

**STUDIES ON GENETIC DIVERSITY FOR
YIELD AND QUALITY TRAITS IN PAPRIKA
(*Capsicum annuum* L.)**

BY

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B.Sc. (Hons.) Horticulture

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DECLARATION

I, Ms. T. LAKSHMI TIRUPATHAMMA, hereby declare that the thesis entitled **“STUDIES ON GENETIC DIVERSITY FOR YIELD AND QUALITY TRAITS IN PAPRIKA (*Capsicum annuum* L.)”** submitted to the Dr. Y.S.R. Horticultural University, Venkataramannagudem, for the degree of Master of Science in Horticulture (Vegetable Science) is the result of original research work done by me. I declare that no material contained in the thesis has been published earlier in any manner.

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CERTIFICATE

Ms. T. LAKSHMI TIRUPATHAMMA has satisfactorily prosecuted the course of research and that the thesis entitled “**STUDIES ON GENETIC DIVERSITY FOR YIELD AND QUALITY TRAITS IN PAPRIKA (*Capsicum annuum* L.)**” submitted is the result of original research work and is of sufficiently high standard to warrant its presentation to the examination.

I certify that neither the thesis nor its part thereof has been previously submitted by her for a degree of any university.

Place : Venkataramannagudem

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Chairman

CERTIFICATE

This is to certify that the thesis entitled “**STUDIES ON GENETIC DIVERSITY FOR YIELD AND QUALITY TRAITS IN PAPRIKA (*Capsicum annuum* L.)**” submitted in partial fulfillment of the requirements for the degree of Master of Science in Horticulture (Vegetable Science) of Dr. Y.S.R. Horticultural University, Venkataramannagudem, is a record of the bonafide research work carried out by **Ms. T. LAKSHMI TIRUPATHAMMA** under our guidance and supervision.

No part of the thesis has been submitted by the student for any other degree or diploma. The published part and all assistance received during the course of investigation have been duly acknowledged by the author of the thesis.

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LIST OF SYMBOLS AND ABBREVIATIONS

%	:	per cent
@	:	at the rate of
&	:	and
⁰ C	:	Degree Celsius
AA	:	Ascorbic Acid
A	:	Absorbance
ANOVA	:	Analysis of variance
AP	:	Andhra Pradesh
ASTA	:	American Spice Trade Association
CD	:	Critical Difference
cm	:	centimetre
COV	:	Co-Variance
CC	:	Capsaicin content
CV	:	Coefficient of variation
df	:	Degrees of freedom
DFF	:	Days to Fifty per cent Flowering
DM	:	Days to Maturity
Dr.Y.S.R.H.U	:	Dr Y S R Horticultural University
DFYP	:	Dry fruit yield per Plant
EC	:	Electrical Conductivity
ESS	:	Error sum of squares
EMSS	:	Error Mean sum of squares
<i>etc.</i>	:	and so on; and other people/things
<i>et al.</i>	:	and others
Fig	:	Figure
F test	:	Fishers test
FD	:	Fruit Diameter
FL	:	Fruit Length
FPL	:	Fruit Pedicel Length
FYM	:	Farm Yard Manure

g	:	gram
G	:	Genotype
GA	:	Genetic Advance
GAM	:	Genetic Advance as per cent of Mean
GCV	:	Genotypic Coefficient of Variation
HC & RI	:	Horticulture College and Research Institute
HRS	:	Horticultural Research Station
h^2 (b)	:	Heritability in broad sense
<i>i.e.</i>	:	that is
k	:	Selection differential
kg	:	kilogram
kg/ ha	:	kilogram per hectare
l	:	litre
LCA	:	Lam Capsicum Annuum
ml	:	millilitre
min	:	minutes
mm	:	millimetre
m	:	meter
mg	:	milligram
m.mhos/cm	:	millimhos per centimeter
MAS	:	Marker Assisted Selection
MSL	:	mean sea level
MSS	:	Mean Sum of Squares
nm	:	nanometre
no.	:	Number
NaOH	:	Sodium Hydroxide
NPBP	:	Number of Primary Branches per Plant
NFP	:	Number of Fruits per Plant
NSF	:	Number of seeds per fruit
OC	:	Oleoresin content
P	:	Phenotype
PCV	:	Phenotypic Coefficient of Variation

PH	:	Plant height
PS	:	Plant spread
pH	:	puissance de hydrogen
RBD	:	Randomised Block Design
RH	:	Relative humidity
r	:	Correlation coefficient
rpm	:	Rotations per minute
RC	:	Red Carotenoids
RSS	:	Replication Sum of Squares
RMSS	:	Replication Mean Sum of Squares
SE(d)	:	Standard error difference
S.Em	:	Standard error mean
SS	:	Sum of Squares
t	:	Treatments
TEC	:	Total extractable colour
T _r SS	:	Treatment Sum of Squares
TSS	:	Total Sum of Squares
T _r MSS	:	Treatment Mean Sum of Squares
t / ha	:	tonne per hectare
ug / ml	:	Microgram per millilitre
<i>viz.</i>	:	namely
V _g	:	Genotypic variance
V _p	:	Phenotypic variance
W.G.Dist.	:	West Godavari District
WSF	:	Weight of seeds per fruit
X	:	General mean
YC	:	Yellow Carotenoids

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ABSTRACT

An investigation was carried out during *kharif* 2016-17 at Horticultural Research Station, Lam, Guntur with 44 genotypes of paprika (*Capsicum annum* L.) in a randomized block design with two replications to study variability, heritability, genetic advance as per cent of mean, genetic divergence, character association and the magnitude of direct and indirect effects of 20 different quantitative and qualitative traits with dry fruit yield per plant.

The study revealed significant differences among genotypes for different characters studied. The genotypic coefficients of variation for all the characters studied were lesser than the phenotypic coefficients of variation indicating the masking effect of the environment. High heritability coupled with high genetic advance as per cent of mean was observed for all the characters excepting plant height, plant spread, number of primary branches per plant and days to 50 per cent flowering. This indicated the predominance of additive gene action in case of all the characters other than the aforesaid four characters suggesting direct phenotypic selection may be useful with respect to these traits.

Correlation and path analysis revealed that number of fruits per plant and fruit length had positive significant association and positive direct effects on yield per plant indicating the use of these attributes in selection to evolve high yielding varieties of paprika.

The results of multivariate analysis indicated the presence of considerable genetic divergence among the 44 genotypes studied. The 44 genotypes were

grouped into 6 clusters in D^2 analysis and 7 clusters in Ward's minimum variance method. This analysis clearly indicated that the genetic diversity and geographical diversity were not related.

By Mahalanobis' D^2 statistic, it could be inferred that total extractable colour followed by red carotenoids and yellow carotenoids contributed maximum towards genetic divergence.

Principal component analysis identified eight principal components (PCs) and has contributed 83.62 per cent of cumulative variance. The significant factors loaded in PC_1 towards maximum genetic divergence were weight of seeds per fruit, fruit diameter, number of seeds per fruit, 1000 seed weight, number of fruits per plant and fruit length. 2D and 3D graphs showed wide divergence between Warangal chappatta double patti and Byadagi kaddi, which are also distantly placed with LCA 512 and Warangal chappatta single patti signifying their usefulness in paprika breeding to develop high heterotic hybrids.

Agglomerative cluster analysis revealed wide genetic distance between the genotypes of cluster VII (LCA 511, Warangal chappatta single patti, LCA 512, Warangal chappatta double patti) and cluster IV (LCA 466, LCA 480, Jangareddy gudem local).

The genotypes Warangal chappatta double patti, LCA 511, LCA 512 and Warangal chappatta single patti showed maximum inter-cluster distance in Mahalanobis' D^2 analysis, principal component analysis and cluster analysis. So they can be exploited for the development of heterotic hybrids in future breeding programmes.

Chapter I

Introduction

Chapter I

INTRODUCTION

Paprika (*Capsicum annum* L. $2n = 24$) is one of the important commercial vegetable as well as spice crops grown all over the world. The genus *Capsicum* belongs to family Solanaceae which comprises of about 20 to 30 species of the new world tropics and subtropics. It is native to tropical areas of the Western Hemisphere, including Mexico, Central America, South America and West Indies.

Modern taxonomists recognize five major cultivated species of capsicum. In India, only two species viz., *Capsicum annum* L. and *Capsicum frutescence* L. are well known and most of the cultivated varieties belong to *Capsicum annum* L. This cultivated species has its unique place in the diet as a vegetable cum spice crop (Gadaginmath, 1992).

Capsicum annum is cultivated for its pods, often called chilli peppers, or chilies. The species includes most of the sweet peppers and many of the pungent, strong-flavoured types. Depending on the variety, the pods may be 0.5 inch to 12 inch (1.25 cm to 30 cm) in length, with round or conical shape and yellow, brown, purple or red colour. A spongy central column bears the flat, kidney-shaped seeds.

Paprika, a form of chilli is mainly valued for its high colour, low or no pungency and oleoresins. In chilli, three major products viz., paprika, oleoresins and dried chilli (both in whole and powder form) are traded in the world market. The pungent principle of paprika is capsaicin, an acid amide of Vanillylamine. They are widely used in curry powder, paste, pickles, sauces and ketchups for its characteristic pungency, colour and aroma (Shiva *et al.*, 2006).

Chilli besides imparting pungency and red colour to dishes, is also rich source of vitamin C, A and E and assists in good digestion. The vitamin C content (150-200 mg/100g) of chilli is the highest among that of all vegetables. There is considerable demand for paprika powder in the western countries.

There is a great demand for the natural colour from paprika fruits and is used in processed foods in place of synthetic colours. The demand for paprika oleoresin as a colouring agent has increased in international market especially in

Europe and USA due to ban on artificial colouring substances (Joshi *et al.* 1995). Capsanthin and Capsorubin are the red pigments and yellow includes beta-carotene, cryptoxanthin and zeaxanthin. Out of the total number of pigments isolated and identified from capsicum, capsanthin is the major one contributing to the colour value. Chilli varieties with high colour value and less pungency are preferred by the food industry.

Globally, chilli and paprika (dry) are grown in a total area of 1.94 million hectares with global production of 3.35 million tonnes. The global productivity of chilli and paprika (dry) is 1.73 metric tonnes/ha (Kumari *et al.* 2014) and the value of the total chilli and paprika is estimated at 3.42 million USD. India is the world's leading producer occupying an area of 0.76 million hectares with a production of 1.6 million tonnes and productivity of 2109 kg/ha (NHB, 2015).

Andhra Pradesh is the leading producer of the crop in the country with an annual production of 0.73 million tonnes from 0.13 million ha while the productivity is 5480 kg ha⁻¹ (Spice India, 2015). The state shares major portion of the exports from our country. Guntur, Prakasam, Kurnool and Krishna districts contribute nearly 80 per cent of chilli production in the state.

India has greater potential to increase the chilli production in order to promote exports which may help in price stabilization of the commodity within the country, particularly during the peak periods of production. Despite continuous efforts by the researchers and other stake holders of the crop at various levels, the productivity of the crop has not gained momentum, considering its potential. The low productivity is often attributed to many limiting factors such as lack of superior genotypes / improved cultivars for use in breeding programme to develop potential hybrids, severe incidence of insect pests (thrips, mites and borers) and diseases (anthracnose, leaf spots and viral diseases) resulting in tremendous reduction in yield and quality. Further, high variability present in the crop has so far not been fully exploited in the crop improvement programme.

The global demand for this crop and its value added products is ever increasing and there is need to develop varieties/ hybrids to meet the requirements of the industry. Improvement in quantitative as well as qualitative

traits needs precise information on the nature and degree of genetic divergence, which helps in choosing the right parents for an efficient breeding programme. The success of selection and hybridization programme depends upon the extent of variability, heritability and association among yield contributing characters and quality traits and their effects upon yield and quality.

Adequate knowledge on variability, genetic divergence, character association and the extent of contribution of each character to fruit yield is a prerequisite to plan appropriate breeding programme and evolve high yielding cultivars or hybrids with suitable traits. To develop such breeding programmes, the breeders need to evaluate the available germplasm for variability and divergence and to understand the performance of genotypes in terms of yield and yield attributing characters. This facilitates identification of promising genotypes and the stable ones can either be released as a variety or used in further breeding programmes.

The genus *Capsicum* is often cross pollinated one and the natural cross pollination may go up to 70 per cent depending on the extent of style exertion, time of dehiscence of anthers, wind direction and insect population (Murthy and Murthy, 1962 and Hosmani, 1993). Hence, breeding methods of both self and cross pollinated crops could be employed for crop improvement. A comprehensive knowledge of available variability within the breeding material of a crop species for desired characters enables the breeders to identify most potential genotypes. The phenotypic variation arises as a result of genotypic and interaction between genotypic and environmental variation. But for making effective selection, the heritable component *i.e.*, the genetic variation is more important. The genetic variability along with heritability should be considered for assessing the maximum and accurate effect of selection (Burton, 1952). Thus, success in a crop improvement programme depends, chiefly on the availability of genetic variability in the crop.

Genetic diversity is an important factor for any heritable improvement. Therefore, genetic divergence analysis is highly essential to estimate the extent of diversity existed among selected genotypes. Genetic diversity is used for discriminating divergent populations, which are reinstated by more scientific and

advanced biometrical techniques viz., multivariate analysis based on Mahalanobis D^2 -statistic (Mahalanobis, 1936).

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 methods. Therefore, heritability studies are of foremost importance to judge whether the observed variation for a particular character is due to genotype or due to environment.

Correlation and path coefficient analysis furnishes information regarding the nature and magnitude of various associations and help in the measurement of direct influence of one variable on other. Correlation coefficient analysis measures the mutual relationship between various plant characters and determines the component characters on which selection can be based for improvement in yield.

Genetic improvement mainly depends upon the amount of genetic variability in the population. Crop improvement in paprika has so far been achieved by exploiting the available sources of variability. Naturally, the genetic variation or diversity for most of the yield attributes is considerably high in paprika. As a result of exchange of paprika germplasm, lot of introgression of characters has taken place in many local paprika cultivars resulting in enhancement of variability and new genetic combination.

There is need for development of paprika (*Capsicum annuum* L.) in view of its increasing demand in the domestic and export sectors. Hence a genetic divergence study which is a basic requirement for effective selection is proposed with the following objectives.

1. To study the genetic variability in paprika germplasm for quantitative and qualitative traits.
2. To study phenotypic and genotypic correlations among yield, its component characters and quality traits.
3. To estimate direct and indirect effects of different component characters on yield.

4. To assess the magnitude of genetic divergence and to classify the genotypes under different groups.

Chapter II

Review of Literature

Chapter II

REVIEW OF LITERATURE

The plant breeder is primarily concerned with the improvement of both quantitative and qualitative characters. It is necessary to understand the genetic architecture of the various characters of importance and interrelationship among them. In the present investigation, an attempt has been made to study genetic variability, heritability, genetic advance, character association, path coefficient analysis and genetic divergence in paprika. A brief review of available literature pertaining to the investigation is presented in this chapter under the following heads.

- Genetic Variability, Heritability and Genetic advance
- Character association
- Path coefficient analysis
- Genetic divergence

2.1 GENETIC VARIABILITY

A critical estimate and study of genetic variability is a pre-requisite for initiating appropriate breeding procedures in crop improvement programmes which demands wide range of variability in a population. The improvement in any crop is proportional to the magnitude of its genetic variability present in the germplasm. Greater the variability in a population, greater is the chance for effective selection for desirable types (Vavilov, 1951).

The variability observed in any population could be due to two factors, the genetic and environmental, which further decide the genetic gain possible through selection in the given population. The genetic and environmental components of variation were discussed in the early part of last century by Johannsen (1909), who attributed the variation in a segregating population to

both heritable and non-heritable factors and variation within pure line to only environmental factors. Nelson-Ehle (1909) and East (1916) later confirmed Johannsen's work and showed that, continuous variation also confirms to Mendelian genetics.

The phenotypic variability is a measure of variability due to genotype, environment, and their interaction. The genetic variability is the real measure of variability concealed in a population. It indicates the relative magnitude of genetic diversity existing in the breeding population and helps to compare the genetic variability present for different characters.

The success of breeding programme for high yield and quality depends on the nature and magnitude of variation available in the genotypes. Selection from quantitative characters is less efficient, if it is based on phenotypic expression. Hence, it is necessary to assess the relative extent of genetic and non-genetic variability exhibited by individual characters. So, partitioning of overall variability into heritable and non-heritable components by calculating genetic parameters such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) is necessary (Chadha and Sindhu, 1983 and Singh and Singh, 1994).

HERITABILITY AND GENETIC ADVANCE

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 methods. Therefore, heritability studies are of foremost importance to judge whether the observed variation for a particular character is due to genotype or due to environment. The ratio of genotypic variance to total variance in non segregating population is known as heritability in broad sense (Hanson *et al.*, 1956) whereas, the ratio of additive variance to the total or phenotypic variance is referred to as narrow sense heritability (Lush, 1949). Thus, heritability denotes the proportion of phenotypic variance that is due to genotype which is heritable.

Genetic advance is the measure of improvement that can be achieved by practicing selection in a population. Genetic advance under selection is the improvement in the mean genotypic value of selected plants over parental population which further depends upon the genetic variability present in the population, heritability of the characters and the intensity of selection. Heritability estimates may not provide clear predictability of the breeding value. Therefore, estimation of heritability accompanied with genetic advance is generally more useful than heritability alone in prediction of the resultant effect for selecting the best individuals (Johnson *et al.*, 1955). This is due to the fact that, a character having high heritability may have very less phenotypic variation thus leading to low genetic advances. But, in the presence of additive gene effects high genetic advances can be expected (Panse, 1957).

Hence, study on components of variance and heritable components with suitable genetic parameters such as genotypic and phenotypic coefficients of variation, heritability and genetic advance are important tools for the breeders in selection of elite genotypes from diverse population.

A brief review of the nature of genetic variability, heritability and genetic advance in paprika investigated by several workers is presented in Table 2.1.

2.2 CHARACTER ASSOCIATION

The correlation coefficient analysis measures the mutual relationship between various characters and it determines the component traits on which selection can be made upon to improve the yield. There are three types of correlations viz., phenotypic, genotypic and environmental correlations.

Phenotypic correlation is the observable correlation between two variables and includes both genotypic and environmental effects. Genotypic correlation on the other hand, is the inherent association between two variables which may be either due to pleiotropic action of genes or linkage or more likely both are developmentally induced relationships (Harland, 1939). Genotypic

correlation measures the magnitude of relationship between various characters that determines the component characters on which selection can be made for improvement in yield (Johnson *et al.*, 1955).

A brief review on the nature of correlation of different characters with yield in paprika investigated by several workers is presented in Table 2.2.

2.3 PATH COEFFICIENT ANALYSIS

The path analysis is a standardized partial regression coefficient as it measures the direct influence of one variable upon other and permits the separation of correlation coefficient into components of direct and indirect effects of a set of independent variables on a dependent variable.

The concept of path analysis developed by Wright (1921), but the technique was first used for plant selection by Dewey and Lu (1959). Basically the technique aims to improve a dependent character like yield when the independent characters have a significant relation in desirable direction and positive direct effect or indirect effect through other traits on the dependent characters. The use of this technique requires cause and effect situation among the variables (Singh and Choudhary, 1979).

If the correlation coefficient between a causal factor and its effect is almost equal to its direct effects, the correlation explains the true relationship through this trait and the selection will be effective. If the correlation coefficient is positive, but the direct effect is negative or negligible, the indirect effects seem to be cause of positive correlation. In such situations, the indirect causal factors are to be considered simultaneously for selection. When the correlation coefficient is negative and the direct effect is positive and high, a restricted simultaneous selection model is to be followed i.e. restrictions to be imposed to nullify the undesirable indirect effects in order to make use of the direct effect. If the correlation coefficient as well as direct effect is negative, the selection based on that character should not be considered. The residual effect determines how best the causal factors account for the variability of the dependent factor. If

residual effect is high, some other factors, which have not been considered here, need to be included in this analysis to account fully for the variation in yield.

Brief review of direct effects of component characters on yield is presented in Table 2.3.

2.4 GENETIC DIVERGENCE:

The magnitude of divergence between two groups under consideration is provided by D^2 statistic developed by Mahalanobis (1936). For the first time D^2 statistic was applied for biological population by Nair and Mukharji (1960) to classify the natural and plantation teak tree types. Its application was extended later to taxonomic studies. Murthy and Pavate (1962) observed that D^2 analysis can be extended to the situations where overlapping species need to be discriminated and also when the discrimination at subspecies level is needed. This technique was subsequently used in different vegetable crops.

Karad *et al.* (2002) grouped 40 chilli genotypes into eight clusters and the D^2 values ranged between 0.1032 and 8.7702. Cluster I was the largest containing 23 genotypes, followed by cluster II (4 genotypes). Inter-cluster distance (D^2) ranged between 7.45 (clusters II and V) and 1.15 (clusters III and VII).

Begum (2002) grouped 46 chilli genotypes into 13 clusters which showed inter cluster D^2 values ranging between 18.91 and 87.12. Seed number per fruit, dry fruit yield per plant and number of fruits per plant were the chief contributors towards diversity. Maximum diversity as revealed by inter cluster distance was observed between cluster VI and XIII with D^2 value of 82.21.

Twenty diverse chilli genotypes studied for 11 characters were grouped into 6 clusters by Senapati *et al.* (2003). Cluster I was the largest with 13 genotypes followed by cluster III and IV with 2 genotypes each. They observed maximum genetic distance between cluster II and cluster VI, suggesting wide diversity between these groups and four characters viz., fresh fruit weight, fruit girth, fruit length and fruit number per plant were the chief contributors towards genetic divergence.

Prabhudeva (2003) grouped 36 genotypes into 11 clusters with D^2 values ranging from 34.02 to 102.13. According to him genetic diversity was not an index of geographical diversity. Fruits per plant, fruit weight and plant height were the characters which contribute maximum towards diversity. He observed maximum inter cluster distance between cluster I and II, suggesting that the genotypes belonging to these clusters form ideal pairs for developing hybrids.

Based on cluster analysis of Manju and Sreelathakumary (2004) revealed that 32 accessions were classified into 6 clusters. Cluster I was the largest with 21 accessions, followed by cluster II with 6 accessions. Cluster I had the highest intracluster distance (229.93). Maximum divergence was obtained between clusters I and cluster VI, followed by cluster I and V, as indicated by their high intercluster distances (1965.74 and 1640.10, respectively.)

Sreelathakumary and Rajmony (2004) evaluated 35 chilli genotypes of different geographical origin were assessed to know the nature and magnitude of genetic divergence using Mahalanobis D^2 statistics. The population was grouped into six clusters. The clustering pattern indicated that there was no association between geographical distribution of genotypes and genetic divergence. Fruits per plant, yield per plant, fruit length, fruit girth and fruit weight contributed for maximum divergence.

Smitha and Basavaraja (2006b) based on Mahalanobis D^2 analysis, revealed that 40 genotypes were grouped into 8 clusters, cluster-B having 17 entries. The maximum intra and inter cluster distances were observed for cluster A, cluster E and H respectively. Maximum relative contribution to the total divergence was recorded by fruits per plant, fruit yield per plant, number of primary branches, number of secondary branches, seeds per fruit, plant spread, fruit weight, and fruit length.

Gogate *et al.* (2006) grouped the genotypes into 11 clusters based on D^2 values. The genotypes were distributed randomly irrespective of geographic origin. The intra cluster distances ranged from 0.00 to 875.95. Number of fruits per plant, chlorophyll content, green fruit yield and ascorbic content largely

influenced genetic discrimination of genotypes. Genotypes Jwala, RHRC 16-5, ACG 349, ACS 98-8, ACS 92-4, S 49 and ACS 2000-02 were identified as promising parents for breeding programme.

Chatterjee *et al.* (2006) evaluated sixty chilli genotypes for 18 different characters to study divergence using PCA and cluster analysis. Out of 18 principal components, first seven PCs accounted for 77.42 per cent of the total variability. The first PC that explained the maximum variability was significantly correlated with 50% flowering and fresh fruit weight. Hierarchical cluster analysis by Ward's minimum variance method classified the genotypes into eight clusters based on their PCA scores. Wide genetic distance was observed between cluster V and VII.

Vani *et al.* (2007b) evaluated fifty-five accessions of chilli (*C. annuum*) for 15 quantitative characters, including yield. Plant height, yield per plant, contributed maximum towards diversity. D^2 analysis grouped all the genotypes into XIV clusters with 10 solitary clusters, and the D^2 values varied between 14.38 and 85.01. Cluster I was the largest containing 32 genotypes, followed by clusters II and IV with five genotypes each. The maximum intra-cluster distance was reported in cluster I, where as inter-cluster distance was maximum between clusters VII and XI. Cluster mean analysis showed that solitary clusters, i.e. cluster XI (IC-32), cluster XII (Pusa Jwala) and cluster XIV (IC-16) were having high mean values for yield per plant, average fruit weight, seeds per fruit and fruit length.

Dutonde *et al.* (2008) studied genetic diversity in 40 genotypes of chilli for various characters revealed substantial differences for all the characters. The accessions were grouped into 7 clusters with Cluster-I comprising of 17 genotypes followed by Cluster IV (11) and Cluster III (8). The maximum intercluster distance ($D=104.98$) was observed between Cluster-IV and Cluster-VII. Intercrossing among the genotypes belonging to Cluster-II, IV and VII was suggested to develop high yielding varieties with other desirable characters.

Ajjapplavara (2009) grouped 36 chilli genotypes into 11 clusters on the basis of genetic distance. Cluster-II was the largest, consisting of 16 genotypes, while cluster, IV, V, VI, VII, VIII, IX and XI contained single genotype each and the maximum inter cluster distance was 125.45 (between the II and X). Among the different characters studied, fruits per plant, fruit yield per plant, plant height and green fruit weight contributed significantly for the genetic diversity. The genotypes Phule Sai, LCA-206, Pant C-1, KDC-1 and AD-5 from these clusters were suggested as parental donors for future hybridization programme to improve fruit yield.

Thul *et al.* (2009) evaluated 24 accessions for 12 quantitative and qualitative traits and grouped all 24 accessions into six clusters. Cluster I consisted of 33.3% of accessions (8) and cluster II of 29.17% of accessions (7), while clusters V and VI consisted of single genotypes. The three characteristics that played the greatest role in differentiation were fruit diameter, number of fruits per plant and leaf diameter.

Sudre *et al.* (2010) grouped 55 *Capsicum* spp accessions into five groups (G1, G2, G3, G4, G5) using Ward-MLM procedure. Group G1 was formed by 12 accessions of *C. annuum* var. *annuum* and only one accession of *C. baccatum* var. *pendulum*. Group G2 was represented by six accessions, five of *C. frutescens* and one of *C. chinense*. Group G3 consisted of 13 accessions of *C. baccatum*, of which 11 belonged to *C. baccatum* var. *pendulum* and two to *C. baccatum* var. *baccatum*

Farhad *et al.* (2010) grouped 45 chilli genotypes into six clusters. Cluster I and cluster III had maximum number (11) and cluster II had the minimum number (3) of genotypes. The highest inter-cluster distance was observed between cluster II and IV and the lowest between cluster I and IV. Cluster II (D=4.91) recorded the highest intra-cluster distance and the lowest was observed in cluster I (D=3.41).

Kumar *et al.* (2010) evaluated 25 chilli genotypes and clustered them into eight constellations. Cluster I contained nine genotypes followed by cluster-II

(four) cluster IV and V (two each). The maximum inter cluster distance ($D=12.75$) was observed between cluster VI and cluster VIII. The cluster IV recorded maximum intra cluster distance ($D=5.91$). Intercrossing among the genotypes belonging to cluster III, IV and I were suggested to develop high yielding varieties with desirable characters.

Kumari *et al.* (2010) evaluated ninety four paprika (*Capsicum annuum*) accessions for 17 characters and grouped them into 10 clusters through Mahalanobis D^2 analysis. The largest group was cluster I which comprised of 24 genotypes. The cluster distances ranged from 15789.6 (between cluster II and cluster X) to 856.7 (between cluster 1 and cluster II).

Forty nine diverse materials of chilli were studied by Pandit *et al.* (2010) for estimation of genetic divergence through multivariate analyses using D^2 statistic. Grouping of genotypes was done based on the divergence (D^2 values) between any two genotypes. The genotypes were grouped into 17 clusters with cluster 1 having the maximum number of genotypes (nine genotypes). The intra and inter cluster distance represented the index of genetic diversity in clusters. The intra cluster distance was low, revealing homogeneity in the genotypes in a particular cluster for expression of the 12 characters under consideration. The inter cluster divergence was maximum between cluster 11 and 16 (32.40) suggesting wide diversity between them.

Fifty chilli germplasm lines were grouped into four and three clusters in first and second years respectively by Singh and Singh (2010). Highest intra-cluster D^2 values (468.96) and genetic distance (21.85) in first year was estimated for cluster III and maximum inter-cluster D^2 values (984.71) and genetic distance (31.38) were recorded between cluster II and III followed by cluster I and III (816.43 and 28.57). In second year, cluster I had maximum intra-cluster D^2 values and distance of 121.00 and 11.00, respectively. Maximum inter-cluster D^2 values (824.91) and genetic distance (28.72) were recorded between cluster II and III followed by cluster I and II (747.37 and 27.34).

Misra *et al.* (2011) grouped thirty eight accessions into 7 clusters, wherein substantial diversity among accessions was indicated by the wide range of D^2

values (752.901 - 1918683.00). Five accessions labelled for high capsaicin content (%), six for high capsanthin content (%) and two for dual purpose had characteristics desirable.

Lahbib *et al.* (2012) studied eleven populations grouped into three clusters and reported that the accessions FTC-1, FTC-2, FTC-5, FTC-7, FTC-8 and FCT-9 belonged to group 1. The accessions FTC-3, FTC-4, FTC-10 and FTC-11 belonged to group 2 and the accession FTC-6 formed the third group.

Srinivas *et al.* (2015) evaluated 78 chilli (*Capsicum frutescens*L.) genotypes for fifteen quantitative characters and one qualitative character. Mahalanobis D^2 statistics was employed to study genetic divergence among 78 genotypes and they were grouped into nine clusters on the basis of relative magnitude of D^2 values using Euclidean² method. Cluster II accommodated maximum number (24) of genotypes and minimum with cluster III (1 genotype). The inter cluster distances (D values) ranged between 3.90 to 12.68. Minimum inter cluster distance was between cluster II and IV (3.90) and maximum inter cluster distance was observed between cluster VII and VIII (12.68). The intra cluster divergence varied from 3.32 to 5.45. Maximum intra cluster distance was achieved in cluster VIII (5.45) and minimum divergence was observed in cluster V (3.32). Cluster III was showed zero intra cluster distance as it contains only one genotype. The maximum relative contribution to the total divergence was made by fruit yield per plant (61.07 %) and cluster VIII and cluster IX may be taken into consideration as better parents for an efficient hybridization programme of chilli.

Datta and Das (2013) evaluated 23 genotypes of chilli. Based on the D^2 value 53 genotypes were grouped into 17 clusters and results indicated that Cluster I and Cluster VII comprised with 29 and 9 genotypes respectively. Rest of clusters consisted of one genotype in each case. Among the different clusters maximum intra cluster distance (5.90) was recorded in cluster VII. Maximum inter Cluster distance (12.89) was observed in between Cluster XVII (CA-28) and Cluster XVI (CA-20), followed by 12.13 in Cluster XVII (CA- 28) and Cluster V (CA-14) and 11.89 in Cluster XVII (CA-28) and Cluster IX (CA- 42).

Tasso *et al.* (2014) evaluated 30 chilli (*Capsicum annuum* L.) genotypes for twelve quantitative characters. Cluster analysis was used for grouping of 30 chilli genotypes into six clusters. Cluster III had maximum (14) and cluster IV and V had the minimum number (1) of genotypes. The highest (459.81) inter cluster distance was observed between cluster II and IV and the lowest (36.04) between cluster I and IV. Cluster III ($D^2 = 67.66$) have exhibited highest intra cluster distance and the lowest was observed in cluster II ($D^2 = 11.19$). The characters capsaicin content and ascorbic acid contributed maximum towards divergence.

Hasan *et al.* (2014) evaluated 54 chilli (*Capsicum annuum* L.) genotypes for twelve quantitative characters. The genotypes were grouped into seven clusters. Cluster II had maximum (13) and cluster III had the minimum number (1) of genotypes. The highest inter-cluster distance was observed between cluster I and III and the lowest between cluster II and VII. The characters yield per plant, canopy breadth, secondary branches per plant, plant height and seeds per fruit contributed most for divergence in the studied genotypes.

Janaki *et al.* (2015b) grouped 63 genotypes of chilli with 8 clusters based on hierarchical cluster analysis. Among the clusters, cluster II was the largest containing 18 genotypes followed by cluster III with 15 genotypes and cluster VIII had only one genotype. The highest inter cluster distance was observed between cluster IV and VIII (7941.635) whereas the lowest between cluster VI and VIII (2836.497). The Cluster VII exhibited highest intra cluster distance (614.548) and the lowest was observed in cluster VIII (0.00).

