrical	Intermediate	Green	Lanceolate	Sparse	Intermediate	Intermediate
UBC4	Green	Cylindrical	Sparse	Dark green	Lanceolate	Sparse	Intermediate	Sparse
UBC5	Green with purple stripes	Cylindrical	Intermediate	Dark green	Lanceolate	Sparse	Intermediate	Intermediate
UBC6	Green	Cylindrical	Intermediate	Dark green	Ovate	Sparse	Intermediate	Intermediate
UBC7	Green	Cylindrical	Sparse	Dark green	Lanceolate	Sparse	Prostrate	Dense
UBC8	Green with purple stripes	Cylindrical	Intermediate	Dark green	Ovate	Sparse	Prostrate	Intermediate
UBC9	Green	Cylindrical	Sparse	Green	Lanceolate	Sparse	Intermediate	Intermediate
UBC10	Green	Cylindrical	Intermediate	Green	Lanceolate	Sparse	Intermediate	Intermediate
UBC11	Green	Cylindrical	Sparse	Green	Lanceolate	Sparse	Prostrate	Dense
UBC12	Green	Cylindrical	Sparse	Dark green	Lanceolate	Sparse	Intermediate	Intermediate
UBC13	Green	Angled	Sparse	Green	Ovate	Sparse	Intermediate	Intermediate
UBC14	Green	Cylindrical	Intermediate	Dark green	Lanceolate	Sparse	Intermediate	Sparse
UBC15	Green	Cylindrical	Sparse	Green	Lanceolate	Sparse	Prostrate	Dense
UBC16	Green	Angled	Sparse	Green	Lanceolate	Sparse	Prostrate	Dense
UBC18	Green	Cylindrical	Sparse	Green	Lanceolate	Sparse	Prostrate	Intermediate
UBC19	Green	Cylindrical	Intermediate	Green	Lanceolate	Sparse	Intermediate	Intermediate
UBC20	Green	Cylindrical	Intermediate	Light Green	Lanceolate	Sparse	Intermediate	Dense
UBC22	Green	Cylindrical	Intermediate	Dark green	Lanceolate	Sparse	Intermediate	Dense
UBC23	Green	Cylindrical	Sparse	Green	Lanceolate	Sparse	Prostrate	Intermediate
UBC24	Green	Cylindrical	Sparse	Green	Lanceolate	Sparse	Erect	Sparse
UBC25	Green	Cylindrical	Sparse	Dark green	Ovate	Sparse	Intermediate	Sparse
UBC26	Green	Cylindrical	Sparse	Light Green	Lanceolate	Sparse	Intermediate	Intermediate
UBC27	Green	Cylindrical	Intermediate	Green	Lanceolate	Sparse	Intermediate	Intermediate
UBC28	Green	Cylindrical	Dense	Dark green	Lanceolate	Sparse	Prostrate	Intermediate

Table 4.1(cont.,)

UBC29	Green	Cylindrical	Sparse	Dark green	Lanceolate	Sparse	Prostrate	Dense
UBC30	Green	Cylindrical	Sparse	Green	Lanceolate	Sparse	Intermediate	Intermediate
UBC31	Green	Cylindrical	Intermediate	Green	Lanceolate	Sparse	Intermediate	Intermediate
UBC32	Green	Cylindrical	Sparse	Green	Lanceolate	Sparse	Intermediate	Intermediate
UBC33	Green	Cylindrical	Sparse	Dark green	Lanceolate	Sparse	Intermediate	Intermediate
UBC34	Green	Cylindrical	Sparse	Light Green	Lanceolate	Sparse	Intermediate	Sparse
UBC35	Green	Cylindrical	Sparse	Green	Lanceolate	Sparse	Intermediate	Intermediate
UBC37	Green with purple stripes	Cylindrical	Sparse	Green	Lanceolate	Sparse	Intermediate	Intermediate
UBC38	Green with purple stripes	Cylindrical	Intermediate	Green	Lanceolate	Sparse	Prostrate	Dense
CBC39	Green	Cylindrical	Sparse	Light Green	Lanceolate	Sparse	Intermediate	Intermediate
UBC40	Green	Cylindrical	Sparse	Dark green	Lanceolate	Sparse	Intermediate	Intermediate
UBC42	Green	Cylindrical	Sparse	Dark green	Lanceolate	Sparse	Intermediate	Intermediate
UBC44	Green	Cylindrical	Intermediate	Dark green	Lanceolate	Sparse	Intermediate	Intermediate
UBC45	Green with purple stripes	Cylindrical	Intermediate	Dark green	Ovate	Sparse	Intermediate	Intermediate
UBC46	Green	Cylindrical	Sparse	Dark green	Lanceolate	Sparse	Intermediate	Intermediate
UBC47	Green	Cylindrical	Intermediate	Green	Lanceolate	Sparse	Intermediate	Sparse
UBC48	Green	Cylindrical	Sparse	Green	Lanceolate	Sparse	Prostrate	Intermediate
UBC49	Green with purple stripes	Angled	Sparse	Green	Lanceolate	Sparse	Intermediate	Sparse
UBC52	Green	Cylindrical	Intermediate	Dark green	Lanceolate	Sparse	Intermediate	Intermediate
UBC53	Green	Cylindrical	Intermediate	Green	Lanceolate	Sparse	Intermediate	Sparse
UBC54	Green	Cylindrical	Sparse	Green	Lanceolate	Sparse	Prostrate	Intermediate
UBC56	Green	Cylindrical	Intermediate	Green	Lanceolate	Sparse	Intermediate	Sparse
UBC57	Green	Cylindrical	Sparse	Dark green	Lanceolate	Sparse	Intermediate	Sparse
UBC58	Green	Cylindrical	Sparse	Dark green	Lanceolate	Sparse	Prostrate	Intermediate
UBC59	Green	Cylindrical	Sparse	Green	Lanceolate	Sparse	Intermediate	Intermediate
UBC60	Green with purple stripes	Angled	Sparse	Green	Lanceolate	Sparse	Intermediate	Sparse
UBC61	Green	Cylindrical	Intermediate	Dark green	Lanceolate	Sparse	Prostrate	Intermediate
UBC62	Green	Cylindrical	Intermediate	Dark green	Lanceolate	Sparse	Prostrate	Intermediate

Table 4.2 Floral and Fruit characters

Code	CCL	CS	ACL	FCL	SE	FS	FCIS	FCMS
UBC1	White	Campanulate	Purple	White	Exserted	Elongate	Green	Red
UBC2	White	Rotate	Purple	White	Exserted	Elongate	Green	Light red
UBC3	White	Campanulate	Purple	White	Exserted	Elongate	Green	Red
UBC4	White	Campanulate	Purple	White	Exserted	Elongate	Green	Dark red
UBC5	White	Rotate	Purple	White	Exserted	Elongate	Green	Dark red
UBC6	White	Campanulate	Purple	White	Exserted	Elongate	Green	Light red
UBC7	White	Rotate	Blue	White	Inserted	Elongate	Green	Light red
UBC8	White	Rotate	Purple	White	Exserted	Elongate	Green	Red
UBC9	White	Rotate	Purple	White	Inserted	Elongate	Green	Dark red
UBC10	White	Rotate	Purple	White	Inserted	Elongate	Green	Orange
UBC11	White	Rotate	Purple	White	Inserted	Elongate	Green	Red
UBC12	White	Campanulate	Purple	White	Same level	Elongate	Green	Light red
UBC13	White	Campanulate	Purple	White	Exserted	Elongate	Green	Red
UBC14	White	Rotate	Purple	Light Purple	Exserted	Elongate	Green	Light red
UBC15	White	Rotate	Blue	White	Exserted	Elongate	Light Green	Light red
UBC16	White	Rotate	Pale blue	White	Exserted	Elongate	Green	Dark red
UBC18	White	Rotate	Purple	White	Exserted	Elongate	Green	Red
UBC19	White	Rotate	Purple	White	Exserted	Elongate	Green	Light red
UBC20	White	Campanulate	Purple	White	Exserted	Elongate	Green	Light red
UBC22	White	Rotate	Purple	White	Exserted	Elongate	Light Green	Red
UBC23	White	Rotate	Pale blue	White	Inserted	Elongate	Green	Light red
UBC24	White	Rotate	Purple	White	Same level	Elongate	Green	Red
UBC25	White	Rotate	Purple	White	Inserted	Elongate	Light Green	Red
UBC26	White	Rotate	Purple	White	Exserted	Elongate	Green	Dark red
UBC27	White	Rotate	Pale blue	White	Exserted	Elongate	Green	Red
UBC28	White	Rotate	Purple	White	Inserted	Elongate	Light Green	Red
UBC29	White	Rotate	Purple	Purple	Exserted	Elongate	Green	Light red
UBC30	White	Rotate	Purple	White	Exserted	Elongate	Green	Red
UBC31	White	Rotate	Pale blue	Purple	Same level	Elongate	Green	Dark red

CCL: Corolla colour, CS: Corolla shape, ACL: Anther colour, FCL: Filament colour, SE: Stigma exertion, FS: Fruit shape, FCIS: Fruit colour at intermediate stage, FCMS: Fruit colour at mature stage

Table 4.2(Cont.,)

UBC32	White	Rotate	Purple	Purple	Inserted	Elongate	Green	Red
UBC33	White	Rotate	Purple	White	Exserted	Elongate	Green	Red
UBC34	White	Rotate	Pale blue	White	Inserted	Elongate	Light Green	Red
UBC35	White	Rotate	Purple	Yellow	Inserted	Elongate	Green	Dark red
UBC37	White	Campanulate	Blue	White	Exserted	Elongate	Green	Light red
UBC38	White	Rotate	Purple	White	Inserted	Elongate	Green	Light red
UBC39	White	Rotate	Purple	White	Inserted	Elongate	Green	Red
UBC40	White	Rotate	Purple	White	Inserted	Elongate	Light Green	Light red
UBC42	White	Rotate	Blue	Yellow	Exserted	Elongate	Green	Light red
UBC44	White	Rotate	Purple	White	Exserted	Elongate	Green	Dark red
UBC45	White	Rotate	Purple	White	Inserted	Sunken	Light Green	Red
UBC46	White	Campanulate	Blue	White	Exserted	Sunken	Green	Red
UBC47	White	Campanulate	Blue	White	Exserted	Elongate	Green	Red
UBC48	White	Campanulate	Pale blue	White	Inserted	Elongate	Green	Light red
UBC49	White	Campanulate	Blue	White	Exserted	Elongate	Green	Dark red
UBC52	White	Campanulate	Pale blue	Yellow	Inserted	Elongate	Green	Light red
UBC53	White	Rotate	Blue	Purple	Inserted	Elongate	Green	Red
UBC54	White	Rotate	Blue	Light Purple	Inserted	Elongate	Light Green	Red
UBC56	White	Campanulate	Pale blue	White	Exserted	Elongate	Green	Red
UBC57	White	Rotate	Pale blue	Purple	Exserted	Elongate	Green	Light red
UBC58	White	Campanulate	Blue	White	Inserted	Elongate	Green	Light red
UBC59	White	Campanulate	Blue	White	Exserted	Elongate	Green	Red
UBC60	White	Rotate	Purple	White	Inserted	Elongate	Green	Red
UBC61	White	Rotate	Purple	White	Exserted	Elongate	Light Green	Dark red
UBC62	White	Rotate	Blue	Purple	Exserted	Elongate	Green	Light red

CCL: Corolla colour, CS: Corolla shape, ACL: Anther colour, FCL: Filament colour, SE: Stigma exertion, FS: Fruit shape, FCIS: Fruit colour at intermediate stage, FCMS: Fruit colour at mature stage

4.1.1 Stem characters

Based on stem colour genotypes are classified into two categories. Whereas 45 genotypes noted green stem colour. Rest 8 genotypes UBC-2, UBC-5, UBC-8, UBC-37, UBC-38, UBC-45, UBC-49, and UBC-60 noted green with purple stripes. Based on stem shape genotypes were categorized into 2 groups. Where are 51 genotypes were noted cylindrical shape. Rest 3 genotypes UBC-13, UBC-49 and UBC-60 noted angled shape stem. Stem pubescence were classified into three categories. Whereas UBC-28 had dense pubescence. Whereas 30 genotypes had sparse pubescence. Rest 23 genotypes had intermediate pubescence.

4.1.2 Leaf characters

All 54 genotypes had shown sparse leaf pubescence. Leaf shape were categorized into two classes. Whereas 49 genotypes noted lanceolate leaf shape. Remaining 5 genotypes UBC-1, UBC-6, UBC-13, UBC-25, and UBC-45 noted ovate leaf shape. Genotypes were categorized into two groups for leaf colour. Out of 54 genotypes 24 genotypes UBC-1, UBC-2, UBC-4, UBC-5, UBC-6, UBC-7, UBC-8, UBC-12, UBC-14, UBC-22, UBC-25, UBC-28, UBC-29, UBC-33, UBC-40, UBC-42, UBC-44, UBC-45, UBC-46, UBC-52, UBC-57, UBC-58, UBC-61, and UBC-62 were observed dark green in colour. While 4 genotypes UBC-20, UBC-26, UBC-34, and UBC-39 genotypes observed light green in leaf colour. Whereas rest 26 genotypes noted green leaf colour.

4.1.3 Growth characters

All 54 genotypes were grouped into 3 groups based on growth habit. 17 genotypes UBC-1, UBC-6, UBC-7, UBC-8, UBC-11, UBC-15, UBC-16, UBC-18, UBC-23, UBC-28, UBC-29, UBC-38, UBC-48, UBC-54, UBC-58, UBC-61, UBC-62 had shown prostrate growth habit. While, erect type of growth habit was noted in UBC-24. Rest 34 genotypes had shown intermediated growth habit. 54 genotypes were grouped into 3 groups based on branching habit. 8 genotypes UBC-28, UBC-22, UBC-29, UBC-20, UBC-16, UBC-15, UBC-11, UBC-7 had noted dense habit. 11 genotypes UBC-2, UBC-4, UBC-25, UBC-24, UBC-34, UBC-47, UBC-49, UBC-52, UBC-54, UBC-56 and UBC-60 had shown sparse branching habit. Rest 35 genotypes had shown intermediate growth habit.

