EXPLORATION OF GENETIC VARIABILITY IN CHILLI (*Capsicum annuum* L.) PRESENT IN SUBTROPICAL REGION OF HIMACHAL PRADESH

Thesis

by

SACHIN BHARDWAJ

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Dr B S Dogra
(Principal Scientist)

Department of Vegetable Science
College of Horticulture and Forestry, Neri
Dr YS Parmar University of Horticulture and Forestry, Nauni, Solan - 173 230 HP

CERTIFICATE-I

This is to certify that the thesis entitled, **"Exploration of genetic variability in chilli *(capsicum annuum* l*.)* present in subtropical region of Himachal Pradesh"** submitted in partial fulfillment of the requirements for the award of degree of **MASTER OF SCIENCE (HORTICULTURE) VEGETABLE SCIENCE** in the discipline of **HORTICULTURAL SCIENCES** of Dr. Yashwant Singh Parmar University of Horticulture and Forestry, (Nauni) Solan (HP) - 173230 is a bonafide research work carried out by **Mr. Sachin Bhardwaj (NH- 2017-25-M)** son of Shri Jai Chand Sharma under my supervision and that no part of this thesis has been submitted for any other degree or diploma.

The assistance and help received during the course of investigations has been fully acknowledged.

Place: Neri, Hamirpur
Dated:

(Dr B S Dogra)
Chairman, Advisory Committee

CERTIFICATE-II

This is to certify that the thesis entitled, **"Exploration of genetic variability in chilli *(capsicum annuum* L*)* present in subtropical region of Himachal Pradesh"** submitted by **Mr Sachin Bhardwaj (NH-2017-25-M)** son of Shri Jai Chand Sharma to Dr Yashwant Singh Parmar University of Horticulture and Forestry, (Nauni) Solan (HP) – 173230 India in partial fulfillment of the requirements for the degree of **MASTER OF SCIENCE (HORTICULTURE) VEGETABLE SCIENCE** in the discipline of **HORTICULTURAL SCIENCES** has been approved by the Advisory Committee after an oral examination of the student in collaboration with an External Examiner.

4/11/19

Dr B S Dogra
Major Advisor

4.11.2019

Dr Sandeep Kumar
(Scientist)
External Examiner

4/11/2019

Dean's Nominee

Members of Advisory Committee:

4/11/19

Dr Deepa Sharma
(Scientist)
Department of Vegetable Science

4/11/19

Dr Kumud Jarial
(Asstt. Professor)
Department of Plant Pathology

4/11/19

Head of the Department

Countersigned

Dean of the College

CERTIFICATE - III

This is to certify that all the mistakes and errors pointed out by external examiner have been incorporated in the thesis entitled **"Exploration of genetic variability in chilli *(capsicum annuum* l*.)* present in subtropical region of Himachal Pradesh"** submitted by **Mr. SACHIN BHARDWAJ (NH-2017-25-M)** son of Shri Jai Chand Sharma to Dr. Yashwant Singh Parmar University of Horticulture and Forestry, Nauni, Solan (HP)-173230 in partial fulfilment of the requirements for the award of degree of **MASTER OF SCIENCE (HORTICULTURE) VEGETABLE SCIENCE.**

_____

Dr. B S Dogra
Chairman
Advisory Committee

_____

Professor and Head
Department of Vegetable Science
College of Horticulture and Forestry
Neri, Hamirpur (H.P.)

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Place: Neri, Hamirpur
Dated: ***(Sachin Bhardwaj)***

CONTENTS

ABBREVIATIONS

%	:	Per cent
=	:	Equal to
×	:	Multiplication
^{0}C	:	Degree Celsius
ANNOVA	:	Analysis of Variance
C.V.	:	Coefficient of Variation
CD	:	Critical Difference
Cm	:	Centimeter
et al.	:	co –workers
etc.	:	*et cetera*
G	:	Gram
HP	:	Himachal Pradesh
i.e.	:	that is
m^2	:	Meter square
Max	:	Maximum
Mg	:	Milli gram
Min	:	Minimum
Mm	:	Milli meter
NHB	:	National Horticulture Board
RHS	:	Royal Horticulture Society
SE	:	Standard error
UHF	:	University of Horticulture and Forestry
CoH&F	:	College of Horticulture and Forestry
viz.	:	Videlicet (namely)
PCV	:	Phenotypic coffecient of variation
GCV	:	Genotypic coffecient of variation
TSS	:	Total Soluble Solids
DAT	:	Days after transplanting
GAM	:	Genetic Advance as per cent of mean
°B	:	Brix
ha	:	Hectare
MT	:	Metric Tonne
m	:	Meter
cm	:	Centimeter
ERMA	:	Electronic Recording Machine Accounting
F_1	:	First Filial generation
F_2	:	Second Filial generation
DAT	:	Days after transplanting
pH	:	Pouvoir hydrogen

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Chapter-1

INTRODUCTION

Chilli *(Capsicum annuum* L., 2n=24) belongs to family Solanaceae, is a vegetable, spice and one of the most important cash crop of India. The domestication of chilli first occurred in Central America, most likely in Mexico, with secondary centres in Guatemala and Bulgaria (Salvador, 2002). It was introduced to Europe by Columbus in 15th century and spread to rest of the globe along the spice trading routes to Africa, India, China and Japan. In 17th century, Portuguese introduced it into India and was incorporated into national cuisines instantly (Bosland and Votava, 2000). The genus Capsicum originated in the American tropics. Chilli has been classified under often cross pollinated crops and the extent of natural out crossing has also reported up to 66.4 per cent (Singh *et al.,* 1994*).*

Chilli crop performs well in warm humid tropical and subtropical regions extending from equator 45º latitude on both Southern and Northern hemisphere. It can do well up to an altitude of 2000 meter above sea level. A frost free period of about 130-150 days with temperature range of 25-35º C is optimum for chilli cultivation. It thrives in areas having a moderate rainfall within the range of 60-120 cm. Chilli crop is grown on practically all types of soils except on salty land provided the soil is well drained and well aerated.

In India green chilli occupies an area of 309 thousand ha with a production of 3592 MT. The major chilli growing states are Andhra Pradesh, Karnataka, West Bengal, Madhya Pradesh and Odisha. In Himachal pradesh chilli occupies an area of 1.22 thousand ha with a production of 14.53 MT. The total export of chillies from India is 44.90 thousand MT (NHB, 2017- 18).

Chilli has diverse uses as spice, condiment, culinary supplement, medicine, vegetable and ornamental plant. Chilli is the most economic and popular additive to improve food acceptability. Particularly in India, there is no home which does not consume chilli. It is grown for use as a vegetable and spice under tropical, subtropical and temperate climates (Hazra, 2014*).* Chilli is valued for pungency and high colouring material, besides is the source of protein, carbohydrates, minerals, vitamin C and A, sugars and carotenes. The active principle of pungency is due to the presence of a crystalline volatile alkoloid called as capsaicin. Chilli is also a rich source of red pigments namely capsorubin, cryptoxanthin and related carotenoids which are esters of capsanthin.

A wide range of genetic variability and large number of distinct forms distributed all over the country provides the maximum opportunity for genetic improvement not only for high yield but also for better quality, resistance to various biotic and abiotic stresses and consumer acceptability (Maurya, 2015).

Genetic diversity is an important factor for any heritable improvement. Knowledge of genetic diversity, its nature and degree is useful for selecting desirable genotypes from a germplasm for the successful breeding programme. The value of germplasm collection depends not only on the number of accessions but also depend upon the magnitude of genetic diversity present in those accessions. The wide genetic diversity that exists in the available genotypes provides ample scope for further improvement. Yield being a complex quantitative character, direct selection for yield may not result in successful improvement. Information on character association and direct and indirect effects of component traits on yield would greatly help in formulating the selection criteria and using them effectively in crop improvement programme. Therefore, it is necessary to partition the observed variability into heritable and non-heritable components by calculating genetic parameters such as genotypic and phenotypic coefficient of variation, heritability and genetic advance (Vanitha, 2017).

Co-efficient of variation is useful in the assessment of genetic variability for the particular characters. Heritability denotes the proportion of phenotypic variation due to genotypes thus help the breeders to select the elite variety for a character. Genetic advance denotes the improvement in the mean genotypic values of selected families over base population and thus helps the breeder to select the progenies in the earlier generation itself (Murmu, 2017).

Correlation and path coefficient analysis gives an insight into the genetic variability present in population. Correlation coefficient analysis measure the mutual relationship between various plant characters and determines the component characters on which selection can be based for improvement in yield. Path analysis splits the correlation coefficients into direct and indirect effects of a set of dependent variables on the independent variable thereby aids in the selection of elite genotype. All the above mentioned parameters are the pre-requisites to formulate the sound and successful breeding programme (Bijalwan, 2016).

Keeping in view the above facts, the present investigation was undertaken to estimate magnitude of components of variation, heritability and genetic advance in 20 genotypes of

chilli. Keeping these factors in view, the present investigation entitled **"Exploration of genetic variability in chilli (*Capsicum annuum* L.) present in subtropical region of Himachal Pradesh"** is being conducted with following objectives:

- To study the performance and extent of genetic variability in the chilli genotypes.
- To estimate heritability and genetic advance.
- To study the character association and path analysis for different traits.
- To identify the best genotype with desirable horticultural traits.

Chapter-2

REVIEW OF LITERATURE

The relevant literatures available on various aspects pertaining to the present study are briefly reviewed under the following heads:

1. **Variability studies**
2. **Heritability and genetic advance**
3. **Correlation coefficient analysis**
4. **Path coefficient analysis**
5. **Genetic divergence studies**

1. Variability studies:-

Sreelathakumary and Rajamony (2004) evaluated thirty-five chilli (*Capsicum annuum* L.) genotypes to assess genetic variability. Higher phenotypic and genotypic coefficients of variation were observed for leaf area, fruits per plant, fruit weight, fruit length, fruit girth and yield per plant.

Ukkund *et al.*, (2007) conducted a study on eighty genetically diverse chilli accessions comprising of established varieties and advanced breeding lines. The difference between phenotypic coefficient of variation and genotypic coefficient of variation were found to be narrow for most of the traits except primary and secondary branches, tertiary branches, fifty per cent flowering and early & late fruit yield per plant.

Sarkar *et al.*, (2009) investigated forty-nine genotypes of chilli to study the genetic variability. Proximities between GCV and PCV for all the characters except fruit width indicated that these characters were controlled by the genetic makeup of the genotypes. High GCV values for fruit yield/plant, number of fruits/plant, plant height, fruit length, placenta length, fruit weight, number of seeds/fruit, and days to 50% flowering was observed.

Singh *et al.*, (2009) inspected thirty genotypes of chilli pepper (*Capsicum annuum* L.) and sufficient variability was observed for all horticultural and quality traits studied; that is, days to 50% flowering, days to first harvest, primary structural branches per plant, secondary branches per plant, fruit length, fruit diameter, average fruit weight, number of seeds per

fruit, 100-seed weight, pericarp:seed ratio, number of marketable fruits per plant, total number of fruits per plant, plant height, marketable yield per plant, total soluble solids, and oleoresin, capsanthin, and capsaicin content.

Kumar *et al.,* (2012) conducted a study on 20 chilli genotypes to evaluate the extent of variability with respect to fourteen characters in different genotypes measured in terms of range, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV). The considerable amount of variation was observed for all the characters. The phenotypic coefficient of variability (PCV) was higher than the genotypic co efficient of variability in all the characters. The estimates of PCV and GCV were high for fruit yield per plant, number of fruits per plant, capsaicin content and average fruit weight, moderate for days to first harvest and low for ascorbic acid content.

Jogi *et al.,* (2013) conducted a research on fifty chilli accessions and observed that, the difference between the genotypic co-efficient of variation (GCV) and phenotypic co-efficient of variation (PCV) were found to be narrow for most of the characters. The results suggest that these traits are least affected by environment and selection for these traits on phenotypic would be rewarding. For rest of the characters, the estimates of PCV were greater than GCV. This indicates that the variation for these traits is not only by genotypes but also due to environment.

Datta and Das (2013) collected fifty three genotypes of *Capsicum annuum L.* and these genotypes upon cataloguing showed distinct variations with respect to vegetative, inflorescence, fruit and quality characters. A wide range of variation was also observed among the genotypes for several morphological, fruit and quality characters. Among the different characters, white corolla colour showed 100 % frequency and higher frequency was also recorded in single flower per axil, number pigmentation at node and green fruit colour at intermediate stage.

Kannan *et al.,* (2016) evaluated eight diverse genotypes of chilli. Analysis of variance revealed significant differences among the genotypes for all the characters studied. The higher estimates of genotypic coefficient of variation (GCV) were observed for flowers per branch, clusters per plant, flower per branch and stem diameter. While the higher estimates of phenotypic coefficient of variation (PCV) were found for flowers per branch, fruits per branch, clusters per plant and stem diameter.

Meena *et al.,* (2016) studied genetic variability in chilli during *Rabi* season involving 20 genotypes showing wider variation for all traits. Result revealed that the highest genotypic and phenotypic coefficients of variation were noted for fruit width, leaf area and number of branches per plant. The highest phenotypic coefficient of variation were observed for fruit width, pedicel length and leaf area. The highest genotypic and phenotypic coefficients of variation were noted for fruit width, leaf area and number of branches per plant. The highest phenotypic coefficient of variation were observed for fruit width, pedicel length and leaf area.

Rosmaina *et al.,* (2016) evaluated sixteen local chilli pepper genotype. Analysis of variance revealed that there are highly significant difference among the genotypes tested for all characters studied indicating the presence of variability. In this study, PCV value was relatively greater than GCV for all traits; however, GCV values were near to PCV values for the characters like plant height, stem length, leaf width, fruit Length, fruit diameter, day to flowering, day to first harvest, and single fruit weight indicating high contribution of genotypic effect for phenotypic expression of such characters.

Sahu *et al.,* (2016) conducted a variability studies on nineteen genotypes of chilli. The highest genotypic and phenotypic coefficient of variation was recorded for number of fruit per plant, fruit yield per plot and fruit yield per ha. The phenotypic coefficients of variation were higher than the genotypic coefficient of variation.

Janaki *et al.,* (2017) inspected seventy one chilli genotypes comprising fifty four F1 hybrids, fifteen parents and two commercial checks. The considerable amount of variation was observed for all the characters. The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation for all the characters indicating the influence of environment on these characters. The estimates of PCV and GCV were high (>20%) and the difference between PCV and GCV was narrow for all the traits indicating the existence of wide range of genetic variability in the material studied. This also indicated that broad genetic base, less environmental influence and these traits are under the control of additive genes and hence there is a good scope for the further improvement of these characters through simple selection.

Pujar *et al.,* (2017) evaluated sixty three chilli genotypes and observed that the genotypic and phenotypic coefficients of variation were moderate to high for all the characters studied except green and dry fruit weight. Fruit yield had positive and highly significant association with number of fruits per plant and fruit set percentage. Strong

association of these traits revealed that selection based on these traits would ultimately improve the fruit yield and it is also suggested that hybridization of genotypes possessing combination of such characters is most useful for obtaining desirable high yielding segregants.

Singh *et al.,* (2017) performed an experiment on eighteen genotypes of chilli. Analysis of variance revealed highly significant difference among the genotypes for all the characters studied. The PCV was higher than the GCV for all the traits. High magnitude of PCV and GCV were observed for number of fruit plant-1 followed by average fruit weight, fruit yield per plant, while it was low for number of branches per plant.

Nahak *et al.,* (2018) conducted a study on eleven genotypes of chilli to determine the magnitude of variability, eleven genotypes of chilli were evaluated. Through analysis of variance, a high significant difference was found for almost all characters indicating a greater opportunity of exploit variability. Genotypic and phenotypic variances were highest for fruit yield /plant followed by fruit weight and no. of fruits/plant. Phenotypic co- efficient of variation (PCV) and genotypic co- efficient of variation (GCV) were maximum in case of number of plants affected by leaf curl/plot followed by fruit weight and no. of wilted plants/plot.

2. Heritability and genetic advance:-

Sreelathakumary and Rajamony (2004) conducted a study on thirty five chilli genotypes and reported high heritability coupled with high genetic advance observed for leaf area, fruits per plant, fruit weight, fruit length, fruit girth and yield per plant imply the potential for crop improvement through selection.

Ukkund *et al.,* (2007) evaluated eighty chilli accessions and observed high estimates of heritabilty was found for plant height, days to first flowering, percent fruit set, number of fruits per plant, fruit length, ten fruit weight and total green fruits per plant. Most of these characters also had moderate to high estimates of genetic advances as a percent over mean except days to first flowering.

Tembhurne *et al*., (2008) inspected eleven elite advanced lines of chilli and reported high genetic advance over mean coupled with higher heritability was observed for number of fruits per plant, indicating the least influence of environment on these traits so that improvement could be made through selection. Days to 50% flowering showed highest

heritability coupled with low genetic advance indicating predominance of non-additive gene effects which happens due to low genotypic coefficient of variation. However, yield and number of secondary branches per plant and fruit weight recorded moderate genetic advance over mean.

Sarkar *et al.,* (2009) evaluated forty nine chilli genotypes and noticed high heritability in broad sense coupled with high GA in % grand mean for fruit yield/plant, number of fruits/plant, fruit length, days to 50% flowering and plant height indicating such characters were controlled by additive gene action.

Singh *et al.,* (2009) conducted a study on thirty chilli genotypes and discoverd high heritability coupled with high genetic advance for marketable fresh and dry yield per plant, average fruit weight, numbers of marketable fruit, fruit diameter, and oleoresin and capsaicin content, which indicated the role of additive gene action for the inheritance of these traits. These traits are likely to respond better to selection.

Kannan *et al.,* (2016) evaluated eighty genotypes of chilli and noted higher estimates of broad sense heritability along with genetic advance recorded for flowers per branch, fruits per plant, cluster per plant, stem diameter, plant weight and days to 50% flowering indicated the scope for improvement of these characters through selection.

Kumar *et al.,* (2012) performed an experiment on twenty genotypes of chilli and reported high estimates of heritability and genetic advance (as per cent of mean) in case of fruits yield plant, capsaicin content, number of fruits per plant. High heritability along with moderate to low genetic advance was observed for average fruit weight, days to first harvest, days to flower anthesis, number of branches, fruit length and fruit diameter.

Datta and Das (2013) investigated a study on fifty three genotypes of chilli and found that high heritability along with higher genetic advance (as a %age of mean) in capsaicin content in fruit, number of fruits per plant, yield per plant and primary branches per plant. These characters may be considered as reliable selection indices as they are possibly governed by additive gene effect.

Meena *et al.,* (2016) evaluated twenty chilli genotypes and recorded the highest heritability for plant height. High heritability with high genetic advance were obtained for leaf area, days to first harvest, days to 50% flowering, red ripe fruit yield per plant, number of fruits per plant, pedicel length, dry fruit width, fruit yield per plant, fruit length, plant height

and number of branches per plant which indicated additive gene action for these traits.

Rosmaina *et al.,* (2016) conducted a research on sixteen genotypes and reported high heritability coupled with high genetic advance per percent of mean was obtained for, plant height, stem length; leaf width; plant canopy width, days to flowering, fruit length; fruit diameter, single fruit weight, number of fruit per plant, fruit weight per plant reflecting the presence of additive gene action for the expression of these traits, and improving of these characters could be done through selection.

Sahu, *et al.,* (2016) studied nineteen genotypes of chilli and found highest heritability in characters like fruit weight per plant, days to first flowering and days to first picking. Whereas, highest heritability coupled with highest genetic advance were observed for characters viz., fruit weight per plant, days to first flowering and days to first picking. Hence, these characters might be improved by simple selection.