Hasan *et al.* (2015) grouped thirteen genotypes of chilli (*Capsicum annuum* L.) into 5 clusters by non-hierarchical clustering using Mahalanobis's D^2 statistics. 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 (24.483) and the lowest inter-cluster distance was observed between the clusters II and V (11.633). The trait fruits per plant (35.8%) contributed maximum to the total divergence followed by fruit length (21.6%) and yield per plant (21.1%). Cluster IV produced highest

mean for fruit weight (4.48), fruits per plant (149.90) and yield per plant (676.03). Cluster V produced highest mean for fruit length (10.23), pedicel length (4.94) and fruit diameter (10.36). Cluster I and III produced lowest mean for most of the characters. Therefore, genotypes belonging to the cluster IV and V was suggested as potential parents for future hybridization programme to develop superior chilli variety with desired traits.

Rana *et al.* (2015) evaluated 24 genotypes of capsicum (*Capsicum annuum* L.) with respect to nine morphological characters. Based on D^2 values for all the possible pairs, 24 genotypes were grouped into 3 clusters, indicates a large amount of genetic diversity. Maximum number of genotypes were grouped in cluster-II (10) followed by cluster-III (9) and cluster-I (5). The average intra cluster distance was maximum (1.80) in cluster III and minimum (1.58) in cluster I whereas, highest inter cluster distance was recorded between cluster I and II.

Razzaq *et al.* (2016) evaluated 25 genotypes of chilli and grouped them into five clusters. Among the different clusters maximum inter cluster distance (59.2612) was observed in between Cluster II and Cluster IV followed in Cluster V and Cluster II (39.5281). Minimum inter cluster distance (16.0230) was observed in Cluster V and Cluster I. Clusters with large inter cluster distance showed that the genotypes included in these clusters have the greater diversity and hence the crossings between the genotypes in these clusters were expected to give desirable combinations.

Janaki *et al.* (2016) evaluated 63 genotypes of chilli for 16 characters. The genotypes grouped into 8 clusters of which the clusters III and V were the largest containing 17 genotypes each followed by cluster IV (11) whereas the clusters VI, VII and VIII were mono genotypic. The highest inter cluster distance was observed between clusters IV and VIII (4139.41) whereas the lowest was observed between clusters I and III (117.25). Cluster V (434.43) has exhibited highest intra cluster distance and the lowest was observed in clusters VI, VII and VIII (0.00).

2.5 QUALITY STUDIES

2.5.1 Ascorbic acid (mg / 100g)

Chilli is considered to be rich source of ascorbic acid (Vit-C) and minerals. It is the source for commercial preparation of Vit-C.

The ascorbic acid content was highest at ripening stage of chilli (Havaladar and Hossain, 1997) while Betlach (1967) found no marked difference between parents and F1 pongency for ascorbic acid content. Alpatiev and Kherenova (1970) reported that the ascorbic acid content in hybrid was close to that of the better parent. Nawalagatti *et al.* (1999) reported that the ascorbic acid content was highest in the hybrids followed by the cultivars and was least in the lines.

Kumar *et al.* (2003) evaluated thirty chilli genotypes and reported that the mean ascorbic acid content was lowest in genotype DCL 344 (78.30 mg/100 g) and highest in genotype ACS 2000-02 (188 mg/100 g). The total mean ascorbic acid content was 130.01 mg/100 g fresh fruit weight. Longer fruits contained higher ascorbic acid content than the shorter fruits.

The highest vitamin C content of 221.5 mg/100g was observed in cv.Phule Jyothi and the lowest (93.00mg/100g) in cv. Achari among the seven genotypes studied (Cheema and Pant, 2011).

Janaki *et al.*(2015d) reported the highest ascorbic acid content in the genotype Aparna (223.22) and the lowest in Phule Jyoti (43.99) among the 63 genotypes evaluated.

2.5.2 Oleoresin content (%)

Chilli is a good source of chilli oleoresin, which is the total flavour extract of dried and ground chillies. Nawalagatti *et al.* (1999) reported the highest oleoresin content in the hybrids followed by the cultivars and was the least in the lines.

Among 17 parents and 42 hybrids of chilli the highest oleoresin content was observed in MS 12x2529 (Singh *et al.* 2003).

Pandey *et al.* (2008) evaluating twenty-one genotypes of chilli reported seasonal variation in respect of oleoresin content which varied from 9.0 to 21.8 per cent.

Jyothi *et al.* (2008) studied twenty three cultivars and reported the highest oleoresin content in DCL 352 (13.82%) and the lowest in PC-7 (6.91%), while Shiva *et al.* (2014) reported a range of 11.28-22.23% for the same trait. The highest was observed in ICB-11 followed by ICB-15, ICB-19 (Arka Abhir) and ICB-10 and the lowest in CC-3.

Janaki *et al.* (2015d) evaluated 63 genotypes and reported highest oleoresin content in the genotype LCA-724 (12.31) and the lowest in Pandava (5.17).

2.5.3 Capsaicin content (SHU)

Pungency of chilli is due to a crystalline acrid volatile alkaloid called capsaicin.

Boronat *et al.* (1999) reported that the ratio of capsaicin to dihydrocapsaicin to be in the range of 0.64 to 1.94.

Mathur *et al.* (2000) reported Tejpur cultivar (*C.frutescence*) containing highest amount of capsaicin and dihydrocapsaicin (4.28 & 1.42%) to be the most pungent.

The capsaicin content varied with the variety (Dabrowska *et al.* 2000) and has been reported to accumulate uniformly with progressive fruit development (Jha *et al.* (2001).

Kumar *et al.* (2003) evaluated thirty chilli genotypes and reported that capsaicin content showed a narrow range of variation from 0.33 mg/100 mg in genotype Rajasthan local to 0.49 mg/100 mg in genotype KDCS-810, with an

overall mean of 0.41 mg/100 mg. Short fruits which were small and thin contained more capsaicin compared to long fruits.

According to evaluation studies of Singh *et al.* (2003) on 17 parents and 42 hybrids of chilli, the cv. Punjab Lal recorded the highest capsaicin concentration in powder (0.70%) and capsaicin level in oleoresin (3.05%).

Prasanth *et al.* (2007) reported six chilli genotypes with high capsaicin content (>1) and 3 genotypes with low capsaicin value (<0.20) while evaluating twenty seven accessions of chilli.

The capsaicin content of twenty-one genotypes of chilli evaluated in two seasons was in the range of 0.18 to 2.01%. (Pandy *et al.* 2008)

Jyothi *et al.* (2008) studied twenty three cultivars and reported that the capsaicin content among the entries was in the range of 0.256% (SKAU-C-101) to 0.528% (BC-40-2).

Janaki *et al.* (2015d) evaluated 63 genotypes and reported that the highest capsaicin content was recorded by the genotype Pusa Sadabahar (0.64) and lowest was in G-4 (0.14).

Lekshmi and Sreelathakumary (2016) evaluated 53 accessions of paprika and reported capsaicin content to be in the range of 0.88 per cent (CA 10) to 0.10 per cent (CA 34 and CA 40).

2.5.4 Total extractable colour (ASTA units)

The intensity of green colour at immature stage and that of red colour at ripening in chilli are important quality characters for domestic and export purposes. The red colour of chilli fruit is mainly due to capsanthin and capsorubin while chlorophyll pigment is responsible for green colour. Extractable pigment expressed in American Spice Trade Association (ASTA) units indicates colour intensity. Extractable colour in chilli is measured by measuring the absorbance of an acetone extract by a spectrophotometer at 460 nm. A number of varieties of chilli have been screened for colour and quality by

Derrera (2000). The average of 2 years data of extractable colour in ASTA revealed the highest content of pigments 269 ASTA units Buncion 50. Hungary has produced very high quality condiment paprika (*Capsicum annuum Longum* group) unparalleled in the world market, its bouquet, taste and color are supreme. It is reported that under Australian environmental conditions, Hungarian cultivars generate considerably higher pigment content. Milled paprika and its extract, oleoresin are used as a natural colouring source in a wide variety of foods, cosmetics and drugs. Development of cultivars with high pigment content and the ability to produce high pigment yield per unit area has to be given importance (Reves *et al.*, 1987) in breeding programmes of paprika in view of its advantage over chilli powder.

Singh *et al.* (2003) evaluated 17 parents and 42 hybrids of chilli (*C. annuum*) and reported that S 2529 exhibited the maximum colouring matter in powder (185.18 ASTA units) and colouring matter in oleoresin (883.86 ASTA units).

Prasanth *et al.* (2007) studied twenty-seven accessions of chilli (26 belonging to *Capsicum annuum* and one to *Capsicum baccatum*) and reported the colour value in the range of 32.82 to 208.56 ASTA units, with a mean value of 117.05 ASTA units.

Pandey *et al.* (2008) evaluated twenty-one genotypes of chilli for two seasons and reported that the mean extractable colour of the two seasons ranged from 53.3 to 346.0 ASTA units.

Jyothi *et al.* (2008) studied twenty three cultivars of which PC-7 and PC-6 from Pantnagar recorded the highest colour value of 50782 and 49456 EOA colour value respectively and the lowest colour value was recorded by DCL-352(19932 EOA).

Shiva *et al.*(2013) evaluated the performance of 30 paprika lines and reported ICB-5, ICB-7, ICB-4, PBC- 171, IMI-5, EC-71 for high colour value.

Gobinath *et al.*(2014) evaluated 24 paprika like chillies (*Capsicum annuum L.*) and were reported the colour range of 109 (ICBD-11) to 353 ICBD-19 ASTA units.

Janaki *et al.*(2015d) reported maximum colour value in the genotype LCA-713 (128) and the minimum in Aparna (20.58).

The among the 63 genotypes studied maximum per cent of red carotenoids was observed for genotypes LCA-357 and KT-1 (0.22) while the genotype Aparna had no red carotenoids. They reported maximum per cent of yellow carotenoids in the genotype HC-28 (0.15) and the minimum in LCA-724 and LCA-620 (0.01). (Janaki *et al.*2015d)

A brief review of literature on variability, heritability and genetic advance, correlation and path analysis related to ascorbic acid content, oleoresin content, color value and capsaicin content are presented in table 2.1, 2.2 & 2.3.

Table 2.1: Review of literature on variability, heritability and genetic advance for quantitative and qualitative parameters in *Capsicum annuum* L.

Character	Materials used for study	GCV (%)	PCV (%)	h ² (b) (%)	GA (%)	GAM (%)	References
1. Plant height (cm)	52 genotypes	Moderate 16.51	Moderate 18.66	78.33 High	-	30.11 High	Gogoi and Gautam (2002)
	32 accessions	Moderate 18.82	High 20.09	87.77 High	-	36.32 High	Manju and Sreelathakumary (2002)
	46 genotypes	Low 6.13	Moderate 11.90	26.56 Low	-	6.52 Low	Begum (2002)
	27 genotypes	Moderate 18.00	Moderate 18.97	90.00 High	-	35.16 High	Kashinath (2003)
	48 genotypes	Moderate 11.51	Moderate 12.77	81.20 High	-	21.36 High	Khurana <i>et al.</i> (2003)
	36 genotypes	Moderate 16.14	High 21.90	56.18 Moderate	-	25.35 High	Prabhudeva (2003)
	35 genotypes	High 22.44	High 22.78	96.98 High	-	45.52 High	Sreelathakumary and Rajamony (2004)
	12 genotypes	High 27.80	High 29.97	86.09 High	-	96.19 High	Verma <i>et al.</i> (2004)
	13 genotypes	Moderate 13.44	Moderate 13.90	93.50 High	-	8.82 Low	Rao (2005)
	31 genotypes	High 25.20	High 27.93	81.00 High	-	42.04 High	Singh <i>et al.</i> (2005)
	80 accessions	Moderate 19.89	High 20.57	93.5 High	23.19 High	39.62 High	Krishna <i>et al.</i> (2007a)
	40 genotypes	Moderate	Moderate	94.92	28.46	35.90	Smitha and Basvaraja

		17.89	18.36	High	High	High	(2007)
	80 accessions	Moderate	Moderate	High	-	High	Ukkund <i>et al.</i> (2007)
	45 genotypes	High 26.78	High 28.52	88.17 High	21.75 High	16.69 Moderate	Farhad <i>et al.</i> (2008)
	11 genotypes	Moderate 10.52	Moderate 13.98	56.60 Moderate	-	16.30 Moderate	Tembhurne <i>et al.</i> (2008)
	37 genotypes	Low 14.06	Low 14.22	97.80 High	17.53 Moderate	28.66 High	Sandeep <i>et al.</i> (2008)
	30 genotypes	Moderate	Moderate	-	-	-	Singh <i>et al.</i> (2009)
		Moderate	Moderate	High	-	High	Pandit <i>et al.</i> (2009)
	49 genotypes	High 24.15	High 25.07	92.80 High	29.12 High	47.92 High	Sarkar <i>et al.</i> (2009)
	94 paprika accessions	Moderate 14.84	Moderate 15.23	95.00 High	28.37 High	29.79 High	Kumari <i>et al.</i> (2010)
	20 genotypes	High	High	High	-	High	Kumar <i>et al.</i> (2010)
	30 genotypes	High	High	High		High	Munshi <i>et al.</i> (2010)
	23 bell pepper genotypes	Moderate 10.44	Moderate 11.98	75.88 High	9.89 Low	18.72 Moderate	Sharma <i>et al.</i> (2010)
	20 capsicum genotypes	Moderate 11.50	Moderate 14.69	61.26 High	9.21 Low	18.55 Moderate	Berhamu <i>et al.</i> (2011a)
		High	High	High	-	High	Singh and Singh (2011)
	10 genotypes	Low 8.76	Moderate 11.16	61.19 High	12.11 Moderate	14.07 Moderate	Jyothi <i>et al.</i> (2011)
	20 genotypes	High 21.08	High 21.17	99.10 High	20.67 High	43.23 High	Kumar <i>et al.</i> (2012)
		Moderate	Moderate	High	-	High	Nehru <i>et al.</i> (2012)
	9 varieties	Moderate 15.14	Moderate 16.69	82.27 High	22.50 High	28.29 High	Lakshmi and Padma (2012)
	53 genotypes	Moderate 15.44	Moderate 16.44	86.10 High	23.64 High	37.81 High	Datta and Das (2013)
	50 accessions	Moderate	Moderate	Moderate	Moderate	Moderate	Mahantesh <i>et al.</i> (2013a)

		12.32	16.12	58.37	11.37	19.39	
	23 genotypes	High 23.29	High 23.68	96.72 High	41.03 High	47.18 High	Amit <i>et al.</i> (2014)
	22 genotypes	High 22.27	High 25.84	74.30 High	17.87 Moderate	39.54 High	Sharma <i>et al.</i> (2014)
	24 genotypes	Moderate 18.10	Moderate 19.76	83.92 High	-	34.16 High	Vijaya <i>et al.</i> (2014)
	63 genotypes	Moderate 18.49	Moderate 19.98	85.65 High	30.73 High	35.25 High	Janaki <i>et al.</i> (2015a)
	30 genotypes	Moderate 18.06	High 20.75	75.77 High	-	32.39 High	Ashish <i>et al.</i> (2015)
	24 genotypes	Low 5.24	Low 5.60	87.60 High	5.84 Low	10.10 Moderate	Rana <i>et al.</i> (2015)
	76 genotypes	Low 5.63	Low 6.37	79.68 High	-	57.62 High	Ajith and Manju (2015)
	40 genotypes	Moderate 15.21	Moderate 17.73	73.6 High	-	26.9 High	Patel <i>et al.</i> (2015)
	20 germplasm lines	Low 2.02	Low 2.93	67.50 High	4.40 Low	12.76 Moderate	Meena <i>et al.</i> (2016)
	16 genotypes	High 20.12	High 20.74	94.15 High	26.46 High	40.22 High	Rosmaina <i>et al.</i> (2016)
	25 accessions	Low 0.21	Low 0.21	99.49 High	29.10 High	43.51 High	Razzaq <i>et al.</i> (2016)
	25 genotypes	Low 8.38	Low 8.92	87.71 High	-	21.13 High	Satish <i>et al.</i> (2016)
	16 genotypes	Low 9.15	Low 9.25	97.85 High	7.4 Low	18.66 Moderate	Priyanka and Madhvi (2016)
	43 genotypes	Low 9.19	Low 7.87	73 High	13.98 Moderate	13.89 Moderate	Kranthi <i>et al.</i> (2016)
2. Plant spread (cm)	52 genotypes	Moderate	Moderate	58.95	-	21.11	Gogoi and Gautam (2002)

		17.38	13.35	Moderate		High	
	32 accessions	Moderate 13.28	Moderate 15.66	71.87 High	-	23.18 High	Manju and Sreelathakumary (2002)
		Moderate 17.38	Moderate 15.33	73.94 High	-	27.15 High	Mallikarjun <i>et al.</i> (2003b)
		Moderate 17.82	Low 6.91	36.78 Moderate	-	8.63 Low	Nehru <i>et al.</i> (2003)
	12 genotypes	High	Low	High	-	High	Verma <i>et al.</i> (2004)
	97 genotypes	High 34.94	High 30.84	77.89 High	-	56.01 Moderate	Prabhakaran <i>et al.</i> (2004)
		Moderate 19.66	Moderate 19.54	98.80 High	-	10.88 Moderate	Rao (2005)
	40 genotypes	Moderate 19.07	Moderate 13.72	51.80 Moderate	-	20.10 High	Smitha and Basavaraja (2006a)
	25 genotypes	High 24.52	High 22.54	84.52 High	-	42.69 High	Karad <i>et al.</i> (2006)
	60 genotypes	Moderate 14.63	Moderate 13.55	84.70 High	-	25.85 High	Chatterjee (2006)
	37 genotypes	Low 16.18	Low 16.61	-	-	-	Sandeep <i>et al.</i> (2008)
	94 paprika accessions	High 20.83	High 21.09	97.5 High	52.94 High	High 42.37	Kumar <i>et al.</i> (2010a)
	10 genotypes	Low 7.25	Moderate 10.96	43.63 Moderate	10.51 Moderate	9.87 Low	Jyothi <i>et al.</i> (2011)
	20 genotypes	Moderate 12.85	Moderate 13.77	87.00 High	9.91 Low	24.69 High	Kumar <i>et al.</i> (2012)
	50 accessions	Moderate 14.54	Moderate 17.97	65.47 High	10.96 Moderate	24.24 High	Mahantesh <i>et al.</i> (2013a)
	53 genotypes	Low 7.24	Low 8.17	78.50 High	6.79 Low	16.94 Moderate	Datta and Das (2013)
	24 genotypes	High	High	86.64	-	47.72	Vijaya

		26.74	24.89	High		High	<i>et al.</i> (2014)
	43 genotypes	Moderate 13.29	Moderate 11.50	75 High	20.69 High	20.48 High	Kranthi <i>et al.</i> (2016)
3. Number of primary branches per plant	17 genotypes	Moderate 15.21	Moderate 15.36	98.12 High	-	69.05 High	Ibrahim <i>et al.</i> (2001)
	52 genotypes	Low 8.64	Moderate 15.93	29.39 Low	-	9.65 Low	Gogoi and Gautam (2002)
	80 genotypes	High 20.57	Moderate 19.89	93.50 High	-	39.62 High	Krishna (2002)
	32 accessions	Moderate 19.17	High 30.56	39.35 Moderate	-	24.77 High	Manju and Sreelathakumary (2002)
	46 genotypes	Low 8.32	Moderate 13.47	38.18 Moderate	-	10.59 Moderate	Begum (2002)
	70 genotypes	Moderate 18.22	Moderate 18.69	95.69 High	-	36.61 High	Sreelathakumary and Rajamony (2002)
	27 genotypes	Moderate 13.38	Moderate 14.56	84.40 High	-	25.36 High	Kashinath (2003)
	36 genotypes	Moderate 14.31	Moderate 16.39	76.22 High	-	25.82 High	Prabhudeva (2003)
	13 genotypes	High 23.84	High 24.24	96.70 High	-	20.03 High	Rao (2005)
	31 genotypes	Moderate 13.90	High 21.74	41.00 Moderate	-	1.28 Low	Singh <i>et al.</i> (2005)
		Moderate	Moderate	Moderate	-	Moderate	Bendale <i>et al.</i> (2006)
	40 genotypes	High 24.60	High 27.33	81.00 High	3.85 Low	45.02 High	Smitha and Basvaraja (2007)
	45 genotypes	High 41.06	High 41.51	97.86 High	2.79 Low	83.684 High	Farhad <i>et al.</i> (2008)
	11 genotypes	Low 5.55	Moderate 12.46	19.80 Low	-	5.09 Low	Tembhurne <i>et al.</i> (2008)

	37 genotypes	Low 8.63	Moderate 11.73	54.20 Moderate	0.54 Low	13.17 Moderate	Sandeep <i>et al.</i> (2008)
	30 genotypes	High	High	-	-	-	Singh <i>et al.</i> (2009)
		High	High	High	-	High	Kumar <i>et al.</i> (2010)
	30 genotypes	High	Moderate	High	-	High	Munshi <i>et al.</i> (2010)
	20 capsicum genotypes	High 21.02	High 25.01	70.62 High	-	36.38 High	Berhanu <i>et al.</i> (2011a)
		Moderate	Moderate	High	-	Low	Singh and Singh (2011)
	53 genotypes	Moderate 11.98	Moderate 12.47	92.30 High	1.45 Low	30.39 High	Datta and Das (2013)
	50 accessions	Moderate 15.56	Moderate 18.54	70.45 High	1.57 Low	26.97 High	Mahantesh <i>et al.</i> (2013a)
	22 genotypes	Moderate 14.00	Moderate 17.21	66.20 High	1.87 Low	23.56 High	Sharma <i>et al.</i> (2014)
	30 genotypes	Moderate 16.82	Moderate 17.89	88.48 High	-	32.60 High	Ashish <i>et al.</i> (2015)
	24 genotypes	Moderate 12.53	Moderate 13.81	82.35 High	-	23.42 High	Vijaya <i>et al.</i> (2014)
	40 genotypes	High 24.88	High 26.47	88.31 High	-	48.17 High	Patel <i>et al.</i> (2015)
	63 genotypes	Moderate 18.55	High 22.64	67.11 High	1.13 Low	31.30 High	Janaki <i>et al.</i> (2015a)
	25 accessions	Low 0.24	Low 0.27	79.38 High	1.95 Low	44.52 High	Razzaq <i>et al.</i> (2016)
	25 genotypes	Moderate 10.23	Moderate 17.29	64.89 High	-	20.48 High	Satish <i>et al.</i> (2016)
	20 germplasm lines	High 33.10	High 34.02	63.60 High	1.68 Low	34.43 High	Meena <i>et al.</i> (2016)
	43 genotypes	Moderate 12.60	Moderate 17.23	53 Moderate	0.68 Low	18.98 Moderate	Kranthi <i>et al.</i> (2016)

4. Days to 50 % flowering	46 genotypes	Low 6.28	Moderate 11.41	30.34 Moderate	-	7.13 Low	Begum (2002)
	27 genotypes	Low 7.42	Low 9.76	57.80 Moderate	-	11.63 Moderate	Kashinath (2003)
	36 genotypes	Low 4.17	Low 9.78	76.19 High	-	7.48 Low	Prabhudeva (2003)
		Low	Low	High	-	Low	Choudhary and Samadia (2004)
	12 genotypes	Low 3.76	Low 4.05	86.04 High	-	7.18 Low	Verma <i>et al.</i> (2004)
		Low	Low	Low	-	Low	Wasule <i>et al.</i> (2004)
	13 genotypes	Low 6.07	Low 6.30	92.60 High	-	3.20 Low	Rao (2005)
	31 genotypes	Moderate 16.56	High 20.47	65.00 High	-	21.55 High	Singh <i>et al.</i> (2005)
	40 genotypes	Moderate	Moderate	High	-	High	Dutonde <i>et al.</i> (2006)
	27 genotypes	Low	Low	Low	-	Moderate	Bharadwaj <i>et al.</i> (2007)
	80 accessions	Low 5.07	Moderate 13.79	13.50 Moderate	-	1.70 Low	Krishna <i>et al.</i> (2007a)
	72 genotypes and 3 varieties	Low 4.20	High 7.34	32.70 Moderate	-	1.73 Low	Shirshat <i>et al.</i> (2007)
	40 genotypes	High 33.13	Low 43.71	54.06 Moderate	19.08 Moderate	50.32 High	Smitha and Basvaraja (2007)
	45 genotypes	Low 6.42	Low 8.86	52.60 High	7.262 Low	9.59 Low	Farhad <i>et al.</i> (2008)
	37 genotypes	Low	Low	High	-	Low	Patil <i>et al.</i> (2008)
	37 genotypes	Low 7.34	Low 9.18	63.90 High	5.51 Low	12.08 Moderate	Sandeep <i>et al.</i> (2008)
	11 genotypes	Low 7.95	Low 8.06	97.20 High	-	16.14 Moderate	Tembhurne <i>et al.</i> (2008)

	49 genotypes	High 22.97	High 23.41	96.30 High	21.93 High	46.43 High	Sarkar <i>et al.</i> (2009)
		Low	Low	High		High	Wilson and Philip (2009)
	94 paprika accessions	Low 5.24	Low 5.62	87.02 High	7.57 Low	10.01 Moderate	Kumari <i>et al.</i> (2010)
	23 bell pepper genotypes	Low 4.59	low 8.18	31.50 High	2.06 Low	5.30 Low	Sharma <i>et al.</i> (2010)
	34 genotypes	High 25.47	High 27.97	96.50 High	-	25.33 High	Arup <i>et al.</i> (2011)
	23 genotypes	Low 9.04	Low 9.20	96.51 High	14.99 Moderate	18.29 Moderate	Amit <i>et al.</i> (2014)
	50 accessions	Moderate 11.32	Moderate 15.51	53.28 Moderate	6.32 Low	17.04 Moderate	Mahantesh <i>et al.</i> (2013a)
	24 genotypes	Low 10.00	Moderate 10.75	86.49 High	-	19.16 Moderate	Vijaya <i>et al.</i> (2014)
	22 genotypes	Low 6.28	Low 8.13	59.60 Moderate	5.73 Low	10.00 Low	Sharma <i>et al.</i> (2014)
	51 genotypes	Moderate 24.50	Moderate 26.6	87.5 High	22.57 High	46.3 High	Pandit and Adhikary (2014)
	30 genotypes	High 20.20	High 20.37	98.32 High	-	41.25 High	Ashish <i>et al.</i> (2015)
	63 genotypes	Moderate 10.42	Moderate 12.19	73.09 High	5.77 Low	18.36 Moderate	Janaki <i>et al.</i> (2015a)
	24 genotypes	Low 5.74	Low 6.11	88.20 High	5.22 Low	11.10 Moderate	Rana <i>et al.</i> (2015)
	20 germplasm lines	Moderate 16.02	Moderate 16.29	96.70 High	13.50 Moderate	32.46 High	Meena <i>et al.</i> (2016)
	80 genotypes	Low 4.15	Low 5.89	50 Moderate	43.44 High	57.72 High	Kannan <i>et al.</i> (2016)
	25 accessions	High	High	High	-	High	Razzaq <i>et al.</i> (2016)
	25 genotypes	Low	Low	87.29	-	13.58	Satish <i>et al.</i> (2016)

		7.05	7.55	High		Moderate	
	43 genotypes	Low 9.84	Moderate 11.18	78 High	5.57 Low	17.86 Moderate	Kranthi <i>et al.</i> (2016)
5. Days to maturity		Low	Low	Moderate	-	Low	Chaim and Paran (2000)
	30 genotypes	Low 5.50	Low 5.32	93.60 High	-	10.60 Moderate	Munshi and Behera (2000)
	52 genotypes	Moderate 10.43	Low 6.95	44.31 Moderate		9.53 Low	Gogoi and Gautam (2002)
	32 accessions	Moderate 11.89	Moderate 12.44	91.32 High	-	23.41 High	Manju and Sreelathakumary (2002)
		Low 5.11	Low 3.81	70.59 High	-	4.40 Low	Acharya and Rajput (2003)
		Low 3.35	Low 3.16	89.25 High	-	6.16 Low	Mallikarjun <i>et al.</i> (2003 b)
		Low 3.41	Low 3.18	87.00 High	-	6.10 Low	Choudhary and Samadia(2004)
	13 genotypes	Low 3.17	Low 2.92	84.50 High	-	1.30 Low	Rao (2005)
	25 genotypes	Low 9.41	Low 6.41	46.32 Moderate	-	8.98 Low	Karad <i>et al.</i> (2006)
	60 genotypes	Low 8.03	Low 7.96	98.30 High	-	16.26 Moderate	Chatterjee (2006)
	37 genotypes	High 33.95	High 34.18	98.70 High	109.06 High	69.47 High	Sandeep <i>et al.</i> (2008)
	23 bell pepper genotypes	Low 8.63	Low 9.83	77.10 High	10.97 Moderate	15.60 Moderate	Sharma <i>et al.</i> (2010)
	20 genotypes	Moderate 10.12	Moderate 11.64	75.60 High	11.74 Moderate	18.13 Moderate	Kumar <i>et al.</i> (2012)
	22 genotypes	Moderate	Moderate	61.30	Moderate	22.13	Sharma <i>et al.</i> (2014)

		10.21	13.04	High	18.80	High	
	25 genotypes	Low 6.59	Low 6.77	94.88 High	-	Moderate 13.23	Satish <i>et al.</i> (2016)
	20 germplasm lines	Low 8.56	Low 8.77	96.80 High	22.47 High	28.83 High	Meena <i>et al.</i> (2016)
	16 genotypes	Low 8.59	Low 8.66	98.51 High	Moderate 12.87	Moderate 17.57	Rosmaina <i>et al.</i> (2016)
	16 genotypes	Low 3.83	Low 3.87	97.61 High	-	8.63 Low	Priyanka and Madhvi (2016)
	43 genotypes	Low 8.88	Low 9.55	86 High	13.36 Moderate	16.99 Moderate	Kranthi <i>et al.</i> (2016)
6. Number of fruits per plant	30 genotypes	High 54.94	High 57.05	95.8 High	52.26 High	108.98 High	Munshi and Behara (2000)
	17 genotypes	Moderate 19.93	Moderate 13.28	96.18 High	-	13.76 Moderate	Ibrahim <i>et al.</i> (2001)
	52 genotypes	High 37.64	High 40.37	86.94 High	-	72.30 High	Gogoi and Gautam (2002)
	32 accessions	High 89.54	High 90.08	98.82 High	-	183.37 High	Manju and Sreelathakumary (2002)
	46 genotypes	High 24.76	High 25.95	91.07 High	-	48.71 High	Begum (2002)
	70 genotypes	High 24.76	High 72.39	99.34 High	-	148.14 High	Sreelathakumary and Rajamony (2002)
	27 genotypes	High 29.29	High 36.90	63.00 High	-	47.88 High	Kashinath (2003)
		High	High	High		-	Cherian <i>et al.</i> (2003)
	48 genotypes	High 54.05	High 59.51	82.51 High	-	101.14 High	Khurana <i>et al.</i> (2003)
	36 genotypes	High 42.49	High 44.32	91.92 High	-	83.93 High	Prabhudeva (2003)

	25 genotypes	High	High	High		High	Mini and Khader (2004)
	35 genotypes	High 63.70	High 63.88	99.42 High	-	130.84 High	Sreelathakumary and Rajamony (2004)
	97 genotypes	High 34.50	High 31.09	81.21 High	-	High 57.72	Prabhakaran <i>et al.</i> (2004)
		High	High	High	-	High	Wasule <i>et al.</i> (2004)
	22 genotypes	High 40.14	High 39.39	96.30 High		79.63 High	Mishra <i>et al.</i> (2005)
	13 genotypes	High 36.50	High 36.84	98.20 High	-	48.51 High	Rao (2005)
	31 genotypes	High 30.90	High 33.88	83.00 High		52.51 High	Singh <i>et al.</i> (2005)
		High	High	High	-	High	Varkey <i>et al.</i> (2005)
	22 genotypes	High	High	High		High	Sood <i>et al.</i> (2006)
	20 genotypes	High	High	High	-	High	Bendale <i>et al.</i> (2006), Sharma and Sharma (2006)
	27 genotypes	High	High	High	High	-	Bharadwaj <i>et al.</i> (2007)
	80 accessions	High 35.63	High 37.96	88.1 High	122.6 High	70.05 High	Krishna <i>et al.</i> (2007a)
	72 genotypes and 3 varieties	High 32.36	High 48.72	44.10 Moderate	33.10 High	44.29 High	Shirshat <i>et al.</i> (2007)
	40 genotypes	High 39.02	High 40.04	95.00 High	59.54 High	77.93 High	Smitha and Basvaraja (2007)
	55 genotypes	High	High	High	High	High	Vani <i>et al.</i> (2007a)
	80 accessions	Moderate	Moderate	High	-	High	Ukkund <i>et al.</i> (2007)
	45 genotypes	High 35.58	High 37.19	91.53 High	8.320 Low	70.134 High	Farhad <i>et al.</i> (2008)
	37 genotypes	Low	Low	High	-	Moderate	Patil <i>et al.</i> (2008)
	11 genotypes	High 33.70	High 37.68	80.00 High	-	62.08 High	Tembhurne <i>et al.</i> (2008)