4.1.4 Floral characters

All 54 genotypes had shown white corolla colour. Corolla shape is categorized into two groups. 16 genotypes UBC1, UBC3, UBC4, UBC6, UBC12, UBC13, UBC20, UBC37, UBC 46, UBC47, UBC48, UBC49, UBC52, UBC56, UBC58 and UBC59. Rest 38 genotypes had shown rotate shape. Anther colour is classified into 3 groups. 12 genotypes UBC7, UBC15, UBC37, UBC42, UBC 46, UBC47, UBC49, UBC53, UBC54, UBC58, UBC59 and UBC62 had shown blue anther colour. Whereas 10 genotypes UBC56, UBC57, UBC48, UBC52, UBC34, UBC31, UBC16, UBC23, UBC27 and UBC31 had shown pale blue anther colour. Rest 32 genotypes had shown purple anther colour. Filament colour was classified into four groups. 6 genotypes had shown purple colour UBC29, UBC31, UBC53, UBC57, UBC32 and UBC62. While, 2 genotypes UBC 14 and UBC 54 noted Light purple colour. UBC 52, UBC 42 and UBC 35 had shown yellow filament colour. Rest 45 genotypes had shown white colour.

4.1.5 Fruit characters

Out of 54 genotypes 52 genotypes had shown elongate shape. While, 2 genotypes UBC 45 and UBC 44 had shown sunken shape. Based on fruit colour at intermediate stage genotypes were categorized into two groups. 9 genotypes UBC 15, UBC 22, UBC25, UBC 28, UBC34, UBC40, UBC45, UBC54, UBC 61 were observed light green in colour. Whereas rest 45 genotypes observed green in colour. Based on fruit colour at mature stage genotypes were categorized into four groups. 9 genotypes UBC5, UBC9, UBC16, UBC26, UBC31, UBC35, UBC49, UBC61 were observed dark red in colour. 19 genotypes UBC 2, UBC6, UBC7, UBC12, UBC14, UBC15, UBC19, UBC20, UBC23, UBC29, UBC37, UBC38, UBC40, UBC42, UBC48, UBC52, UBC57, UBC58, UBC62 were observed light red in colour. Whereas UBC10 noted orange in colour. Rest 25 genotypes noted red in colour.

4.2 Mean performance of genotypes

4.2.1 Growth and earliness character

4.2.1.1 Plant height(cm)

The plant height of chilli genotypes observed was presented in the table 4.3. The average plant height was recorded between (40.30 to 72.75). The maximum plant height was recorded in UBC 62(72.75), followed by UBC33(72.60) and UBC28(71.69). Whereas UBC 23(40.30) is recorded for minimum plant height. The results clearly indicate significant variation in plant height. Therefore, highest range of variation for the trait plant height indicate wide range of variability among genotypes. Similar findings were noticed by Chopra *et al.*, (2005), J Jyothi *et al.*, (2011), Amit *et al.*, (2014), Srinivas *et al.*, (2017) (76.17 -46.57), Purad *et al.*, (2019) (75.43cm-32.02 cm) and Farwah *et al.*, (2020) (49.16-86.00).

4.2.1.2 Primary branches per plant

The number of primary branches per plant was presented in the table 4.3. The maximum number of primary branches was recorded in UBC 60(9.8), UBC 38(9.8) followed by UBC 1(8.8). While UBC 26 (4) recorded for minimum number of primary branches. Highest range of variation for the trait indicate wide range of variability. Results are in conformity with the earlier findings of Nagaraju *et al.*, (2018) (2.20-5.33) and Srinivas *et al.*, (2017) (7-4.33).

4.2.1.3 Days to first flowering (days)

The data pertaining to number of days taken from transplanting to first flower opening in each genotype was recorded. It was presented in the table 4.3. Minimum days to first flowering was recorded in UBC 1(33.6) followed by UBC 62(34) and UBC 36(35.6). Whereas maximum days to first flowering was recorded in UBC 33(57.6). Results were accordance with the findings of Srinivas *et al.*, 2017 (39-63.3), Farwah *et al.*, (2020) (24.40-38.60), Yatagiri *et al.*, (2017) (41.50- 74.50), Manju and Sreelathakumary (2002) and Amit *et al.*, (2014).

4.2.2 Fruit characters

4.2.2.1 Fruit length(cm)

Among all fifty-four genotypes studied maximum variation with respect to fruit length was observed which ranged from 3.72-14.66 and presented in the Table 4.3. Genotype UBC-13 has recorded highest fruit length (14.66) followed by UBC-10 (12.90) and UBC-9(12.6). Whereas UBC -47(3.72) recorded lowest fruit length. Highest range of variation for the trait fruit length indicate wide range of variability among genotypes. Above findings are in close conformity with Sreelatha kumary and Rajamony (2004), Chopra *et al.*, (2005), Smitha and Basavaraja (2006), Dhaliwal *et al.*, (2014), Vijaya *et al.*, (2014), Arup *et al.*, (2011), Singh *et al.*, (2022) (5.70-10.59), Nagaraju *et al.*, (2.15-14.48), Purad *et al.*, (2019) (2.34-15.2) and Mamatha *et al.*, (2017) (3.40 -9.69).

4.2.2.2 Fruit diameter(cm)

The data pertaining to fruit diameter of five replications from each genotype was presented in the table 4.3. The average fruit diameter was recorded between (1.68-3.44). The highest fruit diameter was expressed in genotypes UBC 8(3.44) followed by UBC-16(3.32) and UBC-4(3.30) whereas UBC-12(1.68) has recorded lowest diameter. The results are in line with findings of Janaki *et al.*, (2015) (0.76cm to 3.17cm) and Mamatha *et al.*, (2017) (2.43 cm -4.28 cm).

4.2.2.3 Fruit wall thickness(mm)

The data pertaining to fruit wall thickness was presented in the table 4.3. The highest fruit wall thickness was recorded in genotypes UBC-3(0.84), followed by UBC-61(0.55) and UBC-11(0.55) while, UBC-32(0.32) recorded lowest fruit wall thickness.

4.2.2.4 Days to first red ripe (days)

The observation on days to first red ripe appearance was presented in the table 4.3 UBC 9-(92) taken shorter duration for days to red ripe, followed by UBC-24 (99.40), UBC -10(100.4). Whereas UBC -16 (143.20) taken longer duration for days to red ripe Similar wide range in days to first red ripe was noticed by Singh *et al.*, (2022) (87.67-126.33).

4.2.2.5 Fruit weight (gm)

The data pertaining to fruit weight of matured green fruits were recorded and presented in the Table 4.4. Significant variation in fruit weight of chilli genotypes and it was ranged from 1.39-8.32. The highest fruit weight was recorded in UBC-8(8.32), followed by UBC-60(6.34) and UBC-20(6.25). Whereas UBC-49(1.39) has recorded lowest fruit weight. Findings were in accordance with earlier reports of Singh *et al.*, (2009), Gupta *et al.*, (2009), Farwah *et al.*, (2020) (1.38-9.28), Puradh *et al.*, (2019) (10.62 - 1.74 fruit), Mamatha *et al.*, (2017) (1.75 - 5.45)).

4.2.2.6 Fruits per plant

The observation on number of fruits per plant of five replications from each genotype was presented in the table 4.4. The maximum number of fruits per plant was recorded in genotypes UBC-48(86.0) followed by UBC-49(82.0) and UBC 62(71.4) were as UBC-37 (12.8) recorded for minimum number of fruits per plant. The results are in line with the findings of Puradh *et al.*, (2019) (128.71 - 3.57), Farwah *et al.*, 2020 (29.66-99.86), Mohanty (2003), Chopra *et al.*, (2005), Smitha and Basavaraj (2006), Sandeep *et al.*, (2008), Jyothi *et al.*, (2011), and Chattopadhyay *et al.*, (2011).

Table 4.3 Mean performance of Chilli genotypes for growth parameters and fruit characters

CODE	Plant height(cm)	Primary branches	Days to flowering(days)	Fruit length(cm)	Fruit diameter(cm)	Fruit wall Thickness(mm)	Days to first red ripe (days)
UBC1	53.92	8.8	33.6	10.40	2.80	0.54	120.60
UBC2	64.30	6.8	42.4	6.86	2.30	0.40	122.00
UBC3	48.87	6.8	44.8	12.50	2.60	0.84	135.40
UBC4	65.43	7.2	39.4	9.60	3.30	0.42	124.20
UBC5	53.13	5.2	41.6	9.30	3.20	0.42	114.60
UBC6	59.69	5.6	44.6	15.00	2.76	0.50	118.80
UBC7	53.54	5.2	49.6	8.86	2.88	0.38	120.20
UBC8	65.36	7.2	38.4	11.70	3.44	0.38	130.40
UBC9	54.24	6.8	50.0	12.66	2.10	0.42	92.00
UBC10	57.17	5.8	45.8	12.90	2.96	0.42	100.40
UBC11	42.39	3.8	51.8	8.78	2.20	0.36	120.80
UBC12	56.41	4.6	41.8	5.10	1.68	0.36	139.00
UBC13	66.01	8.2	38.2	14.66	3.04	0.38	124.60
UBC14	48.77	4.6	48.2	7.96	2.38	0.46	122.00
UBC15	59.87	6.8	42.2	7.90	3.22	0.42	133.20
UBC16	40.58	5.2	46.0	8.90	3.32	0.30	143.20
UBC18	68.35	4.0	51.6	7.52	2.96	0.50	136.20
UBC19	45.74	5.0	39.8	9.00	3.00	0.42	124.80
UBC20	60.54	5.8	40.0	8.10	2.24	0.34	134.60
UBC22	55.84	4.8	42.4	6.98	3.22	0.38	132.40
UBC23	40.30	4.4	52.8	10.00	3.18	0.44	119.60
UBC24	58.20	7.2	40.6	10.88	2.84	0.48	99.40
UBC25	53.82	4.2	47.6	12.14	3.10	0.50	123.00
UBC26	42.53	4.0	55.8	7.98	3.28	0.52	132.00
UBC27	51.80	4.4	54.2	9.66	2.70	0.34	120.20
UBC28	71.69	7.4	35.4	7.26	2.84	0.42	130.40
UBC29	54.34	5.6	45.2	8.78	2.38	0.38	138.60
UBC30	42.42	5.0	52.6	7.48	2.56	0.48	138.00
UBC31	59.53	5.8	47.8	9.34	2.06	0.42	129.00

Table 4.3.,

UBC32	40.83	4.4	55.8	11.34	2.08	0.26	133.00
UBC33	72.60	6.6	57.6	7.26	2.72	0.38	133.40
UBC34	53.41	5.5	51.6	6.68	2.26	0.38	141.40
UBC35	58.94	7.1	43.4	9.26	2.08	0.34	142.20
UBC37	42.09	5.4	57.0	7.20	2.52	0.34	136.40
UBC38	71.28	9.8	35.6	9.48	2.42	0.36	137.60
UBC39	61.14	7.2	41.2	12.32	3.10	0.44	143.20
UBC40	48.60	4.0	53.2	9.02	2.08	0.38	141.60
UBC42	64.93	4.6	52.2	7.48	2.30	0.42	145.00
UBC44	45.29	4.2	54.2	6.40	2.20	0.40	141.80
UBC45	52.89	8.0	42.2	4.52	2.12	0.40	139.40
UBC46	69.28	8.4	44.4	3.94	2.00	0.28	131.40
UBC47	69.79	8.5	36.2	3.72	2.28	0.38	133.60
UBC48	56.74	7.8	44.2	4.52	2.14	0.38	142.40
UBC49	58.83	4.8	48.0	6.14	2.44	0.36	136.20
UBC52	56.52	6.6	42.8	5.98	2.30	0.34	142.40
UBC53	55.37	6.0	47.8	7.26	2.84	0.34	141.60
UBC54	65.00	7.6	43.2	6.08	2.92	0.38	133.60
UBC56	65.33	8.4	42.4	6.28	2.66	0.38	138.00
UBC57	55.87	4.6	49.2	6.50	2.88	0.36	142.80
UBC58	51.24	5.9	52.8	7.50	2.18	0.40	131.40
UBC59	55.19	8.7	43.0	7.58	2.26	0.42	135.40
UBC60	69.56	9.8	36.0	8.80	2.10	0.38	130.00
UBC61	60.22	6.8	43.8	8.36	2.40	0.58	132.20
UBC62	72.75	8.4	34.0	5.74	2.72	0.42	142.40
SE _M	0.64	0.33	0.818	0.41	0.13	0.03	0.69
CD at 0.05%	1.80	0.92	2.27	1.15	0.36	0.10	1.94

4.2.2.7 Number of seeds per fruit

The observation on number of seeds per fruit was recorded and presented in the Table 4.4. The highest number of seeds per fruit was recorded in genotypes UBC 35(89.5) followed by UBC 52(83.1) and UBC 10(82.8). Whereas lowest number of seeds per fruit was recorded in the genotype UBC 11(34.4). Similar results were reported by Singh *et al.*, (2022) (57.47-100.40), Nagaraj *et al.*, (2018) (24-153.2) and Jyothi *et al.*, (2011) (39.2-84.2).

4.2.2.8 Seed weight (g/1000seeds)

The data pertaining to seed weight of chilli genotypes. It has been presented in the table 4.4. UBC- 1(7.95) has recorded highest seed weight followed by UBC 22-(7.87), and UBC- 8(7.17). While, UBC -37(4.01) was recorded for lowest seed weight. Results are in accordance with the earlier findings of Nagaraj *et al.*, (2018) (3.38-10.07) and Singh *et al.*, (2022) (2.77-5.1).

4.2.2.9 Fruit yield per plant (gm)

The data pertaining for fruit yield per plants of five replications from each genotype was recorded and presented in the table 4.4. The highest fruit yield per plant was recorded in the genotypes UBC-28(273.74) followed by UBC-62(254.10) and UBC-1(246.1). Whereas UBC- 37 was recorded for lowest fruit yield (36.64). Highest range of variation for fruit yield per plant indicate wide range of variability among genotypes. Above findings are in close conformity with Amit *et al.*, (2014), Jaisankar *et al.*, (2015) Srinivas *et al.*, (2017), Puradh *et al.*, (2019) (37.46-369.24).