Kerketta*, et al*., (2017) studied seventeen accessions of chilli and observed high heritability coupled with high genetic advance (% of mean) for characters like fruit length, fruit diameter , fruit weight, no. of seeds per fruit, no. of fruits per plant, total soluble solids, fruit yield per plant, fruit yield per ha. High heritability with moderate genetic advance was observed for days to flower anthesis, days to 50 % flowering , weight of seeds per fruit, whereas high heritability with low genetic advance was found for days to fist harvest , 100 seeds weight , ascorbic acid.

Janaki *et al.,* (2017) evaluated seventy one chilli genotypes comprising fifty four F_1 hybrids, fifteen parents and two commercial checks. High heritability coupled with high genetic advance (as % of mean indicated) indicated that there is an existence of wide range of genetic variability among the all seventy one genotypes studied and suggested that predominance of additive gene action and lower influence of environmental factors in the expression of all biochemical traits making the selection more effective in their improvement.

Jogi *et al.,* (2017) assessed fifty genotypes of chilli and reported that most of the characters exhibited high estimates of heritability except for plant height at 60 and 120 days, primary and secondary branches at 60 days and plant spread (E-W) at 120, days to 50% flowering and days to fruit set. The high estimates of heritability for days to first flowering, number of fruits per plant at first picking and early yield. High heritability was accompanied with high values of genetic advance for early yield of green chilli indicating predominance of

additive gene component. Thus, there is ample scope for improving these characters based on direct selection. High heritability with moderate genetic advance noticed for plant height at 120 days, tertiary branches at 60 and 120 days, plant spread (N-S) at 60 and 120 days, number of fruits per plant at first picking implied equal importance of additive and non-additive gene action.

Pujar *et al.,* (2017) evaluated sixty three genotypes of chilli and observed high heritability for all characters, except 1000-seed weight and high genetic advance as per cent mean indicating that simple selection would be sufficient for these traits to bring genetic improvement.

Singh *et al.,* (2017) conducted a study on eighteen genotypes of chilli and recorded high heritability coupled with high genetic advance as percentage of mean for average fruit weight, number of fruit plant-1 suggested that the predominance of additive gene action indicating better scope for improvement of these traits by an effective selection programme.

Nahak *et al.,* (2018) investigated eleven genotype of chilli and observed that, heritability was highest for fruit weight followed by no. of fruits/plant and no. of borer affected fruits /plant. The maximum genetic advance (% of mean) was observed in case of no. of plants affected by leaf curl/plot followed by fruit weight and fruit borer/plant suggesting that additive gene action is responsible for expression of these characters.

3. Correlation coefficient analysis:-

Tembhurne *et al*., (2008) evaluated eleven elite advanced lines of chilli. The Correlation studies indicated that the yield showed significantly positive association with most of the traits except plant height, fruit length and fruit width.

Kumar *et al*., (2012) performed an experiment on twenty genotypes of chilli and reported that the genotypic correlation coefficient was larger than the phenotypic correlation. Number of fruits per plant significantly positive correlated with number of branches at 150 DAT, days to flower initiation, number of fruits per plant, average fruit weight, ascorbic acid con tent, fruit length, capsaicin content.

Bijalwan *et al.,* (2013) studied correlation studies in sixteen genotypes of chilli. Correlation coefficients at genotypic and phenotypic levels indicated that fruit yield per plant was positively and significantly correlated with fruit weight at edible maturity, number of

fruits per plant, fruit length, number of branches per plant and ascorbic acid content but negative and significant association was found with days to50% flowering indicating that early flowering and early picking might be associated with increasing the fruits yield per plant.

Yatung *et al.,* (2014) conducted a study on thirty chilli genotypes and reported that fruit yield per plant was positively and significantly correlated with number of branch per plant, number of fruit per plant and chlorophyll content while negative and significant association was established with ascorbic acid content acid content. Maximum positive direct effect on fruit yield per plant was imposed by fruit weight, number of fruit per plant, number of seed per fruit and capsaicin content.

Dolkar *et al.,* (2015) evaluated twelve advanced breeding lines of chilli and revealed that the genotypic correlation was higher than the corresponding phenotypic correlation for all the character combinations establishing predominant role of heritable factors. Among the growth parameters, the phenotypic and genotypic associations of fruit yield were significantly positive with number of secondary branches, plant height and number of primary branches.

Kerketta, *et al*., (2017) inspected seventeen genotypes of chilli and observed that fruit yield per plant, days to flower anthesis, days to 50% flowering, days to first harvest, fruit length, fruit diameter, number of seeds per fruit, seed weight fruit, 100 seeds weight, ascorbic acid content, total soluble solids, number of fruits plant showed positive correlation at genotypic level with fruit yield per plant(g), while at phenotypic level days to flower anthesis, days to 50% flowering, days to first harvest), fruit length, fruit diameter , number of seeds fruit 1, seed weight fruit , 100 seeds weight, ascorbic acid content, total soluble solids, number of fruits plant showed positive correlation with fruit yield per plant(g) and negative correlation at genotypic and phenotypic level was observed for fruit yield per plant (g).

Jogi *et al.,* (2017) conducted a study on fifty genotypes of chilli and revealed that the difference between the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were narrow for most of the characters. The results suggest that these traits are least affected by environment and selection for these traits on phenotype would be rewarding. For rest of the characters, the estimates of PCV were greater than GCV. This indicates that the variation for these traits is not only by genotypes but also due to environment. Selection based on phenotype may not be rewarding as their expression depends more on environmental factors.

Pujar *et al.,* (2017) evaluated sixty three genotypes of chili and observed a narrow difference between the genotypic and phenotypic correlation coefficients for various traits and this indicates the lesser influence of environment in the expression of the traits and presence of strong inherent association among the traits. Fruit set percentage had highly significant and positive correlation with green fruit yield per plant. Highly significant and negative correlation was obtained by 1000- seed weight with green fruit yield per plant.

Manikandan, *et al.,* (2018) conducted an experiment on chilli (Capsicum annuum L) to study the correlation and path coefficient for nine traits of F2 population obtained from the cross of K-1 x China type. Correlation indicated that dry fruit yield per plant was significant and positively associated with plant height, number of branches per plant, number of fruits per plant, pod length, single dry fruit weight, number of seeds per fruit, relative water content and capsaicin. Number of fruits per plant and single dry fruit weight showed the highest positive direct effect on fruit yield per plant. Direct selection may be executed considering these traits as the main selection criteria to reduce indirect effect of other characters during development of high yielding chilli variety.

Vidya *et al.,* (2018) studied twenty genotypes of chilli and reported that plant spread, fruit length, fruit diameter, fruit stalk length showed highly significant and positive genotypic and phenotypic correlation coefficient with fruit yield per plant. Reducing and non- reducing sugar showed highly significant and positive genotypic and phenotypic correlation coefficient with total sugar.

4. Path coefficient analysis:-

Sarkar *et al.,* (2009) studied forty nine genotypes of chilli and observed that number of fruits/plant, fruit weight and 1000 seed weight had positive and high direct effect on fruit yield indicating their reliability as selection criteria to improve yield of chilli.

Singh *et al.,* (2009) conducted a study on path analysis and observed that average fruit weight, numbers of total and marketable fruits per plant, and fruit length contributed to marketable fresh yield. Average dry fruit weight, numbers of t otal and marketable fruits per plant, seed weight per fruit, and harvest duration played a predominant role for predicting dry yield.

Bijalwan *et al.,* (2013) evaluated sixteen genotypes of chilli and reported highest positive direct effect on fruit yield per plant by fruit weight at edible maturity followed by

number of fruits per plant and fruit length, while as highest negative direct effect on fruit yield per plant was exerted by number of branches per plant and pedicel length. Therefore, selection should be practiced for fruit weight at edible maturity, number of fruits per plant and fruit length for direct improvement of fruit yield per plant.

Yatung *et al.,* (2014) investigated thirty chilli genotypes and reported that number of fruit per plant and average fruit weight had strong influence on fruit yield and the main determiners of fruit yield per plant. Therefore, improvement in yield can be achieved by selecting the genotypes which have more number of fruit per plant with more fruit weight.

Dolkar *et al.,* (2015) inspected twelve genotypes of chilli and observed that number of fruits per plant and pericarp weight had the highest positive direct effect on yield per plant indicating their true positive and significant association wi th total yield. Plant height, fruit weight, total fruit chlorophyll content and number of primary branches had highly significant positive correlation with total yield. But, they had low to negligible direct positive effects indicating that their association with the yield was not strong and true.

Sahu *et al.,* (2016) performed a research on nineteen genotypes of chilli and revealed that fruit weight showed the highest positive direct effect on days to first flowering followed by fruit length, number of fruits, fruit weight, days to last picking, number of branches and fruit girth. On the other hand days to first picking, stem girth, fruit length, fruit weight, plant height and days to 50% flowering.

Pujar *et al.,* (2017) evaluated sixty three genotypes of chilli and observed that fruit set percentage and fruit weight had the highest positive direct effect on fruit yield both at genotypic and phenotypic levels and most of the fruit related traits contributed to fruit yield mainly through fruit girth and fruit weight. Hence, it would be rewarding to lay stress on these characters in selection programmes for increasing yield.

Manikandan *et al.,* (2018) conducted an experiment on chilli (Capsicum annuum L) to study the correlation and path coefficient for nine traits of F_2 population obtained from the cross of K-1 x China type The path coefficient analysis in revealed that high positive direct effect on fruit yield per plant was exerted by number of fruits per plant and single dry fruit weight The negligible direct effect on fruit yield per plant was exerted by plant height, number of branches per plant, number of seeds per fruit relative water content and capsaicin. The plant height exerted lowest positive indirect effect on fruit yield per plant through

number of fruits per plant. The number of branches per plant recorded highest positive indirect effect on fruit yield per plant through number of fruits per plant. The indirect effect of number of fruits per plant was lowest and positive on fruit yield per plant through single dry fruit weight. The highest indirect effect of fruit length through single dry fruit weight and number of fruits per plant was positive and moderate.

Vidya *et al.,* (2018) evaluated twenty genotypes of chilli and recorded that plant spread, fruit diameter, weight of seeds per fruit, was found positive and direct effect on fruit yield per plant, while stem girth, primary branches, days to first flowering was found high negative direct effect on fruit yield per plant. Fruit diameter was very high positive direct effect on fruit yield per plant. Stem girth and primary branches had very high negative direct effect on fruit yield per plant. Plant spread and weight of seeds per fruit was medium positive direct effect on fruit yield per plant. Days to first harvesting had low positive direct effect on fruit yield per plant. Plant height and days to first harvesting had negligible effect on fruit yield per plant.

5. Genetic divergence studies:-

Kumar *et al.,* (2010) conducted a study of genetic diversity in 25 chilli genotypes and based on D^2 values, the genotypes were clustered into eight constellations. Cluster I contained nine genotypes fallowed by cluster-II (four) cluster IV and V (two each). The maximum inter cluster distance was observed between cluster VI and cluster VIII. The cluster IV recorded maximum intracluster distance. Intercrossing among the genotypes belonging to cluster III, IV and I was suggested to develop high yielding varieties with other desirable characters or may be used as potential donors for future hybridization programme to develop better chilli variety with good fruit yield.

Hasan *et al.,* (2015) investigated thirteen genotypes of chilli (*Capsicum annuum* L.) to understand the extent of genetic diversity through 6 yield attributing characters. Based on Mahalanobis's D^2 statistics genotypes were grouped into five different clusters by non-hierarchical clustering. The cluster I had the maximum number (5) of genotypes while cluster IV and V each contained only one genotype. The highest inter-cluster distance was observed between cluster I and IV and the lowest inter-cluster distance was observed between the clusters II and V. The results indicated that fruits/plant contributed maximum to the total divergence followed by fruit length and yield/plant. Cluster IV produced highest mean for fruit weight, fruits/plant and yield/plant. Cluster V produced highest mean for fruit length,

pedicel length and fruit diameter. Cluster I and III produced maximum lowest mean for almost all characters.

Janaki *et al.,* (2016) conducted a study sixty three genotypes of chilli was using Mahalanobis D^2 and grouped sixty three genotypes into 8 clusters. The maximum contribution towards genetic divergence was by fruit diameter followed by yellow carotenoids, red carotenoids, ascorbic acid and capsaicin. The mutual relationships between the clusters revealed that inter-cluster distance values were greater than intra-cluster values. Among the clusters, clusters III and V were the largest containing 17 genotypes followed by cluster IV whereas the clusters VI, VII and VIII were mono genotypic. The highest inter cluster distance was observed between clusters IV and VIII whereas the lowest was observed between clusters I and III. Cluster V has exhibited highest intra cluster distance and the lowest was observed in clusters VI, VII and VIII.

Kumari *et al.,* (2018) tested genetic divergence using D^2 analysis and based on fruit yield and its component characters sixteen genotypes were grouped into three clusters. The maximum number of nine genotypes was included in cluster-III followed by five genotypes in cluster-I. The highest inter-cluster divergence was observed between the clusters II and III which indicated maximum exploitation of heterosis on hybridization. The contribution of various characters towards the total divergence was recorded the highest for fruit girth (, dry weight of fruits, fruit yield per plant and dry matter % of fruits.

Pradhan *et al.,* (2017) conducted a genetic divergence study on 12 chilli and based on D2 values, the genotypes were clustered into five constellations. Cluster I, II and III contained three genotypes each followed by cluster-IV (two) and cluster V (one). The intra and inter cluster distances indicated that the statistical distance between clusters III and IV was the highest and this was followed by the distance between clusters IV and V. Cluster I had the highest mean value for branches/plant. Cluster II had the maximum mean values for plant girth and plant height. Cluster III had the highest mean values for average fruit weight, fruit girth, plant spread (e-w), plant spread (n-s) and fruit yield/plant. Cluster IV had the highest mean value for fruit length, fruits/plant, days to 50% flowering and crop duration. Cluster V had the lowest mean values for days to 50% flowering and crop duration. Relative contribution of fruit yield per plant to genetic divergence of genotypes in chilli was the maximum, followed by days to 50% flowering and plant height.

Pujar *et al.,* (2017) estimated genetic divergence study using Mahalanobis's D^2 statistics method on sixty three genotypes of chilli was. These 63 genotypes were grouped into 5 clusters based on similarity of D^2 values. It is desirable to select genotypes from clusters having high inter-cluster distance and with high fruit yield as parents in the recombination breeding programmes.

Chapter-3

MATERIALS AND METHODS

The present investigation on entitled, "**Exploration of genetic variability in chilli (*Capsicum annuum* L.) present in subtropical region of Himachal Pradesh"** was undertaken to access the extent of genetic variability, heritability and genetic advance, correlation coffecient and path coefficient analysis, was carried out during the months of june to december, 2018 at experimental vegetable farm of College of Horticulture and Forestry, Neri, Hamirpur, H.P. The details of the materials used, experimental methods followed and techniques adopted during the course of present investigation are described below in this chapter.

3.1 GENERAL

3.1.1 Location

Vegetable Research farm, Neri, is located in the Sub montane low hills zone (Zone-I) of Himachal Pradesh. Geographically, it is situated at an altitude 650 meters above mean sea level between $31^{o}41'47.6"$ N & $72^{o}28'^{0}6.3"$ E. It falls under the subtropical zone having hilly and mountainous relief in Himachal Pradesh.

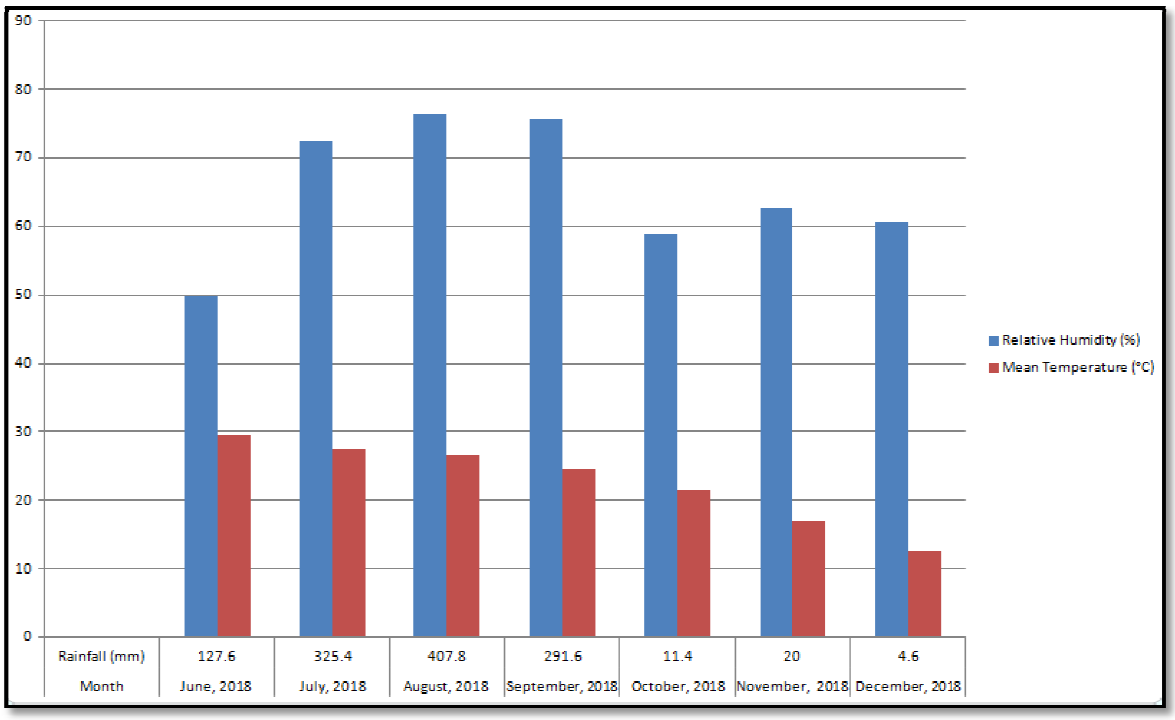
3.1.2 Climatic and weather conditions

The climate of the Experimental Farm is generally characterized as sub-tropical with cool winters during the crop period. Weather conditions which prevailed during growing conditions were recorded and have been presented in Appendix-I. November and December were the coldest months, while June and July were hottest. Maximum mean rainfall was observed for August month (407.8 mm). Maximum mean relative humidity recorded was 76.43 per cent and minimum was 49.87 per cent during the growing season. Graphical representations of monthly data pertaining to the temperature, rainfall and relative humidity during the crop growing season have been given in Fig. 3.1.

3.1.3 Soil

The soil structure of experimental site is sandy clay loamy soil with pH ranging from 7.02 - 7.28.

Fig 3.1 Graphical representation of monthly data pertaining to the temperature, relative humidity and rainfall during the growing season (2018).



Source: Meteorological Observatory, Department of Soil Science and Water Management, College of Horticulture and Forestry, Neri, Hamirpur (HP) 177001

3.2 Experimental material

The experimental materials used for present investigation comprised of 20 genotypes of chilli (*Capsicum annuum* L.) including Surajmukhi as standard check which were maintained at experimental farm, College of Horticulture and Forestry, Neri, Hamirpur, (H.P). The genotypes were diverse with respect to morphological and important economical traits. List of genotypes is given in Table 3.1.