	37 genotypes	Low 18.62	Low 19.47	91.40 High	18.02 Moderate	36.68 High	Sandeep <i>et al.</i> (2008)
	49 genotypes	High 42.33	High 44.85	89.10 High	39.65 High	82.27 High	Sarkar <i>et al.</i> (2009)
	40 genotypes	High 30.35	High 31.38	93.55 High	-	High 60.47	Gupta <i>et al.</i> (2009)
		High	High	High	-	High	Wilson and Philip (2009)
	94 paprika accessions	High 32.46	High 32.82	97.80 High	83.36 High	66.13 High	Kumari <i>et al.</i> (2010)
	23 bell pepper genotypes	High 24.82	High 29.47	70.95 High	2.80 Low	43.07 High	Sharma <i>et al.</i> (2010)
	34 genotypes	High 82.02	High 86.05	97.60 High	-	74.75 High	Arup <i>et al.</i> (2011)
	20 capsicum genotypes	High 48.47	High 50.44	92.32 High	27.10 High	95.93 High	Berhanu <i>et al.</i> (2011 a)
		High	High	High	-	High	Singh and Singh (2011)
	10 genotypes	High 40.15	High 40.67	97.45 High	127.36 High	81.64 High	Jyothi <i>et al.</i> (2011)
	20 genotypes	High 39.93	High 40.34	98 High	92.68 High	81.43 High	Kumar <i>et al.</i> (2012)
	7 varieties	High 30.34	High 32.30	88.24 High	53.76 High	58.7 High	Lakshmi and Padma (2012)
	50 accessions	High 77.68	High 78.39	98.20 High	18.92 Moderate	158.59 High	Mahantesh <i>et al.</i> (2013a)
	53 genotypes	High 25.62	High 26.56	93.00 High	57.35 High	66.21 High	Datta and Das (2013)
	23 genotypes	High 34.14	High 35.57	92.13 High	82.63 High	67.51 High	Amit <i>et al.</i> (2014)
	24 genotypes	Moderate	-	High	-	High	Dipak <i>et al.</i> (2014)
	22 genotypes	High 37.81	High 38.90	94.50 High	218.86 High	75.72 High	Sharma <i>et al.</i> (2014)

	51 genotypes	High 38.86	High 36.16	72.8 High	26.28 High	58.2 High	Pandit and Adhikary (2014)
	24 genotypes	High 33.32	High 36.57	83.01 High	-	62.53 High	Vijaya <i>et al.</i> (2014)
	30 genotypes	High 34.31	High 37.35	84.36 High	-	64.92 High	Ashish <i>et al.</i> (2015)
	76 genotypes	High 31.56	High 32.86	94.70 High	-	76.39 High	Ajith and Manju (2015)
	40 genotypes	High 45.19	High 46.29	95.29 High	-	90.88 High	Patel <i>et al.</i> (2015)
	63 genotypes	High 37.77	High 40.50	87.00 High	125.19 High	72.58 High	Janaki <i>et al.</i> (2015a)
	24 genotypes	Moderate 20.76	Moderate 21.57	92.70 High	6.80 Low	41.17 High	Rana <i>et al.</i> (2015)
	16 genotypes	High 39.77	High 40.11	High 98.31	-	81.24 High	Priyanka and Madhvi (2016)
	20 germplasm lines	Low 9.52	Low 9.63	81.90 High	5.40 Low	17.73 Moderate	Meena <i>et al.</i> (2016)
	25 genotypes	High 41.77	High 42.0	98.93 High	-	45.59 High	Satish <i>et al.</i> (2016)
	19 genotypes	High	High	-	High	High	Leeladhar <i>et al.</i> (2016)
	80 genotypes	Moderate 11.14	Moderate 13.90	64.00 High	65.04 High	53.55 High	Kannan <i>et al.</i> (2016)
	63 genotypes	High	High	High	-	High	Razzaq <i>et al.</i> (2016)
	16 genotypes	High 32.95	High 36.56	81.21 High	58.81 High	61.16 High	Rosmaina <i>et al.</i> (2016)
	49 accessions	Moderate 10	High 38	38 High	3.09 Low	8 Low	Shimeles <i>et al.</i> (2016)
	43 genotypes	High 23.03	High 26.67	75 High	147.57 High	40.98 High	Kranthi <i>et al.</i> (2016)

7. Fruit length (cm)	30 genotypes	Low 5.32	Low 5.50	93.6 High	9.69 Low	10.60 Moderate	Munshi and Behara (2000)
	17 genotypes	High 26.21	High 26.64	96.74 High	-	47.31 High	Ibrahim <i>et al.</i> (2001)
	52 genotypes	High 34.29	High 35.53	93.18 High	-	68.19 High	Gogoi and Gautam (2002)
	32 accessions	Moderate 17.51	Moderate 18.07	93.95 High	-	34.97 High	Manju and Sreelathakumary (2002)
	46 genotypes	Moderate 15.54	Moderate 16.94	84.11 High	-	29.30 High	Begum (2002)
	70 genotypes	High 47.45	High 47.52	99.74 High	-	97.63 High	Sreelathakumary and Rajamony (2002)
	27 genotypes	Moderate 19.68	High 20.51	92.10 High	-	38.87 High	Kashinath (2003)
	48 genotypes	High 22.33	High 27.73	88.57 High	-	43.29 High	Khurana <i>et al.</i> (2003)
	97 genotypes	High	High	High	High	High	Prabhakaran <i>et al.</i> (2004)
	35 genotypes	High 38.50	High 38.56	99.68 High	-	79.19 High	Sreelathakumary and Rajamony (2004)
	12 genotypes	High 38.41	High 42.11	83.19 High	-	72.92 High	Verma <i>et al.</i> (2004)
	22 genotypes	High	High	-	-		Mishra <i>et al.</i> (2005)
	31 genotypes	High 34.35	High 35.21	95.00 High	-	30.85 High	Singh <i>et al.</i> (2005)
	27 genotypes	High	High	High	High		Bharadwaj <i>et al.</i> (2007)
	80 accessions	High 26.66	High 27.74	92.40 High	4.62 Low	52.80 High	Krishna <i>et al.</i> (2007a)
	70 genotypes and 3 varieties	High 21.28	High 23.88	79.50 High	2.79 Low	39.08 High	Shirshat <i>et al.</i> (2007)
	40 genotypes	High 224.58	High 29.45	69.70 High	3.75 Low	41.57 High	Smitha and Basvaraja (2007)

	80 accessions	Moderate	Moderate	High		High	Krishna <i>et al.</i> (2007a)
	45 genotypes	High 25.97	High 27.16	91.41 High	3.115 Low	51.156 High	Farhad <i>et al.</i> (2008)
	11 genotypes	Low 9.81	Moderate 14.19	47.80 Moderate	-	13.96 Moderate	Tembhurne <i>et al.</i> (2008)
	37 genotypes	Moderate 18.19	Moderate 18.67	94.92 High	3.38 Low	36.46 High	Sandeep <i>et al.</i> (2008)
	40 genotypes	High 21.81	High 22.83	91.29 High	-	42.94 High	Gupta <i>et al.</i> (2009)
	49 genotypes	High 28.50	High 28.75	94.90 High	3.54 Low	56.19 High	Sarkar <i>et al.</i> (2009)
	30 genotypes	High	High	High	-	High	Singh <i>et al.</i> (2009)
	94 paprika accessions	High 22.69	High 24.37	86.88 High	3.74 Low	43.50 High	Kumari <i>et al.</i> (2010)
	50 genotypes	High	High	High	-	High	Padhar and Zaveri (2010)
	23 bell pepper genotypes	Low 7.88	Low 9.31	71.70 High	1.31 Low	11.85 Moderate	Sharma <i>et al.</i> (2010)
	34 genotypes	High 38.75	High 38.85	99.50 High	-	6.05 Low	Arup <i>et al.</i> (2011)
	20 capsicum genotypes	Moderate 19.69	High 21.61	83.05 High	3.52 Low	36.94 High	Berhanu <i>et al.</i> (2011a)
	10 genotypes	High 22.29	High 24.57	82.27 High	3.42 Low	41.66 High	Jyothi <i>et al.</i> (2011)
	20 genotypes	High 29.21	High 29.90	95.40 High	4.68 Low	58.79 High	Kumar <i>et al.</i> (2012)
	7 varieties	High 38.50	High 38.56	93.69 High	1.77 Low	27.7 High	Lakshmi and Padma (2012)
	50 accessions	High 35.14	High 36.80	91.22 High	Low 4.26	10.79 Moderate	Mahantesh <i>et al.</i> (2013a)
	30 paprika lines	Moderate	Moderate	-	-		Shiva <i>et al.</i> (2014)
	23 genotypes	High	High	99.86	6.30	72.12	Amit <i>et al.</i> (2014)

		35.04	35.06	High	Low	High	
	24 genotypes	Moderate		Low		Low	Dipak <i>et al.</i> (2014)
	22 genotypes	High 31.06	High 32.25	92.80 High	5.14 Low	61.91 High	Sharma <i>et al.</i> (2014)
	24 genotypes	High 19.62	High 21.73	81.49 High	-	36.48 High	Vijaya <i>et al.</i> (2014)
	51 genotypes	High 23.94	High 22.13	85.4 High	2.68 Low	43.1 High	Pandit and Adhikary (2014)
	76 genotypes	High 32.21	High 32.76	96.68 High	-	65.19 High	Ajith and Manju (2015)
	40 genotypes	High 28.69	High 29.99	91.50 High	-	56.60 High	Patel <i>et al.</i> (2015)
	63 genotypes	Moderate 19.64	High 20.42	92.48 High	3.37 Low	38.92 High	Janaki <i>et al.</i> (2015a)
	30 genotypes	High 20.16	High 21.06	91.64 High	-	39.75 High	Ashish <i>et al.</i> (2015)
	24 genotypes	Moderate 15.47	Moderate 16.69	85.90 High	2.06 Low	29.56 High	Rana <i>et al.</i> (2015)
	20 germplasm lines	Moderate 12.89	High 24.13	68.20 High	1.11 Low	16.64 Moderate	Meena <i>et al.</i> (2016)
	16 genotypes	Moderate 16.26	Moderate 16.29	99.50 High	2.93 Low	33.42 High	Priyanka and Madhvi (2016)
	25 genotypes	Moderate 18.48	Moderate 19.13	93.30 High	-	36.78 High	Satish <i>et al.</i> (2016)
	80 genotypes	Low 9.53	Moderate 15.40	38.00 Moderate	52.06 Moderate	55.70 High	Kannan <i>et al.</i> (2016)
	16 genotypes	High 53.94	High 54.04	99.63 High	8.61 Low	110.96 High	Rosmaina <i>et al.</i> (2016)
	25 accessions	Low 0.23	Low 0.23	99.39 High	4.014 Low	48.084 High	Razzaq <i>et al.</i> (2016)
	49 accessions	Moderate	Moderate	74	6.08	6	Shimeles <i>et al.</i> (2016)

		12	17	High	Low	Low	
	43 genotypes	Low 8.86	Moderate 11.27	62 High	1.34 Low	14.34 Moderate	Kranthi <i>et al.</i> (2016)
8. Fruit diameter (cm)	52 genotypes	High 28.68	High 32.96	75.69 High	-	51.39 High	Gogoi and Gautam (2002)
	46 genotypes	Moderate 15.65	Moderate 16.84	86.33 High	-	30.00 High	Begum (2002)
	70 genotypes	High 49.12	High 49.21	99.65 High	-	161.02 High	Sreelathakumary and Rajamony (2002)
	27 genotypes	Moderate 19.14	High 23.09	68.17 High	-	33.18 High	Kashinath (2003)
	48 genotypes	High 33.13	High 38.83	72.81 High	-	58.24 High	Khurana <i>et al.</i> (2003)
	36 genotypes	High 49.57	High 49.50	86.20 High	-	87.70 High	Prabhudeva (2003)
	97 genotypes	High	High	High	High	High	Prabhakaran <i>et al.</i> (2004)
	12 genotypes	High 31.76	High 33.81	88.00 High	-	8.86 Low	Verma <i>et al.</i> (2004)
	31 genotypes	High 20.41	High 21.43	90.00 High	-	40.17 High	Singh <i>et al.</i> (2005)
	40 genotypes	High 30.33	High 36.43	49.30 Moderate	0.57 Low	51.81 High	Smitha and Basvaraja (2007)
	11 genotypes	Moderate 15.08	Moderate 17.64	73.10 High	-	26.55 High	Tembhurne <i>et al.</i> (2008)
	37 genotypes	High 26.17	High 28.31	85.50 High	0.68 Low	49.64 High	Sandeep <i>et al.</i> (2008)
	40 genotypes	Moderate 14.43	Moderate 18.06	63.88 High	-	23.76 High	Gupta <i>et al.</i> (2009)
	49 genotypes	High 20.21	High 25.32	63.70 High	0.39 Low	33.62 High	Sarkar <i>et al.</i> (2009)

	30 genotypes	High	High	High	-	High	Singh <i>et al.</i> (2009)
	30 genotypes	Low	Low	High	Low	Moderate	Munshi <i>et al.</i> (2010)
	23 bell pepper genotypes	Low 9.14	Low 9.95	84.29 High	0.94 Low	9.86 Low	Sharma <i>et al.</i> (2010)
	20 capsicum genotypes	High 37.94	High 39.46	92.43 High	0.82 Low	75.23 High	Berhanu <i>et al.</i> (2011a)
	20 genotypes	18.81 Moderate	19.39 Moderate	94.10 High	3.45 Low	37.59 High	Kumar <i>et al.</i> (2012)
	50 accessions	High 55.39	High 56.47	96.22 High	1.61 Low	111.80 High	Mahantesh <i>et al.</i> (2013a)
	23 genotypes	High 30.09	High 30.54	97.04 High	1.06 Low	61.06 High	Amit <i>et al.</i> (2014)
	24 genotypes	Moderate	-	-	High	High	Dipak <i>et al.</i> (2014)
	22 genotypes	Moderate 17.82	Moderate 19.35	84.90 High	0.32 Low	34.42 High	Sharma <i>et al.</i> (2014)
	51 genotypes	27.23 High	Moderate 19.31	50.3 High	0.29 Low	26.5 High	Pandit and Adhikary (2014)
	24 genotypes	Moderate 19.76	High 21.89	81.46 High	-	36.74 High	Vijaya <i>et al.</i> (2014)
	63 genotypes	High 27.44	High 27.52	99.50 High	0.76 Low	56.39 High	Janaki <i>et al.</i> (2015a)
	40 genotypes	High 22.09	High 23.39	89.21 High	-	42.93 High	Patel <i>et al.</i> (2015)
	30 genotypes	High 13.75	High 14.83	85.88 High	-	26.24 High	Ashish <i>et al.</i> (2015)
	76 genotypes	High 24.30	High 25.04	94.21 High	-	48.38 High	Ajith and Manju (2015)
	20 germplasm lines	High 121.66	High 181.57	72.50 High	0.39 Low	38.23 Moderate	Meena <i>et al.</i> (2016)
	80 genotypes	Low 7.65	Moderate 12.22	39.00 Moderate	64.00 High	52.64 High	Kannan <i>et al.</i> (2016)

	25 accessions	Low 0.35	Low 0.35	99.85 High	8.608 Low	72.100 High	Razzaq <i>et al.</i> (2016)
	16 genotypes	High 20.37	High 21.08	93.33 High	0.33 Low	44.00 High	Rosmaina <i>et al.</i> (2016)
	16 genotypes	Moderate 20.80	Moderate 21.12	96.77 High	0.60 Low	42.21 High	Priyanka and Madhvi (2016)
	49 accessions	Low 10	High 21	61 High	2.38 Low	14 Moderate	Shimeles <i>et al.</i> (2016)
	25 genotypes	High 20.15	High 21.0	92.02 High	-	39.82 High	Satish <i>et al.</i> (2016)
	43 genotypes	Low 8.72	Moderate 14.15	38 Moderate	0.11 Low	11.08 Moderate	Kranthi <i>et al.</i> (2016)
9. Fruit pedicel length (cm)	32 accessions	Moderate 20.07	Moderate 20.37	97.04 High	-	40.72 High	Manju and Sreelathakumary (2002)
	49 genotypes	Moderate 12.44	Moderate 13.67	82.90 High	0.71 Low	23.27 High	Sarkar <i>et al.</i> (2009)
	37 genotypes	Moderate 13.69	Moderate 14.76	86.10 High	0.71 Low	26.30 High	Sandeep <i>et al.</i> (2008)
	45 genotypes	Low 9.66	Moderate 11.88	66.19 High	0.508 Low	16.199 Moderate	Farhad <i>et al.</i> (2008)
	23 bell pepper genotypes	Moderate 11.24	Moderate 12.62	79.39 High	0.89 Low	20.50 High	Sharma <i>et al.</i> (2010)
	41 genotypes	Moderate 17.99	Moderate 13.99	59.7 High	0.69 Low	21.6 High	Pandit and Adhikary (2014)
	16 genotypes	Moderate 16.39	Moderate 16.72	95.38 High	1.59 High	33.10 High	Priyanka and Madhvi (2016)
	20 germplasm lines	High 43.10	High 105.81	73.60 High	0.70 Low	27.28 High	Meena <i>et al.</i> (2016)
10. Number of seeds per	52 genotypes	High	High	74.70	-	49.67	Gogoi and Gautam (2002)

fruit		27.89	32.27	High		High	
	30 accessions	High 37.44	High 38.01	97.04 High	-	75.99 High	Manju and Sreelathakumary (2002)
	46 genotypes	High 25.10	High 34.77	52.13 Moderate	-	37.20 High	Begum (2002)
	27 genotypes	High 22.69	High 24.68	84.50 High	-	42.95 High	Kashinath (2003)
	48 genotypes	High 46.62	High 50.51	85.17 High	-	88.63 High	Khurana <i>et al.</i> (2003)
	22 genotypes	High	High	-	-	-	Mishra <i>et al.</i> (2005)
	13 genotypes	High 27.46	High 27.92	96.70 High	-	22.55 High	Rao (2005)
	31 genotypes	High 32.55	High 34.25	90.00 High	-	43.05 High	Singh <i>et al.</i> (2005)
	72 genotypes and 3 varieties	High 26.37	High 27.77	90.20 High	37.40 High	51.60 High	Shirshat <i>et al.</i> (2007)
	40 genotypes	Moderate 10.19	High 20.91	80.27 High	19.38 Moderate	26.10 High	Smitha and Basvaraja (2007)
	45 genotypes	High 24.41	High 26.84	82.70 High	30.17 High	45.723 High	Farhad <i>et al.</i> (2008)
	37 genotypes	High 26.04	High 30.20	74.40 High	44.84 High	45.69 High	Sandeep <i>et al.</i> (2008)
	49 genotypes	High 24.41	High 26.89	82.40 High	34.88 High	45.65 High	Sarkar <i>et al.</i> (2009)
	30 genotypes	Moderate	Moderate	-	-	-	Singh <i>et al.</i> (2009)
	94 paprika accessions	High 41.81	High 42.30	97.71 High	60.89 High	85.13 High	Kumari <i>et al.</i> (2010)
	34 genotypes	High 34.93	High 35.18	98.60 High	-	53.34 High	Arup <i>et al.</i> (2011)
	10 genotypes	High 23.15	High 26.13	78.46 High	22.13 High	42.23 High	Jyothi <i>et al.</i> (2011)

	50 accessions	High 46.38	High 47.67	94.67 High	88.38 High	92.98 High	Mahantesh <i>et al.</i> (2013a)
	30 paprika lines	High	High	-	-	-	Shiva <i>et al.</i> (2014)
	23 genotypes	High 34.19	High 35.96	90.40 High	-	51.23 High	Amit <i>et al.</i> (2014)
	24 genotypes	Moderate	-	High	-	High	Dipak <i>et al.</i> (2014)
	41 genotypes	High 27.00	High 23.82	77.8 High	31.62 High	43.2 High	Pandit and Adhikary (2014)
	24 genotypes	High 13.00	High 16.26	63.93 High	-	21.42 High	Vijaya <i>et al.</i> (2014)
	30 genotypes	High 20.59	High 22.02	87.40 High	-	39.65 High	Ashish <i>et al.</i> (2015)
	63 genotypes	High 25.76	High 29.61	75.68 High	28.33 High	46.17 High	Janaki <i>et al.</i> (2015a)
	72 genotypes	High 26.30	High 27.79	96.40 High	-	72.43 High	Ajith and Manju (2015)
	24 genotypes	Moderate 15.16	Moderate 17.67	73.05 High	63.01 High	High 26.76	Rana <i>et al.</i> (2015)
	25 accessions	Low 0.218	Low 0.219	99.58 High	34.455 High	44.825 High	Razzaq <i>et al.</i> (2016)
	25 genotypes	Moderate 14.52	Moderate 15.36	89.26 High	-	28.26 High	Satish <i>et al.</i> (2016)
	43 genotypes	Moderate 18.50	High 21.28	76 High	17.55 Moderate	33.12 High	Kranthi <i>et al.</i> (2016)
11.Weight of seeds per fruit (g)	72 genotypes	High 26.00	High 27.46	89.70 High	0.22 Low	50.00 High	Shirshat <i>et al.</i> (2007)
	55 accessions	High	High	High	-	High	Vani <i>et al.</i> (2007a)
	30 genotypes	-	-	High	-	High	Singh <i>et al.</i> (2009)
	30 genotypes	High	High	89.93	-	41.85	Ashish <i>et al.</i> (2015)

		21.42	22.59	High		High	
12.1000 seed weight (g)	22 genotypes	Moderate 14.36	Moderate 14.38	99.64 High	-	29.53 High	Mishra <i>et al.</i> (2001)
	52 genotypes	Moderate 20.50	Moderate 15.26	85.18 High	-	98.84 High	Gogoi and Gautam (2002)
		Low 5.69	Low 5.55	94.91 High	-	11.14 Moderate	Rathod <i>et al.</i> (2002)
	32 accessions	Moderate 14.23	Moderate 14.74	93.16 High	-	28.29 High	Manju and Sreelathakumary (2002)
		Low 3.26	Low 3.21	97.10 High	-	6.25 Low	Acharya and Rajput (2003)
		High	High	High	-	High	Mini and Khader (2004)
		Moderate 16.53	Low 9.69	34.40 Moderate	-	Moderate 11.71	Wasule <i>et al.</i> (2004)
	97 genotypes	Moderate 17.67(M)	Moderate 12.05	46.54 High	-	16.94 Moderate	Prabhakaran <i>et al.</i> (2004)
	22 genotypes	High 26.37	High 24.53	86.55 High	-	47.01 High	Mishra <i>et al.</i> (2005)
		Low 12.25	Low 11.51	88.30 High	-	8.39 Low	Rao (2005)
	40 genotypes	High 28.89	High 27.47	88.91 High	-	53.63 High	Smitha and Basavaraja (2006a)
	60 genotypes	Moderate 16.36	Moderate 15.35	88.10 High	-	29.69 High	Chatterjee <i>et al.</i> (2006)
	49 genotypes	Moderate 15.05	Moderate 16.30	85.30 High	1.45 Low	28.65 High	Sarkar <i>et al.</i> (2009)
	23 genotypes	High 27.71	High 27.97	98.14 High	2.25 Low	56.55 Moderate	Amit <i>et al.</i> (2014)
	51 genotypes	Moderate 16.07	Moderate 17.18	87.5 High	1.55 Low	31.0 High	Pandit and Adhikary (2014)

	72 genotypes	High 28.30	High 28.82	96.08 High	-	55.23 High	Ajith and Manju (2015)
	43 genotypes	Low 9.48	Moderate 12.45	58 High	1.10 Low	14.88 Moderate	Kranthi <i>et al.</i> (2016)
13.Dry fruit yield per plant (g)	30 genotypes	High 53.80	High 55.67	93.4 High	98.10 High	107.7 High	Munshi and Behara (2000)
	17 genotypes	High 53.80	High 55.67	93.40 High	98.10 High	107.07 High	Ibrahim <i>et al.</i> (2001)
	52 genotypes	High 51.06	High 58.30	76.70 High	-	92.11 High	Gogoi and Gautam (2002)
	32 accessions	High 89.12	High 89.39	99.38 High	-	183.01 High	Manju and Sreelathakumary (2002)
	70 genotypes	High 40.03	High 40.29	98.72 High	-	81.93 High	Sreelathakumary and Rajamony (2002)
	97 genotypes	High	High	High	High	High	Prabhakaran <i>et al.</i> (2004)
	35 genotypes	High 38.99	High 39.21	94.45 High	-	79.87 High	Sreelathakumary and Rajamony (2004)
	22 genotypes	High	High	-		-	Mishra <i>et al.</i> (2005)
	31 genotypes	High 35.30	High 40.23	77.00 High		44.78 High	Singh <i>et al.</i> (2005)
	22 genotypes	High	High	High	High	High	Sood <i>et al.</i> (2006)
	27 genotypes	High	High	High	High	-	Bharadwaj <i>et al.</i> (2007)
	72 genotypes and 3 varieties	High 20.31	High 38.10	28.40 Low	10.92 Moderate	22.30 High	Shirshat <i>et al.</i> (2007)
	40 genotypes	High 30.40	High 35.37	73.90 High	160.3 High	52.73 High	Smitha and Basvaraja (2007)
	55 genotypes	High	High	High	High	High	Vani <i>et al.</i> (2007a)
	45 genotypes	High 40.66	High 42.27	92.77 High	4.694 Low	80.682 High	Farhad <i>et al.</i> (2008)
	11 genotypes	High	High	56.30	-	40.44	Tembhurne <i>et al.</i> (2008)

		26.17	34.88	Moderate		High	
	37 genotypes	High 26.56	High 26.85	97.80 High	45.14 Moderate	54.11 High	Sandeep <i>et al.</i> (2008)
	49 genotypes	High 48.92	High 50.22	94.90 High	116.95 High	98.16 High	Sarkar <i>et al.</i> (2009)
	40 genotypes	High 25.98	High 26.79	94.03 High	-	51.89 High	Gupta <i>et al.</i> (2009)
	30 genotypes	High	High	High	-	High	Singh <i>et al.</i> (2009)
		High	High	High	-	High	Wilson and Philip (2009)
	94 paprika accessions	High 30.62	High 30.96	97.82 High	100.0 High	62.39 High	Kumari <i>et al.</i> (2010)
	50 genotypes	High	High	High	-	High	Padhar and Zaveri (2010)
	23 genotypes	High 38.00	High 40.27	89.03 High	298.68 High	73.87 High	Sharma <i>et al.</i> (2010)
	53 genotypes	High 22.34	High 23.42	91.00 High	4.37 Low	56.59 High	Datta and Jana (2010)
	34 genotypes	High 50.60	High 50.87	99.00 High	-	24.59 High	Arup <i>et al.</i> (2011)
	20 capsicum genotypes	High 55.90	High 59.29	88.89 High	0.17 Low	106.25 High	Berhanu <i>et al.</i> (2011a)
	10 genotypes	High 41.17	High 42.16	93.99 High	38.47 High	82.21 High	Jyothi <i>et al.</i> (2011)
	20 genotypes	High 43.28	High 43.36	99.60 High	317.44 High	88.98 High	Kumar <i>et al.</i> (2012)
	50 accessions	High 37.05	High 38.76	93.71 High	180.42 High	72.96 High	Mahantesh <i>et al.</i> (2013a)
	23 genotypes	High 45.41	High 45.98	97.53 High	55.66 High	92.38 High	Amit <i>et al.</i> (2014)
	24 genotypes	Moderate	-	High	-	High	Dipak <i>et al.</i> (2014)
	22 genotypes	High 55.28	High 55.21	99.90 High	55.08 High	138.7 High	Sharma <i>et al.</i> (2014)

	30 genotypes	High 39.57	High 40.98	93.24 High	-	78.51 High	Ashish <i>et al.</i> (2015)
	51 genotypes	High	High	High		High	Pandit and Adhikary (2014)
	24 genotypes	High 37.17	High 33.97	83.52 High	-	63.96 High	Vijaya <i>et al.</i> (2014)
	63 genotypes	High 26.43	High 30.81	73.54 High	68.55 High	46.69 High	Janaki <i>et al.</i> (2015a)
	24 genotypes	High 40.09	High 41.93	91.40 High	720.04 High	High 78.95	Rana <i>et al.</i> (2015)
	23 germplasm lines	Low 4.07	Low 4.68	71.30 High	8.58 Low	23.15 High	Meena <i>et al.</i> (2016)
	16 genotypes	High 47.67	High 48.24	High 97.63	-	High 97.03	Priyanka and Madhvi (2016)
	63 genotypes	High	High	High	-	High	Razzaq <i>et al.</i> (2016)
	25 genotypes	High 29.61	High 30.34	95.24 High	-	39.52 High	Satish <i>et al.</i> (2016)
	49 accessions	Moderate 19	High 35	37 Moderate	4.3 Low	4 Low	Shimeles <i>et al.</i> (2016)
	43 genotypes	High 20.74	High 22.64	84 High	90.21 High	39.11 High	Kranthi <i>et al.</i> (2016)
14. Ascorbic acid (mg/100g)		High	High	High	-	High	Mallikarjun (2001)
	32 accessions	Moderate 17.04	Moderate 17.07	99.71 High	-	35.05 High	Manju and Sreelathakumary (2002)
	22 genotypes	High	High	High	-	High	Mishra <i>et al.</i> (2005)
	27 genotypes	Low	Low	High	Moderate	-	Bharadwaj <i>et al.</i> (2007)
	72 genotypes and 3 varieties	High 35.36	High 36.43	94.20 High	138.2 High	70.70 High	Shirshat <i>et al.</i> (2007)
	40 genotypes	High	High	High		High	Singh <i>et al.</i> (2007)
	40 genotypes	Moderate	Moderate	93.3	54.88	28.43	Smitha and Basvaraja

		14.31	14.84	High	High	High	(2007)
	45 genotypes	High 45.55	High 46.48	96.06 High	1.479 Low	91.983 High	Farhad <i>et al.</i> (2008)
	37 genotypes	Moderate 12.25	Moderate 15.99	55.87 High	19.98 Moderate	19.32 Moderate	Sandeep <i>et al.</i> (2008)
	30 genotypes	Moderate	Moderate	-	-	-	Singh <i>et al.</i> (2009)
	23 bell pepper genotypes	High 26.68	High 27.98	90.89 High	68.98 High	52.39 High	Sharma <i>et al.</i> (2010)
	43 genotypes	Low 6.32	Low 8.47	55.60 High	11.86 Moderate	12.44 Moderate	Datta and Jana (2010)
	34 genotypes	High 61.70	High 61.79	99.00 High	-	102.60 High	Arup <i>et al.</i> (2011)
	20 genotypes	Low 8.73	Low 8.91	96 High	25.93 High	17.61 Moderate	Kumar <i>et al.</i> (2012)
	50 accessions	High 50.43	High 50.86	98.30 High	88.60 High	103.01 High	Mahantesh <i>et al.</i> (2013a)
	40 genotypes	High 22.40	High 22.47	99.31 High	-	45.98 High	Patel <i>et al.</i> (2015)
	16 genotypes	High 22.24	High 22.26	99.78 High	74.37 High	45.76 High	Priyanka and Madhvi (2016)
15. Oleoresin content (%)	32 accessions	High 35.46	High 36.07	96.65 High	-	71.81 High	Manju and Sreelathakumary (2002)
	40 genotypes	Low	Low	High	-	Low	Singh <i>et al.</i> (2007)
	40 genotypes	Moderate 10.63	Moderate 11.14	91.12 High	-	20.90 High	Gupta <i>et al.</i> (2009)
	30 genotypes	High	High	High	-	High	Singh <i>et al.</i> (2009)
	94 paprika accessions	High 36.71	High 36.86	99.20 High	6.13 Low	75.32 High	Kumari <i>et al.</i> (2010)
	34 genotypes	High 40.29	High 40.57	98.60 High	-	17.55 Moderate	Arup <i>et al.</i> (2011)

	24 genotypes	High 27.88	High 28.01	99.08 High	-	57.16 High	Vijaya <i>et al.</i> (2014)
	76 genotypes	Moderate 13.31	Moderate 13.63	95.26 High		26.75 High	Ajith and Manju (2015)
16. Capsaicin content (SHU)	32 accessions	High 27.52	High 27.57	99.62 High	-	56.58 High	Manju and Sreelathakumary (2002)
	48 genotypes	Moderate 18.59	Moderate 19.13	94.46 High	-	37.23 High	Khurana <i>et al.</i> (2003)
	97 genotypes	High	High	High	High	High	Prabhakaran <i>et al.</i> (2004)
	40 genotypes	High	High	High	-	High	Dutonde <i>et al.</i> (2006)
	27 genotypes	High	High	High	-	High	Bharadwaj <i>et al.</i> (2007)
	40 genotypes	Low	Low	High	-	Low	Singh <i>et al.</i> (2007)
		Low	Low	Low	-	Low	Kumar <i>et al.</i> (2008)
	40 genotypes	High 21.23	High 22.41	89.68 High	-	High 41.41	Gupta <i>et al.</i> (2009)
	30 genotypes	High	High	High	-	High	Singh <i>et al.</i> (2009)
	22 genotypes	High	High	High	-	High	Sood <i>et al.</i> (2009)
	65 genotypes	High 45.17	High 45.29	99.48 High	0.64 Low	95.52 High	Datta and Jana (2010)
	94 paprika accessions	High 39.83	High 40.31	97.62 High	0.15 Low	81.05 High	Kumari <i>et al.</i> (2010)
	30 genotypes	Moderate	Moderate	Low	-	Moderate	Munshi <i>et al.</i> (2010)
	34 genotypes	High 45.97	High 46.32	98.50 High	-	0.15 Low	Arup <i>et al.</i> (2011)
	20 genotypes	High 41.60	High 41.79	99.10 High	0.30 Low	85.32 High	Kumar <i>et al.</i> (2012)
	53 genotypes	High 45.17	High 45.29	99.48 High	0.64 Low	95.52 High	Datta and Das (2013)
	30 paprika lines	High	High	-	-	-	Shiva <i>et al.</i> (2013)
	24 genotypes	High	High	98.38	-	62.26	Vijaya <i>et al.</i> (2014)

		30.47	30.72	High		High	
	40 genotypes	High 21.56	High 21.96	96.45 High	-	43.68 High	Patel <i>et al.</i> (2015)
	76 genotypes	High 31.88	High 32.47	96.39 High		64.48 High	Ajith and Manju (2015)
17.Total extractable colour (ASTA units)	48 genotypes	High 21.34	High 21.40	99.44 High	-	43.83 High	Khurana <i>et al.</i> (2003)
	40 genotypes	High	High	High	-	High	Singh <i>et al.</i> (2007)
		Low	Low	Low	-	Low	Kumar <i>et al.</i> (2008)
	40 genotypes	Moderate 18.65	Moderate 18.82	High 98.27	-	High 38.09	Gupta <i>et al.</i> (2009)
	30 genotypes	Moderate	Moderate	High	-	High	Singh <i>et al.</i> (2009)
	94 paprika accessions	High 58.61	High 58.89	99.10 High	-	120.20 High	Kumari <i>et al.</i> (2010)
	65 genotypes	High	High'	High	-	High	Datta and Jana (2010)
	103 genotypes	High 58.47	High 58.50	99.90 High	20 High	121 High	Naresh <i>et al.</i> (2013)
	30 paprika lines	Low	Low	-	-	-	Shiva <i>et al.</i> (2013)
	50 accessions	High 40.84	High 41.28	97.87 High	Low 0.10	81.53 High	Mahantesh <i>et al.</i> (2013a)
	40 genotypes	High 35.43	High 35.87	98.67 High	-	72.89 High	Patel <i>et al.</i> (2015)
18. Red carotenoids (%)	103 genotypes	High 70.82	High 70.90	99.80 High	13 Moderate	139 High	Naresh <i>et al.</i> (2013)
19. Yellow carotenoids (%)	103 genotypes	High 60.31	High 60.90	99.00 High	9 Low	122 High	Naresh <i>et al.</i> (2013)

Table 2.2: Review of literature on character association for quantitative and qualitative characters in *Capsicum annuum* L.