4.2.2.10 Total Yield(t/ha)

The data pertaining on total yield of chilli genotypes was presented in the Table 4.4 Data revealed significant variation in yield it was ranged from (1.02-7.32). The highest total yield was recorded in genotypes UBC- 8 (7.51) followed by UBC-62(7.32) and UBC-59(7.05) UBC- 1(6.96). While UBC-37(1.02) recorded for lowest total yield

Table 4.4 Mean performance of Chilli genotypes for Yield parameters and Fruit characters

CODE	No of seeds	Seed test wt.	Fruit weight(gm)	NFFP	FYPP (gm)	Total yield(t/ha)
UBC1	72.4	7.95	5.01	50.6	246.91	6.96
UBC2	64.0	5.53	3.06	48.2	149.89	4.41
UBC3	67.2	5.50	3.17	42.8	117.28	3.50
UBC4	58.4	5.53	4.00	29.8	237.09	3.40
UBC5	53.6	4.43	3.18	43.4	131.72	4.25
UBC6	85.2	6.59	6.43	32.4	173.19	5.02
UBC7	59.4	5.24	3.09	32.2	123.27	3.10
UBC8	77.2	7.17	8.32	35.4	232.54	7.51
UBC9	56.4	5.55	4.01	40.6	131.94	4.59
UBC10	71.6	6.96	3.70	52.4	149.76	5.61
UBC11	34.4	3.47	2.55	42.4	98.82	3.09
UBC12	41.6	5.21	2.94	49.2	125.71	4.35
UBC13	73.4	6.26	3.65	40.8	221.99	5.35
UBC14	45.8	5.84	4.16	27.4	97.65	3.31
UBC15	64.8	6.37	3.28	55.4	168.62	5.96
UBC16	61.4	5.42	2.68	27.2	72.37	1.94
UBC18	53.2	5.68	1.68	39.8	65.82	2.35
UBC19	63.6	5.92	2.23	42.8	76.34	2.42
UBC20	82.8	6.44	6.25	25.2	193.13	4.12
UBC22	51.6	7.87	5.18	23.6	141.00	3.62
UBC23	70.4	4.17	3.06	27.6	56.62	2.07
UBC24	62.0	6.16	4.32	27.0	156.59	4.12
UBC25	67.4	5.16	2.68	27.4	123.19	2.48
UBC26	79.0	8.05	2.79	21.8	53.86	1.68
UBC27	71.6	5.73	5.42	22.0	60.55	2.81
UBC28	52.8	6.93	5.05	37.4	273.74	5.40
UBC29	48.6	4.33	3.73	45.4	141.22	4.04

NS: Number of seeds, NFFP: Number of fruits per plant, FYPP: Fruit yield/plant(gm), Fruit yield(t/ha)

Table 4.4 (Cont.,) Mean performance of Chilli genotypes for Yield parameters and Fruit characters

UBC30	52.6	4.12	3.66	34.4	70.20	3.76
UBC31	65.5	5.69	4.06	27.4	130.21	2.83
UBC32	51.0	4.35	3.15	31.8	57.56	2.66
UBC33	63.7	5.22	2.08	31.6	66.85	1.84
UBC34	49.6	6.16	1.90	41.4	62.40	2.50
UBC35	89.5	5.19	3.97	42.6	169.57	5.43
UBC37	51.0	4.01	3.95	12.8	36.64	1.20
UBC38	76.8	4.26	5.64	31.8	243.53	5.08
UBC39	57.5	5.63	6.09	30.8	176.03	5.31
UBC40	75.6	6.05	2.44	36.6	66.39	2.53
UBC42	43.6	4.92	3.41	30.6	78.53	2.95
UBC44	38.8	4.37	2.95	26.6	52.98	2.23
UBC45	55.8	5.80	3.19	51.2	149.17	4.30
UBC46	60.0	6.92	2.55	80.2	205.02	5.90
UBC47	53.6	6.62	2.91	78.6	229.99	6.62
UBC48	37.5	6.68	1.56	86.0	139.52	4.02
UBC49	42.2	6.20	1.38	82.0	113.67	3.27
UBC52	83.1	5.07	2.91	52.8	153.88	4.43
UBC53	51.0	6.19	2.44	48.6	118.50	3.41
UBC54	67.4	5.56	3.72	51.0	189.15	5.45
UBC56	69.2	4.70	3.52	54.8	186.28	5.36
UBC57	46.4	4.46	2.99	42.8	127.42	3.67
UBC58	53.8	5.24	2.50	43.2	103.98	2.99
UBC59	74.9	5.08	5.04	35.2	177.45	5.11
UBC60	68.0	5.31	6.34	38.6	244.76	7.05
UBC61	70.5	4.41	3.76	42.8	160.34	4.62
UBC62	64.4	6.39	3.52	71.4	254.10	7.32
SE	0.78	0.07	0.04	4.94	7.16	0.20
CD at 0.05%	2.19	0.20	0.11	13.7	19.9	0.57

NFPP: Number of fruits per plant, FYPP: Fruit yield/plant(gm) Fruit yield(t/ha)

4.3 Variability

For different characters genotypic coefficient variation and phenotypic coefficient variation, Heritability, Genetic advance, Genetic advance as percent over mean were analysed and worked out for 12 traits of chilli and presented in the table. Most of the characters have shown having higher magnitude of GCV and PCV. For the majority of traits, the difference between phenotypic and genotypic coefficients of variation was found to be less. Environmental influence on character expression was low.

4.3.1 High GCV and PCV

High GCV and PCV (>20%) was recorded for primary branches per plant (26.58% and 29.05%), Fruit length (29.95% and 31.94%), Seed number per fruit (21.64% and 21.83%), Fruit weight (37.99 % and 38.08%), Number of fruits per plant (37.39% and 45.46%), Fruit yield per plant gm (47.85 % and 49.08) and Total yield (47.77% and 49.00%) respectively. High estimates for both the GCV and PCV revealed that there is a more contribution of genetic components for total variation as well presence of environmental on these characters. The characters with higher GCV and PCV reported for yield and yield attributing traits were significant, and there is a better potential for genotype improvement. Therefore, having ample scope for improvement of these traits. The difference between PCV and GCV was found to be very less. Therefore, environmental influence on character expression was low.

Results for PCV and GCV were corroborated with findings of Mallikarjun *et al.*, (2003) (29.90% and 28.03%), Amit *et al.*, (2014) (23.67% and 23.63%) and Sran *et al.*, (2019) (26.89% and 12.33%) for number of primary branches. Farhad *et al.*, (2008) (27.16 % and 25.97%), Nahak *et al.*, (2019) (21.27% and 22.0256%), Sran *et al.*, (2019) (22% and 19.89%) and Farwah *et al.*, (2020) (20.49% and 20.16%) for fruit length. Choudhary and Samadia (2004) (37.69% and 37.46%), Amit *et al.*, (2014) (35.57% and 34.14 %), Nahak *et al.*, (2018) (38.59% and 39.93%), and Farwah *et al.*, (2020) (31.44 % and 31.41%) for number of fruits per plant. Jyothi *et al.* (2011) (23.15% and 26.13%) for number of seeds per fruit. Sarkar *et al.*, (2009) (50.22% and 48.92 %), Diwakar *et al.* (2012) (43.36% and 43.2%) and Farwah *et al.*, (2020) (57.91% and 57.62%) for fruit yield per plant. Amit *et al.*, (2014) (35.47% and 35.37%), Farwah *et al.*, (2020) (38.73% and 38.67%) and Sran *et al.*, (2019) (40.29% and 38.36%) for fruit weight.

4.3.2 Moderate GCV and PCV

Moderate GCV and PCV was recorded for plant height (17.01% and 17.19%), Fruit diameter (15.71% and 19.40%), Seed weight (18.25% and 18.45%). Comparatively higher estimates of PCV indicate the importance of the environmental influence for these traits. Existence of less diversity among the genotypes for these traits due to moderate GCV and PCV. Improvement of these traits might not be successful. The results for PCV and GCV are in line with the findings of Mallikarjun *et al.*, (2003) (16.57% and 15.82%), Vijaya *et al.*, (2014) (19.76 % and 18.10%), Nahak *et al.*, (2018) (15.82% and 14.09%) and Pujar *et al.*, (2017) for plant height. Krishnamurthy *et al.*, (2013) (19.89 % and 12.62%) and Chaudhary *et al.*, (2013) (16.33% and 12.18%) for fruit diameter. Singh *et al.*, (2022) (18.17 % and 17.77%) for seed weight.

4.3.3 Moderate GCV and high PCV

High estimates of PCV and moderate estimates of GCV was recorded for days to flowering (10.96% and 21.46%), Fruit wall thickness (18.42% and 28.38%) respectively. Therefore, results indicate that there is a moderate variability among the genotypes. Predominant effect of environment for these traits. Similar findings for days to flowering reported by Farwah *et al.*, (2020) (15.18 % and 15.22%).

4.3.4 Low GCV and Low PCV

Low GCV and PCV (<10%) recorded for the trait days to first red ripe (8.602% and 8.684%). Therefore, results indicate that due to very low variability for this trait. There is very limited scope for improvement of these characters. Similar findings for days to first red ripe agreed with the report given by Singh *et al.*, (2022) (9.85 % and 9.95%).

4.3.6 High Heritability coupled with high genetic advance over mean

High heritability(>60%) coupled with high GAM(>20%) has been recorded for plant height(97.8% and 34.66%), primary branches per plant(83.72% and 50.1%), Fruit length(87.93% and 57.865%), Fruit diameter(65.15% and 26.19%), Number of seeds per fruit(98.3% and 44.2%), Seed weight(97.4% and 37.3%), Fruit weight(99.5% and 78.07%), Number of fruits per plant(67.6% and 63.35%), Fruit yield per plant(95.05% and 96.11%) and total yield(95.03% and 95.92%). Above findings are in close conformity with Nandadevi and Hosamani (2003) (79.80% and 66.30%), Vijaya *et al.*, (2014) (83.01% and 62.53%), Nahak *et al.*, (2018) (93.43% and 76.8541%), Datta and Das (2013) (86.10 % and 37.81%) and Nahak *et al.*, (2018)(88.72 % and 28.91%) for plant height. Patel *et al.*, (2014)

(95.82 % and 62.46%), Nahak *et al.*, (2018) (93.32% and 42.34%) and Sran *et al.*, (2019) (81.74 % and 37.05%) for fruit length. Verkey *etal.*, (2002) (61.36% and 26.57%), Sarkar *et al.*, (2009) (63.70% and 33.62 %) and Vijaya *et al.*, (2014) (81.46% and 36.74%) for fruit diameter. Jyothi *et al.*, (2011) (78.46% and 42.23%) for number of seeds per fruit. Farwah *et al.*, (2020) (99% and 79.53%), Sran *et al.*, (2019) (90.65% and 75.25%) and Amit *et al.*, (2014) (99.42% and 72.66%) for fruit weight. Sarkar *et al.*, (2009) (94.90 % and 98.16%), Nahak *et al.*, (2018) (87.21 % and 57.9079%) and Farwah *et al.*, (2020) (99 % and 118.09%) for fruit yield per plant. Due to additive gene action, hence direct phenotypic selection is mainly useful with respect to these traits. These traits were very less influenced by environmental factors.

4.3.7 High heritability coupled with moderated GAM

High heritability coupled with moderate GAM (10-20%) has been recorded for has been recorded for days to first red ripe (98.12% and 17.55%). Result is mainly due to non-additive gene action coupled with inter-locus effect. Hybridization can be adopted than simple selection. Similar findings for days to first red ripe was reported by Singh *et al.*, (2022) (98.32% and 20.0%).

Table4.5 Genetic variability parameters for different quantitative characters of chilli

Characters	GCV (%)	PCV (%)	Heritability in broad sense (%)	Genetic advance	Genetic advance (%) of mean
Plant height	17.01	17.19	97.8	19.96	34.66
Primary branches per plant	26.58	29.05	83.720	3.152	50.1
Days to first flowering	10.96	21.46	26.000	4.720	11.53
Fruit length	29.95	31.94	87.930	4.850	57.86
Fruit diameter	15.71	19.40	65.510	0.679	26.19
Fruit wall thickness	18.42	28.38	42.110	0.100	24.61
Days to first red ripe	8.602	8.684	98.120	22.96	17.55
Seed number per fruit	21.64	21.83	98.300	27.32	44.21
Seed weight(mg/100gm)	18.25	18.49	97.4	2.091	37.13
Fruit weight	37.99	38.08	99.530	2.852	78.07
Fruit number per plant	37.39	45.46	67.660	27.11	63.35
Fruit yield per plant(gm)	47.85	49.08	95.050	140.88	96.11
Total yield(t/ha)	47.77	49.00	95.030	5.07	95.92

4.4 Character association analysis

The expression of a character in a plant is the result of a series of interrelationships / interactions between characters, either directly or indirectly. Fruit yield is a main trait that is impacted by various other traits in crop. In crop improvement programme studying of association among characters is an important prerequisite for employing effective selection in breeding programme. The correlation characters may be due to genetic linkage or pleiotropy (Harland, 1939). The mutual relationship between various traits are measured by correlation coefficient analysis. Positive correlation or negative correlation measured by correlation coefficients. Yield is considered as a high variable character. We must know the degree of association both at genotypic and phenotypic level.

Yield is taken as dependent variable; remaining traits are taken as independent variable to find out degree and direct association. Genotypic and Phenotypic coefficient analysis were carried out for all the characters and presented in the Table 4.6. It was observed that genotypic correlation coefficient values were higher than phenotypic correlation coefficient.

4.4.1 Phenotypic correlation

From the extract of the result (Table 4.6) it was recorded that yield is positively correlated and significant to plant height (0.752), number of primary branches (0.756), number of seeds per fruit (0.422), seed test weight (0.346), Fruit weight (0.514), number of fruits per plant (0.415). However, days to first flower was significant and negatively correlated with yield (0.819). Fruit length was non-significant and positively correlated with yield (0.027). It was recorded that yield is negatively correlated and non-significant with Fruit diameter (0.017), Fruit wall thickness (0.0608) and days to first red ripe (0.0209).

Plant height is positively correlated and highly significant with number of primary branches (0.639), test weight of seed (0.280), number of fruits per plant (0.385), fruit yield per hectare (0.752) and it is negatively correlated and showed highly significant with character like days to flower (0.582) and it is significant with fruit length (0.137). Number of primary branches showed positive correlation and highly significant with plant height (0.699), number of seeds per plant (0.364), seed weight (0.210), fruit weight (0.350), number of fruits per plant (0.363), fruit yield per hectare (0.756) however it showed negative correlation and highly significant with days to flower (0.678). Days to flower showed negative and highly significant with number of seeds per fruit (0.323), seed weight (0.347), fruit weight (0.426), number of fruits per plant (0.345), fruit yield per hectare (0.819).

Fruit length showed positive correlation and highly significant with fruit diameter (0.279), fruit wall thickness (0.229), number of seeds per plant (0.364), fruit weight (0.422) whereas it showed negative correlation and highly significant with days to first red ripe (0.451), number of fruits per plant (0.406). Fruit diameter showed positive correlation and highly significant with fruit wall thickness (0.171), test weight of seed (0.201) whereas it showed negative correlation and highly significant with days to first red ripe (0.180), number of fruits per plant (0.196). Fruit wall thickness and days to first red ripe showed negative correlation and significant with days to first red ripe (0.129). Number of fruits per plant showed positive correlation and highly significant with fruit yield per hectare (0.415).