3.3 Experimental layout

The experiment was laid out in a randomized complete block design with three replications. The size of each plot was 1.8 m x 2.25 m. Each replication contained 20 plots. Each plot contained 4 rows with 5 plants in each, making a sum total of 20 plants per plot. The seeds were sown on 18 june, 2018 and seedlings were transplanted on 19 july, 2018. The spacings between the row and within the row were 45 cm x 45 cm, respectively. Necessary plant protection measures were provided to the entire experimental material against the diseases and pests as and when needed. The crop was irrigated at frequent intervals depending upon the need. The standard cultural practices were followed as per recommended

in the package of practices for vegetable crops, to ensure a healthy crop stand of chilli (Anonymous, 2017).

Table 3.1 List of genotypes of chilli along with their sources.

Sr. No.	Genotype	Source
1	LC-C-1	Department of vegetable Science COHF, Neri Hamirpur
2	LC-C-9	Department of vegetable Science COHF, Neri Hamirpur
3	LC-C-8	Department of vegetable Science COHF, Neri Hamirpur
4	LC-C-7	Department of vegetable Science COHF, Neri Hamirpur
5	LC-C-15	Department of vegetable Science COHF, Neri Hamirpur
6	LC-C-14	Department of vegetable Science COHF, Neri Hamirpur
7	LC-C-11	Department of vegetable Science COHF, Neri Hamirpur
8	LC-C-23	Department of vegetable Science COHF, Neri Hamirpur
9	LC-C-21	Department of vegetable Science COHF, Neri Hamirpur
10	LC-C-22	Department of vegetable Science COHF, Neri Hamirpur
11	LC-C-19	Department of vegetable Science COHF, Neri Hamirpur
12	LC-C-20	Department of vegetable Science COHF, Neri Hamirpur
13	LC-C-18	Department of vegetable Science COHF, Neri Hamirpur
14	LC-C-29	Department of vegetable Science COHF, Neri Hamirpur
15	LC-C-51	Department of vegetable Science COHF, Neri Hamirpur
16	LC-C-27	Department of vegetable Science COHF, Neri Hamirpur
17	LC-C-24	Department of vegetable Science COHF, Neri Hamirpur
18	LC-C-26	Department of vegetable Science COHF, Neri Hamirpur
19	LC-C-38	Department of vegetable Science COHF, Neri Hamirpur
20	Surajmukhi	CSK HPKV, Palampur

3.4 OBSERVATIONS RECORDED

The observations were recorded on five randomly selected competitive plants from each plot in each replication and tagged to record the observations. Their means were worked out for statistical analysis. The data was recorded as per the standard procedure are listed as under;

3.4.1 Days to 50% flowering.

The number of days taken to complete 50% plant flowering in a plot from the date of transplanting was recorded. Data was recorded on plot basis.

3.4.2 Days to first picking.

Number of days recorded from the date of transplanting to first picking of fruits was recorded.

3.4.3 Pedicel length (cm).

Average pedicel length of five fruits from the point of holding to the stem from the 5 tagged plants was recorded.

3.4.4 Fruit length (cm).

The fruit length of five mature fruits of a plant from each plot was recorded with the help of digital vernier calliper and then average fruit length was calculated.

3.4.5 Fruit diameter (cm).

The fruit used for recording the fruit length were also used for measuring the fruit diameter with the help of digital vernier calliper.

3.4.6 Average fruit weight (g).

The total weight of harvested fruits from 5 tagged plants was divided by total number of fruits to get weight of single fruit in each genotype.

3.4.7 Number of marketable fruits per plant.

The total numbers of marketable fruits harvested from 5 tagged plants were averaged to get number of fruits per plant. The operation was done for each genotype separately.

3.4.8 Marketable fruit yield per plant (kg).

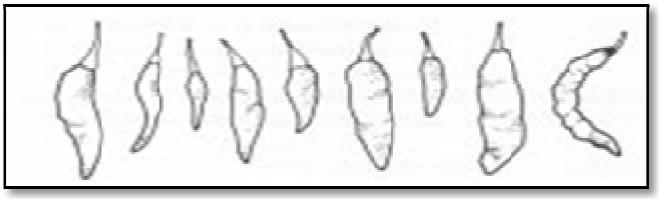
This was recorded as cumulative marketable fruit yield of all pickings from the 5 tagged plants individually and averaged.

3.4.9 Total soluble solids.

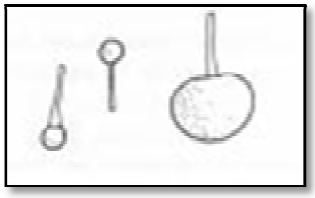
Matured fruits crushed in pestle mortar and the liquid extract obtained was used to record TSS with the help of ERMA hand refractrometer.

3.4.10 Fruit shape and color.

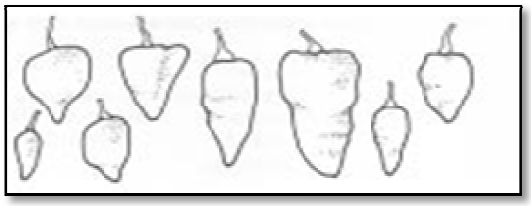
Overall Fruit shape: The fruit shape of the fruits collected from the 5 tagged plants were observed to categorize the genotype into elongate, oblate, round, conical, campanulate, bell or blocky.



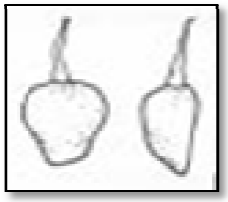
Elongate



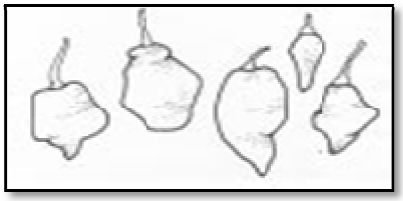
Round



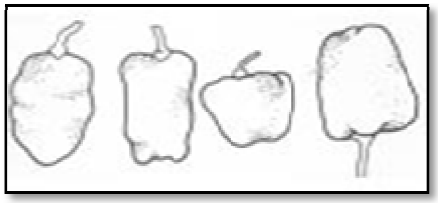
Conical



Oblate



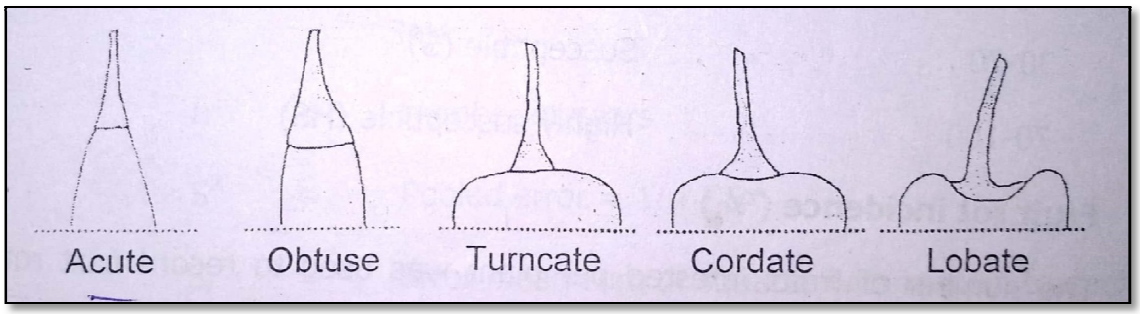
Campanulate



Bell or Blocky

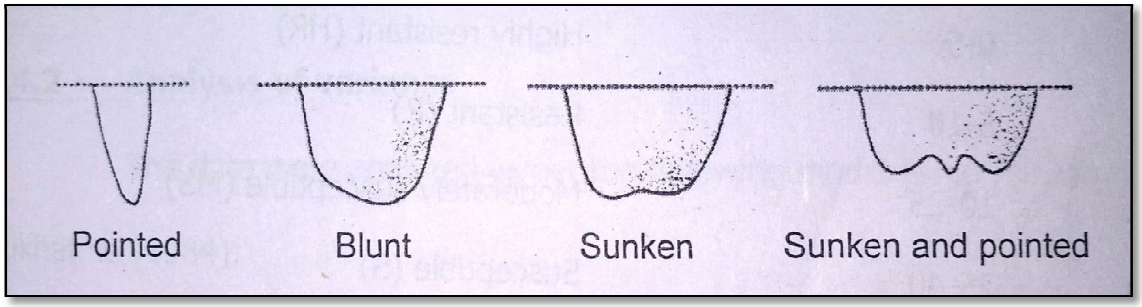
Overall fruit shape

Fruit shape at pedicel attachment: Fruit shape at peduncle attachment of the mature fruits was obsereved to categorize the genotype into acute, obtuse, truncate, cordate and lobate groups.



Fruit shape at pedicel attachment.

Fruit shape at blossom end: Blossom end fruit shape was recorded at mature fruit stage. The genotypes were divided into pointed, blunt, sunken, sunken and pointed group.



Fruit shape at blossom end.

Fruit colour: The fruit colour of the matured fruits was observed to categorize according to Royal Horticultural Society colour charts Edition V (version 2) under the classes yellow-red, purple-blue, turquoise-green and brown-grey.

3.4.11 Number of primary branches per plant.

Number of primary branches arising from the stem were counted in 5 tagged plants was recorded and then mean values were calculated.

3.4.12 Plant height (cm).

Plant height of 5 tagged plants of each genotype was measured with the help of meter scale from the base of the plant to the tip of the main axis at the time of final harvest. Then average plant height was calculated.

3.4.13 Stem length to forking (cm).

Average stem length of five tagged plants of each plot was measured with the help of meter scale from the base of the plant to the point of stem forking at the time of final harvest.

3.4.14 Stem diameter (cm).

The stem girth of five tagged plants from each plot was recorded with the help of digital vernier calliper and then average stem diameter was calculated.

3.4.15 Plant spread (cm).

Plant spread of five tagged plants of each plot was measured with the help of meter scale by measuring the length and breadth of the plant canopy and their average will provide the plant spread of the individual plant.

3.4.16 Number of seeds per fruit.

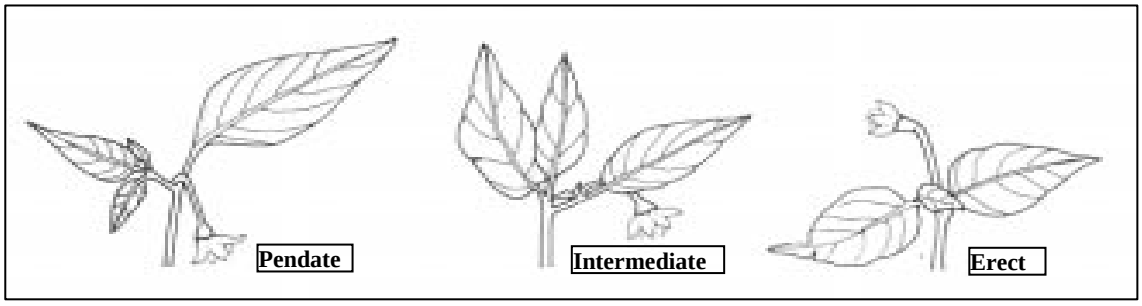
The total number of seeds from five fruits were taken out and counted and then the average value was estimated.

3.4.17 Weight of 100 seeds (g).

Weight of 100 seeds collected from the fruits harvested from the five tagged plants was measured by electronic balance to work out the hundred seed weight**.**

3.4.18 Bearing habit.

Bearing habit was evaluated from flowering habit. Flower per axil were noted as solitary and in cluster and Fruit bearing habit was recorded at mature fruit stage with pendant, intermediate and erect bearing habit as per Bioversity International descriptors in each treatment.



Bearing habit

3.5 STATISTICAL ANALYSIS

Mean of the various observations were subjected to the following statistical analysis for drawing conclusion from present investigation. The statistical analysis was carried out for each observed character by using MS-Excel, OPSTAT and SPAR 1.0 packages.

3.5.1 Analysis of variance (ANOVA)

The statistical analysis for all the characters studied was done by the method recommended by Gomez and Gomez (1983) for Randomized Block Design (RBD) for adopted:

Source of Variation	Degree of Freedom	Sum of Square	Mean Sum of Square	Variation Ratio
Replication (r)	r-1	Sr	$Mr = \frac{Sr}{\mathrm{r}-1}$	$\frac{Mr}{Me}$
Treatments (t)	t-g	Sg	$Mt = \frac{Sg}{g-1}$	$\frac{Mg}{Me}$
Error (e)	(r-1) (g-1)	Se	$Me = \frac{Se}{(r-1)(g-1)}$	

Where,

r = Number of replications.

g = Number of genotypes.

Sr = Sum of squares due to replications.

Sg = Sum of squares due to genotypes.

Se = Sum of squares due to error.

Mr = Mean sum of squares due to replications.

Mg = Mean sum of squares due to genotypes.

Me = Mean sum of square due to error.

The calculated 'F' values were compared with tabulated 'F' value for test of significance. Standard Error (SE), Critical Difference (CD) and Coefficient of Variation (CV) were calculated to find out the superiority of one genotype over the others with the help of following formulae:

SE (m) ± = $\sqrt{\frac{Me}{r}}$

SE (d) ± = $\sqrt{\frac{2Me}{r}}$

$CD_{0.05}$ = S.E. (d) x $t_{(0.05)}$ (r-1) (g-1) df

Where,

SE (m) ± = Standard error of mean

SE (d) ± = Standard error of difference

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

All the characters which showed significant differences among genotypes were further subjected to analysis for the following parameters;

- Coefficients of variability (phenotypic and genotypic)
- Heritability
- Genetic advance
- Genetic gain
- Correlation coefficients
- Path coefficient analysis
- Genetic divergence

3.5.2 Parameters of variability

Variability for different characters was estimated as suggested by **Burton and Devane (1953)**. The coefficient of variability at genotypic (GCV) and phenotypic (PCV) levels were estimated as follows:

A) Genotypic Coefficient of Variability (GCV)

$$\text{GCV (\%)} = \frac{\sqrt{\text{Genotypic Variance (Vg)}}}{\text{General Mean of population } (\mu)} \times 100$$

B) Phenotypic Coefficient of Variability (PCV)

$$\text{PCV (\%)} = \frac{\sqrt{\text{Phenotypic Variance (Vg)}}}{\text{General Mean of population } (\mu)} \times 100$$

Where,

Ve = Me

Vg = Genotypic Variance (Mt-Me)/r

Vp= Phenotypic Variance (Vg+Ve)

PCV and GCV were classified as shown below (Cherian, 2000)

Less than 10 %	=	Low
10-20 %	=	Moderate
More than 20 %	=	High

3.5.3 Heritability:

Heritability in broad sense was estimated as per the formulae suggested by Allard (1960).

$$H\ (\%) = \frac{Vg}{Vp} \times 100$$

Where,

H = Heritability (%)

Vg = Genotypic variance, [$V_g = (M_t - M_e) / r$]

Vp = Phenotypic variance ($V_g + V_e$)

The heritability was categorised as suggested by Johnson *et al.* (1955):

0-30%	=	Low
31-60%	=	Medium
61% and above	=	High

3.5.4 Genetic advance

The expected genetic advance (GA) resulting from selection of five per cent superior individuals was calculated as per Allard (1960).

$$GA = H \times rp \times K$$

Where,

H = Heritability (%)

rp = Phenotypic standard deviation

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

3.5.5 Genetic gain

Genetic gain expressed as per cent ratio of genetic advance and population mean was calculated by the method given by Johanson *et al*. (1955).

$$GG = (GA/\ GM) \times 100$$

Where,

GG = Genetic gain

GA = Genetic advance

GM = Population mean

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

Less than 10%	=	Low
10-20%	=	Moderate
More than 20 %	=	High

3.5.6 Correlations

The genotypic and phenotypic correlations were calculated as per Al-Jibouri *et al.* (1958) by using analysis of variance and covariance matrix in which total variability split into replications, genotypes and errors. All the components of variance were estimated from the analysis of covariance as given below:

3.5.6.1 Analysis of variance and co variance

Source of variance	**Degree of freedom**	**Mean sum of squares**		**Mean sum of products**	**Variance**
		X	**Y**		
Replications (r)	r-1				
Genotypes (g)	g-1	Mg X	Mg Y	Mg XY = MP_1	MP_1/MP_2
Error (e)	(r-1) (g-1)	Me X	Me Y	Me XY = MP_2	

Genotypic, phenotypic and environmental covariances between X and Y characters were worked out as under:

Ve XY = MP_2

Vg XY = $(MP_1-MP_2) / r$

Vp XY = Vg XY + Ve XY

Where,

Ve XY = Environmental covariance between X and Y

Vg XY = Genetic covariance between X and Y

Vp XY = Phenotypic covariance between X and Y

3.5.6.2 Coefficients of correlations

a) Genotypic correlation coefficient between X and Y.

$$r_g = \frac{Vg\ XY}{\sqrt{Vg\ X\ Vg\ Y}}$$

where,

Vg XY = Genotypic covariance between X and Y

Vg X = Genotypic variance of X

Vg Y = Genotypic variance of Y

b) Phenotypic correlation coefficient between X and Y

$$r_p = \frac{Vp\ XY}{\sqrt{Vp\ X\ Vp\ Y}}$$

where,

Vp XY = Phenotypic covariance between X and Y

Vp X = Phenotypic variance of X

Vp Y = Phenotypic variance of Y

Genotypic variance (Vg) = (Mg - Me) / r

Phenotypic variance (Vp) = (Vg + Ve)

The calculated correlation coefficients (r) values were compared with 'r' tabulated values as given by Fisher and Yates (1963) at (n-2) degrees of freedom to test their significance, where 'n' denotes number of genotypes. If calculated 'r' value at 5 per cent level of significance was greater than tabulated value of 'r', the correlation was said to be significant.

3.5.7 Path Coefficients of analysis

The genotypic and phenotypic correlation coefficients were used to finding out their direct and indirect contribution towards marketable fruit yield per plant.

The direct and indirect paths were obtained by following Dewey and Lu (1959). The path coefficients were obtained by simultaneous selection of the following equations, which expresses the basic relationship between genotypic correlation 'r' and path coefficients (P):

$$r14 : P_{14} + P_{24} r_{12} + P_{34} r_{13}$$

$$r24 : P_{14} r_{21} + P_{24} + P_{34} r_{23}$$

$$r34 : P_{14} r_{31} + P_{24} r_{32} + P_{34}$$

Where,

r_{14}, r_{24} and r_{34} are genotypic correlations of component characters with marketable fruit yield per plant (dependent variable) and r_{12}, r_{13} and r_{23} are the genotypic correlations among component characters (independent variables).

The direct effects were calculated by the following set of equations:

$$P_{14} = C_{11} r_{14} + C_{12} r_{24} + C_{13} r_{34}$$

$$P_{24} = C_{21} r_{14} + C_{22} r_{24} + C_{23} r_{34}$$

$$P_{34} = C_{31} r_{14} + C_{32} r_{24} + C_{33} r_{34}$$

Where,

C_{11}, C_{22}, C_{23} and C_{33} are constants derived by using abbreviated Doulittle's technique as explained by Goulden (1959).

$r_{12} P_{24}$, $r_{13} P_{34}$, $r_{21} P_{14}$, $r_{23} P_{34}$, $r_{31} P_{14}$, $r_{32} P_{24}$ are indirect effects.

3.5.7.1 Residual effect

The variation in the dependent variable which remained undetermined by including all the variables was assumed to be due to variable (s) not included in the present investigation. The degree of determination of such variable (s) on dependent variable was calculated as follows:

$$1 = P^2 x_4 + P_{14}^2 + P_{24}^2 + P_{34}^2 + 2P_{14} r_{12} P_{24} + 2P_{14} r_{13} P_{34} + 2P_{24} r_{23} P_{34}$$

3.5.8 Genetic divergence

The genetic divergence in 20 genotypes was estimated by Mahalanobis 'D^2' statistics (generalized distance as suggested by (Rao, 1952) and canonical variate analysis. The calculation of D^2 values involved following steps (Murty and Arunachalam, 1967).