Character	Association	S/NS	Correlated character	References
1. Plant height (cm)	Negative	-	Fruit weight, fruit length and fruit diameter	Chaim and Paran (2000)
	Negative	NS	Number of primary branches per plant	Begum (2002)
	Positive	S	Fruit length, fruit diameter, days to 50 % flowering, number of seeds per fruit and yield per plant	
	Positive	NS	Oleoresin	Manju and Sreelathakumary (2002)
	Positive	S	Ascorbic acid	
	Negative	NS	Capsaicin	
	Positive	S	Number of primary branches per plant, days to 50 % flowering, fruit length and fruit diameter	Acharya and Rajput (2003)
	Negative	NS	Number of fruits per plant	
	Positive	NS	Number of seeds per fruit and per plant	
	Positive	S	Number of fruits per plant, fruit length, number of seeds per fruit, capsaicin and coloring matter	Khurana <i>et al.</i> (2003)
	Negative		Yield per plant	Nehru <i>et al.</i> (2003)
	Negative	NS	Number of fruits per plant and days to 50 % flowering	Choudhary and Samadia (2004)
	Positive	NS	Number of seeds per fruit	

	Positive	-	Yield per plant, number of fruits per plant and fruit diameter	Singh and Singh (2004)
	Positive	S	Yield per plant, number of fruits per plant, fruit length and fruit diameter	Ajjappalavara <i>et al.</i> (2005)
	Negative	NS	Number of primary branches per plant	
	Negative	S	Days to 50 % flowering	
	Positive	NS	Number of primary branches per plant, number of fruits per plant, and number of seeds per fruit, fruit length and fruit diameter.	Rao (2005)
	Positive	S	Yield per plant	
	Negative	S	Days to 50 % flowering	
	Positive	NS	Yield per plant	Ajit and Manju (2006)
	Negative	NS	Yield per plant	Ahmed <i>et al.</i> (2006)
	Positive	S	Number of fruits per plant and number of primary branches per plant	Khader and Mini (2006)
	Positive	S	Yield per plant	Jayashree <i>et al.</i> (2007)
	Positive	NS	Fruit length and number of fruits per plant	Krishna <i>et al.</i> (2007b)
	Negative	NS	Per cent fruit set	
	Positive	-	Yield per plant	Smitha and Basvaraja (2007)
	Positive	NS	Days to 50% flowering, fruit length, fruit weight, number of seeds per fruit and yield per plant.	Farhad <i>et al.</i> (2008)
	Negative	NS	Number of primary branches per plant, number of fruits per plant and ascorbic acid	

	Positive	NS	Yield per plant	Hosamani and Shivkumar (2008)
	Positive	S	Yield per plant, number of primary and secondary branches per plant and number of fruits per plant	Reddy <i>et al.</i> (2008)
	Positive	NS	Fruit length and number of seeds per fruit	
	Negative	NS	Days to 50 % flowering and average fruit weight	
	Positive	NS	Number of primary and secondary branches per plant	Tembhurne <i>et al.</i> (2008)
	Positive	S	Days to 50% flowering and fruit length	
	Negative	S	Fruit diameter	
	Negative	NS	Fruit weight, number of fruits per plant and yield per plant	
	Negative	S	Number of fruits per plant, yield per plant and coloring matter.	Gupta <i>et al.</i> (2009)
	Negative	NS	Fruit length, capsaicin and oleoresin	
	Positive	S	Yield per plant, number of fruits per plant and number of branches per plant	Jabeen <i>et al.</i> (2009)
	Positive	NS	Fruit length,	
	Negative	NS	Average fruit weight	

	Negative	NS	Number of fruits per plant, fruit length and number of seeds per fruit	Kaur and Singh (2009)
	Positive	S	Fruit yield per plant	Kannan <i>et al.</i> (2009)
	Positive	NS	Days to 50% flowering, fruit length and number of fruits per plant	Sharma <i>et al.</i> (2010)
	Negative	S	Average fruit weight, fruit diameter and ascorbic acid	
	Negative	NS	Yield per plant	
	Positive	S	Dry fruit yield per plant and fruit length	Ashok Kumar <i>et al.</i> (2010)
	Positive	NS	Days to 50% flowering and number of seeds per fruit	Hasanuzzaman and Faruq (2011)
	Negative	NS	Fruit length, number of fruits per plant and yield per plant	
	Positive	S	Number of primary and secondary branches per plant and fruit length	Singh and Singh (2011)
	Positive	NS	Fruit length	Berhanu <i>et al.</i> (2011b)
	Negative	NS	Number of fruits per plant, average fruit weight, fruit diameter and yield per plant.	
	Negative	NS	Number of fruits per plant, average fruit weight, ascorbic acid , capsaicin, fruit length and yield per plant.	Kumar <i>et al.</i> (2012)
	Positive	NS	Fruit diameter	
	Positive	S	Dry fruit yield per plant	Srividhya and Ponnuswamy (2012)
	Positive	S	Yield per plant	Mahantesh <i>et al.</i> (2013b)

	Positive	S	Dry pod yield per plant	Rohini and Lakshmanan (2015)
	Positive	S	Yield per plant	Rinchan <i>et al.</i> (2015)
	Positive	S	Fruit width	Satish <i>et al.</i> (2015)
	Negative	S	Days to first picking	
	Negative	S	Dry yield per plant	Hasan <i>et al.</i> (2016)
	Positive	S	Fruit length and inter nodal length	Razzaq <i>et al.</i> (2016)
2. Plant spread (cm)	Negative	S	Days to maturity	Mallikarjun <i>et al.</i> (2003b)
	Positive	S	Number of fruits per plant, Capsanthin (EOA values)	
	Negative	NS	Fruit length (cm) , Fruit girth (cm), Number of seeds per fruit	
	Positive	NS	Oleoresins (%),	
	Negative	NS	Days to maturity	Gogoi and Gautam (2003)
	Positive	NS	Number of fruits per plant, Fruit length (cm)	
	Positive	S	Fruit girth (cm), 1000-seed weight (g), Number of seeds per fruit	
	Positive	S	Number of fruits per plant	Nehru <i>et al.</i> (2003)
	Negative	NS	Fruit length (cm)	

	Positive	NS	Number of fruits per plant	Patil <i>et al.</i> (2004)
	Negative	NS	Fruit length (cm), Fruit girth (cm), Number of seeds per fruit	
	Negative	S	Days to maturity	Hari <i>et al.</i> (2005)
	Positive	NS	Number of fruits per plant, fruit length (cm), Number of seeds per fruit, Oleoresins (%)	
	Negative	NS	Fruit girth (cm)	
	Positive	S	1000-seed weight (g),	
	Positive	S	Number of fruits per plant, Fruit length (cm), Number of seeds per fruit, Oleoresins (%), Capsanthin (EOA values)	Rao <i>et al.</i> (2006)
	Positive	NS	1000-seed weight (g),	
	Negative	NS	Number of fruits per plant, Fruit length (cm), Fruit girth (cm)	Smitha and Basavaraja (2006a)
	Positive	NS	Number of seeds per fruit	
	Negative	NS	Days to maturity	Chatterjee <i>et al.</i> .(2007)
	Negative	S	Number of fruits per plant, Fruit girth (cm), 100-pod weight (g), 1000-seed weight (g), Number of seeds per fruit, Oleoresins (%)	
	Positive	NS	Fruit length (cm)	
	Positive	S	Capsanthin (EOA values)	

	Positive	S	100-pod weight (g) and fruit girth (cm)	Rao <i>et al.</i> (2006)
	Positive	S	Yield per plant	Mahantesh <i>et al.</i> (2013b)
3. Number of primary branches per plant	Positive	S	Number of fruits per plant	Begum (2002)
	Negative	NS	Fruit length, plant height and number of seeds per fruit	
	Positive	NS	Yield per plant	
	Positive	S	Capsaicin	Manju and Sreelathakumary (2002)
	Positive	NS	Oleoresin	
	Negative	NS	Ascorbic acid	
	Negative	NS	Number of fruits per plant	Acharya and Rajput (2003)
	Positive	S	Fruit length, plant height and days to 50 % flowering	
	Negative	S	Fruit diameter	
	Positive	NS	Number of seeds per fruit and yield per plant	
	Positive	S	Yield per plant	Kumar <i>et al.</i> (2003)
	Positive	S	Secondary branches per plant	Ajjappalavara <i>et al.</i> (2005)
	Negative	NS	Number of fruits per plant, plant height and fruit length	
	Positive	NS	Fruit diameter and days to 50 % flowering	
	Negative	S	Yield per plant	

	Positive	S	Number of fruits per plant, days to 50 % flowering and yield per plant	Rao (2005)
	Negative	NS	Fruit length	
	Negative	S	Fruit diameter	
	Positive	NS	Number of seeds per fruit and plant height	
	Positive	NS	Yield per plant	Ahmed <i>et al.</i> (2006)
	Positive	S	Number of fruits per plant	Khader and Mini (2006)
	Positive	-	Yield per plant	Smitha and Basvaraja (2007)
	Positive	S	Secondary branches per plant, number of fruits per plant and number of seeds per fruit	Farhad <i>et al.</i> (2008)
	Positive	NS	Fruit length and yield per plant	
	Negative	NS	Days to 50 % flowering, plant height, fruit weight and ascorbic acid	
	Positive	S	Plant height, number of fruits per plant and yield per plant	Reddy <i>et al.</i> (2008)
	Positive	NS	Average fruit weight and number of seeds per fruit	
	Negative	S	Days to 50 % flowering	
	Negative	NS	Fruit length	
	Positive	NS	Secondary branches per plant	Tembhurne <i>et al.</i> (2008)
	Positive	S	Days to 50% flowering, fruit diameter, number of	

	Negative	NS	fruits per plant and yield per plant	
	Negative	S	Fruit length	
	Positive	S	Fruit weight	
	Positive	S	Secondary branches per plant, number of fruits per plant and yield per plant	Patel <i>et al.</i> (2009)
	Positive	S	Dry fruit yield per plant	Srividhya and Ponnuswamy (2012)
	Positive	S	Yield per plant, plant height and fruit length	Singh and Singh (2011)
	Positive	NS	Number of fruits per plant	
	Positive	S	Dry fruit yield per plant	Vijaya <i>et al.</i> (2014)
	Positive	S	Plant height	Rohini and Lakshmanan (2015)
	Positive	S	Yield per plant	Rinchan <i>et al.</i> (2015)
	Positive	S	Fruit yield per plot, number of seeds per fruits, dry fruit yield per plant	Satish <i>et al.</i> (2015)
	Negative	S	Fruit length, days to 50% flowering	
	Positive	S	Yield per plant	Hasan <i>et al.</i> (2016)
	Negative	S	Inter nodal length	Razzaq <i>et al.</i> (2016)
4. Days to 50% flowering	Positive	S	Plant height, fruit length, fruit diameter and number of seeds per fruit	Begum (2002)
	Negative	S	Yield per plant	
	Positive	S	Plant height and number of primary branches per plant	Acharya and Rajput (2003)

	Positive	NS	Fruit length and number of seeds per fruit	
	Negative	NS	Fruit diameter and yield per plant	
	Negative	S	Yield per plant	Khurana <i>et al.</i> (2003)
	Negative	NS	Plant height , fruit length, yield per plant and number of seeds per fruit	Choudhary and Samadia (2004)
	Negative	S	Plant height and yield per plant	Ajjappalavara <i>et al.</i> (2005)
	Positive	NS	Number of primary branches per plant	
	Negative	NS	Fruit diameter	
	Negative	NS	Yield per plant	Ahmed <i>et al.</i> (2006)
	Negative	S	Yield per plant	Jayashree <i>et al.</i> (2007)
	Positive	S	Yield per plant	Hosamani and Shivkumar (2008)
	Positive	S	Plant height, number of primary branches, yield per plant and number of fruits per plant	Tembhurne <i>et al.</i> (2008)
	Positive	NS	Fruit weight and Fruit length	
	Negative	NS	Fruit diameter	
	Positive	NS	Plant height and ascorbic acid	Farhad <i>et al.</i> (2008)
	Negative	NS	Number of primary branches, fruit weight, number of fruits per plant, number of seeds per fruit and yield per plant	
	Negative	S	Fruit length	
	Negative	S	Number of primary branches per plant	Reddy <i>et al.</i> (2008)

	Negative	NS	Plant height, number of fruits per plant, fruit length, average fruit weight, number of seeds per fruit and yield per plant	
	Positive	NS	Fruit length and average fruit weight	Cankaya <i>et al.</i> (2010)
	Negative	NS	Plant height and fruit width	
	Negative	S	Number of fruits per plant	
	Positive	S	Fruit diameter	Sharma <i>et al.</i> (2010)
	Positive	NS	Plant height and ascorbic acid	
	Negative	S	Fruit length	
	Negative	NS	Number of fruits per plant, average fruit weight and yield per plant	
	Positive	S	Yield per plant	Arup <i>et al.</i> (2011)
	Positive	NS	Plant height, number of fruits per plant, number of seeds per fruit and fruit width	Kumar <i>et al.</i> (2012)
	Negative	NS	Fruit length, fruit weight and yield per plant	
	Negative	S	Dry yield per plant	Mahantesh <i>et al.</i> (2013b)
	Positive	S	Days to maturity	Kumar <i>et al.</i> (2014)
	Positive	S	Days to maturity	Vikram <i>et al.</i> (2014)
	Negative	S	Number of fruits per plant	
	Positive	S	Days to first flowering	Rohini and Lakshmnanan (2015)
	Negative	S	Yield per plant	Rinchan <i>et al.</i> (2015)

	Positive	S	Days to first picking, fruit length	Satish <i>et al.</i> (2015)
	Negative	S	Number of seed per fruit, dry fruit weight, fruit width, seed yield per plant	
	Negative	S	Dry fruit yield per plant	Hasan <i>et al.</i> (2016)
	Negative	S	Dry fruit yield per plant	Priyanka and Mishra (2016)
5. Days to maturity	Negative	S	Number of fruits per Plant	Munshi <i>et al.</i> (2000)
	Positive	NS	Fruit length (cm), Fruit girth (cm)	
	Negative	S	Fruit length (cm)	Chaim and Paran (2000)
	Positive	S	Fruit girth (cm)	
	Negative	NS	Number of fruits per Plant, Number of seeds per fruit, Capsanthin (EOA values)	Mallikarjun <i>et al.</i> (2003b)
	Positive	NS	Fruit length (cm), Fruit girth (cm), Oleoresins (%)	
	Negative	NS	Number of fruits per Plant, Fruit length (cm), Number of seeds per fruit	Acharya and Rajput (2003)
	Positive	NS	Fruit girth (cm) and 1000-seed weight (g)	
	Negative	NS	Number of fruits per Plant, 1000-seed weight (g), Number of seeds per fruit	Gogoi and Gautam (2003)
	Negative	S	Fruit length (cm)	
	Positive	NS	Fruit girth(cm)	
	Negative	S	Green fruit yield per plant	Kumar <i>et al.</i> (2003).

	Positive	NS	Number of fruits per Plant	Choudhary and Samadia (2004)
	Negative	NS	Fruit length (cm), Fruit girth (cm), Number of seeds per fruit	
	Positive	NS	Number of fruits per Plant, Fruit length (cm), Fruit girth (cm), Oleoresins (%)	Hari <i>et al.</i> (2005)
	Negative	NS	1000-seed weight (g), Number of seeds per fruit	
	Positive	NS	Number of fruits per Plant, Fruit length (cm), 1000-seed weight (g), Capsaicin (%)	Chatterjee <i>et al.</i> (2007)
	Negative	NS	Fruit girth (cm), Oleoresins (%)	
	Positive	S	100-pod weight (g), Number of seeds per fruit, Capsanthin (EOA values)	
	Positive	S	Days to 50% flowering	Berhamu <i>et al.</i> (2011b)
	Positive	S	Dry yield fruit per plant	Hasanuzzaman and Faruq (2011)
	Negative	S	Green fruit yield per plant, fruit length, green fruit yield per plant	Vikram <i>et al.</i> (2014)
	Positive	S	Plant weight,	
	Positive	S	Fruit length	Satish <i>et al.</i> (2015)
	Negative	S	Fruit yield per plot, number of seeds per fruits, fruit width	
	Negative	S	Dry fruit yield per plant	Hasan <i>et al.</i> (2016)

5. Number of fruits per plant	Positive	S	Yield per plant	Munshi <i>et al.</i> (2000)
	Negative	S	Fruit weight	
	Positive	-	Number of branches per plant and plant height Fruit length	Ibrahim <i>et al.</i> (2001)
	Positive	S	Fruit length, number of primary branches per plant and yield per plant	Begum (2002)
	Positive	-	Oleoresins	Mini and Vahab (2002)
	Positive	NS	Yield per plant	Acharya and Rajput (2003)
	Negative	NS	Plant height and number of primary branches per plant	
	Positive	S	Number of seeds per fruit, plant height and coloring matter	Khurana <i>et al.</i> (2003)
	Negative	NS	Fruit length and capsaicin	
	Positive		Yield per plant	Nandadevi and Hosamani (2003)
	Positive	S	Fruit length	Choudhary and Samadia (2004)
	Positive	NS	Yield per plant	
	Negative	NS	Plant height	
	Positive	-	Yield per plant	Singh and Singh (2004)
	Positive	S	Fruit length, plant height and yield per plant	Ajjappalavara <i>et al.</i> (2005)
	Negative	NS	Number of primary branches per plant	
	Positive	S	Yield per plant and number of primary branches per plant	Rao <i>et al.</i> (2005)

	Positive	NS	Plant height	
	Negative	NS	Yield per plant	Ahmed <i>et al.</i> (2006)
	Positive	S	Plant height and number of primary branches	Khader and Mini (2006)
	Negative	-	Fruit length	
	Positive	S	Yield per plant and number of branches per plant	Bharadwaj <i>et al.</i> (2007)
	Positive	S	Yield per plant and number of branches per plant	Jayashree <i>et al.</i> (2007)
	Positive	S	Yield per plant	Krishna <i>et al.</i> (2007b)
	Positive	NS	Plant height	
	Negative	S	Fruit length	
	Negative	NS	Fruit set per cent	
	Positive	S	Yield per plant	Singh <i>et al.</i> (2007)
	Positive	S	Yield per plant	Vani <i>et al.</i> (2007a)
	Positive	S	Number of primary and secondary branches per plant and yield per plant	Farhad <i>et al.</i> (2008)
	Positive	NS	Number of seeds per fruit	
	Negative	S	Ascorbic acid	
	Negative	NS	Days to 50 % flowering, plant height, fruit length and fruit weight	
	Positive	S	Yield per plant	Hosamani and Shivkumar (2008)

	Positive	S	Yield per plant, plant height, and number of primary and secondary branches per plant	Reddy <i>et al.</i> (2008)
	Negative	S	Fruit length	
	Positive	NS	Number of seeds per fruit	
	Negative	NS	Days to 50 % flowering and average fruit weight	
	Positive	S	Number of primary branches, yield per plant and fruit diameter	Tembhurne <i>et al.</i> (2008)
	Positive	NS	Days to 50 % flowering	
	Negative	S	Fruit length	
	Negative	NS	Plant height and fruit weight	
	Positive	S	Yield per plant and coloring matter	Gupta <i>et al.</i> (2009)
	Positive	NS	Oleoresin	
	Negative	S	Plant height	
	Negative	NS	Fruit length, fruit weight and capsaicin	
	Positive	S	Yield per plant	Jabeen <i>et al.</i> (2009)
	Negative	S	Fruit length	
	Negative	NS	Average fruit weight	
	Negative	NS	Plant height	Kaur and Singh (2009)
	Positive	S	Yield per plant and number of primary and secondary branches per plant	Patel <i>et al.</i> (2009)

	Positive	S	Yield per plant	Singh <i>et al.</i> (2009)
	Positive	S	Fruit width and plant height	Cankaya <i>et al.</i> (2010)
	Negative	S	Days to 50 % flowering	
	Negative	NS	Fruit length and average fruit weight	
	Positive	S	Yield per plant and number of branches / plant	Padhar and Zaveri (2010)
	Positive	S	Yield per plant	Sharma <i>et al.</i> (2010)
	Positive	NS	Fruit length, fruit diameter, average fruit weight and plant height	
	Negative	NS	Days to 50 % flowering and ascorbic acid	
	Positive	S	Yield per plant	Arup <i>et al.</i> (2011)
	Positive	S	Yield per plant	Hasanuzzaman and Faruq (2011)
	Positive	NS	Days to 50 % flowering, fruit length and number of seeds per fruit	
	Negative	NS	Plant height and fruit width	
	Positive	S	Fruit length and yield per plant	Singh and Singh (2011)
	Positive	NS	Number of primary branches per plant	
	Positive	S	Fruit length, ascorbic acid, capsaicin and yield per plant	Kumar <i>et al.</i> (2012)
	Negative	S	Fruit diameter	
	Negative	NS	Average fruit weight and plant height	

	Positive	-	Yield per plant	Lahbib <i>et al.</i> (2012)
	Positive	S	Dry fruit yield per plant	Srividhya and Ponnuswamy (2012)
	Positive	S	Yield per plant	Mahantesh <i>et al.</i> (2013b)
	Positive	S	Fruit weight	Kumar <i>et al.</i> (2014)
	Positive	S	Dry fruit yield per plant	Pandit and Adhikary (2014)
	Positive	S	Average green fruit weight and dry fruit weight	Vikram <i>et al.</i> (2014)
	Positive	NS	Dry fruit yield per plant	
	Positive	S	Dry fruit yield per plant	Vijaya <i>et al.</i> (2014)
	Positive	S	Fruit length, fruit girth, pedicel length, dry pod yield per plant	Rohini and Lakshmanan (2015)
	Positive	S	Yield per plant	Rinchan <i>et al.</i> (2015)
	Positive	S	Dry fruit yield per plant, seed yield per plant	Satish <i>et al.</i> (2015)
	Positive	S	Dry yield per plant	Hasan <i>et al.</i> (2016)
	Positive	S	Dry yield per plant	Priyanka and Mishra (2016)
7. Fruit length (cm)	Positive	-	Fruit weight	Chaim and Paran (2000)
	Negative	-	Plant height and fruit diameter	
	Positive	S	Fruit weight	Munshi <i>et al.</i> (2000)

	Positive	NS	Fruit diameter and number of seeds per fruit	Begum (2002)
	Positive	S	Yield per plant, plant height and days to 50 % flowering	
	Positive	S	Ascorbic acid	Manju and Sreelathakumary (2002)
	Positive	NS	Oleoresin and capsaicin	
	Negative	S	Fruit diameter	Acharya and Rajput (2003)
	Positive	NS	Number of seeds per fruit, days to 50 % flowering and yield per plant	
	Positive	S	Plant height	
	Positive	S	Plant height	Khurana <i>et al.</i> (2003)
	Positive	NS	Coloring matter	
	Negative	NS	Number of seeds per fruit, number of fruits per plant and capsaicin content	
	Negative	-	Yield per plant	Nehru <i>et al.</i> (2003)
	Positive	NS	Fruit diameter, yield per plant and number of seeds per fruit	Choudhary and Samadia (2004)
	Positive	NS	Days to 50 % flowering	
	Positive	NS	Fruit diameter	Ajjappalavara <i>et al.</i> (2005)
	Positive	S	Yield per plant and plant height	
	Negative	S	Days to 50 % flowering	Rao <i>et al.</i> (2005)
	Positive	NS	Plant height	

	Positive	S	Yield per plant	Ahmed <i>et al.</i> (2006)
	Negative	-	Number of fruits per plant	Khader and Mini (2006)
	Positive	S	Yield per plant	Jayashree <i>et al.</i> (2007)
	Positive	S	Yield per plant	Krishna <i>et al.</i> (2007b)
	Positive	NS	Plant height	
	Negative	S	Number of fruits per plant	
	Negative	NS	Percent fruit set	
	Positive	S	Yield per plant	Singh <i>et al.</i> (2007)
.	Positive	S	Yield per plant	Vani <i>et al.</i> (2007a)
	Positive	S	Fruit weight	Farhad <i>et al.</i> (2008)
	Positive	NS	Plant height, number of primary branches per plant, number of seeds per fruit, ascorbic acid and yield per plant	
	Negative	S	Days to 50 % flowering	
	Negative	NS	Number of fruits per plant	
	Positive	NS	Yield per plant	Hosamani and Shivakumar (2008)
	Positive	NS	Plant height and average fruit weight	Reddy <i>et al.</i> (2008)
	Negative	S	Number of fruits per plant	
	Negative	NS	Yield per plant, days to 50 % flowering, number of	

			primary branches per plant and number of seeds per fruit	
	Positive	NS	Plant height	Tembhurne <i>et al.</i> (2008)
	Negative	S	Number of fruits per plant	
	Negative	NS	Number of primary branches per plant, days to 50 % flowering, fruit weight, yield per plant and fruit diameter	
	Positive	S	Yield per plant, fruit weight and capsaicin	Gupta <i>et al.</i> (2009)
	Negative	NS	Number of fruits per plant, plant height, oleoresin and coloring matter	
	Negative	S	Number of fruits per plant	Jabeen <i>et al.</i> (2009)
	Positive	NS	Average fruit weight and plant height	
	Negative	NS	Yield per plant	
	Negative	NS	Plant height	Kaur and Singh (2009)
	Positive	S	Yield per plant	Patel <i>et al.</i> (2009)
	Positive	S	Fruit width	Sarkar <i>et al.</i> (2009)
	Positive	S	Average fruit weight	Cankaya <i>et al.</i> (2010)
	Positive	NS	Fruit width and days to 50 % flowering	
	Negative	NS	Plant height and number of fruits per plant	
	Positive	S	Yield per plant	Sharma <i>et al.</i> (2010)
	Positive	NS	Fruit diameter, average fruit weight, number of fruits per plant and plant height	

	Negative	S	Fruit length	
	Negative	NS	Ascorbic acid	
	Positive	S	Fruit width, fruit weight and yield per plant	Hasanuzzaman and Faruq (2011)
	Negative	NS	Plant height, number of seeds per fruit and days to 50 % flowering	
	Positive	NS	Number of fruits per plant	
	Positive	S	Yield per plant and plant height	Singh and Singh (2011)
	Positive	S	Yield per plant, fruit weight and fruit diameter	Berhanu <i>et al.</i> (2011b)
	Positive	NS	Plant height	
	Negative	NS	Number of fruits per plant	
	Positive	S	Average fruit weight, number of fruits per plant and yield per plant	Kumar <i>et al.</i> (2012)
	Positive	NS	Fruit diameter	
	Negative	S	Ascorbic acid and capsaicin	
	Negative	NS	Plant height	
	Negative	-	Fruit diameter	Lahbib <i>et al.</i> (2012)
	Positive	S	Dry fruit yield per plant	Srividhya and Ponnuswamy (2012)
	Positive	S	Yield per plant	Mahantesh <i>et al.</i> (2013b)

	Positive	S	Dry yield per plant	Vikram <i>et al.</i> (2014)
	Positive	S	Fruit girth, number of fruits per plant, number of seeds per fruit, 1000 seed weight	Kumar <i>et al.</i> (2014)
	Positive	S	Dry fruit yield per plant	Vijaya <i>et al.</i> (2014)
	Positive	S	Plant height, number of branches per plant, dry pod yield per plant	Rohini and Lakshmanan (2015)
	Negative	S	Fruit diameter, Number of seeds per fruit, dry fruit yield per plant	Satish <i>et al.</i> (2015)
	Positive	S	Dry red fruit weight	Razzaq <i>et al.</i> (2016)
	Positive	S	Dry yield per plant	Priyanka and Mishra (2016)
8.Fruit diameter (cm)	Positive	-	Fruit weight	Chaim and Paran (2000)
	Negative		Plant height	
	Positive	S	Number of seeds per fruit, days to 50 % flowering, plant height and yield per plant	Begum (2002)
	Positive	NS	Fruit length	
	Negative	NS	Number of seeds per fruit, days to 50 % flowering, number of primary branches per plant, plant height and yield per plant	Acharya and Rajput (2003)
	Negative	S	Fruit length	
	Positive	S	Yield per plant	Khurana <i>et al.</i> (2003)
	Negative	S	Number of seeds per fruit and fruit length	

	Positive	NS	Number of seeds per fruit and fruit length	Choudhary and Samadia (2004)
	Positive	S	Yield per plant	
	Positive	S	Yield per plant	Patil <i>et al.</i> (2004)
	Positive	S	Yield per plant	Singh and Singh (2004)
	Negative	S	Yield per plant and days to 50 % flowering	Ajjappalavara <i>et al.</i> (2005)
	Positive	S	Plant height	
	Positive	NS	Number of primary branches per plant and fruit length	
	Positive	S	Yield per plant	Rao <i>et al.</i> (2005)
	Negative	S	Days to 50 % flowering and number of primary branches per plant	
	Positive	NS	Plant height	
	Positive	S	Yield per plant	Singh <i>et al.</i> (2007)
	Positive	-	Yield per plant	Smitha and Basvaraja (2007)
	Negative	NS	Yield per plant	Hosamani and Shivkumar <i>et al.</i> (2008)
	Positive	S	Yield per plant, number of fruits per plant and number of primary branches	Tembhurne <i>et al.</i> (2008)
	Positive	NS	Fruit weight	
	Negative	S	Plant height	
	Negative	NS	Days to 50 % flowering and fruit length	

	Positive	S	Average fruit weight	Jabeen <i>et al.</i> (2009)
	Positive	NS	Yield per plant	
	Negative	NS	Plant height , number of fruits per plant and fruit length	
	Positive	S	Number of fruits per plant and average fruit weight	Cankaya <i>et al.</i> (2010)
	Positive	NS	Fruit length and plant height	
	Negative	NS	Days to 50 % flowering	
	Positive	S	Days to 50 % flowering, average fruit weight and yield per plant	Sharma <i>et al.</i> (2010)
	Positive	NS	Number of fruits per plant, fruit length and ascorbic acid	
	Negative	S	Plant height	
	Positive	S	Dry fruit yield per plant	Ashok Kumar <i>et al.</i> (2010)
	Positive	S	Yield per plant, fruit weight and fruit length	Hasanuzzaman and Faruq (2011)
	Positive	NS	Days to 50 % flowering and number of seeds per fruit	
	Negative	NS	Plant height and number of fruits per plant	
	Positive	S	Fruit length, average fruit weight and yield per plant	Berhanu <i>et al.</i> (2011b)
	Negative	S	Number of fruits per plant	
	Negative	NS	Plant height	