Number of seeds per plant showed positive correlation and highly significant with seed weight (0.279), fruit weight (0.474), fruit yield per hectare (0.422). Test weight of seed having positive correlation and highly significant with fruit weight (0.222), number of fruits per plant (0.181) and fruit yield per hectare (0.346). Fruit weight showed negative correlation and highly significant with number of fruits per plant (0.296) whereas, positive correlation and highly significant with fruit yield per hectare (0.514).

4.4.2 Genotypic correlation

From the extract of the result (Table 4.6) it was observed that yield is positively correlated and significant to plant height (0.779), number of primary branches (0.840), no of seeds per fruit (0.439), seed test weight (0.363), Fruit weight (0.526), number of fruits per plant (0.488). However, days to first flower was significant and negatively correlated with yield (0.881), Fruit length was non-significant and positively correlated with yield (0.028). It was recorded that yield is negatively correlated and non-significant with Fruit diameter (0.0216), Fruit wall thickness (0.0108) and days to first red ripe (0.0307).

Plant height is positively correlated and it showed highly significant with parameters like number of primary branches (0.699), number of fruits per plant (0.469), fruit yield per hectare (0.779) whereas it showed significant with number of seeds per fruit (0.30), test weight of seed (0.293) and fruit weight (0.284). Highly significant and negatively correlated (0.614). Number of primary branches is positively and highly significant with parameters like number of seeds per plant (0.406), fruit weight (0.387), number of fruits per plant (0.476), fruit yield per hectare (0.840) whereas days to flower (0.767) showed negative correlation and highly significant with number of primary branches. Days to flower showed negative correlation with all parameters and highly significant with parameters like number of primary branches (0.767), number of

seeds per fruit (0.340), test weight of seed (0.364), fruit weight (0.446), number of fruits per plant (0.430) and fruit yield per hectare whereas for plant height (0.699) it showed positive correlation and highly significant.

Fruit length showed positive correlation and highly significant with plant height (0.699), fruit diameter (0.374), fruit wall thickness (0.391), number of seeds per fruit (0.392), fruit weight (0.450) whereas, it showed negative correlation and significant with days to flowering (0.767), days to first red ripe (0.485) and number of fruits per plant (0.503). Fruit diameter showed positive correlation and significant with plant height (0.699), fruit length (0.374), fruit wall thickness (0.269) whereas it showed negative correlation with number of primary branches (0.767), number of fruits per plant (0.315). Fruit wall thickness and showed positive correlation and highly significant with plant height (0.699), fruit length (0.374), fruit diameter (0.269) whereas negative correlation and highly significant with number of primary branches (0.767). Days to first red ripe showed positive correlation and highly significant with plant height (0.699), fruit length (0.374), fruit diameter (0.269) whereas, negative correlation and highly significant with number of primary branches (0.767).

Number of seeds per plant showed positive correlation and significant with plant height (0.699), fruit length (0.374), fruit diameter (0.269), seed weight (0.282), fruit weight (0.480), fruit yield per hectare (0.439) whereas, negative correlation and highly significant with number of primary branches (0.767). Seed weight showed positive correlation and significant with plant height (0.699), fruit length (0.374), fruit diameter (0.269), fruit yield per hectare (0.363) whereas, negative correlation and highly significant with number of primary branches (0.767).

Fruit weight showed positive correlation and significant with plant height (0.699), fruit length (0.374), fruit diameter (0.269), number of seeds per fruit (0.282), fruit yield per hectare (0.526) whereas, negative correlation and highly significant with number of primary branches (0.767), number of fruits per plant (0.363). Number of primary branches showed positive correlation and significant with plant height (0.699), fruit length (0.374), fruit diameter (0.269), number of seeds per fruit (0.282), fruit yield per hectare (0.448) whereas, negative correlation and highly significant with number of primary branches (0.767), fruit weight (0.363). Fruit yield per hectare showed positive correlation and significant with plant height (0.699), fruit length (0.374), fruit diameter (0.269), number of seeds per fruit (0.282), fruit weight (0.480), number of fruits per plant (0.488) whereas, negative correlation and highly significant with number of primary branches (0.767).

After probing all findings, thoroughly, it was evident that fruit yield per plant is significant and showed positive correlation with plant height, number of primary branches, fruit weight and number of fruits per plant. The results are in conformity with Lata and Sharma (2022), Srivastava *et al.*, (2018), Minakshi *et al.*, (2017), Mamatha *etal.*, (2016), Hasanuzzaman and Golam (2011), Afroza *et al.*, (2013), Ullah *et al.*, (2011), Chattopadhyay *et al.*, (2011), Kumar *et al.*, (2012), and Yatung *et al.*, (2014). However, fruit length was non-significant and positively correlated to fruit yield the results are in conformity with Bijalwan *et al.*, (2016). Number of seeds per fruit were significant and positively correlated to fruit yield. The results are in conformity with Kumari *et al.*, (2017). Days to first flowering, was significant and it showed negative correlation with fruit yield. The results are in conformity with Chavan *et al.*, (2021) In general, Genotypic correlation coefficient was higher than phenotypic correlation coefficient may be due to masking effect of environment. These findings are in conformation with Sharma *etal.*, (2007) Krishnamurthy *et al.*, (2013), Janaki *et al.*, (2016) and Sharma and Sridevi (2016).

Table4.6 Phenotypic and Genotypic correlation for quantitative traits in chilli genotypes

Characters	PHT	NPB	DTF	FLT	FD	FWLT	DFRR	NSPP	SWT	FWT	NFPP	FYPHA(Pr)
PHT		0.639 **	-0.582 **	-0.137 *	-0.061	-0.109	0.076	0.294 **	0.286 **	0.280 **	0.385 **	0.752 **
NPB	0.699 **		-0.678 **	-0.064	-0.103	0.002	0.036	0.364 **	0.210 **	0.350 **	0.363**	0.756 **
DTF	-0.614 **	-0.767 **		0.001	-0.0601	-0.026	0.032	-0.323**	-0.347**	-0.426**	-0.345**	-0.819 **
FLT	-0.152	-0.084	-0.0016		0.279 **	0.229 **	-0.451 **	0.364**	0.041	0.422 **	-0.406 **	0.027
FD	-0.079	-0.165	-0.094	0.374 **		0.171 **	-0.180 **	0.116 *	0.201 **	0.110	-0.196**	-0.017
FWLT	-0.159	-0.063	-0.034	0.391**	0.269 *		-0.139 *	0.065	0.06	0.009	-0.113	-0.060
DFRR	0.078	0.043	0.036	-0.485**	-0.217	-0.208		-0.0926	-0.095	-0.129 *	0.1037	-0.029
NSPP	0.300*	0.406 **	-0.340 **	0.392**	0.150	0.098	-0.096		0.279 **	0.4749**	-0.072	0.422 **
SWT	0.293 *	0.236	-0.364 **	0.053 NS	0.249	0.096	-0.099	0.282 *		0.222 **	0.181 **	0.346**
FWT	0.284*	0.387 **	-0.446 **	0.450 **	0.138	0.019	-0.131	0.480 **	0.225		-0.296**	0.514 **
NFPP	0.469**	0.476 **	-0.430 **	-0.503 **	-0.315 *	-0.189	0.124	-0.082	0.229	-0.363**		0.415 **
FYHA(Gr)	0.779**	0.840 **	-0.881 **	0.0289	-0.0216	-0.101	-0.0307	0.439 **	0.363 **	0.526 **	0.448**	

*- significant at 5% level

** - significant at 1% level

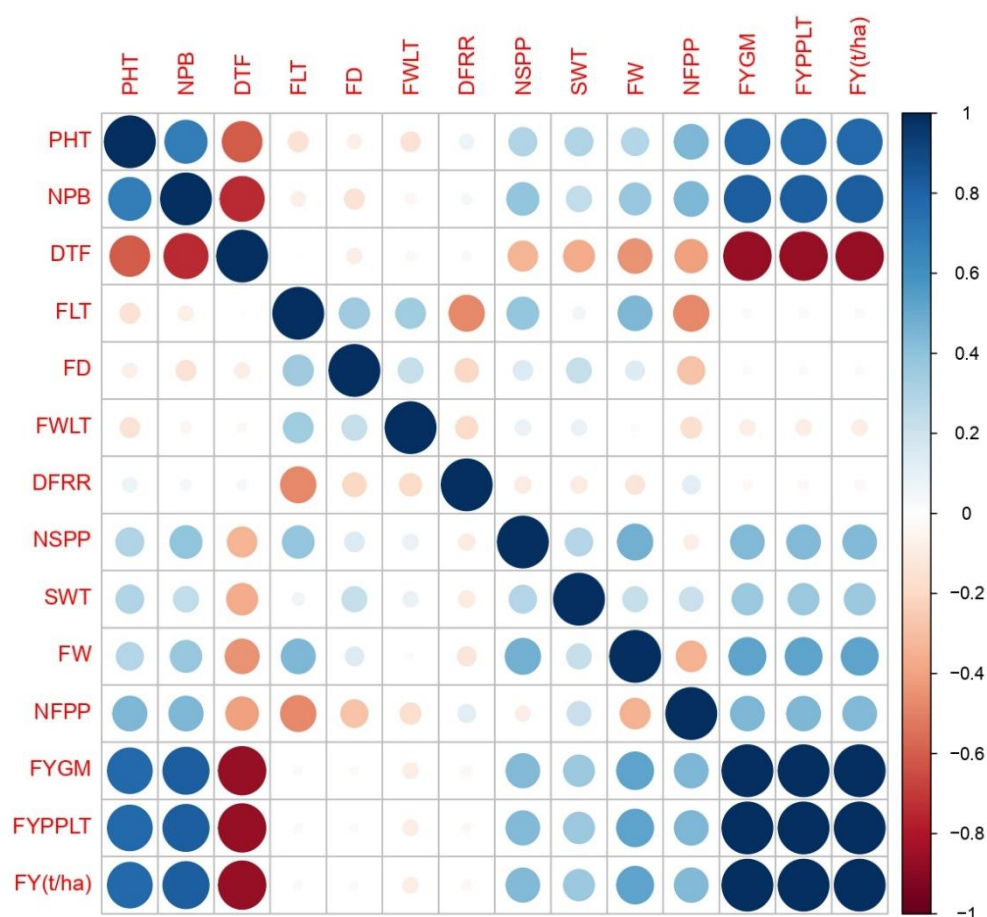
Lower diagonal- Genotypic correlation

Upper diagonal – Phenotypic correlation

Gr=Genotypic correlation coefficient, PR=Phenotypic correlation coefficient

PHT: Plant height, NPB: Number of primary branches, DTF: Days to flower, FLT: Fruit length, FD: Fruit Diameter, FWLT: Fruit wall thickness, NSPP: Number of seeds per fruit, STW: Test weight of seed, DFRR: Days to first red ripe, FWT: Fruit weight, NFPP: Number of fruits per plant, FYPHA: Fruit yield per ha

Fig 4.1 CORRELATION MATRIX FOR QUANTITATIVE TRAITS



Positive correlations are displayed in blue and negative correlations in red colour. Colour intensity and size of the circles are proportional to the correlation coefficients

PHT: Plant height, NPB: Number of primary branches, DTF: Days to flower, FLT: Fruit length, FD: Fruit Diameter, FWLT: Fruit wall thickness, NSPP: Number of seeds per fruit, SWT: Test weight of seed, DFRR: Days to first red ripe, FWT: Fruit weight, NFPP: Number of fruits per plant, FYPHA: Fruit yield per ha

4.5 Path coefficient analysis

Wright (1921) developed path coefficient analysis, but Dewey and Lu (1959) were the first to apply it technically in plant breeding. It is a technique used to improve the efficiency of selection programs by determining the relative contribution of component characters directly on the main characters and indirectly through other characters. To understand the complexity association for contributing traits for both direct and indirect effects towards yield path analysis is the most effective tool and relative importance for each trait is known. Genotypic path is more reliable than phenotypic path in predicting the relationship among both direct and indirect effect. Therefore obtained results for the coefficient path for yield with its contributing traits are divided into direct and indirect effects. Yield was taken as dependent variable with the remaining traits. Results are presented in table 4.7.

4.5.1 Positive direct effect

Based on the results obtained yield shown positive direct effect with the following characters plant height (0.254), Number of fruits per plant (0.1895), Number of primary branches (0.151), fruit length (0.086), Number of seeds per fruit (0.0422), Fruit weight (0.220), These characters which exhibited highest positive direct effect on yield per plant could be taken as major components for improvement of yield.

4.5.2 Negative direct effect

Based on the results obtained yield shown negative direct effect with the following characters days to first flowering (-0.417), Fruit diameter (-0.007), Fruit wall thickness (-0.072), Days to first red ripe (-0.0070), seed test weight (-0.0004).

In the present study residual effect was very low at genotypic level (0.0765), justified the accuracy in inclusion of characters in the present experiment. The characters which exhibited highest positive direct effect on yield per plant could be taken for the improvement of yield. However, the traits having negative direct effect not worthy to consider as selection criteria for yield improvement.

Number of fruits per plant, fruit length, fruit weight and number of primary branches per plant all had a positive direct effect on fruit yield per plant which were in line with the findings of Lata and Sharma (2022), Srinivas *et al.*, (2020), Patil *et al.*, (2009), Gupta *et al.*, (2009), Ullah *et al.*, (2011), Kumar *et al.*, (2012), and Yatung *et al.*, (2014). The findings agreed with report given by Ajjappalavara *et al.*, (2005), Vikram *et al.*, (2014), Hassan *et al.*, (2016), Pandiyaraj *et al.*, (2017), Janaki *et al.*, (2018), Singh *et al.*, (2018), for number of days to flowering had shown negative direct effect on fruit yield. Fruit diameter had shown negative effect on fruit yield. These findings are in conformation with Ahmed *et al.*, (2006), Kulkarni *et al.*, (2006) and Jabeen *et al.*, (2009).