- A set of uncorrelated linear combinations (Y's) was obtained by pivotal condensation of the common dispersion matrix (Rao, 1952) of a set of correlated variable (X's) and this matrix was arranged with the help of error mean sum of square and sum of products.
- Using the relationship between Y's and X's the mean value of different genotypes for different characters (X_1 to X_{10}) were transformed into the mean values of asset of uncorrelated linear combinations (Y_1- Y_{10}).
- The D^2 values between i^{th} and j^{th} genotypes for P^{th} characters was calculated as under:

$$D^2ij = \sum_{i=1}^{k} (Yit - Yjt)^2$$

Where,

Yit = uncorrelated mean value of i^{th} genotype for 't' characters.

Yjt = uncorrelated mean value of j^{th} genotype for 't' characters.

D^2ij = D^2 between i^{th} and j^{th} accessions.

In all combinations each character was ranked based on their contribution towards divergence between two entries (di= Yit- Yjt). Rank 1 is given to the highest mean difference and rank P to the lowest difference, where, P is the total number of characters.

i. The 'P' component and D^2 for each combination were ranked in descending order of magnitude.

ii. The ranks were added up for each component D^2 over all combination and the rank totals were obtained.

3.5.8.1 Group constellation

Varieties were grouped into a number of clusters. D^2 being treated as the square of generalized distance, according to the method described by Tocher (Rao, 1952). The criterion used in clustering by this method is that any two genotypes belonging to the same cluster should, at least on an average, show a smaller D^2 value than those belonging to two different clusters. In other words, if variety V_1 and V_2 are close together and variety V_3 is distinct from both shown by this generalized distance, V_1 and V_2 from one cluster.

The average D^2 values of all possible genotypes combinations in one cluster with those in the other were computed and its square root was used to represent the 'statistical distance' between two clusters.

3.5.8.2 Intra and inter cluster genetic distances

For the analysis of intra-cluster D^2 values, the following formula was used:

Intra and Inter cluster $D^2 = \frac{\sum Di^2}{N}$

N = n (n-1)/2

Where,

$\sum Di^2$ is the sum of D^2 values between all possible combinations (N) within and between clusters, respectively.

n = number of populations included in a cluster

Intra and inter cluster genetic distances (d) where computed square root of average intra-and inter cluster D^2 values *i.e.*, $d = \sqrt{D^2}$

Chapter-4

RESULTS AND DISCUSSION

The present investigation entitled, "**Exploration of genetic variability in chilli *(Capsicum annuum* L.*)* present in subtropical region of Himachal Pradesh"** was undertaken on twenty diverse local collections of chilli including one check cultivar Surajmukhi, to study variability, heritability, genetic advance, correlation coffecient analysis and path coefficient analysis.

The results obtained after the evaluation of genotypes are discussed and supported with relevant or appropriate references in the following headings:

4.1 Variability studies

4.2 Heritability and genetic advance

4.3 Correlation coefficient analysis

4.4 Path coefficient analysis

4.1 VARIABILITY STUDIES

4.1.1 Mean performance of genotypes

Analysis of variance indicated significant variation among all genotypes for all traits tabulated in Appendix-II, which acknowledged the presence of great deal of variability in the genotypes. The mean performances of 20 genotypes for various characters are described and discussed as below:

4.1.1.1 Days to 50% flowering

The major objective in any breeding program is earliness in flowering. Less number of days to 50 % flowering indicated the earliness of the variety while higher number of days revealed the late maturity of the variety. Significant variations were observed among all the genotypes for days to 50% flowering (Appendix-II). The number of days for 50% flowering ranged from 45.33 to 58.00 days (Table-4.1). Grand mean for the character was 50.47 days. Twelve genotypes were earlier in flowering than population mean. The mean value of genotypes illustrated that LC-C-26 was

earliest in flowering (45.33) which was statistically at par with LC-C-1 (45.34) and LC-C-15 (46.33) whereas, the maximum number of days for 50% flowering was noticed in LC-C-27 (58.00). Likewise eight other genotypes were earlier in maturity than standard check Surajmukhi. Tremendous variability with respect to days to 50% flowering were also reported by Smitha *et al*. (2006), Singh *et al.* (2009), Janaki *et al*. (2015), Meena *et al.* (2016) and Sahu *et al*. (2016) and Singh *et al.* (2017) in chilli.

4.1.1.2 Days to first picking

Significant variations among all the genotypes were observed for days to first picking (Appendix-II). General mean for this character was 80.92 days which ranged from 74.33 - 90.00 days (Table 4.1). Ten genotypes were earlier in maturity than population mean. The genotype LC-C-1 took minimum days to first picking (74.33), which was statistically at par with LC-C-26 (75.33) whereas genotype LC-C-27 took maximum days to first picking (90.00). Similarly thirteen genotypes were earlier in maturity than standard check Surajmukhi (81.67). Earliness is determined by one of this parameter and early picking of fruits and several harvesting over wide range of period avoid market glut and fetch higher price during specific parts of the year. Similar findings with respect to days to first picking were also reported by, Singh *et al.* (2009), Kumar et al. (2012), Meena *et al.* (2016), Sahu *et al*. (2016, Kerketta *et al.* (2017) and Singh *et al.* (2017).

4.1.1.3 Average fruit weight (g)

The perusal of data for average fruit weight revealed significant differences among all the genotypes (Appendix-II). It varied from 1.70 – 5.67 (Table 4.1). Grand mean for this trait was found out to be 3.17. Ten genotypes including check weighed higher average fruit weight than population mean. Genotype LC-C-38 (5.67) produced fruits with maximum average fruit weight which was significantly different from other genotypes including check. Considering that, genotype LC-C-23 (1.70) produced fruits with minimum average fruit weight which was found statistically at par with LC-C-21 (1.95). These results are in good agreement with Manju and Sreelathakumary (2002), Tembhurne *et al.* (2008), Singh *et al.* (2009), Dhaliwal *et al.* (2014), Sahu *et al.* (2016), Kerketta *et al.* (2017) and Nahak et al. (2018).

Table 4.1 Mean performance of chilli genotypes for days to 50 % flowering, days to first picking, average fruit weight (g) and fruit diameter (cm).

Genotypes	Days to 50 % flowering	Days to first picking	Average fruit weight (g)	Fruit Diameter (cm)
LC-C-1	45.34	74.33	2.54	0.88
LC-C-9	55.00	81.67	3.21	0.75
LC-C-8	53.00	84.00	3.22	1.12
LC-C-7	52.00	80.33	2.34	0.91
LC-C-15	46.33	76.67	3.39	1.21
LC-C-14	53.33	83.67	3.38	0.98
LC-C-11	48.67	77.67	2.18	0.84
LC-C-23	48.00	77.33	1.70	0.85
LC-C-21	53.33	83.67	1.95	0.94
LC-C-22	48.67	80.33	3.45	1.03
LC-C-19	50.33	81.67	3.40	1.06
LC-C-20	48.33	78.67	3.23	0.90
LC-C-18	49.67	80.67	3.13	1.17
LC-C-51	50.33	81.33	3.93	0.94
LC-C-27	58.00	90.00	3.14	1.73
LC-C-24	53.33	85.67	2.63	1.09
LC-C-26	45.33	75.33	3.12	0.88
LC-C-38	52.67	84.33	5.67	0.80
LC-C-29	48.33	79.33	2.94	0.94
Surajmukhi (check)	49.33	81.67	4.85	1.13
Mean	**50.47**	**80.92**	**3.17**	**1.01**
Range	**45.33 - 58.00**	**74.33 - 90.00**	**1.70 – 5.67**	**0.75 – 1.73**
± SE(m)	**0.44**	**0.37**	**0.17**	**0.04**
CV (%)	**1.49**	**0.80**	**9.24**	**6.33**
C.D. (0.05)	**1.25**	**1.07**	**0.47**	**0.11**

4.1.1.4 Fruit Diameter (cm)

The data observed for fruit diameter showed variability among all the genotypes (Appendix-II). It ranged from 0.75 to 1.73 with a population mean of 1.01 (Table 4.1). Eight genotypes including check recorded higher fruit diameter than population mean. Maximum fruit diameter was recorded in LC-C-27 (1.73) followed by LC-C-18 (1.17), LC-C-15 (1.21) and LC-C-8 (1.12) which were statistically similar to that of check. Three genotypes were found to have larger in fruit diameter than standard check,

Surajmukhi. Results obtained are in close conformity with findings of Tembhurne *et al* (2008), Ukkund *et al*. (2007), Jogi *et al*. (2013), Vijaya *et al.* (2014), Janaki *et al*. (2015), Meena *et al.* (2016) and Singh *et al*. (2017), who have also reported a wide range of fruit diameter in their germplasm.

4.1.1.5 Fruit Length (cm)

Analysis of variance showed the divergence among the genotypes for fruit length (Appendix- II). It varied from 2.01 to 12.07 with a grand mean of 6.02 (Table 4.2). Six genotypes produced longer fruits than population mean (6.02) being maximum value in LC-C-38 (12.07) which was significantly different from other genotypes. Likewise the minimum value for fruit length was observed in genotype LC-C-27 (2.01). Thirteen genotypes had more fruit length than standard check Surajmukhi (5.59). It is one of the major yield determining as well as quality traits of fruits. Similar variations regarding fruit length, among different genotypes were also reported by Smitha *et al*. (2006), Singh *et al.* (2009), Janaki *et al*. (2015), Meena *et al.* (2016), Sahu *et al*. (2016), Singh *et al.* (2017), Singh *et al.* (2017) and Nahak *et al* (2018).

4.1.1.6 Number of marketable fruits per plant

Analysis of variance (Appendix - II) showed genetic diversity among all the genotypes for number of marketable fruits per plant ranging from 10.93 – 61.50 (Table 4.2) with a population mean of 38.29. Eleven genotypes including check produced higher number of marketable fruits per plant than population mean. Three genotype *viz.* LC-C-8 (61.50), LC-C-23 (53.53) and LC-C-22 (50.80) surpasses the standard check Surajmukhi (44.40). These results concurs well with Smitha *et al*. (2006), Singh *et al.* (2009), Datta *et al.* (2013), Jogi *et al*. (2013), Singh *et al.* (2017) and Nahak *et al.* (2018).

4.1.1.7 Number of primary branches per plant

The perusal of data for number of primary branches per plant revealed significant differences among all the genotypes (Appendix-II). It ranged from 2.17–7.13 (Table 4.2) with a grand mean of 3.88. Grand mean for the character was 3.88. Maximum number of primary branches was recorded in LC-C-22 (7.13) which was significantly different from to population other genotypes. Seven genotypes including the check produced more number of primary branches per plant in comparison mean.

Table 4.2 Mean performance of chilli genotypes for fruit length (cm), number of marketable fruits per plant, number of primary branches per plant and number of seeds per fruit.

Genotypes	Fruit length (cm)	Number of marketable fruits per plant	Number of primary branches per plant	Number of seeds per fruit
LC-C-1	6.28	41.53	3.60	58.13
LC-C-9	6.56	41.93	5.00	59.00
LC-C-8	5.61	61.50	2.17	77.07
LC-C-7	5.73	35.53	2.63	55.07
LC-C-15	5.44	37.93	4.27	58.33
LC-C-14	6.78	22.33	3.13	72.73
LC-C-11	5.91	37.87	4.10	64.93
LC-C-23	4.74	53.53	3.47	60.07
LC-C-21	4.66	37.67	3.63	57.40
LC-C-22	8.40	50.80	7.13	55.27
LC-C-19	5.04	37.33	3.33	66.00
LC-C-20	5.82	39.87	3.80	54.67
LC-C-18	5.64	39.27	3.13	71.80
LC-C-51	5.68	10.93	4.13	70.01
LC-C-27	2.01	32.40	3.40	61.60
LC-C-24	5.76	38.60	3.80	77.00
LC-C-26	7.14	39.47	5.20	70.14
LC-C-38	12.07	24.60	3.30	70.13
LC-C-29	5.54	38.40	3.80	56.93
Surajmukhi (check)	5.59	44.40	4.47	64.87
Mean	**6.02**	**38.29**	**3.88**	**64.06**
Range	**2.01 – 12.07**	**10.93 – 61.50**	**2.17 – 7.13**	**54.67 – 77.07**
± SE(m)	**0.27**	**0.91**	**0.21**	**1.15**
CV (%)	**7.71**	**4.14**	**9.28**	**3.11**
C.D. (0.05)	**0.77**	**2.63**	**0.60**	**3.31**

Three genotype *viz.* LC-C-22 (7.13), LC-C-26 (5.20) and LC-C-9 (5.00) recorded significantly higher values for number of primary branches per plant than Surajmukhi while LC-C-15 (4.27), LC-C-51 (4.13) and LC- C-11(4.10) found statistically at par for this horticultural trait. Number of primary branches per plant has a direct effect on the fruit weight. Results obtained are consistent with Manju and Sreelathakumary (2002), Tembhurne *et al.* (2007), Datta *et al.* (2013), Meena *et al.* (2016), Pandiyaraj *et al.* (2017) and Singh *et al*. (2017).

4.1.1.8 Number of seeds per fruit

All the genotypes studied, indicated significant variations for number of seeds per fruit and (Appendix- II). The recorded values are presented in table 4.2 with a general mean of 64.06. Maximum number of seeds per fruit were recorded in LC-C-8 (77.07) followed by LC-C-24 (77.00), LC-C-14 (72.73) and LC-C-18 (71.80). Nine genotypes gave higher number of seeds per fruit than standard check surajmukhi (64.87). The genotypes with more number of seed per fruit can be used as one of the parent in hybrid seed production after its evaluation for GCA and SCA. Results obtained are in close conformity with findings of Manju and Sreelathakumary (2002), Patil *et al.* (2008), Jyothi *et al.* (2011), Vijaya *et al*. (2014), Kerketta *et al.* (2017) and Pandiyaraj *et al.* (2017).

4.1.1.9 Pedicel Length (cm)

All the genotypes studied, indicated significant variations for pedicel length (Appendix- II). It ranged from 1.84 to 4.29 (Table 4.3) with a grand mean 3.12 cm for the parameter. Maximum value was recorded in Surajmukhi (4.29) which is statistically different from all other genotypes except LC-C-9 (3.98) while LC-C-27 depicted the lowest value (1.85). Generally the fruits with long and sturdy pedicel produce longer and bulky fruits. These results are in agreement with the earlier findings of Manju and Sreelathakumary (2002), Sharma *et al.* (2009), Jogi *et al*. (2013), Quresh *et al.* (2015), Meena *et al.* (2016), Mamatha *et al.* (2017) and Murmu *et al.* (2017).

4.1.1.10 Plant height (cm)

As shown in Appendix – II, the data observed for plant height showed wide diversity among all the genotypes. The data presented in table 4.3 revealed that maximum plant height of 80 was recorded in genotype LC-C-8 which is statistically different from all other genotype while genotype LC-C-27 (70.80) and LC-C-9 (67.40) recorded the values that are statistically similar to standard check (68.47). The vigour of the plant has direct effect on most of the yield contributing factors. These results are in agreement with the earlier findings of Manju and Sreelathakumary (2002), Tembhurne *et al*. (2007), Ukkund et al. (2007), Datta *et al.* (2013), Meena *et al.* (2016), Pandiyaraj *et al.* (2017), Nahak et al (2018).

4.1.1.11 Plant spread (cm)

Analysis of variance revealed significant differences among the genotypes for plant spread tabulated in Appendix- II. The statistical data was presented in Table 4.3. Overall mean for the character was 41.43 cm. Maximum plant spread of 55.13 was observed in LC-C-27 followed by LC-C-24 (52.08). Minimum plant spread was recorded in LC-C- 24 (31.24) and was found statistically at par with LC-C-11 (31.47), LC-C-22 (33.52) and LC-C-18 (32.48). Seven genotypes gave higher value of plant spread than standard check Surajmukhi (42.22). Plant spread is the index of plant vigour which in terms provide tolerance to biotic and abiotic stresses. These results share a number of similarities with Patil *et al.* (2008), Sarkar et al. (2009), Datta *et al.* (2013), Vijaya *et al*. (2014) from 18.00 to 48.00, , Aklilu *et al,* (2016) and Zehra *et al.* (2017).

4.1.1.12 Stem diameter (cm)

The analysis of variance showed divergence among all the genotypes (Appendix-II). Data revealed wide variation for diameter Range varied from 0.64 – 0.94 (Table 4.3). Maximum stem diameter of 0.94 cm was recorded in two genotypes i.e. LC-C-27 and LC- C-8 which is statistically at par with LC-C-24 (0.89) followed by LC-C-19 (0.90). Eight genotypes were found statistically at par with for stem diameter in comparision to standard check Surajmukhi (0.72) Stem diameter is an indicative of plant vigour. These results are in complete agreement with Patil *et al.* (2008).

4.1.1.13 Stem length to forking (cm)

The data recorded for stem length to forking showed significant differences among all the genotypes which are tabulated in Appendix-II. It ranged from 12.50–37.47 (Table 4.4). Grand mean for the character was 24.55. Ten genotypes including the check produced longer stem length to forking in disparity to population mean. Maximum value of stem length was observed in LC-C-24 (37.47) followed by LC-C-22 (33.47).Whereas minimum value of stem length to forking was recorded in LC-C-27 (12.50) which was significantly different from others Seventeen genotypes gave higher value of stem length to forking than standard check Surajmukhi (17.43). Stem length to forking is an important character for earliness as, crown bud formation initiates at the point of stem forking.

Table 4.3 Mean performance of chilli genotypes for pedicel length (cm), plant height (cm), plant spread (cm) and stem diameter (cm).

Genotypes	Pedicel length (cm)	Plant height (cm)	Plant spread (cm)	Stem diameter (cm)
LC-C-1	3.07	51.00	48.29	0.85
LC-C-9	3.98	67.40	46.53	0.86
LC-C-8	2.65	80.00	52.31	0.94
LC-C-7	2.97	60.87	39.03	0.80
LC-C-15	3.04	53.93	35.33	0.78
LC-C-14	2.88	48.53	31.24	0.77
LC-C-11	3.25	50.47	31.47	0.75
LC-C-23	3.20	51.07	41.82	0.72
LC-C-21	2.81	54.40	35.86	0.80
LC-C-22	3.36	47.47	33.52	0.70
LC-C-19	3.27	59.33	36.94	0.90
LC-C-20	3.22	56.93	36.48	0.79
LC-C-18	3.03	49.27	32.48	0.64
LC-C-51	2.57	49.60	40.02	0.72
LC-C-27	1.84	70.80	55.13	0.94
LC-C-24	2.86	64.53	52.08	0.89
LC-C-26	3.45	65.80	48.25	0.82
LC-C-38	3.74	58.60	51.20	0.69
LC-C-29	2.93	48.93	38.49	0.71
Surajmukhi (check)	4.29	68.47	42.22	0.72
Mean	**3.12**	**57.87**	**41.43**	**0.79**
Range	**1.84 – 4.29**	**47.47 – 80.00**	**31.24 – 55.13**	**0.64 – 0.94**
± SE(m)	**0.12**	**0.94**	**0.80**	**0.02**
CV (%)	**6.53**	**2.81**	**3.36**	**4.57**
C.D. (0.05)	**0.34**	**2.70**	**2.31**	**0.06**

4.1.1.1 (**Total soluble solids (°Brix)**

Significant variations were obtained among all the genotypes for total soluble solids (appendix- II). Grand mean for this character was 4.99° Brix (Table 4.4). Fifteen genotypes including check gave higher total soluble solids TSS) than population mean. Maximum TSS was recorded in LC-C-27 (5.67) and was significantly different from other genotypes. Likewise, minimum TSS was recorded in LC-C-24 (4.02) and was also

significantly different from other genotypes. Six genotypes showed higher total soluble solids (TSS) than standard check Surajmukhi (5.08). Total soluble solid is one of the quality traits which decide the consumer preference. These results corroborate previous results Afroza *et al*. (2013), Amit et al. (2014), and Khapte *et al*. (2014), Maurya et al. (2017) and Kumar *et al*. (2019).