	Positive	S	Average fruit weight	Kumar <i>et al.</i> (2012)
	Positive	NS	Plant height, fruit length and yield per plant	
	Negative	S	Number of fruits per plant and capsaicin	
	Negative	NS	Ascorbic acid	
	Negative	-	Fruit length	Lahbib <i>et al.</i> (2012)
	Positive	S	Fruit yield per plot and fruit yield per ha	Satish <i>et al.</i> (2015)
	Positive	S	Fresh red fruit weight, dry red fruit weight	Razzaq <i>et al.</i> (2016)
9.Fruit pedicel length(cm)	Positive	S	Seed yield per plant	Gagala <i>et al.</i> (2007)
	Positive	S	Fruit yield per plant	Pandit <i>et al.</i> (2009)
	Negative	S	Dry fruit yield per plant	Hasan <i>et al.</i> (2016)
10.Number of seeds per fruit	Positive	S	Yield per plant, days to 50 % flowering, plant height, number of primary branches per plant, fruit diameter	Begum (2002)
	Positive	NS	Fruit length	Acharya and Rajput (2003)
	Positive	NS	Yield per plant, days to 50 % flowering, plant height, number of primary branches per plant, fruit length	
	Negative	NS	Fruit diameter	

	Positive	S	Number of fruits per plant and plant height	Khurana <i>et al.</i> (2003)
	Negative	NS	Fruit length, capsaicin and coloring matter	
	Positive	S	Yield per plant	Choudhary and samadia (2004)
	Negative	NS	Days to 50 % flowering	
	Positive	NS	Fruit length, plant height and fruit diameter	
	Positive	S	Yield per plant and plant height	Ajjappalavara <i>et al.</i> (2005)
	;Positive	S	Yield per plant	Rao (2005)
	Positive	NS	Days to 50 % flowering, plant height and fruit diameter	
	Positive	S	Yield per plant	Vani <i>et al.</i> (2007a)
	Positive	S	Number of primary and secondary branches , fruit weight and fruit yield per plant	Farhad <i>et al.</i> (2008)
	Positive	NS	Plant height, fruit length and number of fruits per plant	
	Negative	NS	Days to 50 % flowering and ascorbic acid	
	Positive	NS	Plant height, number of primary branches per plant, number of fruits per plant and yield per plant	Reddy <i>et al.</i> (2008)
	Negative	NS	Days to 50 % flowering, fruit length and average fruit weight	
	Negative	NS	Plant height	Kaur and Singh (2009)
	Positive	S	Fruit weight	Sarkar <i>et al.</i> (2009)

	Negative	S	Dry fruit yield per plant	Kannan <i>et al.</i> (2009)
	Positive	S	Number of fruits per plant and dry fruit yield per plant	Ashok kumar <i>et al.</i> (2010)
	Negative	NS	Yield per plant	Arup <i>et al.</i> (2011)
	Positive	NS	Days to 50 % flowering, fruit width, number of fruits per plant and plant height	Hasanuzzaman and Faruq (2011)
	Negative	NS	Fruit length and yield per plant	
	Positive	S	Plant height, number of branches per plant, fruit length, fruit girth, dry pod yield per plant	Rohini and Lakshmanan (2015)
	Positive	S	Weight of pericarp per fruit and fruit length	Shiva <i>et al.</i> (2015)
	Positive	S	Green fruit yield per plant	Satish <i>et al.</i> (2015)
	Negative	S	Number of primary branches	Razzaq <i>et al.</i> (2016)
11. Weight of seeds per fruit (g)	Negative	S	Dry fruit yield per plant	Kannan <i>et al.</i> (2009)
	Positive	S	Individual dry pod weight	Rohini and lakshmanan (2015)
	Positive	S	Weight of pericarp, number of seeds per fruit, fruit girth, fruit length	Shiva <i>et al.</i> (2015)
12. 1000 seed weight (g)	Negative	NS	Number of seeds per fruit	Mishra <i>et al.</i> (2001)
	Positive	S	Number of seeds per fruit	Gogoi and Gautam (2003)

	Positive	S	Number of seeds per fruit	Hari <i>et al.</i> (2005)
	Negative	NS	Capsanthin (EOA values)	
	Positive	NS	Capsaicin (%)	
	Positive	NS	Number of seeds per fruit, Capsanthin (EOA values), Capsaicin (%)	Rao <i>et al.</i> (2006)
	Positive	S	Oleoresins (%)	
	Positive	S	Number of seeds per fruit	Chatterjee <i>et al.</i> (2007)
	Positive	NS	Capsanthin (EOA values)	
	Negative	NS	Capsaicin (%), Oleoresins (%)	
	Positive	S	Fruit weight	Sarkar <i>et al.</i> (2009)
	Negative	S	Fruit yield per plant	Kumar <i>et al.</i> (2014)
	Positive	S	Days to 50% flowering, pedicel length, number of seeds per fruit	Rohini and Lakshmanan (2015)
13. Dry fruit yield per plant (g)	Positive	S	Number of fruits per plant and fruit weight	Munshi <i>et al.</i> (2000)
	Positive	-	Number of fruits per plant	Mishra <i>et al.</i> (2001)
	Negative	-	Number of seeds per fruit	
	positive	-	Number of fruits per plant, Fruit diameter and plant height	Singh and Singh (2001)
	Positive	S	Number of fruits per plant, 1000 seed weight, seed percentage and harvest index.	Rathod <i>et al.</i> (2002)
	Positive	S	Plant height, number of fruits per plant, fruit length, fruit diameter and number of seeds per fruit	Begum (2002)

	Positive	NS	Number of primary branches per plant	
	Negative	S	Days to 50 % flowering	
	Positive	NS	Plant height, number of primary branches per plant, number of fruits per plant, fruit length and number of seeds per fruit.	Acharya and Rajput (2003)
	Positive	NS	Days to 50 % flowering and fruit diameter	
	Positive	S	Plant height, number of fruits per plant, fruit length, fruit diameter, coloring matter and capsaicin	Khurana <i>et al.</i> (2003)
	Negative	S	Days to 50 % flowering	
	Positive	NS	Number of seeds per fruit	
	Positive	S	Number of fruits per plant and number of primary and secondary branches	Kumar <i>et al.</i> (2003)
	Positive	-	Number of fruits per plant	Nandadavi and Hosamani (2003)
	Negative	-	Plant height and fruit length	Nehru <i>et al.</i> (2003)
	Positive	NS	Number of fruits per plant and fruit length	Choudhary and Samadia (2004)
	Positive	S	Fruit diameter and number of seeds per fruit	
	Negative	NS	Days to 50 % flowering	
	Positive	-	Average fruit weight	Patil <i>et al.</i> (2004)
	Positive	-	Plant height, number of fruits per plant and fruit diameter	Singh and Singh (2004)
	Positive	S	Plant height, number of fruits per plant and fruit length	Ajjappalavara <i>et al.</i> (2005)

	Negative	S	Days to 50 % flowering and number of primary branches per plant	
	Negative	NS	Fruit diameter	
	Positive	S	Fruit diameter and number of seeds per fruit	Nazir <i>et al.</i> (2005)
	Negative	NS	Number of fruits per plant	
	Positive	S	Plant height, number of fruits per plant, number of primary branches per plant, fruit diameter, number of seeds per fruit and fruit length	Rao (2005)
	Negative	NS	Plant height, days to 50 % flowering and number of fruits per plant	Ahmed <i>et al.</i> (2006)
	Positive	NS	Number of primary branches per plant	
	Positive	S	Fruit length and Capsaicin	
	Positive	NS	Capsanthin	
	Positive	NS	Plant height	Ajit and Manju (2006)
	Negative	NS	Number of seeds per fruit	
	Positive	S	Number of branches per plant and number of fruits per plant	Bharadwaj <i>et al.</i> (2007)
	Positive	S	Average fruit weight and fruit width	Ahmed <i>et al.</i> (2007)
	Positive	S	Number of branches per plant, plant height, fruit length and number of fruits per plant	Jayashree <i>et al.</i> (2007)
	Negative	S	Days to 50 % flowering	
	Positive	S	Fruit length, fruit breadth and number of fruits per plant	Singh <i>et al.</i> (2007)

	Positive	-	Fruit length, plant height, fruit weight, number of primary branches and fruit diameter	Smitha and Basvaraja (2007)
	Positive	S	Fruit length, number of seeds per plant and number of fruits per plant	Vani <i>et al.</i> (2007a)
	Positive	S	Fruit weight, number of seeds per plant and number of fruits per plant	Farhad <i>et al.</i> (2008)
	Positive	NS	Number of primary branches, fruit length and plant height	
	Negative	S	Ascorbic acid	
	Negative	NS	Days to 50 % flowering	
	Positive	NS	Plant height, number of seeds per fruit and fruit length	Hosamani and Shivkumar (2008)
	Positive	S	Days to 50 % flowering, number of fruits per plant and fruit diameter	
	Positive	S	Plant height, number of primary branches per plant, number of fruits per plant and average fruit weight	Reddy <i>et al.</i> (2008)
	Negative	NS	Days to 50 % flowering and fruit length	
	Positive	NS	Number of seeds per fruit	
	Positive	S	Number of primary branches, fruit diameter, days to 50 % flowering and number of fruits per plant	Tembhurne <i>et al.</i> (2008)
	Positive	NS	Fruit weight	
	Negative	NS	Plant height	

	Positive	S	Number of fruits per plant and fruit length	Gupta <i>et al.</i> (2009)
	Positive	NS	Capsaicin, oleoresin and coloring matter	
	Negative	S	Plant height	
	Negative	NS	Fruit weight	
	Positive	S	Number of branches per plant, plant height and number of fruits per plant	Jabeen <i>et al.</i> (2009)
	Positive	NS	Average fruit weight and fruit breadth	
	Negative	NS	Fruit length	
	Positive	S	Number of primary and secondary branches per plant, fruit length, fruit weight and number of fruits per plant	Patel <i>et al.</i> (2009)
	Positive	S	Average dry fruit weight, Capsanthin and number of fruits per plant	Singh <i>et al.</i> (2009)
	Positive	S	Fruit length, fruit pedicel length, number of fruits per plant , fruit weight and 1000 seed weight	Pandit <i>et al.</i> (2009)
	Positive	S	Number of fruits per plant, fruit length, fruit weight, 100 seed weight , plant height	Wilson and Philip (2009)
	Negative	-	Days to 50% flowering	
	Positive	S	Number of fruits per plant, 100 seed weight , fruit weight	Sarkar <i>et al.</i> (2009)
	Positive	S	Number of branches per plant and number of fruits per plant	Padhar and Zaveri (2010)
	Positive	S	Primary and secondary branches per plant, fruit number and fruit diameter	Datta and Jana (2010)

	Positive	S	Fruit length, fruit diameter, average fruit weight and number of fruits per plant	Sharma <i>et al.</i> (2010)
	Negative	NS	Plant height and days to 50 % flowering	
	Positive	NS	Ascorbic acid	
	Positive	S	Number of fruits per plant, fruit length	Ashok Kumar <i>et al.</i> (2010)
	Positive	S	Ascorbic acid, days to 50 % flowering and number of fruits per plant	Arup <i>et al.</i> (2011)
	Negative	NS	Number of seeds per fruit, average dry fruit weight, oleoresin and capsaicin	
	Positive	S	Fruit length, fruit width and number of fruits per plant	Hasanuzzaman and Faruq (2011)
	Negative	NS	Plant height, number of seeds per fruit and days to 50 % flowering	
	Positive	S	Fruit length, plant height, fruit diameter and fruit weight	Berhanu <i>et al.</i> (2011b)
	Positive	NS	Number of fruits per plant	
	Positive	S	Fruit length, number of fruits per plant and number of branches per plant	Singh and Singh (2011)
	Positive	-	1000 seed weight and fruit length	Rajya and Vijaya (2011)
	Positive	S	Number of fruits per plant, average fruit weight, fruit length, ascorbic acid and capsaicin	Kumar <i>et al.</i> (2012)
	Positive	NS	Fruit diameter	
	Negative	NS	Plant height	

	Positive	S	Number of fruits per plant	Lahbib <i>et al.</i> (2012)
	Positive	S	Number of branches per plant, number of fruits per plant, fruit length and ascorbic acid	Tasso <i>et al.</i> (2014)
	Positive	S	Fruit length, fruit girth, number of fruits per plant, number of seeds per fruit, 100 seed weight.	Kumar <i>et al.</i> (2014)
	Positive	S	Number of fruits per plant, . fruit diameter and fruit length	Vikram <i>et al.</i> (2014)
	Positive	S	Plant height, fruit length, fruit girth, number of fruits per plant, number of seeds per fruit	Rohini and Lakshmanan (2015)
	Positive	S	Green fruit yield per plant	Satish <i>et al.</i> (2015)
	Positive	S	Plant height and number of primary branches per plant	Rinchan <i>et al.</i> (2015)
	Positive	S	Weight of pericarp per fruit, days to 50% flowering	Shiva <i>et al.</i> (2015)
	Negative	S	Plant height	
	Positive	S	Fruit weight , number of fruits per plant ,fruit length, ascorbic acid	Priyanka and Mishra (2016)
	Negative	S	Days to 50% flowering	
14.Ascorbic acid (mg/100g)	Positive	S	Plant height and fruit length	Manju and Sreelathakumary (2002)
	Positive	NS	Fruit weight and oleoresin	
	Negative	NS	Number of primary branches per plant	
	Positive	NS	Days to 50 % flowering and fruit length	Farhad <i>et al.</i> (2008)
	Negative	S	Number of fruits per plant and yield per plant	

	Negative	NS	Plant height, fruit weight, number of primary and secondary branches per plant and number of seeds per fruit	
	Positive	S	Yield per plant	Kannan <i>et al.</i> (2009)
	Positive	NS	Days to 50 % flowering, fruit diameter, average fruit weight and yield per plant	Sharma <i>et al.</i> (2010)
	Negative	S	Plant height	
	Negative	NS	Number of fruits per plant and fruit length	
	Positive	S	Yield per plant	Arup <i>et al.</i> (2011)
	Positive	S	Days to 50% flowering	Cheema and Pant (2011)
	Negative	S	Fruit girth	
	Positive	S	Capsaicin, number of fruits per plant and yield per plant	Kumar <i>et al.</i> (2012)
	Positive	NS	Average fruit weight	
	Negative	S	Fruit length	
	Negative	NS	Plant height	
	Positive	S	Dry fruit yield per plant	Srividhya and Ponnuswamy (2012)
	Positive	S	Yield per plant	Mahantesh <i>et al.</i> (2013b)
	Positive	S	Yield per plant	Priyanka and Mishra (2016)

15.Oleoresin content (%)	Positive	NS	Plant height, fruit length, fruit weight and number of primary branches per plant	Manju and Sreelathakumary (2002)
	Positive	-	Number of fruits per plant	Mini and Vahab (2002)
	Negative	-	Number of days to flowering, fruit set and harvesting	
	Positive	NS	Capsanthin (EOA values)	Mallikarjun <i>et al.</i> (2003 a)
	Negative	NS	Capsanthin (EOA values)	Hari <i>et al.</i> (2005)
	Negative	S	Capsanthin (EOA values)	Rao <i>et al.</i> (2006)
	Negative	S	Capsanthin (EOA values)	Chatterjee <i>et al.</i> (2007)
	Positive	NS	Number of fruits per plant, yield per plant, capsaicin and coloring matter	Gupta <i>et al.</i> (2009)
	Negative	NS	Fruit length, fruit weight and plant height	
	Negative	NS	Yield per plant	Arup <i>et al.</i> (2011)
	Negative	S	Dry fruit yield per plant	Srividhya and Ponnuswamy (2012)
16.Capsaicin content (SHU)	Positive	S	Number of primary branches per plant and oleoresin	Manju and Sreelathakumary (2002)
	Positive	NS	Fruit length	
	Negative	S	Fruit weight	
	Negative	NS	Plant height	

	Positive	S	Plant height and coloring matter	Khurana <i>et al.</i> (2003)
	Negative	NS	Fruit length, number of fruits per plant and number of seeds per fruit	
	Negative	-	Fruit width	Patil <i>et al.</i> (2004)
	Negative	S	Oleoresins (%)	Hari <i>et al.</i> (2005)
	Positive	NS	Capsanthin (EOA values)	
	Positive	S	Oleoresins (%)	Rao <i>et al.</i> (2006)
	Negative	S	Capsanthin (EOA values)	
	Positive	S	Fruit length	Gupta <i>et al.</i> (2009)
	Positive	NS	Fruit weight, yield per plant, oleoresin and coloring matter	
	Negative	NS	Number of fruits per plant and plant height	
	Positive	S	Number of primary branches per plant	Misra <i>et al.</i> (2010)
	Negative	NS	Yield per plant	Arup <i>et al.</i> (2011)
	Positive	S	Ascorbic acid, number of fruits per plant and yield per plant	Kumar <i>et al.</i> (2012)
	Negative	S	Average fruit weight, fruit length and fruit diameter	
	Negative	NS	Plant height	
17. Total extractable colour (ASTA units)	Positive	S	Number of fruits per plant, plant height and capsaicin	Khurana <i>et al.</i> (2003)
	Positive	NS	Fruit length and yield per plant	

	Negative	NS	Number of seeds per fruit	
	Positive	S	Number of fruits per plant	Gupta <i>et al.</i> (2009)
	Negative	S	Plant height	
	Positive	NS	Fruit weight, yield per plant, capsaicin and oleoresin	
	Negative	NS	Fruit length	
	Positive	S	Yield per plant	Singh <i>et al.</i> (2009)
	Positive	S	Dry fruit yield per plant	Srividhya and Ponnuswamy (2012)
	Positive	S	Yellow carotenoids and red carotenoids	Naresh <i>et al.</i> (2013)
	Positive	S	Yield per plant	Rinchan <i>et al.</i> (2015)
	Negative	S	Weight of pericarp, number of seeds per fruit, yield per plant	Shiva <i>et al.</i> (2015)
18.Red carotenoids (%)	Positive	S	Yellow carotenoids and total carotenoids	Naresh <i>et al.</i> (2013)
19.Yellow carotenoids (%)	Positive	S	Red carotenoids and total carotenoids	Naresh <i>et al.</i> (2013)

Table 2.3: Review of literature on direct effects of yield component characters on yield per plant

Character	Positive direct effect	Negative direct effect
1. Plant height (cm)	Khurana <i>et al.</i> (2003), Choudhary and Samadia (2004), Rao (2005), Krishna <i>et al.</i> (2007b), Smitha and Basvaraja (2007), Farhad <i>et al.</i> (2008), Hosamani and Shivakumar (2008), Reddy <i>et al.</i> (2008), Sarkar <i>et al.</i> (2009), Jabeen <i>et al.</i> (2009), Padhar and Zaveri (2010), Berhanu <i>et al.</i> (2011b), Kumar <i>et al.</i> (2012), Vikram <i>et al.</i> (2014), Satish <i>et al.</i> (2015)	Begam (2002), Ajjappalavara <i>et al.</i> (2005), Farhad <i>et al.</i> (2008), Kaur and Singh (2009), Sharma <i>et al.</i> (2010), Hasanuzzaman and Faruq (2011), Mahantesh <i>et al.</i> (2013b), Rohini and Lakshmanan (2015), Rinchan <i>et al.</i> (2015), Satish <i>et al.</i> (2015),
2. Plant spread (cm)	Jabeen <i>et al.</i> (2009), Kumar <i>et al.</i> (2012), Vijaya <i>et al.</i> (2014)	Kumar <i>et al.</i> (2012), Mahantesh <i>et al.</i> (2013b)
3. Number of primary branches per plant	Bhalekar <i>et al.</i> (2002), Begam (2002), Sreelathakumary and Rajamony (2004), Rao (2005), Bharadwaj <i>et al.</i> (2007), Smitha and Basvaraja (2007), Farhad <i>et al.</i> (2008), Reddy <i>et al.</i> (2008), Misra <i>et al.</i> (2010), Datta and Jana (2010), Berhanu <i>et al.</i> (2011b), Satish <i>et al.</i>	Ajjappalavara <i>et al.</i> (2005), Ahmed <i>et al.</i> (2006), Farhad <i>et al.</i> (2008), Rinchan <i>et al.</i> (2015)

	(2015), Hasan <i>et al.</i> (2016).	
4. Days to 50 % flowering	Sreelathakumary and Rajamony (2004), Rao (2005), Ahmed <i>et al.</i> (2006), Smitha and Basvaraja (2007), Farhad <i>et al.</i> (2008), Reddy <i>et al.</i> (2008), Sarkar <i>et al.</i> (2009), Sharma <i>et al.</i> (2010), Ullah <i>et al.</i> (2011), Vikram <i>et al.</i> (2014) Rohini and Lakshmanan (2015), Hasan <i>et al.</i> (2016), Priyanka and Mishra (2016).	Begam (2002), Choudhary and Samadia (2004), Ajjappalavara <i>et al.</i> (2005), Smitha and Basvaraja (2007), Farhad <i>et al.</i> (2008), Hosamani and Shivkumar (2008), Reddy <i>et al.</i> (2008), Sharma <i>et al.</i> (2010), Arup <i>et al.</i> (2011), Hasanuzzaman and Faruq (2011).
5. Days to maturity	Gogoi and Gautam (2003), Berhanu <i>et al.</i> (2011b), Hasanuzzaman and Faruq (2011), Kumar <i>et al.</i> (2014), Hasan <i>et al.</i> (2016)	Farhad <i>et al.</i> (2008)
6. Number of fruits per plant	Munshi <i>et al.</i> (2000), Begam (2002), Khurana <i>et al.</i> (2003), Choudhary and Samadia (2004), Singh and Singh (2004), Sreelathakumary and Rajamony (2004), Ajjappalavara <i>et al.</i> (2005), Rao (2005), Nazir <i>et al.</i> (2005), Ahmed <i>et al.</i> (2006), Krishna <i>et al.</i> (2007b), Singh <i>et al.</i> (2007), Vani <i>et al.</i> (2007a), Smitha and Basvaraja (2007), Kaur and Singh (2007), Farhad <i>et al.</i> (2008), Hosamani and Shivkumar (2008), Reddy <i>et al.</i> (2008), Sarkar <i>et al.</i> (2009),Singh <i>et al.</i> (2009),	Berhanu <i>et al.</i> (2011b), Mahantesh <i>et al.</i> (2013b)

	Jabeen <i>et al.</i> (2009), Padhar and Zaveri (2010), Sharma <i>et al.</i> (2010), Datta and Jana (2010), , Rajya and Vijaya (2010) Arup <i>et al.</i> (2011), Berhanu <i>et al.</i> (2011b), Hasanuzzaman and Faruq (2011), Kumar <i>et al.</i> (2012), Kumar <i>et al.</i> (2014) , Vikram <i>et al.</i> (2014), Tasso <i>et al.</i> (2014), Pandit and Adhikary (2014), Vijaya <i>et al.</i> (2014), Rohini and Lakshmanan (2015), Rinchan <i>et al.</i> (2015), Satish <i>et al.</i> (2015), Patel <i>et al.</i> (2015), Hasan <i>et al.</i> (2016), Priyanka and Mishra (2016).	
7. Fruit length (cm)	Khurana <i>et al.</i> (2003), Ajjappalavara <i>et al.</i> (2005), Krishna <i>et al.</i> (2007b), Singh <i>et al.</i> (2007), Smitha and Basvaraja (2007), Vani <i>et al.</i> (2007a), Kaur and Singh (2007), Reddy <i>et al.</i> (2008), Sarkar <i>et al.</i> (2009), Misra <i>et al.</i> (2010), Berhanu <i>et al.</i> (2011b), Hasanuzzaman and Faruq (2011), Arup <i>et al.</i> (2011), Rajya and Vijaya (2011), Kumar <i>et al.</i> (2012), Kumar <i>et al.</i> (2014), Vikram <i>et al.</i> (2014), Priyanka and Mishra <i>et al.</i> (2016), Hasan <i>et al.</i> (2016)	Munshi <i>et al.</i> (2000), Begam (2002), Sreelathakumary and Rajamony (2004), Rao (2005), Ahmed <i>et al.</i> (2006), Farhad <i>et al.</i> (2008), Hosamani and Shivkumar (2008), Reddy <i>et al.</i> (2008), Jabeen <i>et al.</i> (2009), Sharma <i>et al.</i> (2010), Berhanu <i>et al.</i> (2011b), Mahantesh <i>et al.</i> (2013b), Rohini and Lakshmanan (2015)
8. Fruit diameter (cm)	Munshi <i>et al.</i> (2000), Ajjappalavara <i>et al.</i> (2005),	Begam (2002), Khurana <i>et al.</i> (2003),

	Nazir <i>et al.</i> (2005), Krishna <i>et al.</i> (2007b), Singh <i>et al.</i> (2007), Bharadwaj <i>et al.</i> (2007), Smitha and Basvaraja (2007), Sarkar <i>et al.</i> (2009) Sharma <i>et al.</i> (2010), Misra <i>et al.</i> (2010), Datta and Jana (2010), Berhanu <i>et al.</i> (2011b), Kumar <i>et al.</i> (2012), Vikram <i>et al.</i> (2014), Kumar <i>et al.</i> (2014)	Choudhary and Samadia (2004), Rao (2005), Ahmed <i>et al.</i> (2006), Smitha and Basvaraja (2007), Hosamani and Shivkumar (2008), Satish <i>et al.</i> (2015), Hasan <i>et al.</i> (2016)
9. Fruit Pedicel length (cm)	Nandadevi and Hosamani (2003), Singh and Singh (2004), Farhad <i>et al.</i> (2008), Sarkar <i>et al.</i> (2009), Sharma <i>et al.</i> (2010), Rohini and Lakshmanan (2015)	Hasan <i>et al.</i> (2016), Priyanka and Mishra (2016)
10. Number of seeds per fruit	Smitha and Basvaraja (2007), Hosamani and Shivkumar (2008), Kaur and singh (2007), Reddy <i>et al.</i> (2008), Sarkar <i>et al.</i> (2009), Hasanuzzaman and Faruq (2011), Tasso <i>et al.</i> (2014)	Begam (2002), Khurana <i>et al.</i> (2003), Choudhary and Samadia (2004), Rao (2005), Smitha and Basvaraja (2007), Farhad <i>et al.</i> (2008), Arup <i>et al.</i> (2011), Hasanuzzaman and Faruq (2011), Rohini and Lakshmanan (2015)
11. weight of seeds per fruit (g)	Singh <i>et al.</i> (2009), Rohini and Lakshmanan (2015)	
12.1000 seed weight (g)	Kumar <i>et al.</i> (2003), Leaya and Khader (2002), Verma <i>et al.</i> (2004), Sreelathakumar and	Rohini and Lakshmanan (2015)

	Rajamony (2004), Pandit <i>et al.</i> (2009), Sarkar <i>et al.</i> (2009), Kumar <i>et al.</i> (2014), Vikram <i>et al.</i> (2014), Pandit and Adhikary (2014)	
13.Ascorbic acid content (mg/100g)	Ahmed <i>et al.</i> (2006), Sonia <i>et al.</i> (2007), Singh <i>et al.</i> (2007), Farhad <i>et al.</i> (2008), Sharma <i>et al.</i> (2010), Arup <i>et al.</i> (2011), Kumar <i>et al.</i> (2012), Mahantesh <i>et al.</i> (2013b), Vikram <i>et al.</i> (2014), Priyanka and Mishra (2016)	
14.Oleoresin content (%)	Singh <i>et al.</i> (2007)	Arup <i>et al.</i> (2011)
15.Capsaicin content (SHU)	Khurana <i>et al.</i> (2003), Singh <i>et al.</i> (2007), Misra <i>et al.</i> (2010), Kumar <i>et al.</i> (2012), Tasso <i>et al.</i> (2014)	Singh <i>et al.</i> (2009), Arup <i>et al.</i> (2011)
16. Total extractable colour (ASTA)	Khurana <i>et al.</i> (2003), Singh <i>et al.</i> (2009), Mahantesh <i>et al.</i> (2013b).	Rinchan <i>et al.</i> (2015)

Chapter III

Materials and Methods

Chapter III

MATERIALS AND METHODS

The present investigation on "**Studies on genetic diversity for yield and quality traits in paprika (*Capsicum annuum* L.)**" was undertaken to study the genetic variability, heritability, genetic advance, character association, path coefficient analysis and genetic divergence. Details pertaining to materials used and methodology employed in the investigation are presented in this chapter.

3.1 LOCATION AND CLIMATE

The experiment was conducted at Horticultural Research Station (HRS), Lam, Guntur. The site of the experiment is situated on 16° 2' North latitude and 80°3' East longitude at an altitude of 31.5 m above mean sea level. The meteorological data for the period of experimentation recorded at the meteorological observatory of RARS, Lam are presented in the Annexure I.

3.2 EXPERIMENTAL DETAILS

3.2.1 Layout of experiment

The experiment was laid out in a Randomized Block Design with two replications (Fig 3). Twelve plants of each genotype were transplanted in each replication in one row.

Design	:	Randomized Block Design (RBD)
Number of treatments	:	44
Replications	:	2
Plot size	:	One row of 4 m length

Spacing : 75 cm x 30 cm

Number plants per row : 12

Date of transplanting : 8th September, 2016

Season : *Kharif* , 2016-17

Location : Horticultural Research Station,
Lam farm, Guntur

3.2.2 Experimental material

The experimental material consisted of forty four genotypes of paprika with two check varieties LCA-424 and LCA-436 obtained from germplasm collection of Horticultural Research Station, Lam farm, Guntur (Table 3).

Table 3 : Details of experimental materials used for experiment.

Treatment	Accession Number	Source
T ₁	LCA 445	HRS, Lam farm, Guntur
T ₂	LCA 447	HRS, Lam farm, Guntur
T ₃	LCA 439	HRS, Lam farm, Guntur
T ₄	LCA 442	HRS, Lam farm, Guntur
T ₅	LCA 430	HRS, Lam farm, Guntur
T ₆	LCA 457	HRS, Lam farm, Guntur
T ₇	LCA 443	HRS, Lam farm, Guntur
T ₈	LCA 437	HRS, Lam farm, Guntur
T ₉	LCA 453	HRS, Lam farm, Guntur
T ₁₀	LCA 450	HRS, Lam farm, Guntur
T ₁₁	LCA 441	HRS, Lam farm, Guntur
T ₁₂	LCA 425	HRS, Lam farm, Guntur
T ₁₃	LCA 440	HRS, Lam farm, Guntur
T ₁₄	LCA 446	HRS, Lam farm, Guntur
T ₁₅	LCA 470	HRS, Lam farm, Guntur
T ₁₆	LCA 436-1	HRS, Lam farm, Guntur
T ₁₇	LCA 466	HRS, Lam farm, Guntur
T ₁₈	LCA 472	HRS, Lam farm, Guntur

Treatment	Accession Number	Source
T ₁₉	LCA 476	HRS, Lam farm, Guntur
T ₂₀	LCA 480	HRS, Lam farm, Guntur
T ₂₁	LCA 482	HRS, Lam farm, Guntur
T ₂₂	LCA 498	HRS, Lam farm, Guntur
T ₂₃	LCA 465	HRS, Lam farm, Guntur
T ₂₄	LCA 475	HRS, Lam farm, Guntur
T ₂₅	LCA 488	HRS, Lam farm, Guntur
T ₂₆	LCA 499	HRS, Lam farm, Guntur
T ₂₇	LCA 506	HRS, Lam farm, Guntur
T ₂₈	LCA 503	HRS, Lam farm, Guntur
T ₂₉	LCA 490	HRS, Lam farm, Guntur
T ₃₀	LCA 501	HRS, Lam farm, Guntur
T ₃₁	LCA 504	HRS, Lam farm, Guntur
T ₃₂	LCA 510 (325)	HRS, Lam farm, Guntur
T ₃₃	LCA 510 (RR-42-1)	HRS, Lam farm, Guntur
T ₃₄	LCA 511	HRS, Lam farm, Guntur
T ₃₅	LCA 512	HRS, Lam farm, Guntur
T ₃₆	LCA 513	HRS, Lam farm, Guntur
T ₃₇	Warangal chappatta single patti	HRS, Lam farm, Guntur
T ₃₈	Warangal chappatta double patti	HRS, Lam farm, Guntur
T ₃₉	Byadagi kaddi	HRS, Lam farm, Guntur
T ₄₀	Byadagi dabbi	HRS, Lam farm, Guntur
T ₄₁	Kt-1	HRS, Lam farm, Guntur
T ₄₂	Jangareddy gudem local	HRS, Lam farm, Guntur
T ₄₃	LCA 436	HRS, Lam farm, Guntur
T ₄₄	LCA-424	HRS, Lam farm, Guntur

3.3 CULTURAL PRACTICES

3.3.1 Soil:

The soils of the farm are deep, black clay loams with a depth of 6-7 feet, pH of 8.4, EC of 0.16 m.mhos/cm and have good moisture retentive capacity.