Table 4.7 Genotypic path coefficient analysis for yield as dependent variable for chilli genotypes

Characters	PHT	NPB	DTF	FLT	FD	FWLT	DFRR	NSPP	SWT	FW	NFPP
PHT	0.2547	0.1057	0.2566	-0.0132	0.0006	0.0115	-0.0006	0.0127	-0.0001	0.0626	0.0890
NPB	0.1783	0.1511	0.3207	-0.0074	0.0012	0.0046	-0.0003	0.0172	-0.0001	0.0852	0.0904
DTF	-0.1565	-0.1160	-0.4176	-0.0001	0.0007	0.0025	-0.0003	-0.0144	0.0002	-0.0981	-0.0816
FLT	-0.0387	-0.0128	0.0007	0.0869	-0.0027	-0.0282	0.0034	0.0166	0.0000	0.0992	-0.0954
FD	-0.0202	-0.0250	0.0393	0.0326	-0.0072	-0.0194	0.0015	0.0064	-0.0001	0.0304	-0.0598
FWLT	-0.0406	-0.0097	0.0143	0.0340	-0.0019	-0.0720	0.0015	0.0042	0.0000	0.0044	-0.0358
DFRR	0.0199	0.0066	-0.0151	-0.0422	0.0016	0.0150	-0.0071	-0.0041	0.0000	-0.0289	0.0235
NSPP	0.0767	0.0615	0.1422	0.0341	-0.0011	-0.0071	0.0007	0.0423	-0.0001	0.1057	-0.0157
SWT	0.0747	0.0358	0.1521	0.0046	-0.0018	-0.0069	0.0007	0.0120	-0.0004	0.0496	0.0435
FW	0.0724	0.0585	0.1863	0.0392	-0.0010	-0.0014	0.0009	0.0203	-0.0001	0.2200	-0.0689
NFPP	0.1197	0.0721	0.1799	-0.0438	0.0023	0.0136	-0.0009	-0.0035	-0.0001	-0.0800	0.1895

PHT: Plant height, NPB: Number of primary branches, DTF: Days to flower, FLT: Fruit length, FD: Fruit Diameter, FWLT: Fruit wall thickness, NSPP: Number of seeds per fruit, STW: Test weight of seed, DFRR: Days to first red ripe, FWT: Fruit weight, NFPP: Number of fruits per plant, FYPHA: Fruit yield per ha

4.6 Principal component

4.6.1 To study the genetic divergence for different characters of chilli by principal component analysis

Principal Component Analysis (PCA) is a powerful method for determining the fewest number of components while explaining the most variability out of total variability (Morrison., 1982). In general, principal components that have an eigen value that is greater than or equal to one are regarded to be significant for the inclusion criterion, because eigen value represents variation. whereas principal components that have eigen values that are less than one are considered to be non-significant. In the current study, principal component (PC_s) was performed for morphological and yield traits in fifty-four genotypes of Chilli for a total of fourteen characters. The results showed that only three principal components (PCs) out of the total of fourteen PCs demonstrated an eigen value more than 1.00. These PCs were responsible for 70.17% of the overall variability that was found across all the characteristics. PC1 accounted for the highest variance 43.03 %, followed by PC2, which accounted for 18.72 % and PC3, which accounted 8.42% of the variation.

Table 4.8 Eigen values, Percentage of variance and cumulative percentage of PCs

Principal component	Eigen value	Percentage of variation	Cumulative percentage
PC1	6.02	43.03	43.03
PC2	2.62	18.72	61.7
PC3	1.18	8.42	70.17

Table 4.9 Principal components for 12 yield contributing traits of chilli

Traits	PC1	PC2	PC3
PHT	0.329	0.127	-0.003
NPB	0.353	0.081	0.053
DTF	-0.361	0.009	0.114
FLT	0.009	-0.535	0.072
FD	-0.005	-0.353	-0.370
FWLT	-0.029	-0.282	-0.435
DFRR	-0.010	0.325	0.282
NSPP	0.204	-0.288	0.192
SWT	0.179	-0.112	-0.446
FW	0.218	-0.346	0.423
NFPP	0.185	0.408	-0.395
FYHA	0.400	0.008	0.027

PC1 has the highest loading values fruit yield (0.400), DTF (0.361), NPB (0.353), However days to red ripe has the lowest loading value (0.010), PC2 has the highest loading values for fruit length (0.535), NFPP (0.408), Fruit diameter (0.352) whereas FYPHA has lowest loading value (0.008). PC3 has the highest loading values for SWT (0.446), FWLT (0.435), FW (0.423) whereas lowest loading value for PHT (0.003), based on the loading values traits are related as follows

Table 4.10 Rotated matrix results yield for its related traits

PC1	PC2	PC3
PHT	PHT	DTF
NPB	FLT	FD
DTF	FD	FWLT
NSPP	FWLT	DFRR
SWT	DFRR	NSPP
FW	NSPP	SWT
NFPP	SWT	FW
FYHA	FW	NFPP
	NFPP	

PHT: Plant height, NPB: No of primary branches, DTF: Days to flower, FLT: Fruit length, FD: Fruit Diameter, FWLT: Fruit wall thickness, NSPP: Number of seeds per fruit, STW: Test weight of seed, DFRR: Days to first red ripe, FWT: Fruit weight, NFPP: No of fruits per plant, FYPHA: Fruit yield per ha

Rotated component matrix revealed that. Traits are categorized based on the loading values. The loading values for particular trait should be greater than >0.09 .

PC1(43.03%) had shown maximum variation for the traits Plant height, number of primary branches, days to flowering, number of seeds per fruit, seed test weight, fruit weight, number of fruits per plant and fruit yield per plant. PC2 had shown (18.72%) variation for the traits plant height, fruit length, fruit diameter, fruit wall thickness, days to first red ripe, number of seeds per fruit, seed test weight, fruit weight and number of fruits per plant. PC3 had shown (8.42%) variation for the traits days to flowering, fruit diameter, fruit wall thickness, days to first red ripe, number of seeds per fruit, seed test weight, fruit weight and number of fruits per plant

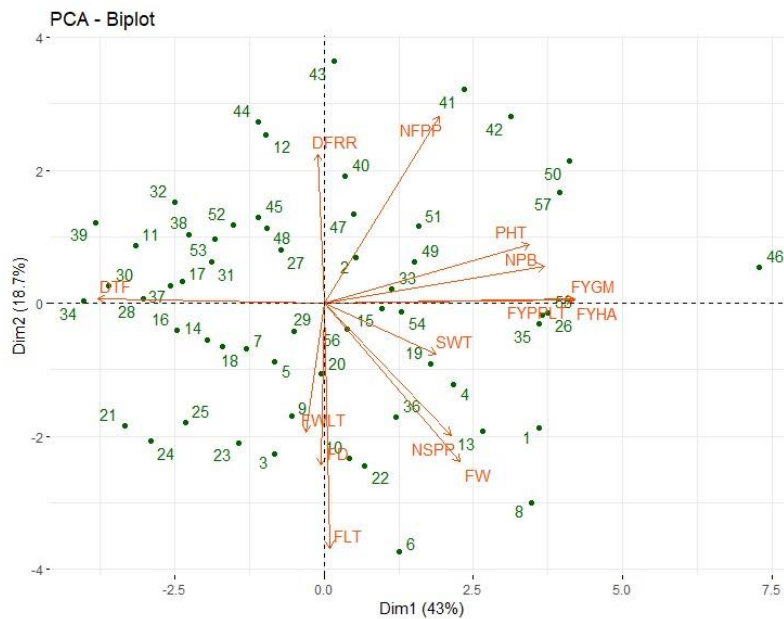


Fig 4.2 PCA-Biplot

It is a merger of PCA score plot and loading values the covariate effect of biplot based on correlation among the traits has been presented in Fig4.2 and the same explained (43.03%) of the total variation and thus can be considered as a good approximation as far as the effect of traits on yield as well as their similarities were concerned. Characters like FW NFPP, FLT, NSPP, PHT, NPB, had relatively longer vector suggesting that the characters had relatively larger effects on fruit yield per plant. On the contrary FD, FWLT, DFRR had shorter vector length indicating that they had little association with fruit yield per plant. The cosine of the angles between the vectors of the two traits measures the similarity between them relative to their effect on number of fruit yield per plant.

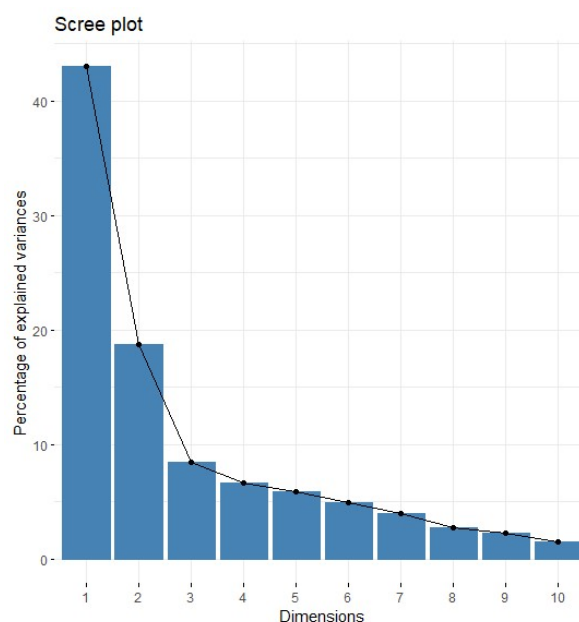


Fig 4.3 Scree plot 1-10

Scree plot graph represents the percentage of variance associated between the eigen values and principal components for each principal component X-axis represent the principal components. Whereas Y-axis represents percentage of explained variables. PC1 has the maximum variation (43.03%) were as it decline gradually for the remaining principal components. The most variable PC were PC1, PC2, PC3.). Similar findings were observed Pugalendi *et al.*, (2020) who studied ten principal components with eigen values greater than one accounted for 98.69% of the total variability. Singh *et al.*, (2020) reported ten principal components and showed around 88.85% variability in the traits. PC1 has accounted for the highest variability (36.93%). Rahevar *et al.*, (2021) reported five principal components accounted for 74.90 total variation. PC1 has the highest variation.

4.7 Genetic divergent analysis

The magnitude of divergence between two groups under consideration is provided by D^2 statistic developed by Mahalanobis (1936). Diversity among different genotypes is positively correlated to heterosis. By selecting the divergent genotypes, we can exploit the heterosis in future breeding programme. Divergence is not parallel to different geographical location it depends upon the performance of the genotype. By using mahala nobis D^2 analysis genetic divergence is carried out for 57 genotypes.

4.7.1 Grouping of genotypes into different clusters

Total 57 genotypes were broadly categorized in 10 clusters. Among 10 cluster groups, cluster one consists highest number of genotypes 34, followed by cluster IV (7), cluster III (5), cluster V (3), cluster II and VI (2), Rest of the clusters composed on one genotype in each cluster VII, VIII, XI and Results obtained through D² analysis presented in the table 4.11.

4.7.2 Mean inter and intra cluster distance

The results obtained for inter and intra cluster distance were presented in the table. Genetic diversity exists higher among the inter cluster groups than intra cluster. Intra cluster distance will be minimum and inter cluster distance will be maximum.

4.7.2.1 Intra cluster distance

Highest intra cluster distance was recorded for cluster V (429.28), followed by cluster I (417.17), cluster III (411.67), cluster IV (391.71), cluster VI (266.64), cluster II (68.34) intra cluster distance for VII, VIII, XI, X is 0 (due to the presence of one genotype).

4.7.2.2 Inter cluster distance

Highest inter cluster distance was recorded for cluster II and VII (6100.48), cluster VIII and X (4060.11), cluster IX and VII (3970.11), cluster X and II (3723.98), cluster IV and II (2988.75). Whereas minimum inter cluster distance was recorded between cluster IV and VI (643.4), cluster VIII and I (652.93), cluster I and V (674.96), cluster II and I (721.50), cluster IX and I (723.40).

Highest inter cluster distance was recorded for cluster II and 7(6100.48), cluster VIII and X (4060.11), cluster IX and VII (3970.11), cluster X and II (3723.98), cluster IV and II (2988.75). Therefore, existence of genetic divergence among genotypes. Multiple crossing programme can be performed involving genotypes from divergent groups having maximum inter cluster distance to develop transgressive segregants in F₂ population and subsequent generations due to existence of high heterogeneity (Mehta and Asati 2008).

Present study in agreement with Thul *et al.*, (2009), Kumari *et al.*, (2010) reported genetic divergence for 92 genotypes and grouped into 10 clusters. Above findings are in conformity with Hasan *et al.*, (2014) studied diversity analysis in chilli and grouped into 7 cluster groups inter cluster distance is higher between cluster III and cluster VI, cluster I and cluster III, cluster III, and cluster VII. Same findings corroborated with Sen *et al.*, (2021) studied divergent

analysis where inter-cluster distance values ranged between 40.404 and 127.530, maximum inter-cluster distance was reported between clusters II and V (127.53).