4.1.1.16 Weight of 100 seeds (g)

The data presented in appendix - II revealed significant differences among all the genotypes. Grand mean for the character was 0.47 (Table 4.4). Seven genotypes had higher weight of 100 seeds in distinction to population mean. Weight of 100 seeds was recorded maximum in LC-C-15 (0.61) and was found statistically at par with LC-C-8 (0.55), LC-C- 19 (0.54), LC-C-18 (0.57) and LC-C-51 (0.59) whereas minimum value for weight of 100 seeds was observed in LC-C-1 (0.39) which was statistically at par with 9 other genotypes *viz.* LC-C-9 (0.44), LC-C-11 (0.40), LC-C-23 (0.40), LC-C-21 (0.41), LC-C-22 (0.42), LC- C-29 (0.41), LC-C-38 (0.41), LC-C-26 (0.45) and LC-C-27 (0.43). Nineteen genotypes gave higher weight of 100 seeds than standard check surajmukhi (0.39). Weight of 100 seeds is also one of the major yield determining factors in chilli crop. Tremendous variations with respect to this trait were also reported by Manju and Sreelathakumary (2002), Farhad *et al.* (2008), Sarkar *et al.* (2009), Abhinaya *et al.* (2016), Pandiyaraj *et al.* (2017) and Zehra *et al.* (2017).

4.1.1.18 Marketable fruit yield per plant (kg)

As shown in appendix – II, the data observed for marketable fruit yield per plant showed significant differences among all the genotypes. Eleven genotypes including check yielded higher marketable fruit yield per plant than population mean (Table 4.4). Maximum marketable fruit yield was harvested from LC-C-22 (0.27). Whereas, minimum marketable fruit yield per plant was recorded in LC-C-51 (0.04) and was significantly different from other genotypes. LC-C-22 produced higher marketable fruit yeild per plant than standard check Surajmukhi. Results obtained are consistent with Singh *et al.* (2009), Datta *et al.* (2013), Janaki *et al*. (2015), Meena *et al.* (2016), Singh *et al.* (2017) and Nahak *et al.* (2018).

Table 4.4 Mean performance of chilli genotypes for stem length to forking (cm), total soluble solids (°brix), weight of 100 seeds (g), marketable fruit yield per plant (kg).

Genotypes	Stem length to forking (cm)	Total soluble solids (°Brix)	Weight of 100 seeds (g)	Marketable fruit yield per plant (kg)
LC-C-1	25.40	5.09	0.39	0.11
LC-C-9	28.53	5.16	0.44	0.14
LC-C-8	26.51	4.70	0.55	0.17
LC-C-7	26.60	4.74	0.48	0.09
LC-C-15	26.67	5.03	0.61	0.13
LC-C-14	28.27	5.07	0.53	0.07
LC-C-11	22.27	4.91	0.40	0.09
LC-C-23	23.03	4.57	0.40	0.09
LC-C-21	29.43	5.07	0.41	0.07
LC-C-22	33.47	5.01	0.42	0.27
LC-C-19	28.47	5.15	0.54	0.13
LC-C-20	23.49	5.08	0.50	0.13
LC-C-18	17.40	5.13	0.57	0.16
LC-C-51	23.47	5.03	0.59	0.04
LC-C-27	12.50	5.67	0.43	0.11
LC-C-24	37.47	4.02	0.51	0.10
LC-C-26	23.47	5.05	0.45	0.13
LC-C-38	17.67	5.17	0.41	0.15
LC-C-29	19.40	5.01	0.41	0.13
Surajmukhi (check)	17.43	5.08	0.39	0.24
Mean	**24.55**	**4.99**	**0.47**	**0.13**
Range	**12.50 – 37.47**	**4.02 – 5.67**	**0.39 – 0.61**	**0.04 – 0.27**
± SE(m)	**0.60**	**0.12**	**0.02**	**0.004**
CV (%)	**4.21**	**4.10**	**8.87**	**5.96**
C.D. (0.05)	**1.72**	**0.34**	**0.07**	**0.01**

4.1.1.19 Fruit shape and Fruit colour

4.1.1.19.1 Overall fruit shape

Observations presented in Table 4.5 revealed that, out of 20 genotypes, the overall fruit shape of 15 genotypes including check was found to be elongate and 3 genotypes *viz.* LC-C-7, LC-C-11 and LC-C-14 produced conical shaped fruit. Genotype

LC-C-21 produced oblate shaped fruit whereas genotype LC-C-27 produced round shaped fruits. The results are in agreement with early findings of Zhigila *et al.* 2014, Quresh *et al.* (2015) and Rahman *et al.* (2017).

4.1.1.19.2 Fruit Shape at pedicel end

The perusal of data presented in Table 4.5 revealed that, fruit shape at pedicel end in all 20 genotypes was found to be obtuse. Conforming the results of present findings the variability in flowering habit were also reported by Dutta and Das (2013), Zhigila *et al.* 2014, Quresh *et al.* (2015) and Rahman *et al.* (2017).

4.1.1.19.3 Fruit shape at blossom end

Observations recorded for fruit shape at blossom end revealed that, all 20 genotypes were found to be obtuse in shape (Table 4.5). The results were in conformity with those reported by Datta and Das (2013), Quresh *et al.* (2015) and Zhigila *et al.* (2014) and Rahman *et al.* (2017).

4.1.1.19.4 Fruit colour

The perusal of data presented in Table 4.5 revealed that two colour intensities *viz.*, Turquoise-green and Brown-grey were observed in fruit at mature green stage. Out of 20 genotypes, 18 genotypes had Turquoise-green group and 2 genotypes had Brown-grey. Fruit colour of different genotypes, as of standard colour chart of Royal Horticultural Society Colour Charts Edition V (version 2), upon visual observation is presented in Table 4.5. Fruit colour is an important trait which decides the consumer preference. Wide variation for this character was also been reported by Datta and Das (2013), Zhigila *et al.* 2014, Kadwey *et al.* (2015), Quresh *et al.* (2015) and Rahman *et al.* (2017).

4.1.1.20 Bearing habit

4.1.1.20.1 Flowering habit

The perusal of data presented in Table 4.5 revealed that out of 20 genotypes, 17 genotypes exhibited solitary flowering habit while three genotypes *viz.* standard check variety (Surajmukhi), LC-C-8 and LC-C-15 had clustered fruiting habit as tabulated in Table 4.5. Conforming the results of present findings the variability in flowering habit were also reported by Datta and Das (2013) and Quresh *et al.* (2015)

Table 4.5 Mean performance of chilli genotypes for fruit shape, fruit colour and bearing habit.

Genotypes	Fruit shape			Fruit colour	Bearing habit	
	Overall fruit shape	At blossom end	At pedicel end		Flowering habit	Fruiting habit
LC-C-1	Elongate	Pointed	Obtuse	Turquoise- green 131C	Solitary	Pendant
LC-C-9	Elongate	Pointed	Obtuse	Turquoise-green 132D	Solitary	Erect
LC-C-8	Elongate	Pointed	Obtuse	Brown-grey 202A	Cluster	Erect
LC-C-7	Conical	Pointed	Obtuse	Turquoise-green 137A	Solitary	Pendant
LC-C-15	Elongate	Pointed	Obtuse	Turquoise-green 132A	Cluster	Erect
LC-C-14	Conical	Pointed	Obtuse	Turquoise-green 131B	Solitary	Pendant
LC-C-11	Conical	Pointed	Obtuse	Turquoise-green 132C	Solitary	Pendant
LC-C-23	Elongate	Pointed	Obtuse	Turquoise-green 131B	Solitary	Erect
LC-C-21	Oblate	Pointed	Obtuse	Turquoise-green 132C	Solitary	Pendant
LC-C-22	Elongate	Pointed	Obtuse	Turquoise-green 132D	Solitary	Pendant
LC-C-19	Elongate	Pointed	Obtuse	Turquoise-green 132C	Solitary	Erect
LC-C-20	Elongate	Pointed	Obtuse	Turquoise-green 134B	Solitary	Pendant
LC-C-18	Elongate	Pointed	Obtuse	Brown-grey200A	Solitary	Intermediate
LC-C-51	Elongate	Pointed	Obtuse	Turquoise- green 137A	Solitary	Pendant
LC-C-27	Round	Blunt	Obtuse	Turquoise- green 132D	Solitary	Pendant
LC-C-24	Elongate	Pointed	Obtuse	Turquoise- green 132A	Solitary	Intermediate
LC-C-26	Elongate	Pointed	Obtuse	Turquoise- green 132C	Solitary	Pendant
LC-C-38	Elongate	Pointed	Obtuse	Turquoise- green 134A	Solitary	Pendant
LC-C-29	Elongate	Pointed	Obtuse	Turquoise- green 132D	Solitary	Pendant
Surajmukhi (check)	Elongate	Pointed	Obtuse	Turquoise- green 134A	Cluster	Erect

4.1.1.20.2 Fruiting habit

Fruiting habit of the genotypes exhibited three types *viz.* pendant, intermediate and erect. The perusal of data presented in Table 4.5 revealed that that 12 genotypes exhibited pendant fruiting habit while six genotypes had erect fruiting habit *viz.* standard check variety (Surajmukhi), LC-C-8 and LC-C-19, LC-C-15, LC-C-9 and LC-C-23. Genotype, LC-C-24 and LC-C-18 had intermediate bearing habit. Confirming the results of present findings by Datta and Das (2013).

4.1.2 Parameters of variability

To initiate any breeding programme, the nature and extent of genetic variability is one of the important criteria. The knowledge of phenotypic and genotypic coefficient of variation is very much helpful in predicting the amount of variation present in a given set of genetic stock. The estimates of PCV and GCV were worked out for all the characters. Heritability in broad sense is a parameter of tremendous significance to the breeder as its magnitude indicates the reliability with which a genotype can be recognized by its phenotypic expression. But, for estimating the real effects of selection, heritability alone is not sufficient and genetic advance along with heritability is more useful. The estimates of genetic parameters *viz.*, phenotypic coefficient of variation (PCV%), genotypic coefficient of variation (GCV%), heritability in broad sense (h^2_{bs}%) and genetic advance (GA) as per cent of mean for different traits are given in Table 4.6 and results pertaining to these parameters are briefly presented below:

4.1.2.1 Coefficients of variability

The observations recorded on magnitude of genotypic and phenotypic variability, the genotypic and phenotypic coefficients of variability are presented in table 4.6. For all the characters studied, phenotypic coefficients of variability were higher in magnitude than genotypic coefficients of variability, though difference was very less in majority of cases. Thus, showing that these traits were less influenced by environmental factors. Coefficients of variability varied in magnitude from character to character, either low or moderate or high. Therefore, it showed that there was greater diversity in the material used in the present study. The wide variations in the characters among all the genotypes are due to effect of genotype and environment. Environmental variations are not heritable.

4.1.2.1.1 Phenotypic coefficient of variation

A perusal of data presented in table 4.6 indicated that wide range of phenotypic variability existed in experimental material. The phenotypic coefficient of variation (PCV) ranged from 7.14 to 41.73%. High phenotypic coefficient of variation existed for marketable fruit yield per plant (41.73%), fruit length (31.66%), average fruit weight (29.87%), number of marketable fruits per plant (28.47%), and number of primary

branches per plant (28.16%), stem length to forking (24.26%) and fruit diameter (21.77%). Moderate phenotypic coefficient of variation (PCV) was exhibited for plant spread (18.65%), pedicel length (17.49%),weight of 100 seeds (17.12%), plant height (15.89%), number of seeds per fruit (11.84%) and stem diameter (11.48%) while Days to 50% flowering (7.75%), total soluble solids (7.14%) and days to first picking (5.64%) showed low magnitude of (PCV).

High PCV for marketable fruit yield per plant (50.05%), fruit length (80.79%), fruit diameter (45.2%) and number of primary branches (21.09%) was recorded by Murmu *et al.* (2012). Similarly, Dhaliwal *et al.* (2014) observed high PCV for marketable fruit yield per plant, fruit length and average fruit weight. Pandiyaraj *et al.* (2017) observed high PCV for fruit length, average fruit weight and number of primary branches. Singh *et al.* (2017) recorded high PCV for number of marketable fruits per plant, Khapte *et al.* (2014) recorded high PCV for number of primary branches and Maurya *et al*. (2017) observed high PCV for number of marketable fruits per plant.

Moderate PCV for pedicel length and plant height was recorded by Murmu *et al.* (2012). Similarly Pandiyaraj *et al.* (2017) recorded moderate PCV for weight of 100 seeds, plant height and number of seeds per fruit). Mamatha *et al.* (2016) observed moderate PCV for pedicel length. Kannan *et al.* (2016) recorded moderate PCV for stem diameter. Sarkar *et al.* (2009) observed moderate PCV for plant spread and weight of 100 seeds. Singh *et al.* (2009) recorded moderate PCV for number of seeds per fruit and weight of 100 seeds. Manju *et al.* (2002) observed moderate PCV for plant spread and Patil *et al.* (2008) recorded moderate PCV for stem diameter.

Low PCV for days to 50% flowering and days to first picking was recorded by Mamatha *et al.* (2016). Singh *et al.* (2017) recorded low PCV for days to 50% flowering, total soluble solids and days to first picking. Kannan *et al.* (2016) recorded low PCV for days to 50% flowering.

4.1.2.1.2 Genotypic coefficient of variation

Phenotypic coefficient of variation alone does not reveal the relative amount of variation; hence different aspects of genetic parameters were worked out. In the experimental material, wide range of genotypic coefficient of variation was observed for characters under study ranging from 5.58 to 41.30 (Table 4.6). High genotypic coefficient of variation existed for marketable fruit yield per plant (41.30%) ,

fruit length (30.70%), average fruit weight (28.41%), number of marketable fruits per plant (28.17%), number of primary branches per plant (26.58%), stem length to forking (23.89%) and fruit diameter (20.83%). Moderate phenotypic coefficient of variation (PCV) was observed for plant spread (18.34%), pedicel length (16.23%), weight of 100 seeds (14.64%), plant height (15.64%), number of seeds per fruit (11.42%) and stem diameter (14.53%), while days to 50% flowering (7.60%), total soluble solids (5.85%) and days to first picking (5.58%) showed low magnitude of genotypic coefficient of variation (GCV).

High GCV for marketable fruit yield per plant, fruit length, fruit diameter was observed by Murmu *et al.* (2012). Similarly Dhaliwal *et al.* (2014) observed high GCV for marketable fruit yield per plant, fruit length and average fruit weight. Pandiyaraj *et al.* (2017) observed high GCV for fruit length, average fruit weight and number of primary branches. Singh *et al.* (2017) recorded high GCV for number of marketable fruits per plant. Khapte *et al.* (2014) recorded high GCV for number of primary branches and Maurya *et al*. (2017) observed high PCV for number of marketable fruits per plant.

Moderate GCV for pedicel length and plant height was recorded by Murmu *et al.* (2012). Similarly Pandiyaraj *et al.* (2017) recorded moderate GCV for weight of 100 seeds, plant height and number of seeds per fruit. Mamatha *et al.* (2016) observed moderate GCV for pedicel length. Kannan *et al.* (2016) recorded moderate GCV for stem diameter. Sarkar *et al.* (2009) observed moderate GCV for plant spread and weight of 100 seeds. Singh *et al.* (2009) recorded moderate GCV for number of seeds per fruit and weight of 100 seeds. Manju *et al.* (2002) observed moderate GCV for plant spread and Patil *et al.* (2008) recorded moderate GCV for stem diameter.

Low GCV for days to 50% flowering and days to first picking was recorded by Mamatha *et al.* (2016). Singh *et al.* (2017) recorded low GCV for days to 50% flowering, total soluble solids and days to first picking. Kannan *et al.* (2016) recorded low GCV for days to 50% flowering.

4.2 Heritability

Heritability in broad sense is a parameter of tremendous significance to breeders as its magnitude indicates the reliability with which a genotype can be recognized by its phenotypic expression. Heritability is the portion of phenotypic variation which is transmitted from parent to progeny. Higher the heritable variation,

greater will be the possibility of fixing the characters by selection. Hence, heritability studies are of foremost importance to judge whether the observed variation for a particular character is due to genotype or due to environment. Johnson *et al.* (1955) stated that heritability estimates together with genetic advance provides better response during selection than either of the parameters alone.

In the present study, high to moderate heritability estimates were obtained for most of the characters. The estimates of heritability (broad sense) varied from 67.11% to 97.96 % for different characters under study (Table 4.6). High heritability estimates were obtained for marketable fruit yield per plant (97.96%), number of marketable fruits per plant (97.89%), days to first picking (97.95%), stem length to forking (96.98%), plant height (96.87%), plant spread (96.76%), days to 50% flowering (96.08%), fruit length (94.07%), number of seeds per fruit (93.11%), fruit diameter (91.55%), average fruit weight (90.43%), number of primary branches per plant (89.13%), pedicel length (86.05%), stem diameter (84.18%), weight of 100 seeds (73.14%) and total soluble solids (67.11%).

High heritability for different traits indicated that large proportion of phenotypic variance was attributed to genotypic variance and therefore, reliable selection could be made for these traits on the basis of phenotypic expression. The results of present investigation were in close agreement with those of Sarkar *et al.* (2009) who recorded high magnitude of heritability for days to 50% flowering, average fruit weight, fruit diameter, fruit length, number of marketable fruits per plant, number of seeds per fruit, pedicel length, plant height, plant spread, weight of 100 seeds and marketable fruit yield per plant. Patil *et al.*(2008) reported high heritability for days to 50% flowering, fruit diameter, fruit length, number of marketable fruits per plant, number of seeds per fruit, pedicel length, plant height and stem diameter. Zehra *et al.* (2017) reported high heritability for days to first picking, average fruit weight, plant spread and weight of 100 seeds. Murma *et al.* (2012) observed high heritability for number of primary branches per plant and marketable fruit yield per plant. Afroza et al. (2013) reported high heritability for total soluble solids.

4.2.1 Genetic advance and genetic gain

The heritability estimates itself may not be solely an useful index of genetic potentiality of a character. Thus, high heritability estimates coupled with high genetic

advance/gain indicates that traits was governed mainly due to additive gene effect and therefore selection might be effective for those traits. Genetic gain is genetic advance as percentage of mean. Genetic gain (expressed as per cent of population mean) was low to high in nature and ranged from 9.88 – 84.21 per cent for different characters inherited (Table 4.6). It was found high for marketable fruit yield per plant (84.21%), fruit length (61.35%), number of marketable fruits per plant (57.42%), average fruit weight (55.65%), number of primary branches per plant (51.70%), stem length to forking (48.47%), fruit diameter (41.06%), plant height (37.71%), plant spread (37.17%), pedicel length (31.02%), weight of 100 seeds (25.80%) and number of seeds per fruit (22.71%). Moderate genetic gain was recorded for stem diameter (19.91%), days to 50% flowering (15.35%) and days to first picking (11.38%) and low in case of total soluble solids (9.88%).