3.3.2 Nursery raising:

Raised beds were prepared after bringing the soil to a fine tilth. Each bed was mixed with 2 kg of FYM. The beds were leveled and seeds of 44 accessions were

T ₂₂	I	T ₄₄	I	T ₃₂	I	T ₄₄
T ₂₁	R	T ₄₃	R	T ₂₃	R	T ₁₀
T ₂₀	R	T ₄₂	R	T ₁₄	R	T ₂₇
T ₁₉	I	T ₄₁	I	T ₃₉	I	T ₅
T ₁₈	G	T ₄₀	G	T ₇	G	T ₄₁
T ₁₇	A	T ₃₉	A	T ₃₅	A	T ₃
T ₁₆	T	T ₃₈	T	T ₉	T	T ₂₀
T ₁₅	I	T ₃₇	I	T ₂₁	I	T ₃₄
T ₁₄	O	T ₃₆	O	T ₃₀	O	T ₂
T ₁₃	N	T ₃₅	N	T ₁₉	N	T ₆
T ₁₂		T ₃₄		T ₄₂		T ₁₃
T ₁₁	C	T ₃₃	C	T ₂₅	C	T ₂₈
T ₁₀	H	T ₃₂	H	T ₁₆	H	T ₃₆
T ₉	A	T ₃₁	A	T₂₉	A	T ₂₄
T ₈	N	T ₃₀	N	T₁₂	N	T ₄
T ₇	N	T ₂₉	N	T ₃₈	N	T ₈
T ₆	E	T ₂₈	E	T ₂₂	E	T ₄₃
T ₅	L	T ₂₇	L	T ₄₀	L	T ₁₇
T ₄		T ₂₆		T ₃₁		T ₁₈
T ₃		T ₂₅		T ₁₅		T ₁₁
T ₂		T ₂₄		T ₂₆		T ₈
T ₁		T ₂₃		T ₁		T ₃₇
R1			R2			

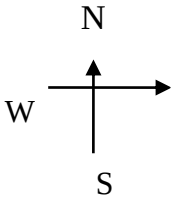


Fig 3. Layout of the experimental plot of paprika



Plate 1 : Field view of experimental plot of paprika, HRS, Lam.

sown in lines at 5 cm spacing on August 8th, 2016. Nursery beds were regularly watered and beds were kept free from weeds. As a precaution against “damping off” disease of the seedlings, the beds were drenched with copper oxychloride (3g/l) on 12th and 21st day after sowing. Thirty days old, uniform and healthy seedlings from each accession were transplanted in the main experimental field.

3.3.3. Preparation of experimental plot

The experimental fields were brought to fine tilth by ploughing thrice followed by harrowing. Before final harrowing, FYM @ 25 tonnes/ha was applied as basal dose and incorporated in the soil. The recommended dose of fertilizers @ 200:60:80 kg NPK/ha in the form of urea, single super phosphate and muriate of potash, respectively were applied. Entire dose of P was applied as basal while N and K were applied in three equal splits during the crop growth.

3.3.4 Transplanting and after care

The seedlings were transplanted in the main field after allotting entries randomly in each replication. They were planted at a spacing of 75 cm between the rows and 30 cm between the plants with in a row. Immediately after transplanting the field was irrigated lightly. The plots were kept free of weeds and irrigated regularly. Need based plant protection measures were taken up to keep the plot free from pests and diseases and raise a healthy crop.

3.4 OBSERVATIONS RECORDED

Five randomly selected plants from each entry were tagged in each replication for recording observations on different characters as described below and the mean values were calculated.

3.4.1 QUANTITATIVE CHARACTERS

3.4.1.1 Plant height (PH)

Height of the plant was measured from the ground level to tip of the plant in centimeters at the time of harvest.

3.4.1.2 Plant spread (PS)(cm)

The plant spread was measured using with the help of a measuring tape over the plant in the direction of maximum spread of the plant.

3.4.1.3 Number of primary branches (NPBP)

The number of branches arising from the main stem above the ground level at final harvest was counted and expressed as number.

3.4.1.4 Days to 50 per cent flowering (DFF)

Number of days taken from the date of transplanting to 50 per cent plants start flowering in a plot was recorded.

3.4.1.5 Days to maturity (DM)

The number of days from the date of transplanting to the date on which fruits are harvested for the first time was expressed as days to first picking.

3.4.1.6 Number of fruits per plant (NFP)

The total number of fruits per plant at harvest on five randomly selected plants was counted and the mean was calculated.

3.4.1.7 Fruit length (FL) (cm)

Average fruit length of five fruits from five randomly selected plants was measured from base to the tip of the fruit and expressed in centimeters.

3.4.1.8 Fruit diameter (FD) (cm)

Average diameter of five fruits from five randomly selected plants was measured at the top shoulder and expressed in centimeters.

3.4.1.9 Fruit pedicel length (FPL) (cm)

The mean length of the pedicel was measured from its tip to the base of the fruit for the randomly selected five fruits.

3.4.1.10 Number of seeds per fruit (NSF)

The number of seeds from five fruits from five randomly selected plants was counted and average was worked out.

3.4.1.11 Weight of seeds per fruit (WSF) (g)

The weight of seeds from five fruits from five randomly selected plants was counted and average was worked out.

3.4.1.12 1000 seed weight (g)

Seeds were extracted from the dried fruits and mean 1000 seed weight was recorded and expressed in grams.

3.4.1.13 Dry fruit yield per plant (DFYP) (g)

The yield in terms of dry fruit weight was recorded in grams on five randomly selected plants and mean was worked out.

3.4.2 QUALITATIVE CHARACTERS

3.4.2.1 Ascorbic acid (mg /100g)

Ascorbic acid content of mature green fruits was estimated by volumetric method described by Sadasivam and Balasubramanian (1987).

Dye solution: 42 mg of sodium bicarbonate was weighed into a 200 ml volumetric flask in distilled water and 52 mg of 2-6 dichlorophenol indophenol was dissolved in it and then the volume was made up with distilled water.

Standard stock solution: Stock solution was prepared by dissolving 100 mg ascorbic acid in 100 ml of 4 % oxalic acid solution. 10 ml of stock solution was diluted to 100 ml with 4 % oxalic acid to get the working standard of 100 mg per ml.

Procedure :

5 ml of the working standard solution was pipetted into a 100 ml conical flask to which 10 ml of 4 % oxalic acid was added. The contents were titrated against the dye (V_1 ml) to get a pink end point which persisted for a few seconds. The chilli sample (5 g) was extracted in 4 % oxalic acid and the volume was made up to 100 ml and the contents were centrifuged. 5 ml of this supernatant was pipetted out, to which 10 ml of 4 per cent oxalic acid was added and titrated against the dye (V_2 ml). The ascorbic acid content was calculated using the formula given below.

Amount of ascorbic acid (mg/100 g) sample

$$\frac{0.5 \text{ mg}}{V_1} \times \frac{V_2}{5 \text{ ml}} \times \frac{100 \text{ ml}}{\text{Wt. of the sample}} \times 100$$

3.4.2.2 Oleoresin content (%)

The oleoresin content was estimated as per the procedure given by Ranganna (1986).

Principle:

Acetone being an organic solvent, dissolves whole content of chillies when passing acetone from chilli powder. Acetone can be evaporated after dissolving by mild heating at 15°C for 15 minutes to separate oleoresin that can be quantified.

Procedure:

Finely mashed 25 g chilli powder was transferred to a glass column, which was plugged by cotton plug on its narrow end. A thin layer of cotton was placed over chilli powder in the glass column and 25 ml of acetone was added. After all the acetone was decanted, 25 ml acetone was added each time till a total of 250 ml acetone was added to the contents. After decantation, the resulting red colored liquid in beaker contains all the principle constituents of chilli. The collected filtrate was transferred to a 250 ml volumetric flask and the volume was made up with acetone.

The chilli extract was transferred to a 250 ml beaker of known weight (W_1 g) and was kept in water bath at 50-60°C for 15-30 minutes so that acetone gets evaporated. Then, weight of the beaker along with contents was recorded as W_2 g. The weight of the oleoresin content in the 25 g chilli powder was calculated and expressed in percentage using the given formula.

$$\text{Oleoresin content (\%)} = \frac{W_2 - W_1}{\text{Weight of sample}} \times 100$$

3.4.2.3 Capsaicin content (%)

The capsaicin content of fruits was estimated by colorimetric method described by Balasubramanian *et al.* (1982).

Principle:

The phenolic group in capsaicin reduces phosphomolybdic acid to lower acids of molybdenum. The resulting component is blue in color and is read at 650 nm. The color intensity is directly proportional to the concentration of capsaicin.

Chemicals:

- 0.4% sodium hydroxide
- 3% phosphomolybdic acid
- Dry acetone (add 25 g anhydrous sodium sulphate to 500 ml of acetone at least one day before use)
- Stock standard capsaicin solution (exactly 50 mg capsaicin was dissolved in 50ml of 0.4% NaOH solution (1000 μ g/ ml)) and working standard (10 ml of the stock standard was diluted to 50 ml with 0.4% NaOH solution (200 μ g/ ml)).

Procedure:

0.5g dry chilli powder was weighed into glass-stoppard test tube; 10ml dry acetone was added into the test tube and kept overnight for extraction. Next day samples were centrifuged at 10000 rpm for 10 min. to get clear supernatant. 1ml of the supernatant was taken into a test tube and evaporated to dryness in a hot water bath. Then, the residue was dissolved in 5ml of 0.4% NaOH solution and 3ml of 3% phosphomolybdic acid was added. The contents were shaken and left undisturbed for 1hr. After 1hr, the solution was quickly filtered into centrifuge tubes to remove any floating debris and then centrifuged at 5000rpm for 15min. The clear blue coloured solution was directly transferred into the cuvette and absorbance was read at 650nm along with a reagent blank.

Preparation of standard graph: A standard graph was prepared using 0-200µg pure capsaicin. Simultaneously 0.2, 0.4, 0.6, 0.8 and 1ml of working standard solution were taken into new test tubes and proceeded as mentioned above.

Per cent capsaicin calculated using the formula mentioned below

$$\text{Capsaicin content (\%)} = \frac{\mu\text{g capsaicin} \times 100 \times 100}{1000000 \times 1 \times 0.5}$$

$$1\% = 1,60,000 \text{ SHU units}$$

3.4.2.4 Total extractable colour value (ASTA units):

Total extractable colour of fruits measured in ASTA (American Spice Trade Association) units was determined using the procedure outlined by ASTA (1986).

Procedure:

100 mg of sieved fine chilli powder was weighed into a volumetric flask. Acetone was added and flask was closed tightly with stopper, then contents were kept for 16 h at room temperature in dark and shaken intermittently. Solution was filtered using Whatman filter paper and final volume was made up to 100 ml. Absorbance of final extract was read at 460 nm using acetone as blank.

ASTA colour units were calculated as per the formula given below,

$$\text{ASTA} = \frac{\text{Absorbance at 460nm} \times 16.4}{\text{Weight of sample in g}}$$

3.4.2.5 Determination of yellow and red fractions in chilli powder:

All the carotenoid pigments present in hot pepper have chromophore properties that allow their grouping in two isochromic families *i.e.* red (R) and yellow (Y). The R fraction contains pigments capsanthin, capsorubin and

capsanthin-5, 6-epoxide, whereas Y fraction contains remaining pigments such as zeaxanthin, violaxanthin, antheraxanthin, β -cryptoxanthin, β -carotene and cucurbitaxanthin A, which acts as precursors of the former (Minguez-Mosquera and Perez-Galvez, 1998). Yellow and red fractions were determined using UV-visible spectrophotometric measurements at two characteristic wavelengths and application of Lambert-Beer law for multi-component mixtures according to procedure developed by Hornero-Mendez and Minguez-Mosquera, (2001).

Procedure:

Dried chilli fruits were ground into a fine powder and 100mg of dried powder was extracted four times with 25 ml acetone until the complete exhaustion of the color. The extract was filtered and transferred to 50 ml volumetric flask and the volume was made up with acetone. The samples absorbance was read at two wave lengths *i.e.*, 472 and 508 nm using acetone as blank. The red and yellow fractions were calculated using the following formulae.

$$C^R (\mu\text{g/ml}) = \frac{A_{508} \times 2144.0 - A_{472} \times 403.3}{270.9}$$

$$C^Y (\mu\text{g/ml}) = \frac{A_{472} \times 1724.3 - A_{508} \times 2450.1}{270.9}$$

Total colour = $C^R + C^Y$

$\mu\text{g/ml}$ values were converted into percentage on dry weight basis.

3.5 STATISTICAL ANALYSIS:

The data obtained in respect of all the characters have been subjected to the following statistical analysis.

3.5.1 Analysis of variance (ANOVA):

Data were analyzed by the methods outlined by Panse and Sukhatme (1985) using the mean values of random plants in each replication from all genotypes to find out the significance of genotypes effect.

$$Y_{ij} = \mu + b_i + t_j + e_{ij}$$

Where,

Y_{ij} = Performance of the j^{th} genotype in the i^{th} block

μ = general mean

b_i = true effect of i^{th} block

t_j = true effect of j^{th} genotype

e_{ij} = random error associated with i^{th} block and j^{th} genotype.

The analysis of variance for each character was carried out as indicated below:

Sources of variation	Df	SS	MSS	F ratio
Replications	r-1	RSS	RMSS	RMSS/EMSS
Treatments	t-1	T_r SS	T_r MSS	T_r MSS/EMSS
Error	(r-1) (t-1)	ESS	EMSS	
Total	(rt-1)	TSS		

Where,

r = Number of replications

t = Number of genotypes or treatments

df = degrees of freedom

SS	=	sum of squares
MSS	=	Mean sum of squares
RSS	=	Replication sum of squares
T _r SS	=	Treatment sum of squares
ESS	=	Error sum of squares
TSS	=	Total sum of squares
RMSS	=	Mean squares due to replications
T _r MSS	=	Mean squares due to treatments
EMSS	=	Mean squares due to error

The test of significance was carried out by 'F' table values given by Fisher and Yates (1963).

3.5.2 Components of variance:

$$\text{Genotypic variance (V}_g \text{ or } \sigma_g^2) = \frac{\text{Genotype MSS} - \text{Error MSS}}{r}$$

$$\text{Environmental variance (V}_e \text{ or } \sigma_e^2) = \frac{\text{Error MSS}}{r}$$

Where,

r = number of replications

$$\text{Phenotypic variance (V}_p \text{ or } \sigma_p^2) = V_g + V_e$$

Significance of treatment MSS was assessed with reference to F table values at 1 and 5 percent probabilities. Further, computation was carried out only when the treatment effects were significant.

3.5.3 Estimation of genetic parameters

The genetic parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense and genetic advance for different characters were worked out by following the standard procedures for all the genotypes under study.

3.5.3.1 Genotypic and phenotypic coefficient of variation

Genotypic and phenotypic coefficients of variation were estimated according to Burton and Devane (1953) by using the following formulae.

$$PCV = \frac{\sqrt{\sigma_p^2}}{\bar{X}} \times 100$$

$$GCV = \frac{\sqrt{\sigma_g^2}}{\bar{X}} \times 100$$

Where,

σ_g^2 = Genotypic variance

σ_e^2 = Environment variance

σ_p^2 = Phenotypic variance

$\bar{X}$ = General mean

PCV and GCV were classified as shown below (Sivasubramanian and Menon, 1973).

Less than 10% = Low

10-20% = Moderate

More than 20 % = High

3.5.3.2 Heritability in Broad sense [$h^2 (b)$]

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

$$h^2 (b) = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Where,

$h^2 (b)$ = Heritability estimates in broad sense

σ_g^2 = Genotypic variance

σ_p^2 = Phenotypic variance

The heritability ($h^2 (b)$) was categorised as suggested by Johnson *et al.* (1955).

0-30% = Low

31-60% = Medium

61% and above = High

3.5.3.3 Genetic advance (GA)

This was estimated as per formula proposed by Allard (1960)

$$GA = K \times \sigma_p \times h^2 (b)$$

Where,

K = Selection differential at 5 per cent selection intensity which accounts to a constant value 2.06

$h^2(b)$ = Heritability in broad sense

σ_p = Phenotypic standard deviation

3.5.3.4 Genetic advance as per cent of mean (GAM)

Genetic advance over mean (GAM) was calculated using the following formula and was expressed in percentage.

$$GAM = \frac{GA}{\bar{X}} \times 100$$

Where,

GA = genetic advance

$\bar{X}$ = general mean of the character

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

3.5.4 Correlation studies

Phenotypic and genotypic correlations were worked out by using formula suggested by Falconer (1964).

Phenotypic coefficient of correlation (r_p)

$$r(x_i, x_j)_p = \frac{\text{COV}(x_i, x_j)_p}{\sqrt{V(x_i)_p \cdot V(x_j)_p}}$$

Where,

$r(x_i, x_j)_p$ = Phenotypic correlation between i^{th} and j^{th} character.

$\text{COV}(x_i, x_j)_p$ = Phenotypic covariance between i^{th} and j^{th} character.

$V(x_i)_p$ = Phenotypic variance of i^{th} character.

$V(x_j)_p$ = Phenotypic variance of j^{th} character.

Genotypic coefficient of correlation (r_g)

$$r(x_i, x_j)_g = \frac{\text{COV}(x_i, x_j)_g}{\sqrt{V(x_i)_g \cdot V(x_j)_g}}$$

Where,

$r(x_i, x_j)_g$ = Genotypic correlation between i^{th} and j^{th} character.

$\text{COV}(x_i, x_j)_g$ = Genotypic covariance between i^{th} and j^{th} character.

$V(x_i)_g$ = genotypic variance of i^{th} character.

$V(x_j)_g$ = genotypic variance of j^{th} character.

Test of significance

Significance of correlation coefficients was tested by comparing phenotypic correlation coefficients with the table values (Fisher and Yates, 1963) at $(n-2)$ degrees of freedom at 5 % and 1 % level where 'n' denotes the total number of pairs of observations used in the calculation.

$$t = \frac{r}{\sqrt{\frac{1-r^2}{n-2}}}$$

Where,

t = test of significance

r = correlation coefficient

n = number of paired observations

3.5.5 Path coefficient analysis

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

Path coefficients were obtained by solving the following simultaneous equations.

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

Where,

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

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

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

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

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

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

$$\text{Residual effect (Pr}_y) = 1 - R^2$$

$$\text{Where, } R^2 = P_{1y}r_{1y} + P_{2y}r_{2y} + P_{3y}r_{3y} + \dots\dots\dots P_{iy}r_{iy}$$

$$Pr_y = \text{Residual effect}$$

$$P_{1y} = \text{Direct effect of } x_1 \text{ on } y.$$

$$r_{1y} = \text{Correlation coefficient of } x_1 \text{ and } y$$

$$P_{2y} = \text{Direct effect of } x_2 \text{ on } y$$

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

$$P_{3y} = \text{Direct effect of } x_3 \text{ on } y$$

$$r_{3y} = \text{Correlation coefficient of } x_3 \text{ and } y$$

$$P_{iy} = \text{Direct effect of } x_i \text{ on } y$$

$$r_{iy} = \text{Correlation coefficient of } x_i \text{ and } y$$

$$Pr_y = \sqrt{1 - P_{1y} r_{1y} + P_{2y} r_{2y} + \dots\dots\dots P_{ky} r_{ky}}$$

$$\text{Where } P_{ry} = \text{residual effect}$$

$$P_{1y} = \text{direct effect of } x_1 \text{ only}$$

$$r_{1y} = \text{correlation coefficient of } x_1 \text{ only}$$

Scales for path coefficients

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

3.5.6 Genetic divergence

3.5.6.1 Mahalanobis' D² analysis

The data collected on different yield contributing characters was analyzed using Mahalanobis' D² analysis to determine the genetic divergence among the genotypes (Mahalanobis, 1936).

3.5.6.1.1 Test of significance

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

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

Where,

Λ = Wilk's criterion

(E) = Determinant of error matrix and

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

n = degree of freedom for error + varieties and

$$\log_e \Lambda' V_{(Stat)} = -m \log_e \Lambda = -\left(n - \frac{P+Q+1}{2}\right) \log_e \Lambda'$$

Where,

m = $n - (P+Q+1)/2 = 2.3026 \log_{10} \Lambda'$

P = number of variables (or) characters (17)

Q = number of varieties –1 (or d.f.) / (or) populations (43)

$V_{(stat)}$ is distributed as χ^2 with PQ (731) degrees of freedom.

Transformation of correlated variables

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

3.5.6.1.2 Computation of D^2 values

For the given combination of i and j genotypes, the mean deviation *i.e.*, $Y_{it} - Y_{jt}$ for $t=1, 2 \dots p$ variables are computed and the D^2 values were calculated as

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

Where,

Y_i^t is uncorrelated mean value of i^{th} genotype for character 't'

Y_j^t is uncorrelated mean value of j^{th} genotype for character 't'

D_{ij}^2 is D^2 between i^{th} and j^{th} genotypes.

3.5.6.1.3 Testing the significance of D^2 values

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

3.5.6.1.4 Contribution of individual characters towards divergence

The character contribution towards genetic divergence was computed using the method given by Singh and Chaudhary (1977). In all combinations, each character was ranked on the basis of their contribution towards divergence between two entries ($d_i = Y_{it} - Y_{jt}$).

Where, d_i = mean deviation

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

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

Rank 1 is given to the highest mean difference and the rank P to the lowest difference, where, P is the total number of characters.

Percentage contribution towards genetic divergence was calculated using the following formula.

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

Where,

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

M = All possible combinations of number of genotypes considered.

3.5.6.1.5 Grouping of genotypes into various clusters

The grouping of genotypes into different clusters was done using the Tocher's method as described by Rao (1952). The criterion was that the two varieties belonging to the same cluster at least on an average show a smaller D^2 value than those belonging to different clusters. For this purpose D^2 values of all combinations of each genotype were arranged in ascending order of magnitude in a tabular form as described by Singh and Chaudhary (1977).

To start with, two populations having the closest distance from each other were considered, to which the third population having the smallest D^2 value from the first two populations was added. Similarly, the next nearest fourth population was considered and this procedure was continued. At certain stage when it was felt that after adding a particular population there was an abrupt increase in the average D^2 , that population was not considered for including in that cluster.

The genotypes of the first cluster were then eliminated and the rest were treated in a similar way. This procedure was continued till all the genotypes were included into one or other cluster.

3.5.6.1.6 Average intra- cluster distance

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

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

Where,

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

n = Number of all possible combinations

3.5.6.1.7 Average inter-cluster distance

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

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

Where,

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

n_i = Number of entries in cluster i

n_j = Number of entries in cluster j

3.5.6.2 Principal component analysis and cluster analysis

Principal component analysis was carried according to procedure described by Banfield (1978). PCA can be performed on two types of data matrices viz., variance-covariance matrix and correlation matrix. With characters of different scale a correlation matrix standardizing the original data set is preferred. If the characters are of same scale, a variance – covariance matrix can be used. In the present study, PCA was performed on the correlation matrix of traits, thereby removing the effects of scale (Jackson, 1991).

3.5.6.2.1 Eigen values and eigen vectors

The eigen values and eigen vectors were computed from data matrix. Eigen values define the amount of total variation that is displayed on principal

components. The proportion of variation accounted for each principal component (PC) is expressed as the eigen value divided by the sum of the eigen values.

$$\text{Per cent variance explained for PC}_1 = \frac{\text{Eigen value (PC}_1\text{)}}{\text{Sum of eigen values}}$$

The eigen vector (loading) defines the correlation of each variable with the principal components.

The principal components were identified by following procedure.

The j^{th} principal component (Y_j) of the observations X is the linear combination given as follows:

$$Y_j = A_{1j}X_1 + \dots + A_{pj}X_p$$

Where,

A_{ij} are found such that Y_j is uncorrelated $Y_1, Y_2, \dots, Y_{j-1}$ the j^{th} largest variance. The A_{ij} are the elements of the normalized eigen vector associated with largest j^{th} eigen value. The variance of the j^{th} principal component of the λ_j and the total system variance trace $(S) = \lambda_1 + \lambda_2 + \dots + \lambda_p$.

The importance of the j^{th} principal component is given by

$$\frac{\lambda_j}{\text{Trace (S)}}$$

This is informative about the proportion of total variation that can be accounted for the i^{th} principal component. The correlation between the i^{th} original variable X_i and the j^{th} principal component Y_j is given by

$$\rho(X_i, Y_j) = A_{ij} \frac{\sqrt{\lambda_j}}{\sqrt{S_i}}$$

Where S_i is the standard deviation of X_i .

Thus, a principal component is linear function of the test variables given as follows

$$\text{Principal component} = ax_1 + bx_2 + \dots + hx_8$$

Where, $a, b, \dots$ are coefficients and $x_1, x_2, \dots$ etc., are the variables in such a way that the principal component has a unit variance as reported by Ehrenberg (1985).

PCA scores for each genotype under concerned PCs were computed and utilized to derive a 2D or 3D (dimensional) scatter plot of individuals.

3.5.6.2.2 Cluster analysis

Agglomerative hierarchical clustering technique was followed as given by Anderberg (1993).

3.5.6.2.2.1. Obtaining data matrix

PCA scores for 44 genotypes were used as input for clustering because principal component analysis provides variable independence and balanced weighting of traits, which leads to an effective contribution of different characters on the basis of respective variation.

3.5.6.2.2.2. Standardizing the data matrix

To compare the similarities among the genotypes the data matrix was standardized with a column standardizing function *i.e.*, Q analysis. The data matrix is standardize in cluster analysis to make the characters contribute more equally to

the similarities among genotypes and to nullify the arbitrarily affect the units chosen for measuring the attributes among the genotypes.

Column standardizing function CA-Q analysis was carried by the following formula.

$$Z_{ij} = \frac{\overline{X}_{ij} - \overline{X}_j}{s_{ij}}$$

Where $\overline{X}_j = \sum_{i=1}^n X_{ij} / n$

$$s_{ij} = \sqrt{\sum_{i=1}^n \frac{X_{ij} - \overline{X}_j}{n-1}}$$

For

i= genotypes *i.e.*, 44

j = total variables *i.e.*,44

The resulting data after standardization is unit less and have mean zero and variance one.

3.5.6.2.2.3. Computing the resemblance matrix

A resemblance coefficient, which measures the overall resemblance (the degree of similarity or distance) between a pair of genotypes, was computed. Here 44 genotypes were taken in data matrix therefore resemblance coefficient was computed for a total of 946 combinations *i.e.*, $^{44}C_2$ ways. The data matrix was transformed to distance matrix (resemblance matrix) based on the dissimilarity coefficients using squared Euclidean distance method.

$$\text{Squared Euclidean distance } [d_{ij}] = \sum_{k=1}^P (X_{ik} - X_{jk})^2$$

Where,

P = Number of genotypes *i.e.*, 44

X_{ik} = Value of i^{th} genotype for k PCA scores

X_{jk} = Value of j^{th} genotype for k PCA scores

3.5.6.2.2.4 Execution of the clustering method

Distance matrix was converted into dendrogram by using Ward's method where the distance between two clusters is the sum of squares between two clusters summed over all variables. At each stage in the clustering procedure within cluster sum of squares is minimized over all partitions obtained by combining 2 clusters from previous stage.

3.5.6.2.3 Complete linkage diagram

This was one of the hierarchical methods as classified by Everitt (1974), starts with the computation of the 'distance' or similarities of each individual with every other individual. A comparison of such similarity coefficients among the pairs of individuals or objects finally leads to a tree diagram, referred as 'Dendrogram'. For the dendrogram, the clusters of homogeneous units can be identified.

Sorenson (1948) first developed the method, complete linkage dendrogram. This method was based on the distance matrix D .

Chapter IV

Results and Discussion

Chapter IV

RESULTS AND DISCUSSION

A systematic study was conducted to know the variability, heritability, genetic advance, character association, path coefficient analysis and genetic divergence at Horticultural Research Station, Lam, Guntur, Andhra Pradesh. The results obtained are presented under the following headings.

- Analysis of variance
- Mean performance of genotypes
- Variability, heritability and genetic advance as per cent of mean
- Character association analysis
- Path coefficient analysis
- Genetic diversity

4.1 ANALYSIS OF VARIANCE

The analysis of variance (Table 4.1) revealed significant differences among the genotypes for all the 20 characters studied indicating the presence of genetic variability among them. These results are in conformity with earlier reports of Nandadevi and Hosmani (2003), Vani *et al.* (2007a), Farhad *et al.* (2008), Patil *et al.* (2008), Jyothi *et al.* (2008), Tembhurne *et al.* (2008), Gupta *et al.* (2009), Kumari *et al.* (2010), Berhanu *et al.* (2011a), Arup *et al.* (2011), Kumar *et al.* (2012) and Lakshmi and Padma (2012), Tasso *et al.* (2014), Pandit and Ahikary (2014), Vijaya *et al.* (2014), Janaki *et al.* (2015c), Janaki *et al.* (2015d) and Leeladhar *et al.* (2016).

Table 4.1 : Analysis of variance for various characters in paprika (*Capsicum annuum* L.)

S.No.	Character	Mean sum of squares		
		Replications	Genotypes	Error
1	Plant height (cm)	0.16	257.11**	122.38
2	Plant spread (cm)	12.45	698.05**	187.34
3	Number of primary branches per plant	0.02	0.17**	0.04
4	Days to 50 per cent flowering	0.40	52.46**	12.59
5	Days to maturity	405.92	840.97**	121.33
6	Number of fruits per plant	78.09	2217.27**	97.27
7	Fruit length (cm)	2.10	10.32**	0.78
8	Fruit diameter (cm)	0.13	2.92**	0.11
9	Fruit pedicel length (cm)	0.20	0.68**	0.13
10	Number of seeds per fruit	192.63	1204.12**	85.28
11	Weight of seeds per fruit (g)	0.001	0.09**	0.004
12	1000 seed weight (g)	1.73	16.86**	0.73
13.	Ascorbic acid (mg/100g)	145.89	4674.56**	151.61
14	Oleoresin content (%)	0.53	16.66**	0.66
15	Capsaicin content (SHU)	1784670.75	36198080.00**	157919.25
16	Total extractable colour (ASTA units)	22.99	2376.67**	115.58
17	Red carotenoids (%)	0.0005	0.02**	0.0007
18	Yellow carotenoids (%)	0.00004	0.015**	0.0009
19	Total carotenoids (%)	0.0003	0.03**	0.0019
20	Dry fruit yield per plant (g)	0.10	2316.47**	178.91

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

4.2 MEAN PERFORMANCE OF GENOTYPES

The data on the mean performance recorded for thirteen quantitative and seven qualitative characters are presented in Table 4.2 and 4.3.

4.2.1 Plant height (cm)

The plant height ranged from 54.80 cm to 119.00 cm with a mean of 88.95 cm. The genotype LCA 446 recorded maximum plant height (119.00 cm) followed by LCA 457 (110.10 cm) while, the genotype LCA 513 recorded minimum plant height (54.80 cm).

4.2.2 Plant spread (cm)

The plant spread ranged from 57.40 cm to 176.00 cm with a mean of 128.89 cm. The genotype LCA 424 recorded maximum plant spread (176.00 cm) followed by LCA 430 (154.00 cm) while, the genotype LCA 513 recorded minimum plant spread (57.40 cm).

4.2.3 Number of primary branches per plant

The number of primary branches per plant was in the range of 2.30 to 4.20 with a mean of 3.57. The genotype LCA 446 recorded the highest number of primary branches (4.20) followed by LCA 425 (4.00), LCA 480 and Byadagi kaddi (4.00) while, the lowest number of branches were observed for LCA 513 (2.30).

4.2.4 Days to 50 per cent flowering

Days to 50 per cent flowering ranged from 41.50 to 65.50 with a mean of 59.97 days. The genotype Warangal chappatta single patti recorded maximum number of days to 50 per cent flowering (65.50) followed by LCA 441 (65.00) while LCA 436-1 (41.50) and LCA 424 (43.50) were the earliest to flower.

Table 4.2 : Mean performance of various quantitative characters in paprika (*Capsicum annuum* L.) genotypes.