Table 4.11 Cluster composition of 57 genotypes of chilli

S.NO	Cluster Num	Total number of genotypes	Name of genotypes
1	I	34	UBC28, UBC34, UBC30, UBC39, UBC27, UBC52, UBC12, UBC53, UBC40, UBC38, UBC48, UBC16, UBC3, UBC7, UBC32 UBC15, UBC45, UBC23, UBC 37 UBC18, UBC 5, UBC2, UBC29, UBC56, UBC 49, UBC51, UBC14, UBC47, UBC21, UBC 4, UBC 31, UBC42, UBC41, UBC 17
2	II	2	UBC42, UBC44
3	III	5	UBC9, UBC22, UBC 10, UBC13, UBC 1
4	IV	7	UBC35, UBC55, UBC19, UBC54 UBC36, UBC 6, UBC 25
5	V	3	UBC50, UBC57, UBC33
6	VI	2	UBC20, UBC26
7	VII	1	UBC8
8	VIII	1	UBC11
9	IX	1	UBC24
10	X	1	UBC46

Table 4.12 Inter and intra cluster distance of chilli

Cluster	1	2	3	4	5	6	7	8	9	10
1	417.2	721.5	980.2	1448.2	675.0	1039.4	3789.3	652.9	723.4	2244.8
2		68.3	1823.0	2988.7	1311.5	1811.1	6100.5	714.7	991.6	3724.0
3			411.7	1031.6	874.0	764.5	2478.8	1528.8	944.9	1572.6
4				391.7	1022.0	643.4	967.6	2423.5	1794.4	821.1
5					429.3	847.9	2906.8	1552.4	1048.5	1028.4
6						266.6	1514.4	1846.6	1283.4	1067.5
7							0.0	5364.0	3970.0	1238.2
8								0.0	1317.0	4060.9
9									0.0	2480.2
10										0.0

Fig 4.4 Dendrogram representing cluster analysis in chilli among 57 genotypes by using Darwin software

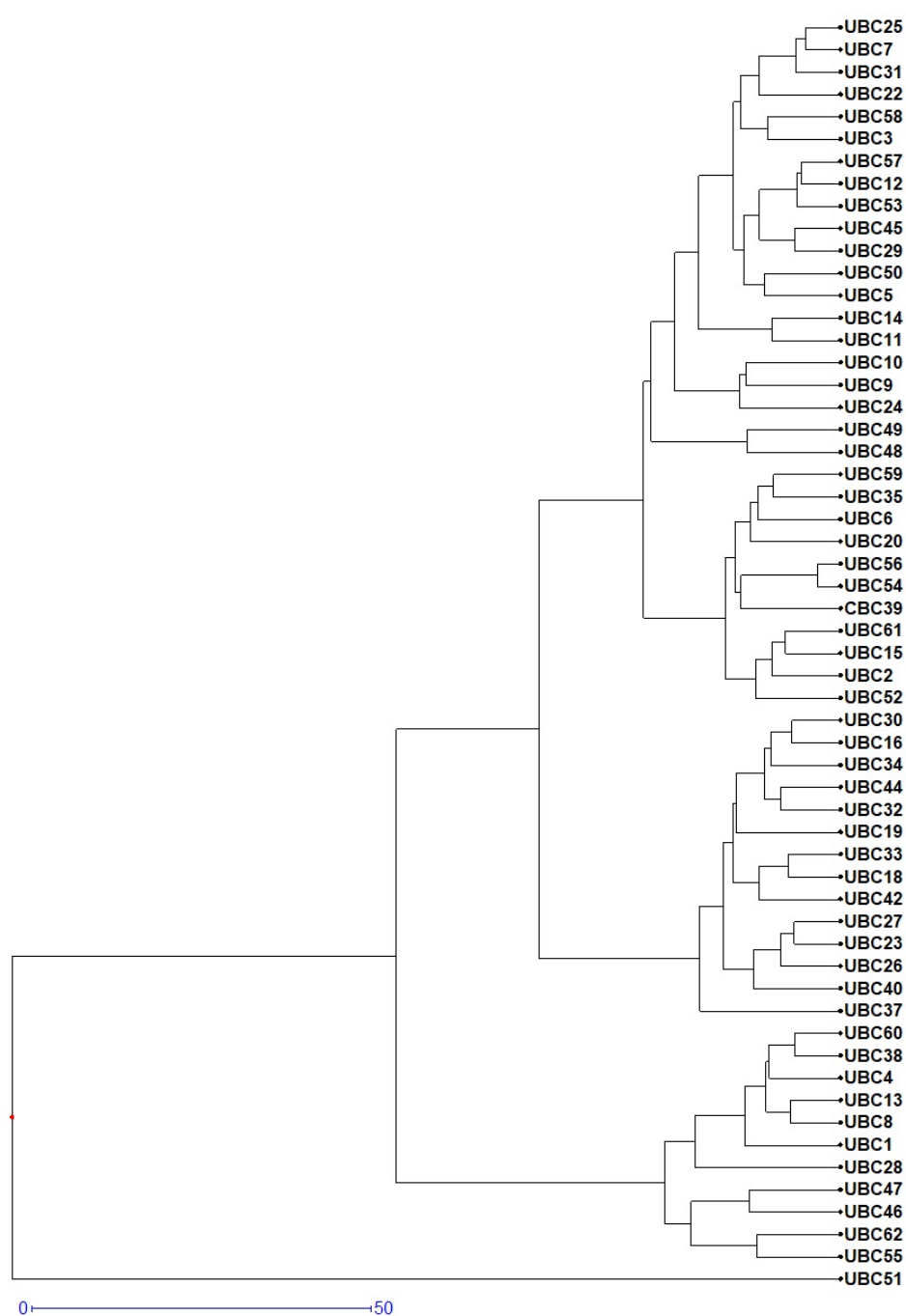


Plate 4 Variation in fruits under study



Plate 4 Variation in fruits under study



Plate 4 Variation in fruits under study



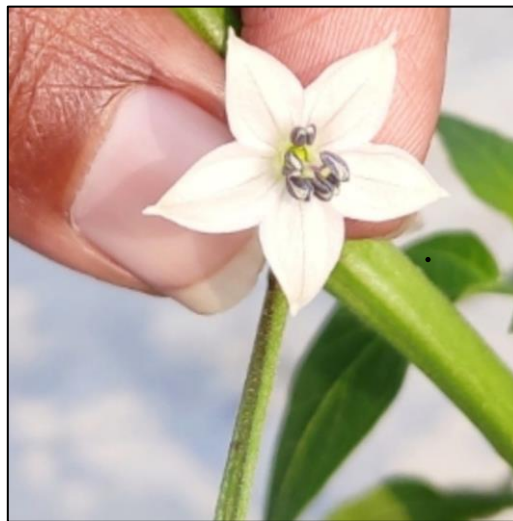
Plate 4 Variation in fruits under study



Plate 5 Variation in anther colour, filament colour, stigma exsertion under study



UBC-42



UBC 35



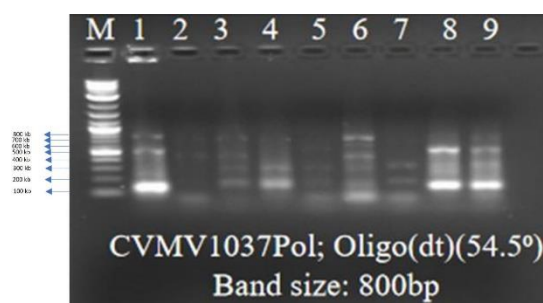
UBC 31

4.8 Molecular detection of ChiVMV

Symptomatic leaves were collected from infected chilli genotypes and RNA was isolated from each genotype using TRIzol method and cDNA was prepared using oligo (dT₁₈). ChiVMV linked molecular markers are used to screen against infected leaf sample of different plants showing typical ChiVMV symptom and confirm the presence of ChiVMV using primers (Table no 3.6). The gel images of screening obtained by PCR using cDNA of each infected genotype were shown below in (Plate 5). The primers used in this screening were reported by (Jiao.Y.*et al.*, (2020) (Chi1-F, Chi1-R). When the results of PCR amplification were observed in 0.8% agarose gel, an amplicon size of 800 bp fragment was observed which is of ChiVMV (comprising of CP gene). This amplification was confirmed using second set of primers (CVMV 1037 Pol F Oligo dt R) reported by (Tsai W. S. *et al.*, 2008) which gave positive results. After confirming the presence of ChiVMV in the studied material particularly ChiVMV plant used as source of inoculum for screening chilli genotypes through artificial sap inoculation method. Presence of ChiVMV in 1,3,4,6,8,9 samples confirmed by using (Chi 1-F, Chi 1- R, CVMV1037 Pol, Oligo dt). Genotypes showed very faint band indicating low viral load or presence.



M-1kb plus ladder, 1 - UBC 52, 2-AICRP chilli ,3-UBC-22, 4-UBC-15,6-UBC34,8-Local white chilli,9-King chilli

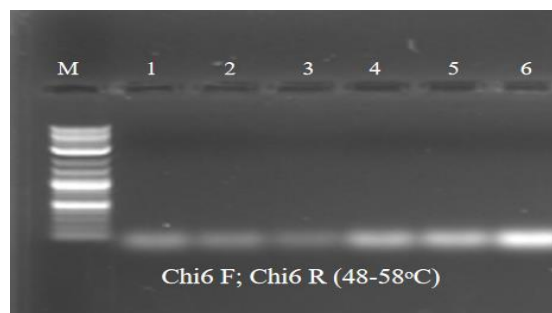


M-1kb plus ladder, 1 - UBC 52, 2-AICRP chilli ,3-UBC-22, 4-UBC-15,6-UBC34,8-Local white chilli,9-King chilli

Plate 6 Gel images for the primers (Chi 1-F, Chi 1-R, CVMV1037 Pol, Oligo dt)

By using the primers Chi5-F -Chi 5-R, Chi6-F, Chi 6-R amplification was not confirmed (Jiao.Y.et *al.*,2 020) Gel image was not shown (Fig) by usings these primers.

Plate- 6 Band image for the primer Chi 6-F, Chi 6-R primer



M-1kb plus ladder, 1 - UBC 52, 2-AICRP chilli ,3-UBC-22,4-UBC-15,6-UBC34,8-Local white chilli,9-King chilli (absence of detection)

4.9 Screening the genotypes against ChiVMV

To identify the resistance total 39 chilli genotypes were screened against ChiVMV. Screening was done in both field level and artificial sap mediated mechanical inoculation method. For both field and artificial screening disease scoring scale stated by Reddy *et al.*, (2001) has been used and disease incidence for each and every genotype noted. Before sap inoculation, the presence of virus is (diseased plant) confirmed through ChiVMV using primers (Table no 3.6). After sap inoculation symptoms were recorded from 2-28 days after post inoculation. Highly susceptible genotypes expressed symptoms after 5-6 days after post inoculation. Symptoms were mostly mosaic mottling, vein banding, shoe string. Dark green vein banding, mosaic mottling, shoe string symptoms were observed in highly susceptible genotypes. In case of immune genotypes there are devoid of symptoms. The percentage of disease incidence recorded based on the symptoms after post inoculation.

Based on disease incidence percentage genotypes are classified had shown in the figure 4.6

1.Immune, highly resistant, Resistant, moderately resistant, Susceptible, highly susceptible



Immune



Highly resistant



Resistant



Susceptible



Highly susceptible

Table 4.13 Disease incidence percentage of genotypes in both field and artificial sap inoculation method

S.NO	Genotype	Code	Disease incidence% (Field)	Disease incidence% mechanical inoculation	Disease reaction	Symptoms
1	CHILLIVAR-1IET-2021	UBC1	0.00	46.67	Susceptible	Mosaic mottling, Shoe string
2	CHILLIVAR-3IET-2021	UBC3	0.00	0.00	Immune	No symptom
3	CHILLIVAR-4IET-2021	UBC4	0.00	0.00	Immune	No symptom
4	CHILLIVAR-6IET-2021	UBC6	0.00	36.67	Moderately resistant	Leaf mottling
5	CHILLIVAR-7IET-2021	UBC7	0.00	53.33	Susceptible	Mosaic mottling, shoestring
6	CHILLIVAR-9IET-2021	UBC9	0.00	46.67	Susceptible	Mosaic mottling, shoestring
7	CHILLIVAR-10IET-2021	UBC10	0.00	37.67	Moderately resistant	Leaf mottling
8	CHILLIVAR-11IET-2021	UBC11	0.00	0.00	Immune	No symptom
9	CHILLICVRRESIST2021/CHILLICVRES-1 (Susceptible Check)	UBC 15	73.33	90.00	Highly susceptible	Mosaic mottling, Shoe string vein banding
10	CHILLICVRRESIST2021/CHILLICVRES-2	UBC 16	0.00	0.00	Immune	No symptom
11	CHILLICVRRESIST2021/CHILLICVRES-4	UBC 19	0.00	0.00	Immune	No symptom
12	CHILLICVRRESIST2021/CHILLICVRES-7 (Susceptible check)	UBC 22	76.66	93.33	Highly susceptible	Mosaic mottling, Shoe string vein banding
13	CHILLICVRRESIST2021/CHILLICVRES-8	UBC 23	0.00	68.67	Highly susceptible	Mosaic mottling, Shoe string
14	CHILLICVRRESIST2021/CHILLICVRES-9	UBC 24	0.00	65.33	Highly susceptible	Mosaic mottling, Shoe string
15	CHILLI-HPAVT-12021 CHILLIVAR-1	UBC 25	0.00	21.67	Resistant	Leaf mottling
16	CHILLI-HPAVT-12021 CHILLIVAR-2	UBC26	0.00	46.67	Susceptible	Mosaic mottling, Shoe string
17	CHILLI-HPAVT-12021 CHILLIVAR-3	UBC27	43.33	53.33	Susceptible	Mosaic mottling, Shoe string
18	CHILLI-HPAVT-12021 CHILLIVAR-4	UBC28	0.00	0.00	Immune	No symptom
19	CHILLI-HPAVT-12021 CHILLIVAR-5	UBC29	0.00	0.00	Immune	No symptom
20	CHILLI-HPAVT-12021 CHILLIVAR-6	UBC30	0.00	53.33	Susceptible	Mosaic mottling, Shoe string

Table 4.13 (Cont.,) Disease incidence percentage of genotypes in both field and artificial sap inoculation method

Genotype	Code	Disease incidence% Field	Disease incidence% mechanical inoculation	Disease reaction	Symptoms
CHILLI-HPAVT-12021 CHILLIVAR-7	UBC31	0.00	0.00	Immune	No symptom
CHILLI-HPAVT-12021 CHILLIVAR-8	UBC32	0.00	0.00	Immune	No symptom
CHILLI-HPAVT-12021 CHILLIVAR-9	UBC33	56.67	62.00	Highly susceptible	Mosaic mottling, Shoe string
CHILLI-HPAVT-12021 CHILLIVAR-10	UBC34	43.33	66.67	Highly susceptible	Mosaic mottling, Shoe string
CHILLI-HPAVT-12021 CHILLIVAR-11	UBC35	0.00	0.00	Immune	No symptom
CHILLI-HPAVT-12021 CHILLIVAR-12	UBC37	0.00	0.00	Immune	No symptom
CHILLI-AVT-2-2019CHILLIVAR-1	UBC38	26.67	26.67	Moderately resistant	Leaf mottling
CHILLI-AVT-2-2019CHILLIVAR-2	UBC39	16.67	33.33	Moderately resistant	Leaf mottling
CHILLI-AVT-2-2019CHILLIVAR-4	UBC40	76.67	86.67	Highly susceptible	Mosaic mottling, vein banding, Shoe string symptom
CHILLI-AVT-2-2019CHILLIVAR-6	UBC 42	0.00	0.00	Immune	No symptom
AP-1G4JAGANATH	UBC45	0.00	0.00	Immune	No symptom
NW-2MITREMORO	UBC46	0.00	0.00	Immune	No symptom
CB-1	UBC47	0.00	0.00	Immune	No symptom
ARKA HARITHA (RESISTANT CHECK)	UBC 50	0.00	0.00	Immune	No symptom
AVT-2 2018-CHILLIVAR-1	UBC 52	72.22	86.67	Highly susceptible	Mosaic mottling, shoe string
IET 2020-CHILLIVAR-12	UBC 54	53.33	83.33	Highly susceptible	Mosaic mottling, shoe string
IET2020/CHIVAR-8	UBC 59	0.00	0.00	Immune	No symptom
AVT-2-2018-CHILLIVAR-5	UBC60	0.00	0.00	Immune	No symptom
PUNDIBARI LOCAL	UBC62	0.00	0.00	Immune	No symptom
CD		5.45	6.57		
SE(m)		1.93	2.33		