These results are similar with the findings of Kumar *et al.* (2019) who reported high genetic gain for marketable fruit yield per plant, average fruit weight, number of marketable fruits per plant, fruit length, number of seeds per fruit fruit diameter, pedicel length. Vijya *et al.* (2014) reported high genetic gain for number of marketable fruits per plant, fruit diameter, plant spread, fruit length, plant height, number of primary branches per plant and number of seeds per fruit. Sarkar *et al*. (2009) reported high genetic gain for marketable fruit yield per plant, average fruit weight, plant spread, weight of 100 seeds and pedicel length. Patil *et al*. (2008) recorded high genetic gain for number of primary branches per plant. Moderate genetic gain was reported by Kumar et al. (2019) for days to 50% flowering.

Mamtha *et al.* (2016) also reported moderate genetic gain for days to first picking on the basis of overall results it was observed that high genotypic coefficient of variation and phenotypic coefficient of variation, heritability and genetic advance as percentage of mean were noted for marketable fruit yield per plant (41.304 and 41.731, 97.96 and 84.21) average fruit weight (28.41 and 29.87, 90.43 and 55.65), (fruit diameter 20.83 and 21.77, 91.55 and 41.06), fruit length (30.70 and 31.66, 94.07 and 61.35) number of marketable fruits per plant (28.17 and 28.47, 97.89 and 57.42), number of primary branches per plant (26.58 and 28.16, 89.13 and 51.70) and stem length to forking (23.89 and 24.26, 96.98 and 48.47). Therefore, selection should be imposed considering these traits for improvement of population in chilli.

Table 4.6 Estimates of phenotypic and genotypic coefficients of variation, heritability, genetic advance and genetic gain for various characters in chilli

Characters	Range	Mean± SE(d)	Coefficients of variability (%)		Heritability (%)	Genetic advance	Genetic gain (%)
			Genotypic	Phenotypic			
Days to 50% flowering	45.33 - 58.00	50.47± 0.62	7.61	7.76	96.09	7.66	15.36
Days to first picking	74.33 - 90.00	80.92± 0.53	5.59	5.64	97.96	9.13	11.39
Average fruit weight (g)	1.70 – 5.67	3.17± 0.24	28.41	29.87	90.44	1.76	55.66
Fruit diameter (cm)	0.75 – 1.73	1.01± 0.05	20.83	21.77	91.55	0.41	41.06
Fruit length (cm)	2.01 – 12.07	6.02± 0.38	30.71	31.66	94.08	3.69	61.36
Number of marketable fruits per plant	22.33 – 61.50	38.29± 1.29	28.18	28.48	97.89	21.99	57.43
Number of primary branches per plant	2.17 – 7.13	3.88± 0.29	26.59	28.16	89.14	2.00	51.71
Number of seeds per fruit	54.67 – 77.07	64.06± 1.63	11.43	11.84	93.11	14.55	22.72
Pedicel length (cm)	1.84 – 4.29	3.12± 0.17	16.23	17.50	86.06	0.97	31.02
Plant height (cm)	47.47 – 80.00	57.87± 1.33	15.64	15.89	96.88	18.35	31.71
Plant spread (cm^2)	31.24 – 55.13	41.43± 1.14	18.35	18.65	96.77	15.40	37.18
Stem diameter (cm)	0.64 – 0.94	0.79± 0.03	10.54	11.48	84.19	0.16	19.91
Stem length to forking (cm)	12.50 – 37.47	24.55± 0.84	23.89	24.26	96.99	11.90	48.47
Total soluble solids (°B)	4.02 – 5.67	4.99± 0.17	5.86	7.15	67.12	0.49	9.88
Weight of 100 seeds (g)	0.39 – 0.61	0.47± 0.03	14.65	17.13	73.15	0.12	25.81
Marketable fruit yield per plant (kg)	0.04 – 0.27	0.13± 0.01	41.30	41.73	97.96	0.11	84.22

4.3 Correlation coefficient analysis

After gaining information regarding the genetic variability available in experimental material, the knowledge of association among different characters within a species is important. As most of the traits of economic importance in the crop plants depend on one or the other traits and the degree of expression of one character increases or decreases with the increase or decrease in the other character and vice-versa. After understanding the nature of variation for yield and related traits, it would be desirable to know the nature and magnitude of associations among these characters in order to bring out improvement. A few of the component traits may be directly and positively associated with marketable fruit yield per plant and often provide chances of crop improvement through selection. Knowledge of association between traits serves two main purposes for breeders, i.e., (1) selection of characters which are not easily observed or genotypic values of which are modified by environment effects and (2) provides information about the nature and extent, and direction of selection pressure among different traits.

The effectiveness of any breeding or selection programme depends upon the nature of association between yield and other component characters, as more directly a character is associated with yield in the desirable direction, more will be the success of the selection programme. Therefore, it is also important to gather information on association of yield with other characters and among themselves, and their basis to identify characters for increasing the efficiency of both direct and indirect selection and thereby defining an ideal plant type.

4.3.1 Genotypic correlations

The data presented in table 4.7 recorded the genotypic correlation coefficients among different characters. Marketable fruit yield per plant had positive and significant association average fruit weight (0.462), fruit length (0.329) number of marketable fruits per plant (0.570), number of primary branches (0.488) and pedicel length (0.528). Number of marketable fruits per plant showed significant negative association with average fruit weight (-0.351).

Total soluble solids had significant positive association with average fruit weight (0.391) and fruit diameter (0.356) while it showed significant negative correlation with number of marketable fruits per plant (-0.327), number of seeds per fruit (-0.321) and stem length to forking (-0.673).

Table- 4.7 Genotypic coefficients of correlation among different traits in chilli.

	DTFF	DTFP	AFW	FD	FL	NMFP	NPBP	NSPF	PL	PH	PS	SD	SLTF	TSS	WHS	MFYP
DTFF	1.000															
DTFP	0.953**	1.000														
AFW	0.317*	0.455**	1.000													
FD	0.404**	0.529**	0.072	1.000												
FL	-0.044	-0.010	0.593**	-0.591**	1.000											
NMFP	-0.167	-0.171	-0.351**	0.019	-0.151	1.000										
NPBP	-0.243	-0.202	0.138	-0.131	0.283*	0.101	1.000									
NSPF	0.360**	0.458**	0.293*	0.117	0.174	-0.158	-0.327*	1.000								
PL	-0.202	-0.222	0.411**	-0.609**	0.580**	0.213	0.433**	-0.110	1.000							
PH	0.462**	0.438**	0.204	0.343**	-0.180	0.346**	-0.231	0.324*	0.017	1.000						
PS	0.426**	0.427**	0.207	0.240	0.020	0.131	-0.190	0.312*	-0.134	0.732**	1.000					
SD	0.343**	0.272*	-0.262*	0.380**	-0.472**	0.220	-0.291*	0.141	-0.418**	0.717**	0.592**	1.000				
SLTF	-0.157	-0.203	-0.338**	-0.325*	0.128	0.189	0.270*	0.038	0.050	-0.079	-0.145	0.268*	1.000			
TSS	0.065	0.052	0.391**	0.356**	-0.075	-0.327*	0.107	-0.321*	-0.060	-0.042	-0.072	-0.047	-0.673**	1.000		
WHS	0.188	0.231	0.103	0.264*	-0.173	-0.280*	-0.270*	0.435**	-0.354**	0.007	-0.213	0.122	0.225	-0.142	1.000	
MFYP	0.020	0.153	0.462**	0.145	0.329*	0.570**	0.488**	-0.098	0.528**	0.229	0.039	-0.207	-0.045	0.131	-0.223	1.000

*Significant at 5% level of significance

**Significant at 1% level of significance Where,

DTFF = Days to 50% flowering, DTFP = Days to first picking, AFW = Average fruit weight, FD = Fruit diameter, FL = Fruit length, NMFP = Number of marketable fruits per plant, NPBP = Number of primary branches per plant, NSPF = Number of seeds per fruit, PL = Pedicel length, PH = Plant height, PS = Plant spread, SD = Stem diameter, SLTF = Stem length to forking, TSS = Total soluble solids, WHS = Weight of 100 seeds and MFYP = Marketable fruit yield per plant.

Stem length to forking showed significant positive association with number of primary branches per plant (0.270) and stem diameter (0.268) whereas it showed negative significant correlation with average fruit weight (-0.388) and fruit diameter (-0.325). Stem diameter showed significant positive association with number of days to 50% flowering (0.343), days to first picking (0.272), fruit diameter (0.380), plant height (cm) (0.717) and plant spread (0.592) while it showed negative significant correlation with average fruit weight (-0.262), fruit length (-0.472), number of primary branches per plant (-0.291) and pedicel length (-0.418).

Plant spread had significant positive association with days to 50% flowering (0.426), days to first picking (0.427), number of seeds per fruit (0.312) and plant height (0.732). Plant height had significant positive association with days to 50% flowering (0.462), days to first picking (0.438), fruit diameter (0.343), number of marketable fruits per plant (0.346) and number of seeds per fruit (0.324). Number of primary branches per plant showed significant positive association with fruit length (0.283).

Fruit length showed significant positive association with average fruit weight (0.593) while it showed negative significant correlation with fruit diameter (-0.591). Fruit diameter showed significant positive association with days to 50% flowering (0.404) and days to first picking (0.529). Pedicel length showed significant positive association with average fruit weight (0.411), fruit length (0.580), number of primary branches per plant (0.433) while it showed negative significant correlation with fruit diameter (-0.609).

Weight of 100 seeds had significant positive association with fruit diameter (0.264) and number of seeds per fruit (0.435), while it had negative significant correlation with number of marketable fruits per plant (-0.280), number of primary branches per plant (-0.270) and pedicel length (-0.354). Number of seeds per fruit showed significant positive association with days to 50% flowering (0.360), days to first picking (0.458) and average fruit weight (0.293) while it showed negative significant correlation with number of primary branches per plant (-0.327).

Further, significant positive correlation of days to first picking was observed with days to 50% flowering (0.953) and average fruit weight had significant positive correlation with days to 50% flowering (0.317) and days to first picking (0.455).

4.3. Phenotypic correlations

The perusal of data from table 4.8 revealed that, the phenotypic correlation coefficients among different characters, marketable fruit yield per plant had positive and significant association with average fruit weight (0.438), fruit length (0.305) number of marketable fruits per plant (0.561), number of primary branches (0.459) and pedicel length (0.482). Number of marketable fruits per plant showed significant negative association with average fruit weight (-0.327).

Total soluble solids had significant positive association with average fruit weight (0.292) and fruit diameter (0.284) while it showed significant negative correlation with number of marketable fruits per plant (-0.264), number of seeds per fruit (-0.293) and stem length to forking (-0.541).

Stem diameter showed significant positive association with number of days to 50% flowering (0.314), fruit diameter (0.320), plant height (0.641) and plant spread (0.548) while it showed negative significant correlation with fruit length (-0.407) and pedicel length (-0.328).

Plant spread had significant positive association with days to 50% flowering (0.455), days to first picking (0.418), number of seeds per fruit (0.287) and plant height (0.710). Plant height had significant positive association with days to 50% flowering (0.414), days to first picking (0.422), fruit diameter (0.319), number of marketable fruits per plant (0.339) and number of seeds per fruit (0.302). Stem length to forking had significant negative correlation with average fruit weight (-0.318) and fruit diameter (-0.310).

Number of seeds per fruit showed significant positive association with days to 50% flowering (0.331), days to first picking (0.429) and average fruit weight (0.299) while negative significant correlation was observed with number of primary branches per plant (- 0.316). Weight of 100 seeds had significant positive association with number of seeds per fruit (0.345) while it had significant negative correlation with pedicel length (-0.341).

Fruit length showed significant positive association with average fruit weight (0.540) while it showed significant negative correlation with fruit diameter (-0.549). Fruit diameter showed significant positive association with days to 50% flowering (0.376) and days to first picking (0.510). Pedicel length showed significant positive

association with average fruit weight (0.381), fruit length (0.524) and number of primary branches per plant (0.360) and showed negative significant correlation with fruit diameter (-0.515).

Further, significant positive correlation of days to first picking was observed with days to 50% flowering (0.930), Average fruit weight had significant positive correlation with days to 50% flowering (0.285) and days to first picking (0.429).

Genotypic correlation coefficients in general were higher than the phenotypic correlations which revealed that though there is a strong inherent association between various characters, the phenotypic expression of the correlation gets modified under the influence of environment. The effective yield improvement would be achieved through the characters which have significant and positive correlation with yield and other economic traits. Genotypic correlation provides measures of genetic association between characters and is more reliable than phenotypic correlation and thus, helps to identify the characters to be utilized in breeding programme.

Corresponding to the result of present investigation, positive and significant association of fruit yield per plant with fruit length, pedincel length, average fruit weight and number of fruits per plant both at genotypic and phenotypic level have also been reported by Bijalwan *et al*. (2013), Rohini *et al.* (2015), Shewta *et al* (2018), Kumari *et al*. (2018), Jogi et al. (2013), Thakur *et al*. (2019). Plant spread showed significant positive association with plant height while number of primary branches had significant positive association with fruit length (Jogi *et al*,. (2013)). Number of marketable fruit yeild per plant showed significant positive association with average fruit weight reported by Ajith and Manju (2015). Chakrabarty *et al.* (2017) reported weight of 100 seeds had significant positive association with number of seeds per fruit. Plant height had significant positive association with days to first picking and number of marketable fruits per plant while average fruit weight had significant negative association with number of marketable fruits per plant.

4.4 Path coefficient analysis

The correlation coefficients provide information regarding the association of different characters among themselves, whereas better insight into the cause of the association is provided by the path coefficient analysis. It depicts the effects of different independent characters individually and in combination with other characters on the

Table 4.8 Phenotypic coefficients of correlation among different traits in chilli.

	DTFF	DTFP	AFW	FD	FL	NMFP	NPBP	NSPF	PL	PH	PS	SD	SLTF	TSS	WHS	MFYP
DTFF	1.000															
DTFP	0.930**	1.000														
AFW	0.285*	0.429**	1.000													
FD	0.376**	0.510**	0.076	1.000												
FL	-0.029	-0.011	0.540**	-0.549**	1.000											
NMFP	-0.166	-0.169	-0.327*	0.017	-0.150	1.000										
NPBP	-0.228	-0.179	0.107	-0.141	0.227	0.099	1.000									
NSPF	0.331**	0.429**	0.299*	0.114	0.158	-0.156	-0.316*	1.000								
PL	-0.182	-0.210	0.381**	-0.515**	0.524**	0.199	0.360**	-0.094	1.000							
PH	0.455**	0.422**	0.178	0.319*	-0.173	0.339**	-0.225	0.302*	0.018	1.000						
PS	0.414**	0.418**	0.189	0.228	0.019	0.133	-0.163	0.287*	-0.109	0.710**	1.000					
SD	0.314*	0.225	-0.243	0.320*	-0.407**	0.196	-0.237	0.121	-0.328*	0.641**	0.548**	1.000				
SLTF	-0.148	-0.200	-0.318*	-0.310*	0.122	0.178	0.246	0.033	0.061	-0.076	-0.141	0.253	1.000			
TSS	0.067	0.041	0.292*	0.284*	-0.062	-0.264*	0.117	-0.293*	-0.035	-0.020	-0.070	-0.049	-0.541**	1.000		
WHS	0.146	0.200	0.101	0.217	-0.128	-0.235	-0.236	0.345**	-0.341**	-0.002	-0.191	0.078	0.185	-0.088	1.000	
MFYP	0.018	0.152	0.438**	0.130	0.305*	0.561**	0.459**	-0.091	0.482**	0.221	0.041	-0.189	-0.042	0.071	-0.183	1.000

*Significant at 5% level of significance

**Significant at 1% level of significance Where,

DTFF = Days to 50% flowering, DTFP = Days to first picking, AFW = Average fruit weight, FD = Fruit diameter, FL = Fruit length, NMFP = Number of marketable fruits per plant, NPBP = Number of primary branches per plant, NSPF = Number of seeds per fruit, PL = Pedicel length, PH = Plant height, PS = Plant spread, SD = Stem diameter SLTF = Stem length to forking, TSS = Total soluble solids, WHS = Weight of 100 seeds and MFYP = Marketable fruit yield per plant.

expression of yield. It allows the partition of the correlation coefficients into direct and indirect effects of the traits contributing towards the dependent variable. In this analysis, green fruit yield per plant was taken as dependant variable and rest of the characters were considered as independent variables. The results of the present study with respect to direct and indirect effects on marketable yield per plant at phenotypic and genotypic level are presented in Table 4.9 and Table 4.10 and described in detail as respectively:

4.4.2 Path analysis at genotypic level

A perusal of genotypic path coefficient analysis indicated that maximum positive direct effect on marketable fruit yield per plant was imposed by average fruit weight (1.216), number of marketable fruits per plant (0.964), days to 50% flowering (0.639), stem length to forking (0.315), fruit diameter (0.241), number of primary branches per plant (0.159) and number of seeds per fruit (0.059). Maximum negative direct effect on marketable fruit yield per plant was registered via average fruit weight, days to first picking (-0.701), weight of 100 seeds (-0.2743), stem diameter (-0.262), fruit length (-0.240), pedicel length (-0.221), plant spread (-0.154), plant height (-0.118) and marketable fruit yield per plant (-0.003).

Days to first picking had maximum positive indirect effect via days to 50% flowering (0.609), fruit diameter had maximum positive indirect effect via days to 50% flowering (0.258), fruit length had maximum positive indirect effect via average fruit weight (0.721), number of marketable fruits per plant had maximum positive indirect effect via days to first picking (0.120), number of primary branches per plant had maximum positive indirect effect via average fruit weight (0.167), number of seeds per fruit had maximum positive indirect effect via average fruit weight (0.356), pedicel length had maximum positive indirect effect via average fruit weight (0.500), plant height had maximum positive indirect effect via number of marketable fruits per plant (0.333), plant spread had maximum positive indirect effect via days to 50% flowering (0.272), stem diameter had maximum positive indirect effect via days to 50% flowering (0.219), total soluble solids had maximum positive indirect effect via average fruit weight (0.475) and weight of 100 seeds had maximum positive indirect effect via average fruit weight (0.125).

On the other hand days to 50% flowering had maximum negative indirect effect via days to first picking (-0.668), average fruit weight had maximum negative indirect

effect via number of marketable fruits per plant(-0.338), fruit diameter had maximum negative indirect effect via days to first picking (-0.371), number of marketable fruits per plant had maximum negative indirect effect via average fruit weight (-0.427), number of primary branches per plant had maximum negative indirect effect via days to 50% flowering (- 0.155), number of seeds per fruit had maximum negative indirect effect via days to first picking (-0.321), plant height had maximum negative indirect effect via days to first picking (-0.307), plant spread had maximum negative indirect effect via days to first picking (-0.299), stem diameter had maximum negative indirect effect average fruit weight (-0.319), stem length to forking had maximum negative indirect effect via average fruit weight (-0.411) and total soluble solids had maximum negative indirect effect via number of marketable fruits per plant (-0.315).