Genotype	PH	PS	NPBP	DFF	DM	NFP	FL	FD	FPL	NSP	WSP	1000SW	DFYP
LCA 445	87.80	138.90	3.50	63.50	157.00	140.05	13.00	5.20	4.30	102.30	0.73	2.50	160.00
LCA 447	89.90	100.60	3.50	62.50	156.00	199.90	14.80	4.30	4.50	63.90	0.49	4.49	148.00
LCA 439	98.30	136.30	3.70	61.00	157.50	214.20	14.95	3.55	3.90	47.20	0.36	2.69	172.50
LCA 442	100.90	133.20	3.60	63.50	156.00	159.80	13.60	4.55	4.55	74.20	0.56	2.41	144.00
LCA 430	90.00	154.00	3.90	61.50	113.00	168.90	13.50	4.15	4.25	74.70	0.48	2.21	112.00
LCA 457	110.10	130.50	3.60	63.00	109.00	158.60	12.50	4.15	3.95	58.30	0.50	7.19	100.00
LCA 443	105.30	118.00	3.70	56.50	152.50	117.20	6.450	6.05	3.40	97.90	0.585	5.38	99.00
LCA 437	89.10	130.90	3.40	61.50	159.00	199.00	11.90	3.85	3.05	70.30	0.53	6.08	102.00
LCA 453	81.80	128.30	3.30	64.50	154.00	108.30	10.40	5.95	4.55	87.50	0.47	6.14	94.50
LCA 450	89.80	134.40	3.40	60.00	138.00	134.00	10.15	4.75	3.35	68.90	0.42	2.29	87.00
LCA 441	96.70	140.80	3.50	65.00	158.50	153.20	12.10	4.25	3.80	64.10	0.39	3.53	112.00
LCA 425	90.50	136.80	4.00	63.00	149.00	168.60	14.75	4.70	4.05	51.80	0.45	2.64	133.50
LCA 440	95.90	149.60	3.80	60.50	143.00	177.10	9.30	4.30	3.35	64.70	0.59	6.78	119.00
LCA 446	119.00	148.00	4.20	58.50	137.00	152.50	12.95	6.95	3.75	69.60	0.51	3.69	139.50
LCA 470	83.40	125.70	3.60	58.50	140.50	190.20	15.15	4.85	4.25	77.10	0.51	2.60	220.00
LCA 436-1	80.20	125.60	3.30	41.50	96.00	168.20	10.55	4.30	3.50	59.40	0.46	5.87	155.00
LCA 466	82.00	122.50	3.40	62.50	126.00	143.50	8.55	4.55	2.75	47.00	0.21	4.82	112.00
LCA 472	75.20	125.90	3.60	59.50	148.00	169.40	10.95	5.60	3.50	85.10	0.56	3.49	195.00

Genotype	PH	PS	NPBP	DFP	DM	NFP	FL	FD	FPL	NSP	WSF	1000SW	DFYP
LCA 476	81.60	127.50	3.50	64.00	137.00	179.85	13.15	4.90	4.05	54.90	0.34	5.61	162.50
LCA 480	83.10	132.40	4.00	61.00	138.00	197.10	11.55	4.85	3.90	53.90	0.32	2.59	144.00
LCA 482	87.40	126.10	3.50	61.00	137.50	138.60	10.95	4.35	3.65	70.90	0.48	7.48	108.00
LCA 498	86.30	133.90	3.60	62.00	140.00	167.00	10.75	5.40	2.90	64.60	0.45	7.47	136.00
LCA 465	82.50	127.80	3.30	61.00	163.50	206.90	11.55	5.25	3.70	45.20	0.33	6.41	135.50
LCA 475	79.50	136.10	3.50	64.00	137.50	163.60	13.65	3.95	3.65	39.50	0.32	7.58	152.00
LCA 488	95.00	139.40	3.80	63.50	127.50	183.00	12.80	4.55	3.45	45.80	0.25	5.05	137.00
LCA 499	77.30	114.00	3.50	56.50	141.00	159.80	12.15	4.70	3.95	56.70	0.37	5.34	129.50
LCA 506	79.40	130.80	3.70	62.00	131.00	161.30	11.80	5.10	3.50	63.30	0.42	7.69	185.00
LCA 503	86.70	136.00	3.50	63.00	108.50	171.60	13.00	4.10	3.65	64.40	0.29	5.87	164.00
LCA 490	86.70	138.60	3.90	61.50	134.50	154.30	12.55	4.50	3.80	73.90	0.47	2.81	174.50
LCA 501	85.20	124.65	3.40	60.00	138.50	206.10	12.60	4.45	3.95	68.10	0.43	6.07	179.00
LCA 504	96.70	133.30	3.70	61.50	149.00	192.80	14.00	3.50	4.00	51.20	0.28	4.53	140.50
LCA 510	78.60	84.60	3.40	59.50	154.50	164.30	8.85	3.30	2.15	37.80	0.35	5.30	92.50
LCA 510-1	75.00	89.20	3.60	62.00	150.00	133.90	8.95	3.35	2.50	41.80	0.43	8.20	84.00
LCA 511	108.80	132.20	3.70	58.50	125.00	108.50	12.05	6.35	3.75	98.80	0.70	9.75	97.00
LCA 512	108	126.10	3.50	63.00	133.50	107.20	10.80	5.35	3.30	137.10	1.05	9.43	103.00
LCA 513	54.80	57.40	2.30	58.50	87.00	113.90	11.90	3.80	3.05	37.30	0.26	8.75	102.50
Warangal chappatta single Patti	86.20	121.30	3.20	65.50	117.00	108.00	11.55	5.70	3.05	102.90	1.02	8.87	105.00
Warangal chappatta double Patti	91.80	117.80	3.40	59.00	112.00	120.50	8.30	9.70	2.40	154.00	1.35	18.10	95.00
Byadagi kaddi	83.0	141.10	4.00	52.50	97.50	118.70	16.80	2.55	3.70	45.40	0.25	8.40	82.00

Genotype	PH	PS	NPBP	DFF	DM	NFP	FL	FD	FPL	NSP	WSF	1000SW	DFYP
Byadagi dabbi	80.80	127.60	3.50	62.00	97.00	116.50	9.25	2.90	2.95	84.50	0.56	7.40	85.00
Kt-1	83.80	141.00	3.70	62.00	111.50	96.50	9.15	2.75	3.00	51.00	0.31	8.30	92.00
Jangareddy gudem Local	99.20	135.20	3.70	59.50	119.00	90.50	5.70	4.45	2.35	92.20	0.65	8.62	87.00
LCA-424	99.90	176.00	3.90	43.50	97.00	197.50	12.20	3.75	3.75	88.60	0.66	4.20	137.00
LCA 436	90.60	141.40	3.60	46.00	112.00	172.65	11.95	4.40	3.75	77.50	0.34	5.60	142.00
Mean	88.95	128.89	3.57	59.97	132.87	155.75	11.67	4.63	3.55	69.66	0.49	5.91	128.55
C.V	12.43	10.61	6.21	5.91	8.29	6.33	7.61	7.33	10.13	13.25	12.95	14.49	10.40
F ratio	2.10	3.72	3.47	4.16	6.93	22.79	13.07	25.29	5.26	14.11	24.19	22.92	12.94
S.E.	7.82	9.67	0.15	2.50	7.78	6.97	0.62	0.24	0.25	6.53	0.04	0.60	9.45
C.D.5%	22.30	27.60	0.44	7.15	22.21	19.89	1.79	0.68	0.72	18.62	0.12	1.72	26.97

*Bold values indicate maximum and minimum mean performance

Note :

PH – Plant height (cm), PS-Plant spread (cm), NPBP – Number of primary branches per plant, DFF – Days to 50 per cent flowering , DM- Days to maturity, NFP – Number of fruits per plant, FL – Fruit length (cm), FD – Fruit diameter (cm), FPL- Fruit pedicel length (cm), NSF – Number of seeds per fruit, WSF- Weight of seeds per fruit (g), 1000 SW- 1000 seed weight (g), DFYP – Dry fruit yield per plant (g).

Table 4.3 : Mean performance of qualitative characters in paprika (*Capsicum annuum* L.) genotypes

Genotype	Ascorbic acid (mg/100g)	Oleoresin content (%)	Capsaicin content (SHU)	Total extractable colour (ASTA)	Red Carotenoids (%)	Yellow carotenoids (%)	Total Carotenoids (%)
LCA 445	48.60	5.50	7673.50	141.87	0.18	0.15	0.33
LCA 447	42.55	7.30	8772.00	72.85	0.18	0.26	0.44
LCA 439	112.86	5.00	14045.50	91.06	0.03	0.12	0.15
LCA 442	39.36	9.00	10550.50	97.72	0.22	0.07	0.30
LCA 430	83.97	6.25	9746.50	136.53	0.26	0.18	0.44
LCA 457	51.55	6.75	7911.50	98.10	0.11	0.12	0.23
LCA 443	26.78	11.00	17994.50	130.00	0.10	0.15	0.26
LCA 437	40.20	9.35	9762.50	145.40	0.05	0.30	0.36
LCA 453	32.92	5.45	20767.50	173.52	0.13	0.17	0.30
LCA 450	95.05	8.50	3406.50	115.00	0.44	0.27	0.72
LCA 441	66.60	11.70	11676.00	94.40	0.07	0.31	0.37
LCA 425	67.08	7.10	3072.00	151.11	0.11	0.03	0.15
LCA 440	64.74	8.70	19498.50	47.50	0.26	0.22	0.48
LCA 446	78.68	7.20	9203.50	163.68	0.08	0.12	0.21
LCA 470	41.73	7.60	5730.00	120.12	0.28	0.16	0.44
LCA 436-1	39.12	7.80	11044.00	160.00	0.17	0.37	0.54
LCA 466	171.95	8.05	11326.00	95.72	0.07	0.27	0.34
LCA 472	51.99	7.05	4624.00	147.68	0.18	0.16	0.34
LCA 476	179.75	4.60	9044.50	37.50	0.31	0.23	0.55
LCA 480	167.31	11.50	4552.00	61.81	0.06	0.13	0.19
LCA 482	150.15	4.50	3002.50	113.64	0.34	0.18	0.53
LCA 498	125.89	7.50	14739.50	93.69	0.36	0.14	0.50
LCA 465	83.61	14.75	5142.50	149.57	0.07	0.34	0.42
LCA 475	126.45	4.90	13628.00	61.11	0.07	0.13	0.20
LCA 488	60.74	7.60	6983.50	56.34	0.12	0.37	0.50
LCA 499	61.65	6.30	7431.50	178.71	0.33	0.27	0.60
LCA 506	39.70	10.05	6308.50	81.60	0.06	0.27	0.32
LCA 503	55.72	7.00	5898.50	136.40	0.33	0.08	0.41
LCA 490	60.44	15.35	7518.50	78.36	0.05	0.07	0.12
LCA 501	82.73	7.30	7568.00	93.90	0.06	0.26	0.33
LCA 504	86.26	8.45	13159.50	100.38	0.16	0.27	0.44
LCA 510	207.30	7.90	16592.00	79.73	0.33	0.15	0.48
LCA 510-1	120.95	7.70	14343.00	67.75	0.46	0.10	0.56
LCA 511	73.39	9.00	8653.00	78.22	0.15	0.24	0.39
LCA 512	112.25	10.10	8660.50	118.14	0.36	0.25	0.62
LCA 513	124.96	9.10	7270.00	105.85	0.06	0.26	0.32
Warangal chappatta single patti	129.51	10.10	10431.50	98.28	0.14	0.26	0.40

Genotype	Ascorbic acid (mg/100g)	Oleoresin content (%)	Capsaicin content (SHU)	Total extractable colour (ASTA)	Red Carotenoids (%)	Yellow carotenoids (%)	Total Carotenoids (%)
Warangal chappatta double patti	72.93	14.55	5463.00	147.35	0.16	0.25	0.41
Byadagi kaddi	181.40	11.35	6052.50	115.00	0.16	0.26	0.42
Byadagi dabbi	138.30	6.70	6121.00	109.00	0.35	0.33	0.68
Kt-1	148.30	12.55	8779.50	141.04	0.27	0.13	0.41
Jangareddy gudem local	174.26	14.25	5072.50	116.60	0.11	0.25	0.36
LCA-424	115.16	13.25	8872.50	111.43	0.33	0.05	0.39
LCA-436	63.54	12.92	9568.50	101.68	0.13	0.08	0.21
Mean	93.14	8.83	9265.02	109.44	0.19	0.20	0.39
C.V	13.22	9.25	13.57	9.82	14.13	15.15	11.19
F ratio	30.83	24.95	22.91	20.56	39.29	16.82	20.36
S.E.	8.71	0.58	888.80	7.60	0.02	0.02	0.03
C.D. 5%	24.83	1.65	2534.89	21.68	0.05	0.06	0.09

*Bold values indicate maximum and minimum mean performance

Note :

SHU - Scoville Heat Unit

ASTA - American Spice Trade Association

4.2.5 Days to maturity

Days to maturity ranged from 87.00 to 163.50 with a mean of 132.87 days. The genotype LCA 465 recorded maximum no. of days to maturity (163.50) followed by LCA 437 (159.00) while, LCA 513 (87.00) was the earliest to mature.

4.2.6 Number of fruits per plant

The number of fruits per plant ranged from 90.50 to 214.20 with a mean of 155.75. The genotype LCA-439 (214.20) recorded the maximum number of fruits per plant followed by LCA-465 (206.90) while, the lowest was recorded for Jangareddy gudem local (90.50) preceded by Kt-1 (96.50).

4.2.7 Fruit length (cm)

The fruit length had the range of 5.70 cm to 16.80 cm with a mean of 11.67cm. The maximum fruit length was observed for the genotype Byadagi kaddi (16.80 cm) followed by LCA 470 (15.15 cm) and LCA 439 (14.95 cm) while, the minimum was recorded by Jangareddy gudem local (5.70cm) preceded by LCA 443 (6.45 cm).

4.2.8 Fruit diameter (cm)

The fruit diameter varied from 2.55 cm to 9.70cm with a mean of 4.63 cm. The maximum diameter was recorded by the genotype Warangal chappatta double patti (9.70 cm) followed by LCA 446 (6.95 cm) whereas, the minimum diameter was recorded by Byadagi kaddi (2.55 cm) preceded by Byadagi dabbi (2.90 cm).

4.2.9 Fruit pedicel length (cm)

The range of fruit pedicel length varied from 2.15cm to 4.55cm with a mean of 3.55 cm. The maximum fruit pedicel length was recorded by the genotype LCA-442 and LCA 453 (4.55cm) followed by LCA 447 (4.50cm). The minimum fruit

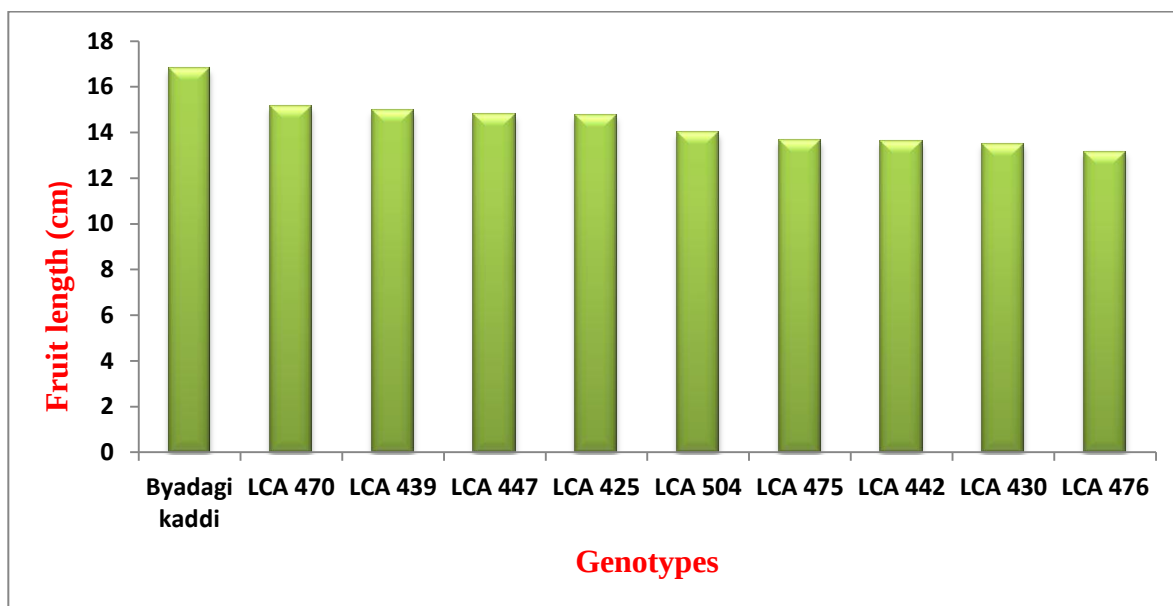


Fig 4.1 : Mean performance of promising paprika genotypes for fruit length

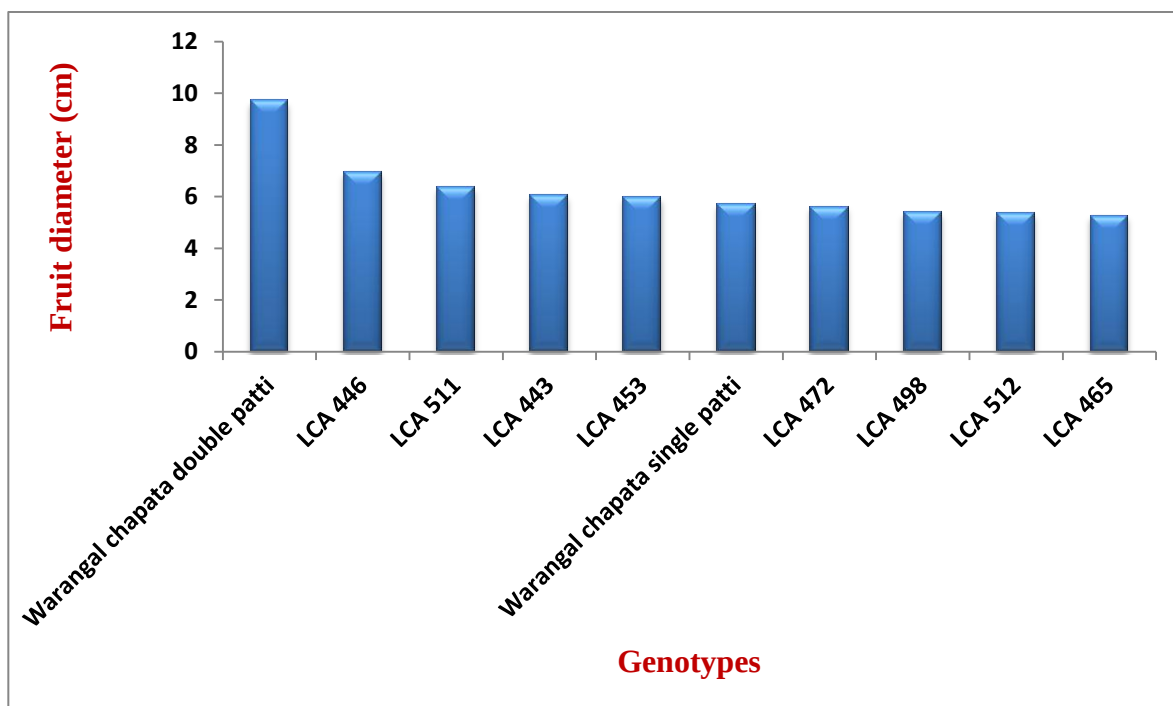


Fig 4.2: Mean performance of promising paprika genotypes for fruit diameter

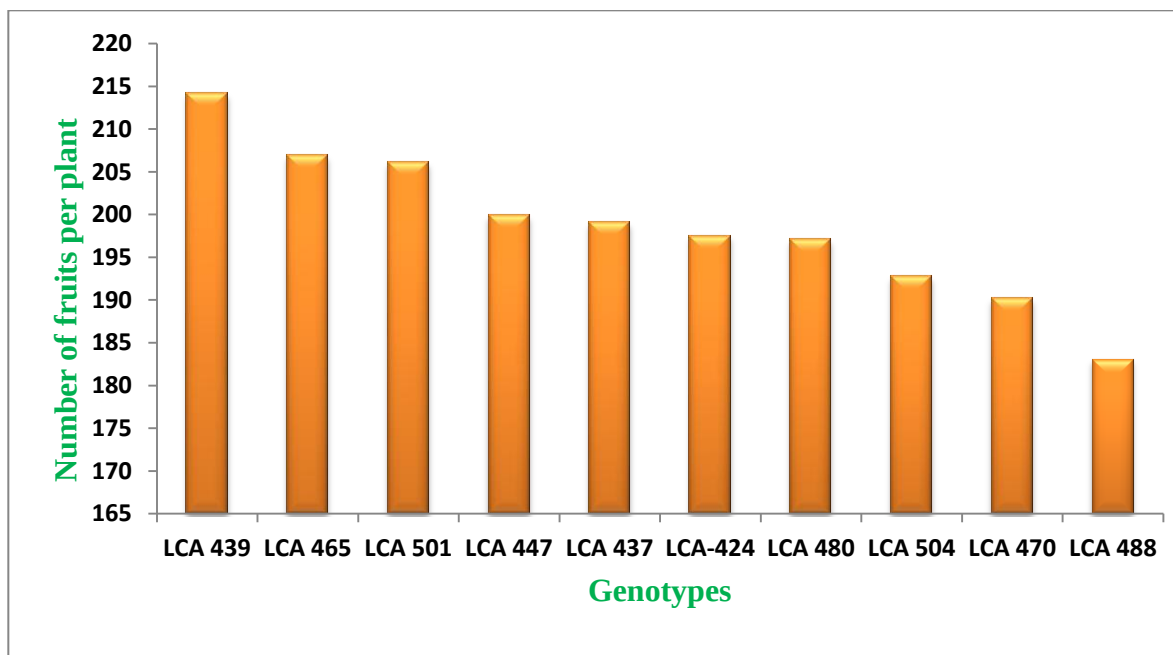


Fig 4.3: Mean performance of promising paprika genotypes for number of fruits per plant

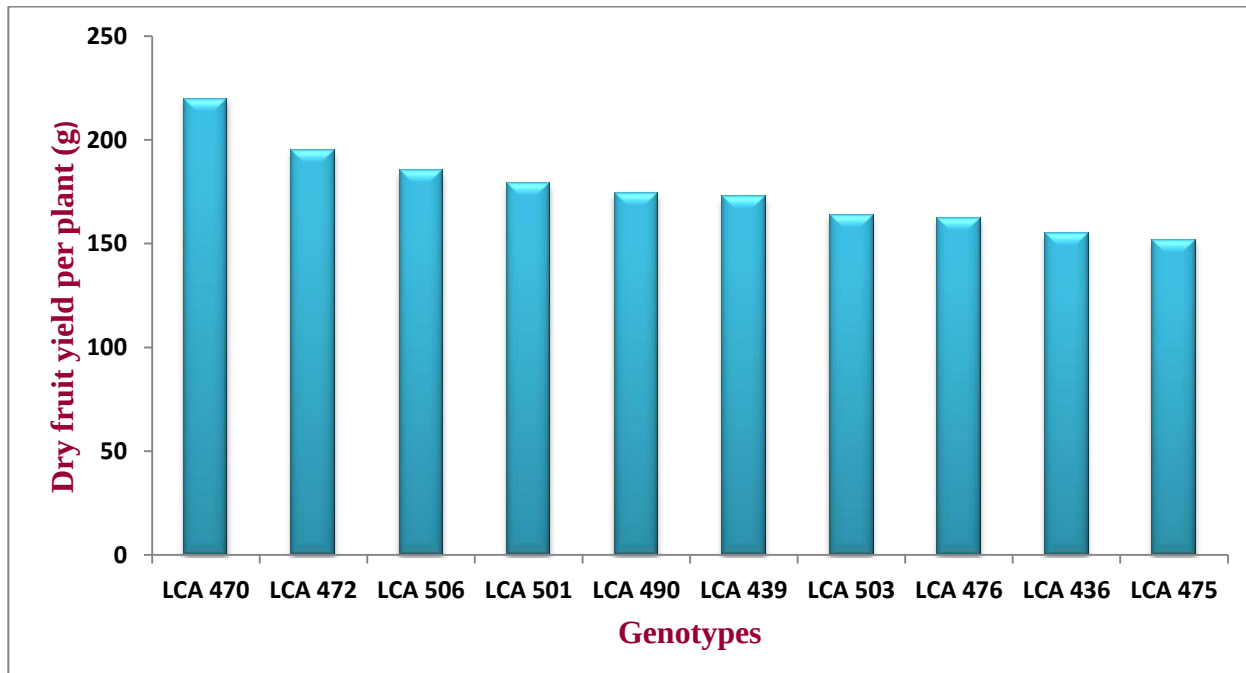


Fig 4.4 : Mean performance of promising paprika genotypes for dry fruit yield per plant



LCA- 439



LCA-465



LCA-501



LCA-447



LCA-437



LCA -424

Plate 2 : Promising paprika genotypes for number of fruits per plant



LCA-470



LCA-472



LCA-506



LCA-501



LCA-490



LCA-439

Plate 3 : Promising paprika genotypes for dry fruit yield per plant

pedicel length was recorded by LCA 510 (2.15 cm) preceded by Jangareddy gudem local (2.35 cm) and Warangal chappatta double patti (2.40 cm).

4.2.10 Number of seeds per fruit

The number of seeds per fruit ranged from 37.30 to 154.00 with a mean of 69.66. The highest mean performance for this trait was recorded by genotype the Warangal chappatta double patti (154.00) followed by LCA-512 (137.10) whereas, the lowest for LCA-513 (37.30) preceded by LCA-510 (37.80).

4.2.11 Weight of seeds per fruit (g)

The weight of seeds per fruit ranged from 0.21 g to 1.35 g with a mean of 0.490g. The highest mean performance for this trait was recorded by genotype Warangal chappatta double patti (1.35 g) followed by LCA 512 (1.05 g) whereas, the lowest by LCA466 (0.21 g) and by LCA 488 (0.25 g).

4.2.12 1000 seed weight (g)

The 1000 seed weight ranged from 2.21 g to 18.10 g with a mean of 5.91 g. The highest mean performance for this trait was recorded for genotype the Warangal Chappatta double patti (18.10 g) followed by LCA 511 (9.75 g) whereas, the lowest for LCA 430 (2.21 g) preceded by LCA 450 (2.29 g).

4.2.13 Dry fruit yield per plant (g)

The range of this character varied from 82.00g to 220.00g with a mean of 128.55 g. The maximum mean performance was observed for genotype LCA 470 (220.00 g) followed by LCA 472 (195.00 g) and LCA 506 (185.00 g) while the minimum value was observed for Byadagi kaddi (82.00 g) preceded by Byadagi dabbi (85.00 g) and Jangareddy gudem local (87.00 g).

4.2.14 Ascorbic acid (mg/100g)

The ascorbic acid content of fruits ranged from 26.78 mg to 207.30 mg with a mean of 93.14 mg. The highest ascorbic acid content was recorded in the genotype LCA 510 (207.30 mg) followed by Byadagi kaddi (181.40 mg) while the lowest was observed in LCA 443 (26.78 mg) preceded by LCA 453 (32.92 mg).

4.2.15 Oleoresin content (%)

The oleoresin content ranged from 4.50% to 15.35% with a mean of 8.83 per cent. The highest oleoresin content was recorded by the genotype LCA 490 (15.35%) followed by LCA 465 (14.75%) while the lowest was observed in LCA 482 (4.50%) preceded by LCA 476 (4.60%) and LCA 475(4.90%).

4.2.16 Capsaicin content (SHU)

The capsaicin content ranged from 3002.50 SHU to 20767.50 SHU with a mean of 9265.02 SHU. The highest capsaicin content was recorded by the genotype LCA-453 (20767.50 SHU) followed by LCA-440(19498.50 SHU) and LCA-443 (17994.50 SHU) while the lowest was observed in LCA-482 (3002.50 SHU) preceded by LCA 425(3072.00 SHU) and LCA-450(3406.50 SHU).

4.2.17 Total extractable colour (ASTA units)

The total extractable colour ranged from 37.50 to 178.71 with a mean of 109.44 ASTA units. The highest colour value was recorded for the genotype LCA-499 (178.71) followed LCA-453 (173.52) and the lowest was observed by LCA-476 (37.50) preceded by LCA-440 (47.50).

4.2.18 Red carotenoids (%)

The range of this character varied from 0.03 % to 0.46 % with a mean of 0.19 per cent. The maximum per cent was observed in genotypes LCA-510 (0.46