Table 4.14 Disease reaction of 39 chilli genotypes

S.NO	Immune	Resistant	Moderately resistant	Susceptible	Highly susceptible
1	CHILLIVAR-3IET-2021	CHILLI-HPAVT-12021 CHILLIVAR-1	CHILLI-AVT-2- 2019CHILLIVAR-1	CHILLIVAR-1IET-2021	CHILLICVRRESIST2021/CHI LLICVRES-1
2	CHILLIVAR-4IET-2021		CHILLI-AVT-2- 2019CHILLIVAR-2	CHILLIVAR-7IET-2021	CHILLICVRRESIST2021/CHI LLICVRES-7
3	CHILLIVAR-11IET-2021		CHILLIVAR-6IET-2021	CHILLIVAR-9IET-2021	CHILLICVRRESIST2021/CHI LLICVRES-8
4	CHILLICVRRESIST2021/CHIL LICVRES-2		CHILLIVAR-10IET-2021	CHILLI-HPAVT-12021 CHILLIVAR-2	CHILLICVRRESIST2021/CHI LLICVRES-9
5	CHILLICVRRESIST2021/CHIL LICVRES-4			CHILLI-HPAVT-12021 CHILLIVAR-3	CHILLI-HPAVT-12021 CHILLIVAR-9
6	CHILLI-HPAVT-12021 CHILLIVAR-4			CHILLI-HPAVT-12021 CHILLIVAR-6	CHILLI-HPAVT-12021 CHILLIVAR-10
7	CHILLI-HPAVT-12021 CHILLIVAR-5				CHILLI-AVT-2- 2019CHILLIVAR-4
8	CHILLI-HPAVT-12021 CHILLIVAR-7				CHILLI-AVT-2-2018- CHILLIVAR-1
9	CHILLI-HPAVT-12021 CHILLIVAR-8				CHILLI-IET-2020- CHILLIVAR-12
10	CHILLI-HPAVT-12021 CHILLIVAR-11				
11	CHILLI-HPAVT-12021 CHILLIVAR-12				
12	CHILLI-AVT-2- 2019CHILLIVAR-6				
13	AP-1G4JAGANATH				
14	NW-2MITREMORO				
15	CB-1				
16	ARKA HARITHA				
17	CHILLI-IET2020/CHIVAR-8				
18	CHILLI-AVT-2-2018- CHILLIVAR-5				
19	PUNDIBARI LOCAL				

Total of 19 immune, 1 resistant and 4 moderately resistant genotypes were identified during field and artificial screening against Chilli Veinal Mottle Virus disease.

4.10 Disease reaction of genotypes during field and artificial screening

Out of 39 genotypes nineteen genotypes UBC3, UBC4, UBC11, UBC16, UBC19, UBC28, UBC29, UBC31, UBC32, UBC35, UBC37, UBC42, UBC45, UBC46, UBC47, UBC50, UBC59, UBC60, UBC62 had shown immune reaction with 0.0% disease incidence in both field level and artificial screening. One genotype UBC-25 had shown resistant reaction with 21.67% disease incidence in artificial screening method. Four genotypes UBC 38, UBC39, UBC6, UBC10 had shown moderately resistant reaction. Whereas UBC 38 and UBC 39 had shown disease incidence in both field and artificial screening method. However, UBC 6 and UBC 10 had shown disease incidence only in artificial screening method.

Out of 39 genotypes nine genotypes UBC11, UBC7, UBC9, UBC26, UBC27, UBC30 had shown susceptible reaction. UBC 27 had shown disease incidence in both field and artificial screening (43.33% and 53.33%). Whereas UBC1, UBC9, UBC 26 had shown disease incidence only in artificial screening method with 46.67%. UBC 30 had shown disease incidence (53.33%) in artificial method. A total of nine genotypes UBC15, UBC22, UBC23, UBC24, UBC33, UBC34, UBC 40, UBC 52, UBC59 had shown highly susceptible disease incidence. Seven genotypes had shown disease incidence in both field and artificial screening method. Highest disease incidence had shown by UBC 22(76.66% and 93.33%), followed by UBC15(73.33% and 90.0%), UBC 40, UBC 52(76.67% and 86.67%), UBC54(53.33% and 83.33%), UBC33(56.67% and 62.0%) UBC34(43.33% and 66.67%). Whereas UBC 23(68.67%) and UBC 24(65.33) had shown disease incidence only in artificial screening method.

A total of 19 immune, 1 resistant and 4 moderately resistant genotypes were identified during field and artificial screening against Chilli Veinal Mottle Virus disease.

Table 4.15 Reaction of genotypes against ChiVMV disease incidence and yield

S.NO	Genotype	Disease reaction	Yield(t/ha)
1	UBC 46	Immune	6.66
2	UBC 62	Immune	7.32
3	UBC 60	Immune	7.05
4	UBC 25	Resistant	2.48
5	UBC 38	Moderately resistant	5.08
6	UBC 39	Moderately resistant	5.31
7	UBC 6	Moderately resistant	5.02
8	UBC 26	Susceptible	1.68
9	UBC 27	Susceptible	2.81
10	UBC 30	Susceptible	1.38
11	UBC 40	Highly susceptible	2.53
12	UBC 34	Highly susceptible	2.5
13	UBC 33	Highly susceptible	1.8
14	UBC 54	Highly susceptible	5.45
15	UBC 15	Highly susceptible	5.9
16	UBC 22	Highly susceptible	2.07

Among immune 3 genotypes recorded highest yield presented in the table 4.14 UBC 62, UBC 60 and UBC 46. While, in highly susceptible genotypes moderate yield was recorded in the genotypes UBC54, UBC 15. So, in future breeding we can go for marker assisted back cross breeding. By using MABC we can transfer of the desired trait (resistant trait) from a donor parent into a recurrent parent. Maximum recovery of recurrent parent genome for yield traits. Complete elimination of donor parent genome, by leaving only desirable targeted gene should be done. Linkage drag can be reduced through MABC where it is a major drawback in conventional method.

Similar findings were noticed by Satyaprakash and Singh (2006) reported that ChiVMV was easily transferred to chilli and other herbaceous hosts by sap inoculation. Results are in line with the findings of Tsai *et al.*, (2008), ie., the viral genomic RNA 3' terminal sequences were determined. In the 3'UTR of all isolates, the inverted repeat sequence GUGGNNCCAC was present. Results were corroborated with findings of Naresh *et al.*, (2016). They screened 50 Capsicum genotypes against Chilli veinal mottle virus (ChiVMV) and Cucumber mosaic virus (CMV), through artificial sap inoculation method to develop the resistance in chilli against (ChiVMV and CMV). Resistance developed by crossing the parents in diallel fashion. Similar results were noticed by Chorgasti *et al.*, (2020) who studied 50 chilli genotypes screened against ChiVMV through both symptomatology and serology, five genotypes were highly resistant, ten genotypes showed resistant, six were moderately resistant and remaining were susceptible. Borah *et al.*, (2022), reported 41 chilli samples (42.70%) were found to be positive for ChiVMV after mechanical inoculation.

PLATE-7 FIELD LEVEL SYMPTOMS



UBC 30



UBC 22



UBC 15



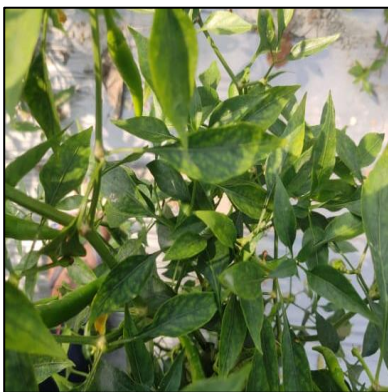
UBC 27



UBC 34



UBC 33



UBC 52



UBC 26

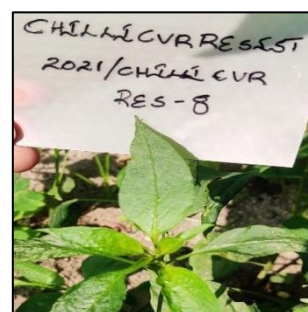


UBC 39

PLATE 8 SYMPTOMS OF ARTIFICIAL SAP INOCULATION



UBC -22(HS)



UBC 23(HS)



UBC 15(HS)



UBC 30(S)



UBC 34(HS)



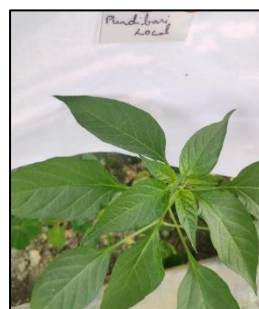
UBC 52(HS)



UBC 54(HS)



UBC 40(HS)



UBC 62 (I)



UBC 46 (I)



UBC 45(I)

I-Immune, HS-Highly susceptible-Susceptible

Table 4.16 Analysis of variance of mean performance in Chilli genotypes with thirteen characters

Characters	Degrees of Freedom (d.f)		Mean sum of square	
	Genotype	Error	Genotype	Error
Plant height	56	224	482.02	2.10
No. of primary branches	56	224	14.61	0.54
Days to 1 st flowering	56	224	200.70	3.34
Fruit length	56	224	32.38	0.86
Fruit diameter	56	224	0.91	0.08
Fruit wall thickness	56	224	0.03	0.007
Days to 1 st red ripe	56	224	635.23	2.42
No. of seeds/fruit	56	224	898.34	3.10
Seed test weight	56	224	5.31	0.02
Fruit weight	56	224	9.64	0.009
No. of fruits/plant	56	224	1402.07	122.36
Fruit yield/plant	56	224	24860.5	256.4
Fruit yield/ha	56	224	20.58	0.21

Significance at 5% Level

PLATE -9 EXPERIMENTAL FIELD



CHAPTER 5

SUMMARY
AND
CONCLUSION

Chilli is an important vegetable-spice which not only adds wonderful colour to Indian dishes but also have medicinal and nutritional properties. Genetic improvement mainly depends upon the amount of genetic variability present in the population. Variability plays an important role in plant breeding because hybrids between lines of different origin generally possess greater heterosis than those closely related species. Information regarding genetic variability provides an information to identify right genotypes that would help plant breeder in breeding programme. Germplasm serves as a valuable source of base population and provides scope for wide variability. Present study was to evaluate and select suitable parents for hybridization to improve yield attributing traits and to identify resistant source against biotic stress (ChiVMV diseases).

The current experiment entitled “Variability, character association and diversity analysis in chilli (*Capsicum annuum* L.) genotypes.” based on morphological, and quantitative traits conducted at Instructional farm, Department of Vegetable and Spice Crops, Faculty of Horticulture, Uttar Banga Krishi Vishwavidyalaya, Pundari, Cooch Behar, during the year 2022-2023. The experiment consists of fifty -seven genotypes with 5 replications. Therefore, the investigation on genetic variability, character association and diversity analysis among different chilli genotypes for various traits have been studied and identification of resistant genotypes against ChiVMV was done with the following objectives

Objectives:

- 1.Characterization, variability, and character association study in chilli genotypes
- 2.Assessment of diversity among genotypes
- 3.Molecular detection and screening of chilli genotypes against ChiVMV

The results summarized which were furnished below.

Mean performance of 54 Chilli genotypes

A total of 14 characters viz. growth, yield and morphological, were studied and significant variation observed among the genotypes collected across the country. This variation may be due to genotype, environment, or their interaction.

The top best genotypes for growth and earliness parameters based on their mean performance

The genotypes UBC 62(72.75 cm), followed by UBC33(72.60 cm) and UBC28(71.69 cm) were recorded for highest plant height based on their mean performance. Whereas genotypes UBC 60(9.8), UBC 38(9.8) followed by UBC 1(8.8) were recorded for highest number of primary branches. Minimum days to first flowering was recorded in UBC 1(33.6 days) followed by UBC 62(34 days) and UBC 36(35.6 days). Whereas minimum days to first red ripe was recorded in UBC 9-(92) followed by UBC-24 (99.40), UBC -10 (100.4).

Best genotypes for fruit characters based on their mean performance

The genotypes UBC-13 (14.66 cm) followed by UBC-10 (12.90 cm) and UBC-9(12.6 cm) were recorded for highest fruit length. For fruit diameter UBC 8(3.44 cm) followed by UBC-16(3.32 cm) and UBC-4(3.30 cm) are the superior genotypes. The highest fruit weight was recorded in UBC-8(8.32 gm), followed by UBC-60(6.34gm) and UBC-20(6.25 gm). The higher number of fruits per plant was recorded in genotypes UBC-48(86.0) followed by UBC-49(82.0) and UBC 62(71.4). The highest number of seeds per fruit was expressed in genotypes UBC 35(89.5) followed by UBC 52(83.1) and UBC 10 (82.8). The highest seed weight per fruit was recorded in UBC 1(7.95 gm), followed by UBC 22(7.87 gm) and UBC 8(7.17gm).

Best genotypes for yield parameters

UBC- 8 (7.51 t/ha) followed by UBC-62(7.32 t/ha) and UBC-59(7.05t/ha) recorded highest yield. These are the superior genotypes for fruit yield

Variability

High GCV and PCV (>20%) was recorded for primary branches per plant (26.58%and 29.05%), Fruit length (29.95% and 31.94%), Seed number per fruit (21.64% and 21.83%), Fruit weight (37.99 %and 38.08%), No of fruits per plant (37.39% and 45.46%), Fruit yield per plant gm (47.85 % and 49.08%), Fruit yield per plot (47.83% and 49.08%), Total yield (47.77% and 49.00%) respectively. High estimates for both the GCV and PCV revealed that there is a more contribution of genetic components for total variation as well presence of environmental on these characters. Therefore, these traits having higher range of variation have better scope of improvement through selection.

Heritability with Genetic advance over mean

High heritability(>60%) coupled with high GAM(>20%) has been recorded for plant height(97.8% and 34.66%),primary branches per plant(83.72% and 50.1%),Fruit length(87.93%and 57.86%),Fruit diameter(65.15%and 26.19%),No of seeds per fruit(98.3% and 44.2%),Seed weight(97.4% and 37.3%),Fruit weight(99.5% and 78.07%),Number of fruits per plant(67.6% and 63.35%),Fruit yield per plant(95.05% and 96.11%),Fruit yield per plot(95.05% and 96.10%) and Total yield(95.03% and 95.92%).Due to additive gene action, hence direct phenotypic selection is mainly useful with respect to these traits. These traits were very less influenced by environmental factors.