Bijalwan *et al.* (2013) reported positive direct effect of days to 50% flowering, fruit length and plant height at genotypic level and days to first picking at phenotypic level while fruit diameter, number of marketable fruits per plant and average fruit weight both at phenotypic and genotypic level in contradiction to negative direct effect for days to first picking, fruit length, pedicel length at genotypic at phenotypic level. Rohini et al. (2015) reported positive direct effect for pedicel length, number of fruits per plant while negative direct effect for plant height, days to 50% flowering, fruit length, number of seed per fruit and weight of 100 seeds. Vikram *et al.* (2014) observed positive direct effect for days to 50% flowering, plant height, number of marketable fruits per plant and fruit length while negative direct effect for number of seeds per fruit. Vidya et al. (2018) recorded positive direct effect for plant height, days to 50 % flowering, days to first picking, fruit length, fruit length, number of marketable fruit and pedicel length whearas negative direct effect for stem diameter. Shweta *et al.* (2018) showed positive direct effect with average fruit weight, number of marketable fruit per plant, fruit diameter and fruit length, while it showed negative values for plant height days to 50 % flowering. Reddy *et al*. (2008) depicted positive direct effect for days to 50% flowering, plant height, number of primary branches per plant, number of marketable fruits per plant, average fruit weight and pedicel length in contrast to negative direct effect on fruit length and weight of 100 seeds.

Table 4.9 Path coefficient analysis showing the direct and indirect effect of fifteen characters on marketable fruit yield per plant genotypic at level

	DTFF	DTFP	AFW	FD	FL	NMFP	NPBP	NSPF	PL	PH	PS	SD	SLTF	TSS	WHS	GCCMYP
DTFF	0.640	-0.669	0.386	0.098	0.011	-0.161	-0.039	0.021	0.045	-0.055	-0.066	-0.090	-0.049	0.000	-0.052	0.020
DTFP	0.610	-0.702	0.553	0.128	0.002	-0.165	-0.032	0.027	0.049	-0.052	-0.066	-0.072	-0.064	0.000	-0.063	0.153
AFW	0.203	-0.319	1.217	0.018	-0.142	-0.339	0.022	0.017	-0.091	-0.024	-0.032	0.069	-0.107	-0.001	-0.028	0.462
FD	0.258	-0.372	0.088	0.242	0.142	0.019	-0.021	0.007	0.135	-0.040	-0.037	-0.100	-0.102	-0.001	-0.072	0.145
FL	-0.028	0.007	0.721	-0.143	-0.240	-0.145	0.045	0.010	-0.129	0.021	-0.003	0.124	0.040	0.000	0.048	0.329*
NMFP	-0.107	0.120	-0.427	0.005	0.036	0.964	0.016	-0.009	-0.047	-0.041	-0.020	-0.058	0.059	0.001	0.077	0.570**
NPBP	-0.155	0.141	0.168	-0.032	-0.068	0.097	0.160	-0.019	-0.096	0.027	0.029	0.076	0.085	0.000	0.074	0.488**
NSPF	0.230	-0.321	0.357	0.028	-0.042	-0.152	-0.052	0.059	0.025	-0.038	-0.048	-0.037	0.012	0.001	-0.119	-0.098
PL	-0.129	0.156	0.500	-0.147	-0.139	0.206	0.069	-0.007	-0.222	-0.002	0.021	0.110	0.016	0.000	0.097	0.528**
PH	0.296	-0.307	0.248	0.083	0.043	0.334	-0.037	0.019	-0.004	-0.118	-0.113	-0.188	-0.025	0.000	-0.002	0.229
PS	0.273	-0.300	0.252	0.058	-0.005	0.126	-0.030	0.019	0.030	-0.086	-0.155	-0.156	-0.046	0.000	0.058	0.039
SD	0.219	-0.191	-0.319	0.092	0.113	0.213	-0.046	0.008	0.093	-0.085	-0.092	-0.263	0.085	0.000	-0.033	-0.207
SLTF	-0.100	0.142	-0.412	-0.078	-0.031	0.182	0.043	0.002	-0.011	0.009	0.023	-0.070	0.315	0.002	-0.062	-0.045
TSS	0.041	-0.037	0.476	0.086	0.018	-0.316	0.017	-0.019	0.013	0.005	0.011	0.012	-0.212	-0.004	0.039	0.131
WHS	0.120	-0.162	0.125	0.064	0.042	-0.270	-0.043	0.026	0.079	-0.001	0.033	-0.032	0.071	0.001	-0.274	-0.223

Where,

DTFF = Days to 50% flowering, DTFP = Days to first picking, AFW = Average fruit weight, FD = Fruit diameter, FL = Fruit length, NMFP = Number of marketable fruits per plant, NPBP = Number of primary branches per plant, NSPF = Number of seeds per fruit, PL = Pedicel length, PH = Plant height, PS = Plant spread, SD = Stem diameter SLTF = Stem length to forking, TSS = Total soluble solids, WHS = Weight of 100 seeds and GCCMYPP = Genotypic correlation coefficient with marketable fruit yield per plant.

Residual effect 0.00495

Diagonal figures represent the direct effect.

4.4.1 Path analysis at phenotypic level

In the present investigation, path analysis at phenotypic level revealed that maximum positive direct effect on marketable fruit yield per plant was registered by number of marketable fruits per plant (0.699), average fruit weight (0.459), days to first picking (0.292), number of primary branches per plant (0.250), fruit diameter (0.242), fruit length (0.222), plant height (0.114) and pedicel length (0.038). Maximum negative direct contribution on marketable fruit yield per plant was made by plant spread (-0.217), days to 50% flowering (-0.182), days to 50% flowering (-0.117), stem diameter (-0.072), weight of 100 seeds (-0.043), total soluble solids (-0.019) and stem length to forking (-0.007).

Days to 50% flowering had maximum positive indirect effect via days to first picking (0.2716), fruit length had maximum positive indirect effect via average fruit weight (0.248), number of seeds per fruit had maximum positive indirect effect via average fruit weight (0.137), pedicel length had maximum positive indirect effect via average fruit weight (0.174), plant height had maximum positive indirect effect via number of marketable fruits per plant (0.237), plant spread had maximum positive indirect effect via days to first picking (0.122), stem diameter had maximum positive indirect effect via number of marketable fruits per plant (0.137), stem length to forking had maximum positive indirect effect via number of marketable fruits per plant (0.124), total soluble solids had maximum positive indirect effect via average fruit weight (0.133) and weight of 100 seeds had maximum positive indirect effect via days to first picking (0.585).

On the other hand days to days to first picking had maximum negative indirect effect via days to 50% flowering (-0.169), average fruit weight had maximum negative indirect effect via number of marketable fruits per plant (-0.228), fruit diameter had maximum negative indirect effect via fruit length (-0.122), fruit length had maximum negative indirect effect via fruit diameter (-0.133), number of marketable fruits per plant had maximum negative indirect effect via average fruit weight (-0.150), number of primary branches per plant had maximum negative indirect effect via days to first picking (-0.052), pedicel length had maximum negative indirect effect via fruit diameter (-0.124), plant height had maximum negative indirect effect via plant spread (-0.154), stem diameter had maximum negative indirect effect via plant spread (-0.119), stem length to forking had maximum negative indirect effect via average fruit weight

Table 4.10 Path coefficient analysis showing the direct and indirect effect of fifteen characters on marketable fruit yield per plant at phenotypic level

	DTFF	DTFP	AFW	FD	FL	NMFP	NPBP	NSPF	PL	PH	PS	SD	SLTF	TSS	WHS	PCCMFYP
DTFF	-0.183	0.272	0.131	0.091	-0.007	-0.116	-0.057	-0.039	-0.007	0.052	-0.090	-0.023	0.001	-0.001	-0.006	0.018
DTFP	-0.170	0.292	0.197	0.123	-0.002	-0.118	-0.045	-0.050	-0.008	0.048	-0.091	-0.016	0.002	-0.001	-0.009	0.152
AFW	-0.052	0.125	0.459	0.018	0.120	-0.228	0.027	-0.035	0.015	0.020	-0.041	0.018	0.002	-0.006	-0.004	0.438**
FD	-0.069	0.149	0.035	0.242	-0.122	0.012	-0.035	-0.013	-0.020	0.037	-0.050	-0.023	0.002	-0.006	-0.010	0.130
FL	0.005	-0.003	0.248	-0.133	0.222	-0.105	0.057	-0.019	0.020	-0.020	-0.004	0.030	-0.001	0.001	0.006	0.305*
NMFP	0.030	-0.050	-0.150	0.004	-0.033	0.699	0.025	0.018	0.008	0.039	-0.029	-0.014	-0.001	0.005	0.010	0.561**
NPBP	0.042	-0.052	0.049	-0.034	0.050	0.069	0.251	0.037	0.014	-0.026	0.036	0.017	-0.002	-0.002	0.010	0.459**
NSPF	-0.060	0.125	0.137	0.028	0.035	-0.109	-0.079	-0.117	-0.004	0.035	-0.063	-0.009	0.000	0.006	-0.015	-0.091
PL	0.033	-0.061	0.175	-0.125	0.116	0.139	0.090	0.011	0.038	0.002	0.024	0.024	0.000	0.001	0.015	0.482**
PH	-0.083	0.123	0.082	0.077	-0.038	0.237	-0.056	-0.035	0.001	0.114	-0.155	-0.047	0.001	0.000	0.000	0.221
PS	-0.076	0.122	0.087	0.055	0.004	0.093	-0.041	-0.034	-0.004	0.081	-0.218	-0.040	0.001	0.001	0.008	0.041
SD	-0.057	0.066	-0.112	0.077	-0.091	0.137	-0.059	-0.014	-0.013	0.073	-0.119	-0.073	-0.002	0.001	-0.003	-0.189
SLTF	0.027	-0.058	-0.146	-0.075	0.027	0.125	0.062	-0.004	0.002	-0.009	0.031	-0.018	-0.008	0.011	-0.008	-0.042
TSS	-0.012	0.012	0.134	0.069	-0.014	-0.184	0.029	0.034	-0.001	-0.002	0.015	0.004	0.004	-0.020	0.004	0.071
WHS	-0.027	0.059	0.046	0.053	-0.029	-0.165	-0.059	-0.040	-0.013	0.000	0.042	-0.006	-0.001	0.002	-0.044	-0.183

Where,

DTFF = Days to 50% flowering, DTFP = Days to first picking, AFW = Average fruit weight, FD = Fruit diameter, FL = Fruit length, NMFP = Number of marketable fruits per plant, NPBP = Number of primary branches per plant, NSPF = Number of seeds per fruit, PL = Pedicel length, PH = Plant height, PS = Plant spread, SD = Stem diameter SLTF = Stem length to forking, TSS = Total soluble solids, WHS = Weight of 100 seeds and PCCMFYP = Phenotypic correlation coefficient with marketable fruit yield per plant

Residual effect 0.0853

Diagonal figures represent the direct effect

(-0.146), total soluble solids had maximum negative indirect effect via number of marketable fruits per plant (-0.184) and weight of 100 seeds maximum negative indirect effect via had maximum negative indirect effect via number of marketable fruits per plant (-0.164).

4.5 Genetic Divergence

In order to measure the genetic distance between populations for number of traits, the genetic divergence in clustering pattern was worked out in the present studies. The analysis of variance revealed highly significant differences among the genotypes for all the characters studied, indicating the existence of wide genetic divergence among them. Information on genetic diversity was also used to identify promising diverse genotypes, which may further be used in breeding programmes.

Clustering pattern based upon Mahalanobis D^2 values for 20 diverse genotypes were presented in table 4.11. All the genotypes were grouped into 3 clusters. Maximum number of genotypes were accommodated in cluster I (11) followed by cluster II (6) with minimum number of genotypes in cluster III (3).

Table 4.11: Clustering pattern of twenty genotypes on the basis of genetic divergence

Cluster	Number of genotypes	Genotypes along with their sources
I	11	LC-C-1 (Neri), LC-C-9 (Neri), LC-C-3 (Neri), LC-C-4 (Neri), LC-C-6 (Neri), LC-C-7 (Neri), LC-C-8 (Neri), LC-C-9 (Neri), LC-C-10 (Neri), LC-C-11 (Neri), LC-C-12 (Neri), LC-C-18 (Neri).
II	6	LC-C-2 (Neri), LC-C-13 (Neri), LC-C-15 (Neri), LC-C-16 (Neri), LC-C-19 (Neri), LC-C-20 (Neri)
III	3	LC-C-5 (Neri), LC-C-14 (Neri), LC-C-17 (CSK HPKV Palampur)

Group constellation of chilli genotypes through genetic divergence has also been reported by Kumar *et al.* (2010), Hasan *et al*. (2015), kumari *et al*. (2018), Pradhan *et al.* (2017), Pujar *et al* (2017) and Janaki *et al.* (2016).

Average inter-cluster and intra-cluster distance (D^2) values are presented in Table 4.12. The diagonal figures in the table represent the intra-cluster distance. The intra-cluster distance varied from 3.83 (cluster I) to 4.47 (cluster III). Since crossing of genotypes belonging to same cluster do not expect to yield superior hybrids or segregants, hence inter cluster distances were also worked out. The inter cluster distance

was maximum to the tune of 5.56 between cluster II and III followed by cluster I and III (5.03). The minimum inter cluster distance was observed for cluster I and II (4.78). The cluster with higher inter cluster distances indicated that the genotypes included in those clusters had high genetic variation and hybridization between genotypes of these cluster may result heterotic progenies because of convergence of diverse genes scattered in parents.

Table 4.12: Average intra (Diagonal) and inter- cluster (Lower half diagonal) distance (D^2).

Clusters	I	II	III
I	**3.83**		
II	4.78	**4.27**	
III	5.03	5.56	**4.47**

A wide range of inter cluster genetic distance among the different cluster of chilli genotypes have also been reported by Kumar *et al*. (2010)), Hasan *et al*. (2015), kumari et al. (2018), Pradhan *et al.* (2017), Pujar *et al* (2017) and Janaki *et al.* (2016).

Further, for getting the reliable conformity on the basis of cluster means, it was calculated for various horticultural traits and has been presented in the table 4.13. For days to 50% flowering lowest mean was recorded in cluster I (49.00) followed by cluster III (52.11) and cluster 11 (52.33). For days to first picking lowest mean was recorded in cluster I (79.15) followed by cluster II (83.06), cluster III (83.11). The average fruit weight was found to be maximum in cluster III (4.33) followed by cluster II (3.36) and cluster I (2.75). Maximum fruit diameter was recorded in cluster II (1.12) followed by cluster I (0.97) and cluster III (0.91) while maximum fruit length was observed in cluster III (8.18) followed by cluster I (5.74) and cluster II (5.45). Maximum number of marketable fruits per plant was recorded in cluster II (43.05) followed by cluster I (40.88) and cluster III (19.29). For number of primary branches per plant highest mean was recorded in cluster II (4.01) followed by cluster I (3.90) and cluster III (3.52). Maximum Number of seeds per fruit was recorded in cluster III (70.96) followed by cluster II (68.28) and cluster I (59.87). For pedicel length highest mean was recorded in cluster II (3.18) followed by cluster I (3.11) and cluster III (3.06) while for plant height highest mean was recorded in cluster II. (69.50) followed by cluster I (53.06) and cluster III (52.24). Maximum plant spread was recorded in cluster II (49.42) followed by cluster

III (40.82) and cluster I (37.25). For Stem diameter highest mean was recorded in cluster II (0.86) followed by cluster I (0.77) and cluster III (0.72) while for stem length to forking highest mean was recorded in cluster I (25.06) followed by cluster II (24.32) and cluster III (23.13). Maximum total soluble solids was recorded in cluster III (5.09) followed by cluster I (4.98) and cluster II (4.95) while maximum weight of 100 seeds was recorded in cluster III (0.51) followed by cluster I (0.47) and cluster II (0.46). Maximum marketable fruit yield per plant was recorded in cluster II (0.15) followed by cluster I (0.13) and cluster III (0.09). Earlier workers like Kumar *et al.* (2010)), Hasan *et al*. (2015), Kumari *et al.* (2018), Pradhan *et al.* (2017), Pujar *et al* (2017) and Janaki *et al.* (2016) have also indicated significance of divergence in chilli.

Table 4.13: Cluster means for different characters among twenty genotypes of chilli

Characters	**Cluster I**	**Cluster II**	**Cluster III**
Days to 50% flowering	49.00	52.33	52.11
Days to first picking	79.15	83.06	83.11
Average fruit weight (g)	2.75	3.36	4.33
Fruit diameter (cm)	0.97	1.12	0.91
Fruit length (cm)	5.74	5.45	8.18
Number of marketable fruits per plant	40.88	43.05	19.29
Number of primary branches per plan	3.90	4.01	3.52
Number of seeds per fruit	59.87	68.28	70.96
Pedicel length (cm)	3.11	3.18	3.06
Plant height (cm)	53.06	69.50	52.24
Plant spread (cm)	37.25	49.42	40.82
Stem diameter (cm)	0.77	0.86	0.72
Stem length to forking (cm)	25.06	24.32	23.13
Total soluble solids(°B)	4.98	4.95	5.09
Weight of 100 seeds (g)	0.47	0.46	0.51
Marketable fruit yield per plant (kg)	0.13	0.15	0.09

Plate 1. Nursery production

Plate 2. Field view experimental chilli crop

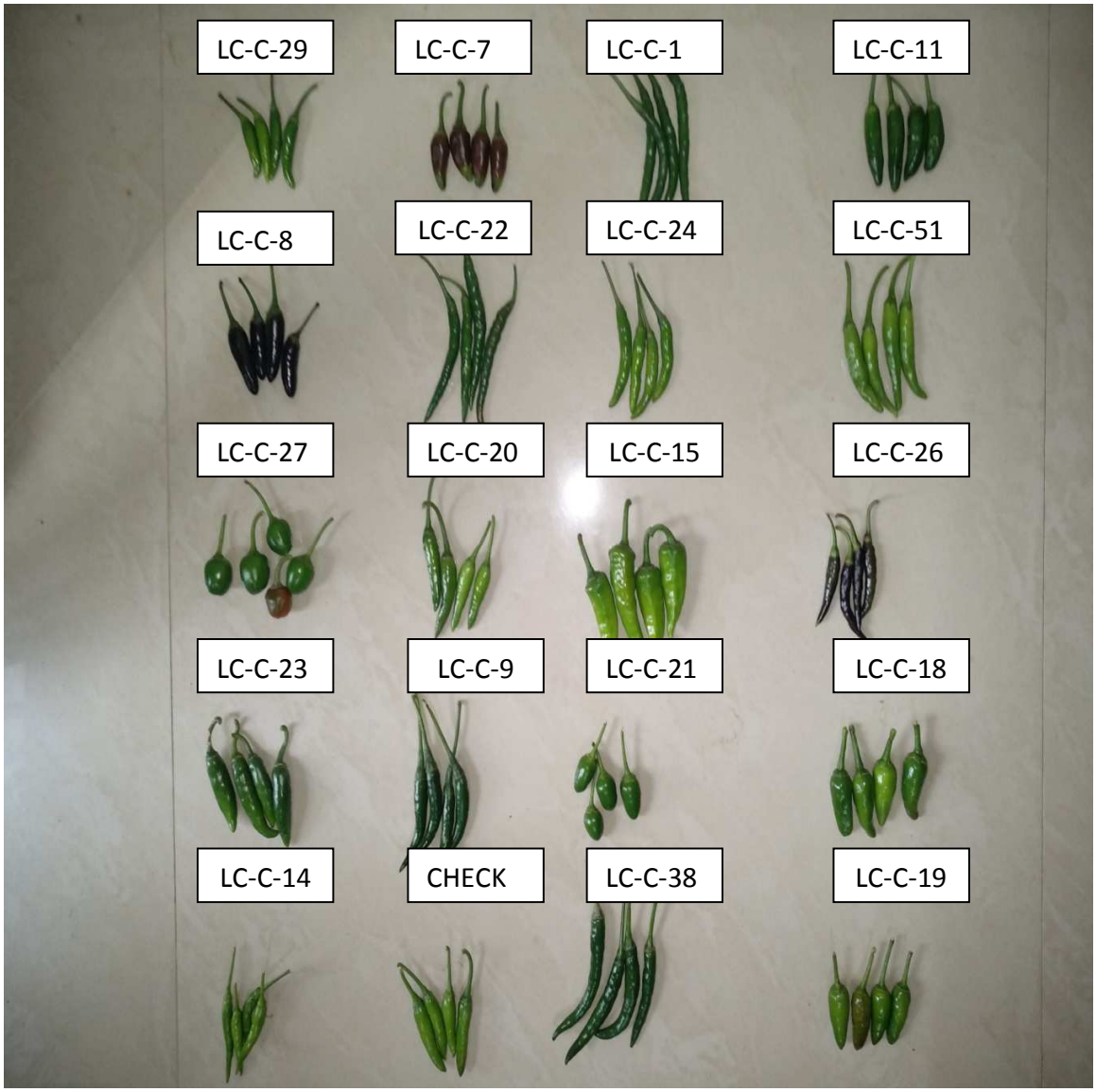


Plate 3. Diversity in 20 chilli genotypes

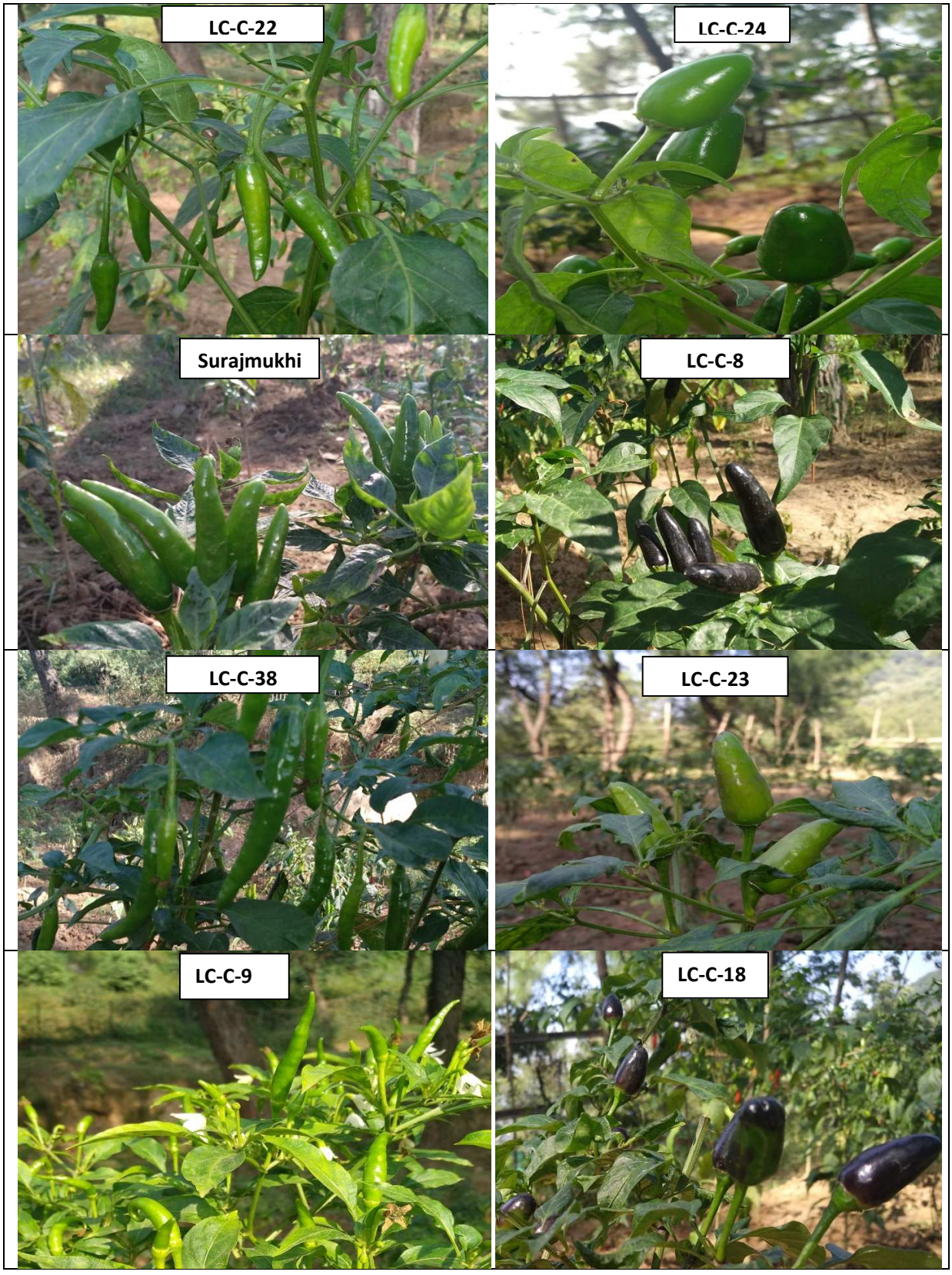


Plate 4. Some elite genotypes of chilli with good overall perfomance

Chapter-5

SUMMARY AND CONCLUSION

The present investigation entitled "**Exploration of genetic variability in chilli (*Capsicum annuum* L.) present in subtropical region of Himachal Pradesh".**" was carried out with 20 genotypes of chilli including Surajmukhi as a standard check to ascertain the variability, heritability, genetic advance, correlations, path coefficient analysis and genetic divergence. The experiment was laid out in Randomized Complete Block Design with three replications at Vegetable Research Farm, Department of Vegetable Science, College of Horticulture and Forestry, Neri, Hamirpur, Dr YS Parmar University of Horticulture and Forestry, Nauni, Solan (HP)) during *kharif* season, 2018. The transplanting was done during third week of july 2018 at a spacing of 45 × 45 cm in a plot size of 1.8× 2.25m. The observations were recorded on various characters *viz.,* days to 50 % flowering, days to first picking, average fruit weight (g), fruit diameter (cm), fruit length (cm), number of marketable fruits per plant, number of primary branches per plant, days to 50% flowering, pedicel length (cm), plant height (cm), plant spread (cm), stem diameter (cm), stem length to forking (cm), total soluble solids(°B), weight of 100 seeds (g) and marketable fruit yield per plant (kg).

Mean performance

The analysis of variance showed highly significant differences among the genotypes for all the horticultural traits under study. The genotype LC-C-26 was the earliest for days to 50% flowering and also exhibited minimum number of days to first picking which was significantly at par with LC-C-1. The genotype LC-C-1 took minimum days to first picking while genotype LC-C-27 took maximum days. The Genotype LC-C-38 produced fruits with maximum average fruit weight while genotype LC-C-23 produced fruits with minimum average fruit weight. Maximum fruit diameter was observed in LC-C-27 followed by LC-C-8, whereas, minimum fruit diameter was recorded in LC-C-9. The maximum value for fruit length was observed in genotype LC-C-38, likewise the minimum value for fruit length was observed in genotype LC-C-27. The genotype LC-C-8 produced maximum number of marketable fruits per plant, whereas, it was observed minimum on genotype LC-C-51. Maximum number of primary branches was observed on LC-C-22 while it was observed minimum on LC-C-8. Maximum number of seeds per fruit was observed in LC-C-8 whereas

it was observed minimum on LC-C-20. Maximum pedicel length was recorded in standard check variety Surajmukhi while it was observed minimum on LC-C-27. Maximum plant height was observed in LC-C-8 while it was observed minimum on LC-C-22. Maximum plant spread was observed in LC-C-27 followed by LC-C-24 while it was recorded minimum on LC-C-24. Maximum value of stem diameter was observed in LC-C-27 while it was recorded minimum on LC-C-18. Maximum value of stem length was observed in LC-C-24 followed by LC-C-22 while it was recorded minimum on LC-C-27. Maximum TSS was recorded in LC-C-27 while it was recorded minimum in LC-C-24. Weight of 100 seeds was recorded maximum on LC-C-15 whereas it was observed minimum on LC-C-1. Maximum marketable fruit yield was harvested from LC-C-22 while it was recorded minimum on LC-C-51.

Parameters of variability

High phenotypic and genotypic coefficient of variation existed for marketable fruit yield per plant, fruit length, average fruit weight, number of marketable fruits per plant, and number of primary branches per plant, stem length to forking and fruit diameter. Moderate phenotypic and genotypic coefficient of variation was exhibited for plant spread, pedicel length, weight of 100 seeds, plant height, number of seeds per fruit and stem diameter while days to 50% flowering, total soluble solids and days to first picking showed low magnitude of phenotypic and genotypic coefficient of variation. High heritability estimates were observed for all the traits among all genotypes while high estimates of genetic gain were observed for marketable fruit yield per plant, fruit length, number of marketable fruits per plant, average fruit weight, number of primary branches per plant, stem length to forking, fruit diameter, plant height, plant spread, pedicel length, weight of 100 seeds and number of seeds per fruit.

Correlation studies

The correlation coefficients among the different characters were worked out at both phenotypic and genotypic levels. The results revealed that marketable fruit yield per plant had positive and significant association with average fruit weight, fruit length, number of marketable fruits per plant, number of primary branches and pedicel length. Thus, from the correlation studies it is concluded that selection should be followed as a criteria for improvement of fruit yield in chilli.

Table 5.1 Best three genotypes with respect to different horticultural traits in chilli

Character	Genotypes	Mean
Days to 50 % flowering (minimum)	LC-C-1	45.34
	LC-C-26	45.33
	LC-C-15	46.33
Days to first picking (mature green stage)	LC-C-1	74.33
	LC-C-26	75.33
	LC-C-15	76.67
Average fruit weight (g)	LC-C-38	5.67
	Surajmukhi	4.85
	LC-C-51	3.93
Fruit diameter (cm)	LC-C-27	1.73
	LC-C-15	1.21
	LC-C-18	1.17
Fruit length (cm)	LC-C-38	12.07
	LC-C-22	8.40
	LC-C-36	7.14
Number of marketable fruits per plant	LC-C-8	61.50
	LC-C-23	53.53
	LC-C-22	50.80
Number of primary branches per plant	LC-C-22	7.13
	LC-C-26	5.20
	LC-C-9	5.00
Number of seeds per fruit	LC-C-8	77.07
	LC-C-24	77.00
	LC-C-14	72.73
Pedicel length (cm)	Surajmukhi	4.29
	LC-C-9	3.98
	LC-C-38	3.74
Plant height (cm)	LC-C-8	80.00
	LC-C-27	70.80
	Surajmukhi	68.47
Plant spread (cm)	LC-C-27	55.13
	LC-C-8	52.31
	LC-C-24	52.08
Stem diameter (cm)	LC-C-8	0.94
	LC-C-27	0.94
	LC-C-19	0.90
Stem length to forking (cm)	LC-C-24	37.47
	LC-C-22	33.47
	LC-C-21	29.43
Total soluble solids (°B)	LC-C-27	5.67
	LC-C-9	5.16
	LC-C-19	5.15
Weight of 100 seeds(g)	LC-C-15	0.61
	LC-C-51	0.59
	LC-C-18	0.57
Marketable fruit yield per plant(kg)	LC-C-22	0.27
	Surajmukhi	0.24
	LC-C-8	0.17

Path coefficient analysis

The path coefficient analysis at phenotypic and genotypic level revealed that the maximum positive direct effect on marketable fruit yield per plant was registered by number of marketable fruits per plant, average fruit weight, number of primary branches per plant and fruit diameter while maximum negative direct contribution on marketable fruit yield per plant was made by plant spread, stem diameter and weight of 100 seeds. Therefore, selection should be exercised to increase the marketable fruit yield per plant which was directly affected by number of marketable fruits per plant, average fruit weight, number of primary branches per plant and fruit diameter for direct improvement of green fruit yield per plant.

Genetic divergence

For those traits, where selection is not responsive and non-additive gene action plays major role in the expression, hybridization between diverse parents on the basis of their cluster mean performance to get superior hybrids or transgressive segregants in F_2 or subsequent generations. In the present studies, on the basis of genetic divergence, 20 genotypes were grouped in to three clusters and maximum intercluster distance was recorded between II and III clusters. Therefore, the hybridization between the genotypes of cluster II and III can be utilized for getting superior hybrids or recombinants in segregating population.

CONCLUSION

- On the basis of overall performance, out of 20 genotypes, LC-C-22, LC-C-8 and Surajmukhi were found superior for marketable fruit yield and other important characters.
- The estimates of PCV and GCV were high for marketable fruit yield per plant, fruit length, average fruit weight, number of marketable fruits per plant, and Number of primary branches per plant, stem length to forking and fruit diameter.
- High heritability was observed for all the characters among all genotypes.
- Genetic advance was observed high for marketable fruit yield per plant, fruit length, number of marketable fruits per plant, average fruit weight, number of primary branches per plant, stem length to forking, fruit diameter, plant height, plant spread, pedicel length, weight of 100 seeds and number of seeds per fruit.

- A positive and significant correlation coefficient of marketable fruit yield was observed for fruit length, average fruit weight, number of marketable fruits per plant, number of primary branches and pedicel length.
- In path coefficient analysis at genotypic level, days to fifty per cent flowering, average fruit weight, fruit diameter, no. of marketable fruits per plant, no. of primary branches and stem length to forking had positive and direct effects on marketable fruit yield per plant.
- In path coefficient analysis at phenotypic level days to first picking, average fruit weight, fruit diameter, fruit length, no. of marketable fruits per plant, no. of primary branches, pedicel length and plant height had positive and direct effects on marketable fruit yield per plant.
- The intra-cluster distance varied from cluster I to cluster III. The inter cluster distance was maximum to the tune of between cluster II and III followed by cluster I and III. The minimum inter cluster distance was observed for cluster I and II.
- For quality traits like total soluble solids, genotypes LC-C-9, LC-C-18 and LC-C-38 were found significantly superior to all other genotypes.

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APPENDIX-I

Mean meteorological data during the study period (*Kharif*, 2018)

Month	Rainfall (mm)	Relative Humidity (%)	Mean Temperature (°C)
June, 2018	127.6	49.87	29.49
July, 2018	325.4	72.51	27.56
August, 2018	407.8	76.43	26.54
September, 2018	291.6	75.67	24.65
October, 2018	11.4	58.87	21.36
November, 2018	20	62.59	17.03
December, 2018	4.6	60.67	12.65

Source: Meteorological Observatory, Department of Soil Science and Water Management, College of Horticulture and Forestry, Neri, Hamirpur HP 177 001

APPENDIX- II

Analysis of variance for various horticultural traits in chilli

Source	**Mean sum of squares**			
Character	**Replications**	**Genotypes**	**Errors**	**Total**
Df	2	19	38	59
Days to 50% flowering.	2.433	32.996	0.568	650.933
Days to first picking	0.133	42.251	0.418	818.583
Pedicel length (cm)	0.035	0.811	0.042	17.032
Fruit length (cm)	2.853	10.466	0.215	209.886
Fruit diameter (cm)	0.033	0.136	0.004	2.776
Average fruit weight (g)	0.182	2.519	0.086	51.300
Number of marketable fruits per plant	0.902	351.756	2.508	6779.557
Marketable fruit yield per plant (kg)	0.002	0.008	0.002	0.160
Total soluble solids	0.628	0.298	0.042	7.869
Number of primary branches per plant.	0.217	3.314	0.129	68.093
Plant height (cm)	10.241	248.428	2.638	4830.607
Stem length to forking (cm)	2.523	104.262	1.068	2024.089
Stem diameter (cm)	0.007	0.022	0.001	0.475
Plant spread (cm^2)	1.811	175.295	1.932	3405.845
Number of seeds per fruit	22.974	164.723	3.969	3303.523
Weight of 100 seeds (g)	0.008	0.016	0.002	0.378

***Significant at 5% level of significance**

Department of Vegetable Science
College of Horticulture and Forestry, Neri
Dr Yashwant Singh Parmar University of Horticulture and Forestry (Nauni) Solan (HP) - 173 230 India

Title of Thesis	**:**	**Exploration of genetic variability in chilli (*Capsicum annuum* L.) present in subtropical region of Himachal Pradesh"**
Name of the Student	**:**	Sachin Bhardwaj
Admission Number	**:**	NH-2017-25-M
Major Advisor	**:**	Dr BS Dogra
Major Field	**:**	Vegetable Science
Minor Field(s)	**:**	i) Genetics and Plant Breeding
	:	ii) Plant Pathology
Degree Awarded	**:**	M.Sc. (Horticulture) Vegetable Science
Year of Award of Degree	**:**	2019
Number of pages in thesis	**:**	75+ii
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Date of thesis submission	**:**	

ABSTRACT

The present investigation entitled "Exploration of genetic variability in chilli (*Capsicum annuum* L.) present in subtropical region of Himachal Pradesh" was carried out at Vegetable Research Farm, Department of Vegetable Science, College of Horticulture and Forestry, Neri, Hamirpur (HP) during *Kharif* season, 2018. Twenty genotypes including check variety Surajmukhi were evaluated in Randomized Complete Block Design with three replications to ascertain extent of variability, heratibility, genetic advance and gain, correlation and path coefficient analysis for yield and other horticulture traits along with the estimation of genetic divergence among the genotypes. Analysis of variance showed significant differences among all the genotypes for all the characters under study. Three genotypes namely LC-C-22, LC-C-17 and LC-C-8 were found to be high yielding as well as better from consumer's point of view. They could be the promising parents for utilization in further breeding programmes. High PCV and GCV existed for marketable fruit yield per plant, Fruit length, average fruit weight, Number of marketable fruits per plant, and Number of primary branches per plant, Stem length to forking and Fruit diameter. High heritability estimates were observed for all the traits among all genotypes while high estimates of genetic gain were observed for. high for Marketable fruit yield per plant, fruit length, number of marketable fruits per plant, average fruit weight, number of primary branches per plant, stem length to forking, fruit diameter, plant height, plant spread, pedicel length, weight of 100 seeds and number of seeds per fruit. The correlation studies at phenotypic and genotypic level revealed that marketable fruit yield per plant had positive and significant association with average fruit weight, fruit length, number of marketable fruits per plant, number of primary branches and pedicel length. Path analysis revealed that average fruit weight, fruit diameter, number of marketable fruits per plant and number of primary branches had positive and direct effects on marketable fruit yield per plant. Genetic divergence studies revealed that the intra-cluster distance varied from cluster I to cluster III whereas, the inter cluster distance was maximum to the tune of between cluster II and III and therefore hybridization between genotypes of cluster II and III will be more rewarding for getting superior progenies.

Signature of Student
Name: Sachin Bhardwaj
Date:

Signature of the Major Advisor
Name: Dr B S Dogra
Date:

Head of the Department

BRIEF BIO-DATA

Name : Sachin Bhardwaj

Father's Name : Sh Jai Chand Sharma

Mother's Name : Smt Kamlesh Sharma

Date of Birth : 12- November, 1995

Permanent Address : Vill Sheera, PO Poabo, Teh Shimla & Distt Shimla (HP) – 171 001

Educational Qualifications:

Certificate/ degree	Year	University/ Board	Marks (%)	Division
Matriculation	2011	CBSE	85.50	FIRST
10+2	2013	CBSE	68.06	FIRST
Graduation	2017	Dr Y S Parmar University of Horticulture and Forestry, Nauni, Solan (HP)	75.40	FIRST

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Dated: **(Sachin Bhardwaj)**