Correlation

In phenotypic correlation yield is positively correlated and significant to plant height (0.752), number of primary branches (0.756), no of seeds per fruit (0.422), seed test weight (0.346), Fruit weight (0.514), number of fruits per plant (0.415).In genotypic correlation yield is positively correlated and significant to plant height (0.779), number of primary branches (0.840), no of seeds per fruit (0.439), seed test weight (0.363), Fruit weight (0.526), number of fruits per plant (0.488).

Genotypic correlation coefficient where higher than the phenotypic correlation coefficient It is may be due to masking effect of environment causing differential genotypic and phenotypic expression of these traits. Strong association of these positively related traits revealed that selection based on these traits would ultimately useful in the improvement of fruit yield and Combination of these traits in hybridization programme is useful for obtaining higher yield segregants

Path coefficient analysis

Based on the results obtained yield shown positive direct effect with the following characters plant height (0.254), Number of primary branches (0.151), fruit length (0.086), Number of seeds per fruit (0.0422), Fruit weight (0.220), Number of fruits per plant (0.1895). The characters which exhibited highest positive direct effect on yield per plant could be taken for the improvement of yield. The direct selection of these traits would be useful for the improvement of fruit yield per plant in chilli.

Principal component analysis

PCs component analysis for different genotypes revealed that out of 10 principal components only 3 components have eigen value >1% with 70.17% variability. Among different PC components highest percentage of variability was recorded in PC1(43.03%) followed by PC2(18.72%), PC3(8.42%). Total 3 PCs out of 10 accounted for 70.17 % variability. The traits accounts in PC-1 such as plant height, number of primary branches, days to flowering, number of seeds per fruit, seed test weight, number of fruits per plant and fruit yield/ha. The highly variable traits plays an important role in explaining diversity in genotypes. Traits account in PC-2 plant height, fruit length, fruit diameter, fruit wall thickness, days to first red ripe, number of seeds per fruit, seed test weight, fruit weight and number of fruits per plant. Traits account in PC-3 days to flowering, fruit diameter, fruit wall thickness, days to first red ripe, number of seeds per fruit, seed test weight, fruit weight and number of fruits per plant.

Genetic divergent analysis

Highest intra cluster distance was recorded for cluster V (429.28), followed by cluster I (417.17), cluster III (411.67), cluster IV (391.71), cluster VI (266.64), cluster II (68.34). Highest inter cluster distance was recorded for cluster II and VII (6100.48), cluster VIII and X (4060.11), cluster IX and VII (3970.11), cluster X and II (3723.98), cluster IV and II (2988.75). Therefore, existence of genetic divergence among the genotypes was noted. Multiple crossing programme can be performed involving genotypes from divergent groups having maximum inter cluster distance to develop transgressive segregants in F₂ population and subsequent generations due to existence of high heterogeneity.

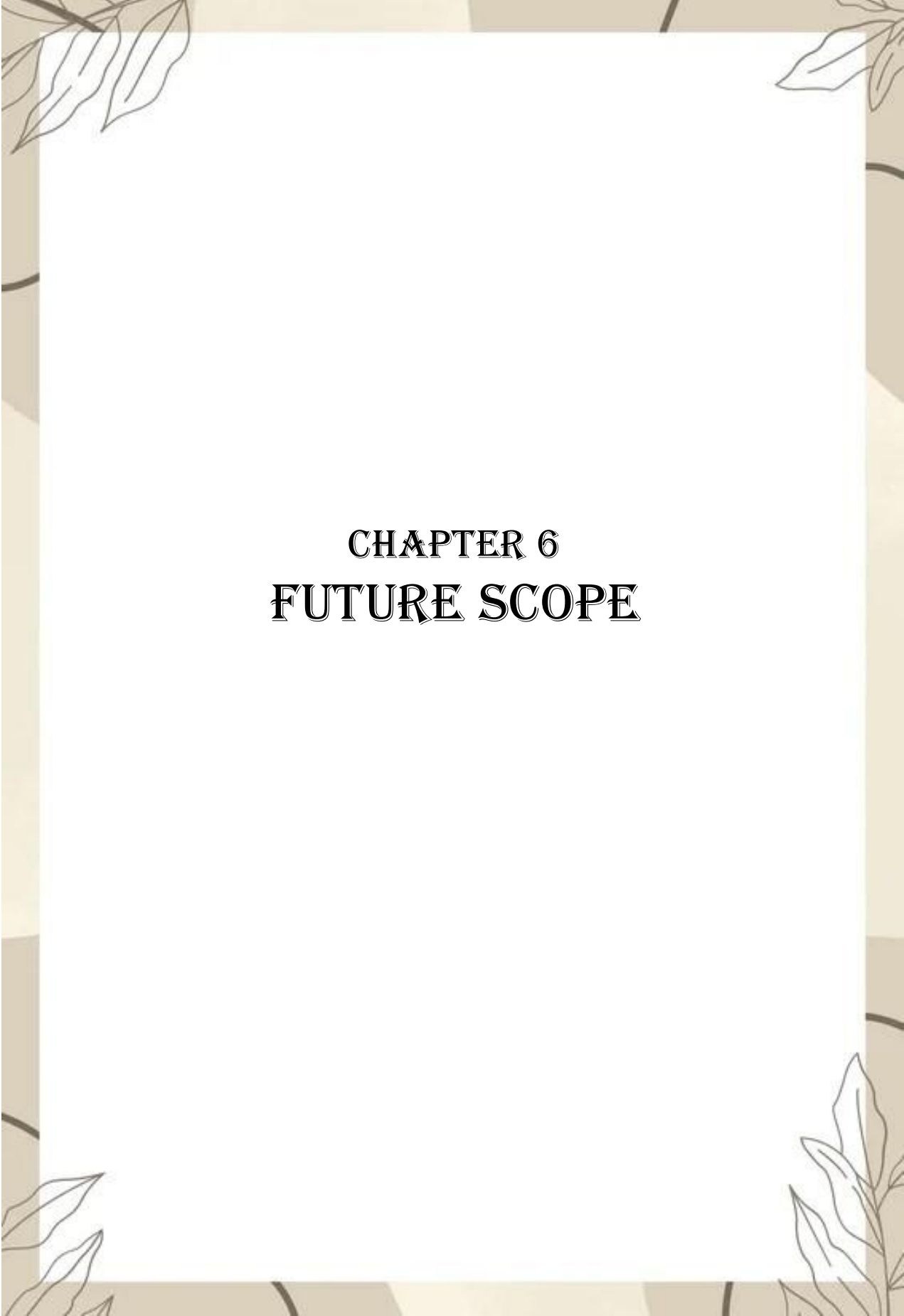
Molecular detection and screening of chilli genotypes against ChiVMV

The primers used in this screening were reported by (Jiao.Y.*et al.*, 2020 Chi1-F, Chi1-R). When the results of PCR amplification were observed in 0.8% agarose gel, an amplicon size of 800 bp fragment was observed which is of ChiVMV (comprising of CP gene). This amplification was confirmed using second set of primers (CVMV 1037 Pol F Oligo dt R) reported by (Tsai W. S. *et al.*, 2008) which confirmed the ChiVMV presence.

Screening of chilli genotypes against ChiVMV

Screening of 39 genotypes against ChiVMV through both field and mechanical inoculation have been performed in 2022. A total of 19 immune, 1 resistant and 4 moderately resistant genotypes were identified during field and artificial screening against chilli veinal Mottle Virus

disease. Highly susceptible genotypes were recorded for moderate yield, so in future breeding we can go for marker assisted back cross breeding. By using MABC we can Transfer of the desired trait (resistant trait) from a donor parent into a recurrent parent. Maximum recovery of recurrent parent genome for yield traits. Complete elimination of donor parent genome, by leaving only desirable targeted gene should be done. Linkage drag can be reduced through MABC

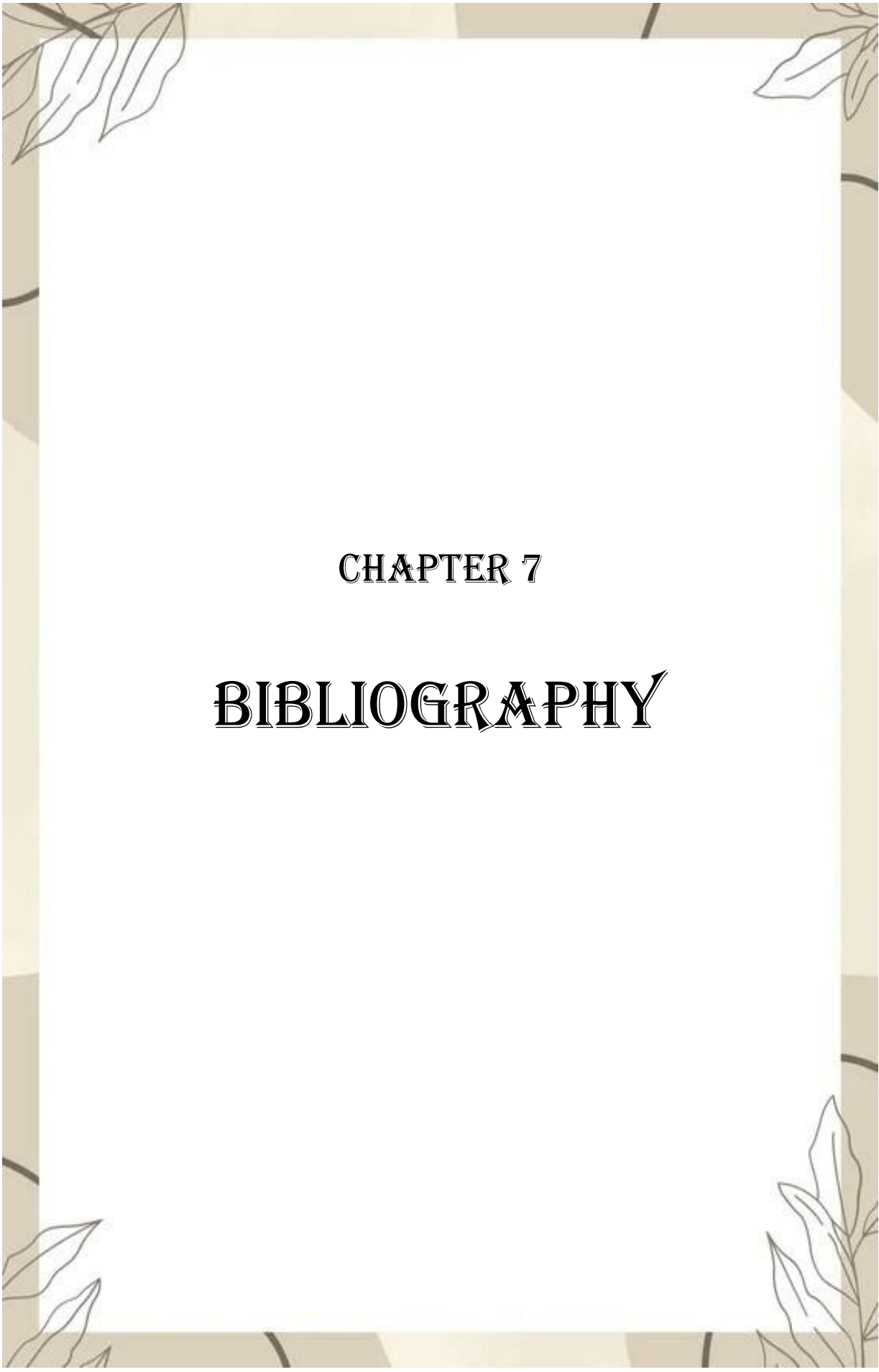


CHAPTER 6

FUTURE SCOPE

Future Scope

1. Further evaluation of identified promising high yielding genotypes in larger area over different location and season could be done for their commercial utilization
2. The traits which exhibited high GCV, PCV, Heritability coupled with high GAM/moderate may be taken care for further selectioning in breeding and crop improvement of chilli
3. The characters showed desirable, high correlation and direct effects with yield/plant should be given utmost importance for genetic improvement of chilli
4. Highly diversified genotypes can be used in the hybridization and pedigree programme
5. The identified molecular marker linked with ChiVMV can be used for further disease detection experiment and validation
6. Immune, Resistant and Moderately resistant genotypes can be used for developing hybrids or varieties resistant to ChiVMV.
7. Mechanism of ChiVMV disease resistance and vector virus relationship can be studied in the broader way
8. Simple marker-assisted backcross breeding is the best breeding approach method due to monogenic recessive nature of ChiVMV.



CHAPTER 7

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%	Per cent
Σ	Summation of
δ^2	Variance
/	Per
R.B.D	Randomized Block Design
b s	Broad sense
$^{\circ}\text{C}$	Degree Celsius
C.D	Critical difference
C.V	Coefficient of variation
Df	Degrees of freedom
cm	Centimetre
G	Gram
Kg	Kilogram
mm	Milli meter
Ha	Hectare
T	Tonnes
Mg	Milligram
ml	Millilitre
μg	Microgram
No.	Number
<i>i.e.</i>	That is
GA	Genetic advance
GAM	Genetic advance as per cent of mean
GCV	Genotypic coefficient of variation
PCV	Phenotypic coefficient of variation
PCA	Principal Component Analysis
h^2	Heritability
$T_a^{\circ}\text{C}$	Annealing temperature
TAE	Tris-acetate EDTA
dNTPs	Deoxynucleotide triphosphates
PCR	Polymerase chain reaction
Rpm	Revolutions per minute
Iso P	Iso propanol
C DNA	Complimentary DNA
RT enzyme	Reverse transcriptase
DEPC	Diethyl pyro carbonate
Nm	Nanometer
pH	Potential of Hydrogen
ChiVMV	Chilli veinal mottle virus
MABC	Marker assisted Back cross breeding

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NAME OF THE UNIVERSITY	PONDICHERRY UNIVERSITY
OGPA	8.70
YEAR OF AWARD	2021

MASTER'S DEGREE

NAME OF THE UNIVERSITY	UTTAR BANGA KRISHI VISWAVIDYALAYA, WEST BENGAL
OGPA	8.86
TITLE OF MASTER'S THESIS	Variability, character association and diversity analysis in chilli (<i>Capsicum annuum</i> L.) genotypes.
ACHIEVEMENTS/ SCHOLARSHIP	ASRB NET qualified with 59.78%
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