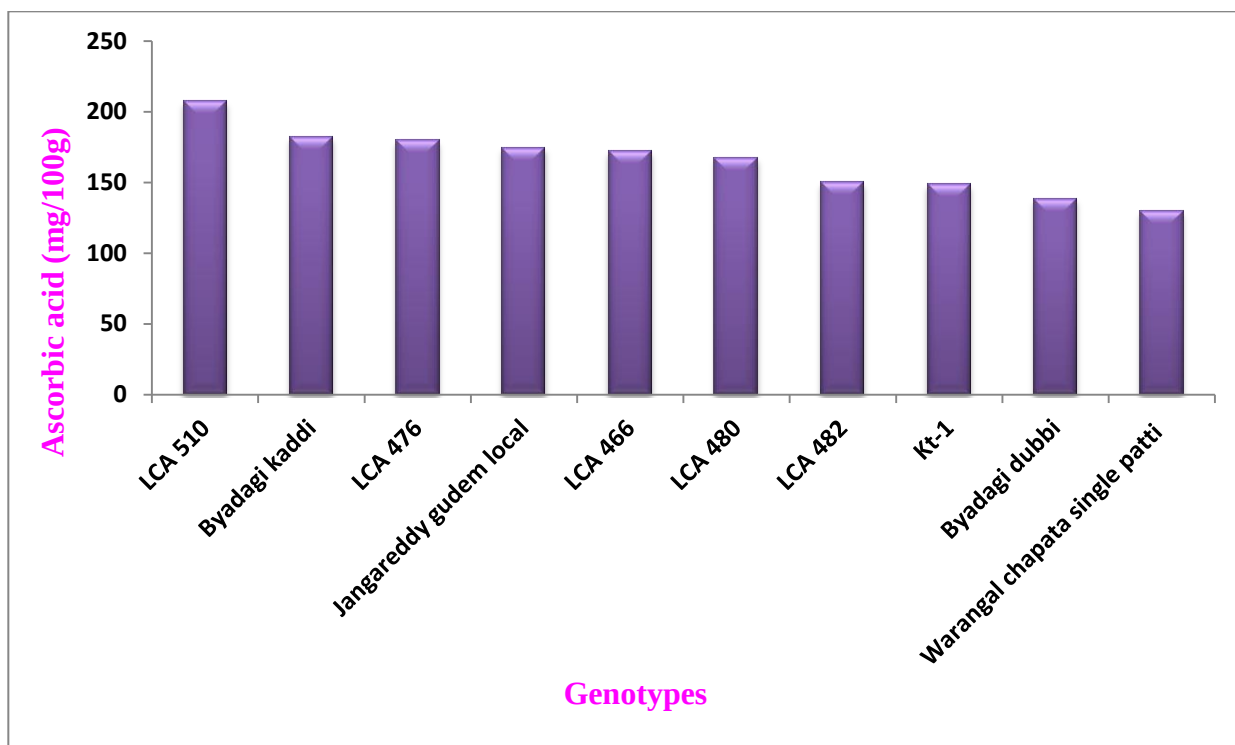


Fig 4.5 : Mean performance of promising paprika genotypes for ascorbic acid

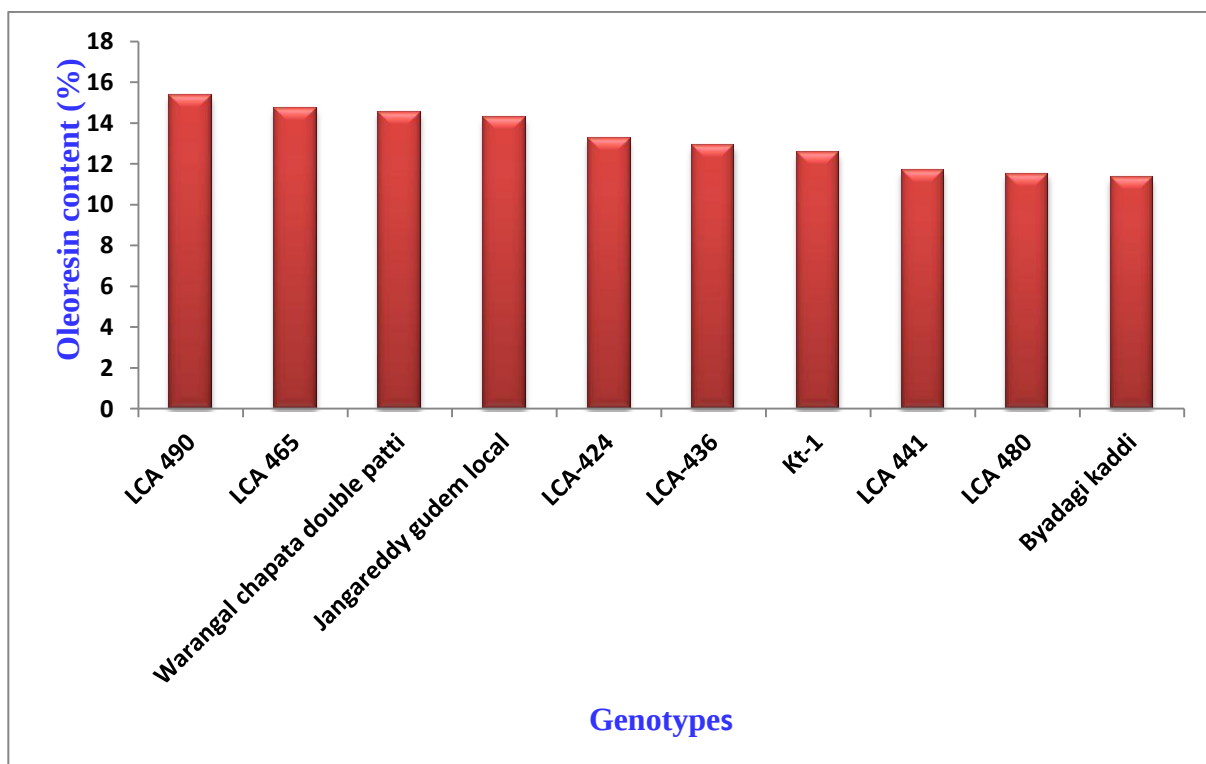


Fig 4.6 : Mean performance of promising paprika genotypes for oleoresin

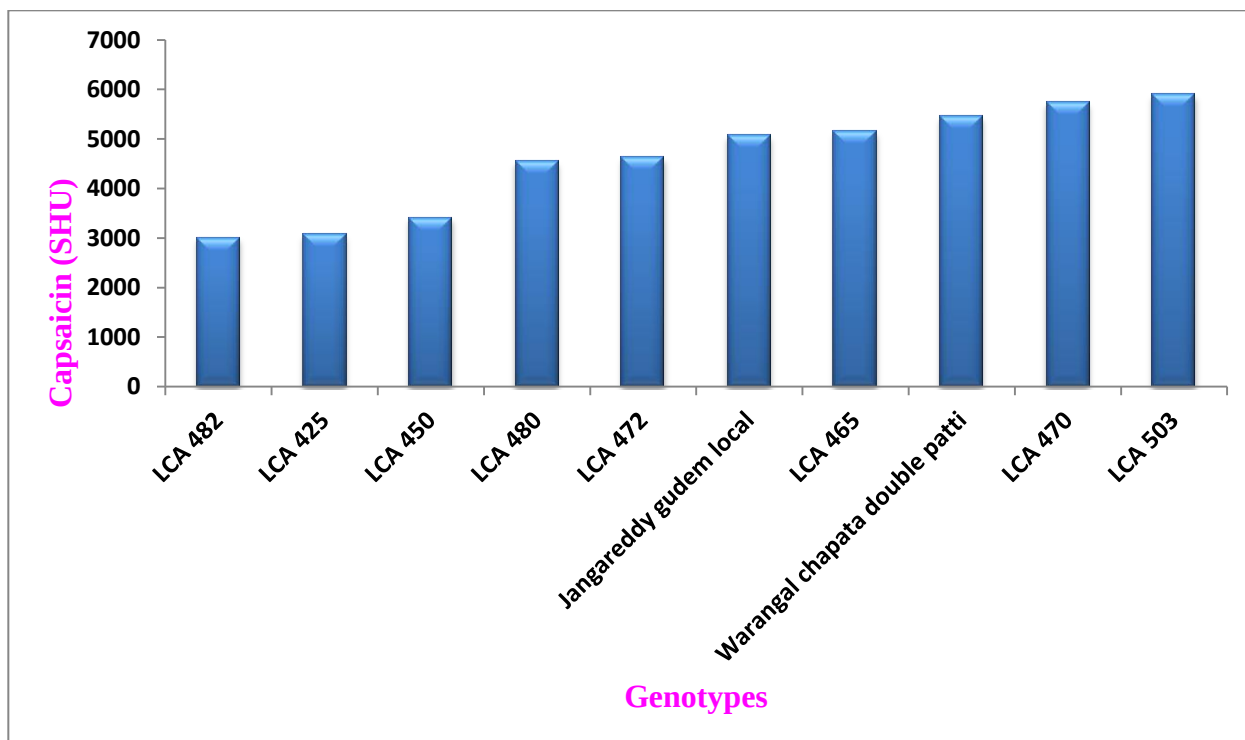


Fig 4.7 : Mean performance of promising paprika genotypes for capsaisin

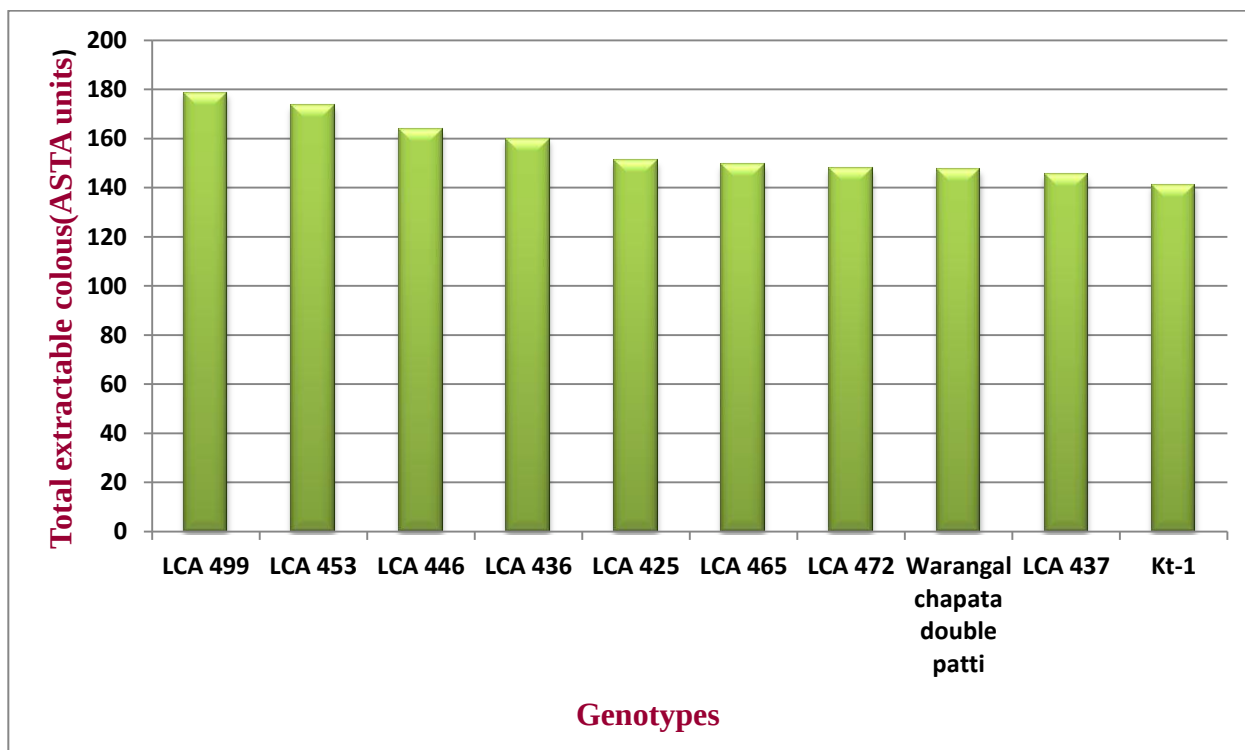


Fig 4.8 : Mean performance of promising paprika genotypes for total extractable colour



LCA-482



LCA-425



LCA-450



LCA-480



LCA-472



Jangareddy gudem local

Plate 4 : Promising paprika genotypes for capsaicin



LCA-499



LCA-453



LCA-446



LCA-436



LCA-425



LCA-465

Plate 5: Promising paprika genotypes for total extractable colour

%) followed by LCA 450 (0.44 %) while the minimum was recorded in LCA 439 (0.03 %) preceded by LCA 437 and LCA 490 (0.05 %).

4.2.19 Yellow carotenoids (%)

The range of this character varied from 0.03 % to 0.37 % with a mean of 0.20 per cent. The maximum per cent was observed for the genotype LCA-488 and LCA-436 (0.37 %) closely followed by LCA-465 (0.34 %) and Byadagi dabbi (0.33 %) while the minimum was observed in LCA-425(0.03 %) preceded by LCA-424 (0.05 %).

4.2.20 Total carotenoids (%)

The range of this character varied from 0.12% to 0.72% with a mean of 0.39 per cent. The maximum per cent was observed for the genotype LCA-450 (0.72%) closely followed by Byadagi dabbi (0.68%) and LCA-512 (0.62%) while the minimum per cent was recorded for LCA-490 (0.12%) preceded by LCA-439 and LCA-425 (0.15%).

In the present study, a high range of variability was observed for all the characters. It was maximum for capsaicin content (3002.50 to 20767.50) and minimum for yellow carotenoids (0.03% to 0.37%). The characters showing wide range of variation provide an ample scope for selecting desired types. These results are in accordance with those reported by earlier workers like Vani *et al.* (2007a), Farhad *et al.* (2008), Jyothi *et al.* (2008), Gupta *et al.* (2009), Thul *et al.* (2009), Kumari *et al.* (2010), Kumar *et al.* (2012), Lakshmi and Padma (2012), Naresh *et al.* (2013), Janaki *et al.*(2015c) and Shiva *et al.*(2015). These findings suggest that it is possible to isolate superior genotypes during the selection process.

4.3 VARIABILITY, HERITABILITY AND GENETIC ADVANCE AS PER CENT OF MEAN

In the present investigation estimates of mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in broad sense (h^2 (b)) and genetic advance as per cent of mean (GAM) were calculated and are presented in Table 4.4 and described character-wise here under.

4.3.1 Plant height (cm)

The observed PCV and GCV were moderate and low with 15.48 per cent and 9.23 per cent, respectively. The heritability (35.51%) as well as genetic advance as per cent of mean (11.33%) were moderate for this character indicating the operation of both additive and non-additive gene action and further improvement of this character would be easier through mass selection, progeny selection or any modified selection procedure aiming to exploit the additive gene effects rather than simple selection. Similar results are also reported by Begum (2002), Temdhurne *et al.* (2008), Jyothi *et al.* (2011) and Mahantesh *et al.* (2013a).

4.3.2 Plant spread (cm)

The observed PCV and GCV were moderate with 16.32 per cent and 12.40 per cent, respectively. The heritability (57.68%) as well as genetic advance as per cent of mean (19.40%) for this trait were also moderate indicating the operation of both additive and non-additive gene action and further improvement of this character would be easier through mass selection, progeny selection or any modified selection procedure aiming to exploit the additive gene effects rather than simple selection as suggested by earlier workers like similar results are also reported by Gogi and Gautam (2002), Manju and Sreelathakumary (2002), Rao (2005), Smitha and Basavaraja (2006a), Kumar *et al.* (2012) and Mahantesh *et al.* (2013a).

Table 4.4 : Estimates of mean, range, components of variance, heritability and genetic advance for yield and it's component Characters in paprika (*Capsicum annuum* L.)

S.No.	Character	Mean	Range	V _g	V _p	GCV (%)	PCV (%)	h ² (b) (%)	GA @ 5%	GAM @ 5%
1	PH	88.95	54.80- 119.00	67.38	189.74	9.23	15.48	35.51	10.08	11.33
2	PS	128.89	57.40-176.00	255.35	442.70	12.40	16.32	57.68	25.00	19.40
3	NPBP	3.57	2.30-4.20	0.06	0.11	6.92	9.30	55.31	0.38	10.60
4	DFP	59.97	41.50-65.50	19.93	32.53	7.44	9.51	61.28	7.20	12.00
5	DM	132.87	87.00-163.50	359.82	481.16	14.28	16.51	74.78	33.79	25.43
6	NFP	155.75	90.50-214.20	1060.00	1157.27	20.90	21.84	91.59	64.19	41.21
7	FL	11.67	5.70-16.80	4.77	5.56	18.71	20.20	85.79	4.17	35.69
8	FD	4.63	2.55-9.70	1.40	1.52	25.55	26.58	92.39	2.35	50.60
9	FPL	3.55	2.15-4.55	0.28	0.41	14.79	17.93	68.07	0.89	25.14
10	NSF	69.66	37.30-154.00	559.42	644.71	33.95	36.45	86.77	45.39	65.15
11	WSF	0.49	0.21-1.35	0.05	0.05	44.14	46.00	92.06	0.43	87.24
12	1000 SW	5.91	2.21-18.10	8.06	8.80	48.00	50.14	91.64	5.60	94.65
13	AA	93.14	26.78-207.30	2261.47	2413.09	51.05	52.74	93.72	94.84	101.81
14	OC	8.83	4.50-15.35	8.00	8.67	32.02	33.33	92.29	5.60	63.37
15	CC	9265.02	3002.50-20767.50	173090.80	188890.00	44.90	46.91	91.64	8204.21	88.55
16	TEC	109.44	37.50-178.71	1130.55	1246.13	30.72	32.26	90.72	65.97	60.28
17	RC	0.19	0.03-0.46	0.01	0.01	61.85	63.44	95.04	0.24	124.20
18	YC	0.20	0.03-0.37	0.01	0.01	42.60	45.21	88.77	0.17	82.68
19	TC	0.39	0.12-0.72	0.02	0.02	34.82	36.57	90.63	0.27	68.28
20	DFYP	128.55	82.00-220.00	1068.78	1247.69	25.43	27.48	85.66	62.33	48.48

Note :

PH – Plant height (cm), PS-Plant spread (cm), NPBP – Number of primary branches per plant, DFP – Days to 50 per cent flowering, DM –Days to maturity, NFP – Number of fruits per Plant, FL – Fruit length (cm), FD – Fruit diameter (cm), FPL- Fruit pedicel length (cm), NSF – Number of seeds per fruit, WSF- Weight of seeds per fruit (g), 1000 SW- 1000 seed weight (g), AA-Ascorbic acid(mg/100mg), O- Oleoresin content (%), CC- Capsaicin content (SHU), TEC- Total extractable colour (ASTA units), RC- Red carotenoids (%), YC- Yellow carotenoids (%), DFYP – Dry fruit yield per plant (g),

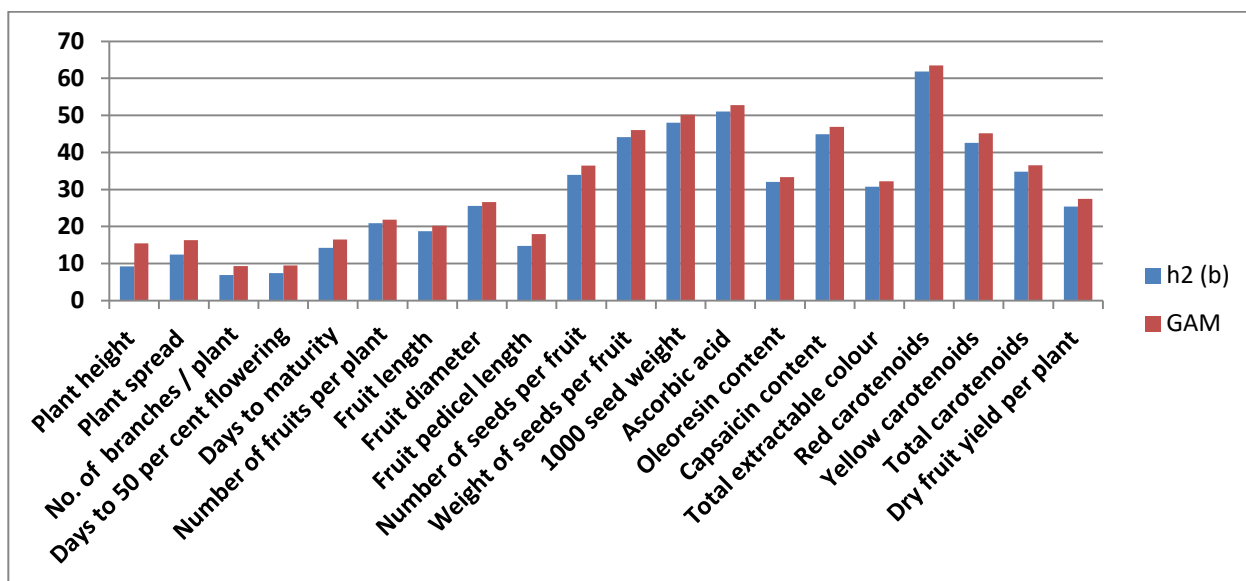


Fig 4.9: Phenotypic and genotypic coefficient of variation for different characters of paprika (*Capsicum annuum* L.)

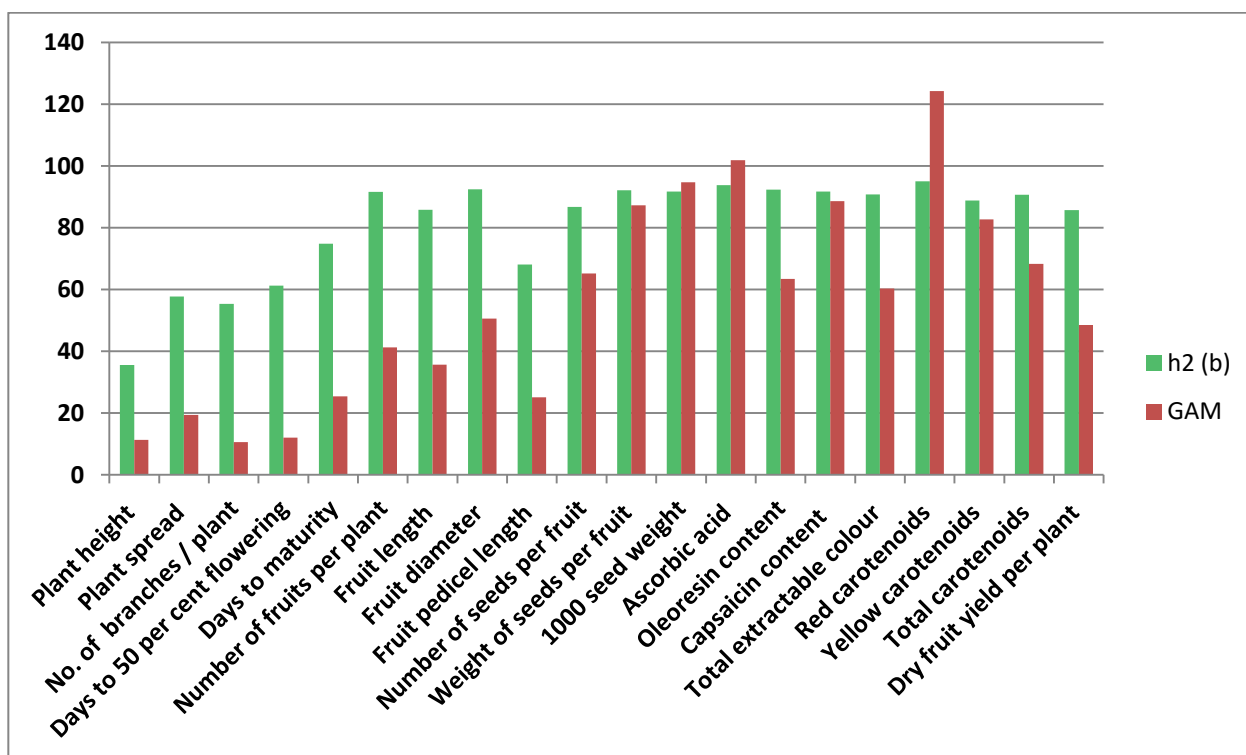


Fig 4.10 : Heritability and genetic advance as per cent of mean for different characters of paprika (*Capsicum annuum* L.).

4.3.3 Number of primary branches per plant

The estimates of PCV and GCV were low with 9.30 per cent and 6.92 per cent, respectively. These results are in conformity with those reported by Razzaq *et al.* (2016). The heritability (55.31%) as well as genetic advance as per cent of mean (10.60%) for this trait were also moderate. These results are in conformity with those reported by Begum (2002) and Bendale *et al.* (2006).

4.3.4 Days to 50 per cent flowering

The observed PCV and GCV were low with 9.51 per cent and 7.44 per cent respectively. The heritability recorded was high (61.28%) coupled with moderate genetic advance as per cent of mean (12%) for this character indicating the operation of both additive and non-additive gene action and further improvement of this character would be easier through mass selection, progeny selection or any modified selection procedure aiming to exploit the additive gene effects rather than simple selection. Similar results are also reported by Ajit and Manju (2006), Bendale *et al.* (2006), Bharadwaj *et al.* (2007), Kumar (2008), Tembhurne *et al.* (2008), Sandeep *et al.* (2008), Kumari *et al.* (2010), Amit *et al.* (2014), Vijaya *et al.* (2014), Janaki *et al.* (2015a), Rana *et al.* (2015), Satish *et al.* (2016) and Kranthi *et al.* (2016).

4.3.5 Days to maturity

The estimates of PCV and GCV were moderate with 16.51 per cent and 14.28 per cent, respectively. High heritability (74.78%) coupled with high genetic advance as per cent of mean (25.43%) were recorded for this trait. These results are in agreement with earlier workers (Manju and Sreelathakumary, 2002 and Sharma *et al.*, 2014).

4.3.6 Number of fruits per plant

The estimates of PCV and GCV were high with 21.84 per cent and 20.90 per cent, respectively. The heritability (91.59%) as well as genetic advance as per cent of mean (41.21%) for this trait were also high. These results are in agreement with those reported by many earlier workers viz., Smitha and Basavaraja (2007), Farhad *et al.* (2008), Tembhurne *et al.* (2008), Gupta *et al.* (2009), Sarkar *et al.* (2009), Kumari *et al.* (2010), Padhar and Zaveri (2010), Sharma *et al.* (2010), Munshi *et al.* (2010), Arup *et al.* (2011), Berhanu *et al.* (2011a), Singh and Singh (2011), Jyothi *et al.* (2011), Kumar *et al.* (2012), Lakshmi and Padma (2012), Mahanatesh *et al.* (2013a), Datta and Das (2013), Amit *et al.* (2014), Sharma *et al.* (2014), Pandit and Adhikary (2014), Vijaya *et al.* (2014), Ajith and Manju (2015), Satish *et al.* (2016), Patel *et al.* (2015), Janaki *et al.* (2015a), Priyanka and Madhvi (2016), Razzaq *et al.* (2016), Rosmaina *et al.* (2016) and Kranthi *et al.* (2016).

4.3.7 Fruit length (cm)

The estimates of PCV and GCV were high and moderate with 20.20 per cent and 18.71 per cent, respectively. The heritability (85.79%) and the genetic advance as per cent of mean (35.69%) were also high for this trait. Similar results are reported by Gogoi and Gautam (2002), Sreelathakumary and Rajamony (2002), Khurana *et al.* (2003), Prabhakaran *et al.* (2004), Verma *et al.* (2004), Mishra *et al.* (2005), Singh *et al.* (2005), Bharadwaj *et al.* (2007), Krishna *et al.* (2007a), Shirshat *et al.* (2007), Smitha and Basavaraja (2007), Sandeep *et al.* (2008), Farhad *et al.* (2008), Tembhurne *et al.* (2008), Gupta *et al.* (2009), Singh *et al.* (2009), Sarkar *et al.* (2009), Kumari *et al.* (2010), Padhar and Zaveri (2010), Sharma *et al.* (2010), Arup *et al.* (2011), Berhanu *et al.* (2011a), Jyothi *et al.* (2011), Kumar *et al.* (2012) and Lakshmi and Padma (2012), Amit *et al.* (2014), Sharma *et al.* (2014), Vijaya *et al.* (2014), Pandit and Adhikary (2014), Rana *et al.* (2015), Ajith and Manju (2015), Patel *et al.* (2015), Janaki *et al.* (2015a), Ashish *et al.* (2015) and Rosmaina *et al.* (2016).

4.3.8 Fruit diameter (cm)

The estimates of PCV and GCV were high with 26.58 per cent and 25.55 per cent, respectively. High heritability (92.39 %) coupled with high genetic advance as per cent of mean (50.60 %) was recorded for this trait. These findings are in agreement with reported by Gogoi and Gautam (2002). Sreelathakumary and Rajamony (2002), Khurana *et al.* (2003), Prabhudeva (2003), Prabhakaran *et al.* (2004), Verma *et al.* (2004), Bendale *et al.* (2006), Dutonde *et al.* (2006), Bharadwaj *et al.* (2007), Krishna *et al.* (2007a), Smitha and Basvaraja (2007), Sandeep *et al.* (2008), Sarkar *et al.* (2009), Singh *et al.* (2009), Berhanu *et al.* (2011a), Mahantesh *et al.* (2013a), Amit *et al.* (2014), Janaki *et al.* (2015a), Patel *et al.* (2015), Ashish *et al.* (2015), Ajith and Manju (2015), Satish *et al.* (2016), Meena *et al.* (2016) and Rosmaina *et al.* (2016).

4.3.9 Fruit pedicel length (cm)

The estimates of PCV and GCV were moderate with 17.93 per cent and 14.79 per cent, respectively. High heritability (68.07%) coupled with high genetic advance as per cent of mean (25.14%) was recorded for this trait. These findings are in agreement with Manju and Sreelathakumary (2002), Sarkar *et al.* (2009), Sandeep *et al.* (2008), Sharma *et al.* (2010), Pandit and Adhikary (2014) and Priyanka and Madhvi (2016).

4.3.10 Number of seeds per fruit

The estimates of PCV and GCV were high with 36.45 per cent and 33.95 per cent, respectively. The high heritability (86.77%) coupled with high genetic advance as per cent of mean (65.15%) recorded for this trait indicated the preponderance of additive gene action. Similar results are reported by Gogoi and Gautam (2002), Manju and Sreelathakumary (2002), Kashinath (2003), Khurana *et al.* (2003), Mishra *et al.* (2005), Rao (2005), Singh *et al.* (2005), Bendale *et al.* (2006), Shirshat *et al.* (2007), Farhad *et al.* (2008), Sandeep *et al.* (2008), Sarkar *et al.* (2009),

Kumari *et al.* (2010) and Arup *et al.* (2011), Jyothi *et al.* (2011), Shiva *et al.* (2014), Mahantesh *et al.* (2013), Amit *et al.* (2014), Pandit and Adhikary (2014), Vijaya *et al.* (2014), Ashish *et al.* (2015), Janaki *et al.* (2015a) and Ajith and Manju (2015).

4.3.11 Weight of seeds per fruit (g)

The estimates of PCV and GCV were high with 46.00 per cent and 44.14 per cent, respectively. The high heritability (92.06%) coupled with high genetic advance as per cent of mean (87.24 %) recorded for this trait. Similar results are reported by Shirshat *et al.* (2007), Vani *et al.* (2007a), Singh *et al.* (2009) and Ashish *et al.* (2015).

4.3.12 1000 seed weight (g)

The estimates of PCV and GCV were high with 50.14 per cent and 48.00 per cent, respectively. The high heritability (91.64%) coupled with high genetic advance as per cent of mean (94.65%) recorded in this study are in accordance with those reported by Mini and Khader (2004), Mishra *et al.* (2005), Smitha and Basavaraja (2006a), Sarkar *et al.* (2009), Pandit and Adhikary (2014) and Ajith and Manju (2015).

4.3.13 Dry fruit yield per plant (g)

The estimates of PCV and GCV were high with 27.48 per cent and 25.43 per cent, respectively. The heritability (85.66%) as well as genetic advance as per cent of mean (48.48%) were high for this trait. These results are in agreement with earlier workers viz., Bharadwaj *et al.* (2007), Vani *et al.* (2007a), Farhad *et al.* (2008), Sandeep *et al.* (2008), Sarkar *et al.* (2009), Gupta *et al.* (2009), Singh *et al.* (2009), Kumari *et al.* (2010), Padhar and Zaveri (2010), Sharma *et al.* (2010), Datta and jana (2010), Arup *et al.* (2011), Berhanu *et al.* (2011a), Jyothi *et al.* (2011), Kumar *et al.* (2012), Mahantesh *et al.* (2013a), Amit *et al.* (2014), Sharma *et al.* (2014), Ashish *et al.* (2015), Pandit and Adhikary (2014), Vijaya *et al.* (2014),

Janaki *et al.* (2015a), Rana *et al.* (2015), Satish *et al.* (2016), Meena *et al.* (2016), Priyanka and Madhvi (2016), Razzaq *et al.* (2016) and Kranthi *et al.* (2016).

4.3.14 Ascorbic acid (mg/100g)

The estimates of PCV and GCV were high with 52.74 per cent and 51.05 per cent, respectively. High heritability (93.72%) coupled with high genetic advance as per cent of mean (101.81%) recorded for this trait. Similar results were reported from earlier works of Mallikarjun (2001), Mishra *et al.* (2005), Shirshat *et al.* (2007), Farhad *et al.* (2008), Sharma *et al.* (2010), Arup *et al.* (2011), Mahantesh *et al.* (2013a), Patel *et al.* (2015) and Priyanka and Madhvi (2016).

4.3.15 Oleoresin content (%)

The estimates of PCV and GCV were high with 33.33 per cent and 32.02 per cent, respectively. High heritability (92.29%) coupled with high genetic advance as per cent of mean (63.37%) was recorded for this trait also. Similar results were reported by Mallikarjun (2001), Manju and Sreelathakumary (2002), Singh *et al.* (2009), Kumari *et al.* (2010) and Vijaya *et al.* (2014).

4.3.16 Capsaicin content (SHU)

The estimates of PCV and GCV were high with 46.91 per cent and 44.90 per cent, respectively. The heritability (91.64 %) and the genetic advance as per cent of mean (88.55 %) recorded for this trait were high. Similar results were observed by Manju and Sreelatha kumary (2002), Prabhakaran *et al.* (2004), Dutonde *et al.* (2006), Bharadwaj *et al.* (2007), Gupta *et al.* (2009), Singh *et al.* (2009), Sood *et al.* (2009), Datta and jana (2010), Kumari *et al.* (2010), Kumar *et al.* (2012), Datta and Das (2013), Vijaya *et al.* (2014), Patel *et al.* (2015) and Ajith and Manju (2015).

4.3.17 Total extractable colour (ASTA units)

The estimates of PCV and GCV were high with 32.26 per cent and 30.72 per cent, respectively. High heritability (90.72%) coupled with high genetic advance as

per cent of mean (60.28%) was recorded for this trait indicating the preponderance of additive gene action making selection effective. These results are in agreement with the earlier reports of Mallikarjun (2001), Khurana *et al.* (2003), Singh *et al.* (2007), Gupta *et al.* (2009), Kumari *et al.* (2010), Datta and Jana (2010), Naresh *et al.* (2013), Mahantesh *et al.* (2013a) and Patel *et al.* (2015).

4.3.18 Red carotenoids (%)

The estimates of PCV and GCV were high with 63.44 per cent and 61.85 per cent, respectively. The heritability (95.04 %) as well as genetic advance as per cent of mean (124.20 %) were high for this trait.

4.3.19 Yellow carotenoids (%)

The estimates of PCV and GCV were high with 45.21 per cent and 42.60 per cent, respectively. High heritability (88.77 %) coupled with high genetic advance as per cent of mean (82.68%) was recorded for this trait.

4.3.20 Total carotenoids (%)

The estimates of PCV and GCV were high with 36.57 per cent and 34.82 per cent, respectively. High heritability (90.63 %) coupled with high genetic advance as per cent of mean (68.28 %) was recorded for this trait and these findings are in agreement with those reported by Naresh *et al.* (2013) who also recorded high PCV and GCV estimates for red, yellow and total carotenoids in chilli

As indicated by the results on variability and heritability, the estimates of phenotypic variance were higher than the corresponding genotypic variance for all the characters studied indicating the influence of environment in the expression of these traits. Since these estimates alone do not provide means to assess the nature of genetic variability, the phenotypic and genotypic coefficients of variation are also estimated to draw conclusions. In the present study, the PCV was significantly

higher than GCV for all the traits. It is obvious because PCV includes variability due to genotype and genotype and environment interaction.

The difference between the phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was found to be narrow for number of fruits per plant suggesting that these traits were least affected by the environment and selection for these traits based on phenotypic would be rewarding. The difference between PCV and GCV was found wide for rest of the characters indicating that the apparent variation was not only due to genotypes but also due to influence of environment.

High heritability coupled with high genetic advance as per cent of mean was recorded for all the characters except plant height, plant spread, number of primary branches per plant and days to 50 per cent flowering indicating the preponderance of additive gene action making the selection more effective. However, operation of both additive and non-additive gene action was indicated for plant height, plant spread, number of primary branches per plant and days to 50 per cent flowering through moderate genetic advance. Further improvement of this character would be easier through mass selection, progeny selection or any modified selection procedure aiming to exploit the additive gene effects rather than simple selection.

Similar observations were made by Gogoi and Gautam (2002), Begum (2002), Manju and Sreelathakumary (2002), Mallikarjun *et al.* (2003b), Sreelathakumary and Rajamony (2004), Rao (2005), Bendale *et al.* (2006), Smitha and Basavaraja (2006a), Chatterjee (2006), Bharadwaj *et al.* (2007), Kumar (2008), Temdhurne *et al.* (2008), Sandeep *et al.* (2008), Kumari *et al.* (2010), Jyothi *et al.* (2011), Kumar *et al.* (2012), Mahantesh *et al.* (2013a), Amit *et al.* (2014), Vijaya *et al.* (2014), Janaki *et al.* (2015a), Rana *et al.* (2015), Satish *et al.* (2016), Kranthi *et al.* (2016) and Meena *et al.* (2016) who also suggested selection based on phenotypic characters which are less influenced by environment.

4.4 CHARACTER ASSOCIATION

In the present investigation, phenotypic and genotypic correlation coefficients between dry fruit yield per plant and other related component characters and among themselves were estimated and are presented in Table 4.5 and 4.6.

4.4.1 Character association analysis among ten quantitative characters

4.4.1.1 Plant height (cm)

Plant height showed significant and positive correlation with plant spread (0.5853** and 0.4851**), primary branches per plant (0.5515** and 0.6215**), fruit diameter (0.2308** and 0.4234**), number of seeds per fruit (0.3307** and 0.5477**) and weight of seeds per fruit (0.3115** and 0.4517**) at both phenotypic and genotypic levels, where increase in one character will lead to increase in second and *vice versa* thus indicating possibility of simultaneous selection for these traits. Plant height showed significant and positive correlation with fruit pedicel length (0.2748**) at genotypic level indicating that there is strong association between these two traits genetically, where the phenotypic value is lessened by significant interaction of environment. At both phenotypic and genotypic levels plant height showed negative and non- significant association with yield per plant (-0.1532 and -0.0438) which clearly indicated the independent nature of two characters and selection for high dry fruit yield based on plant height is not reliable. Similar results were also reported by Begum (2002), Acharya and Rajput (2003), Khurana *et al.* (2003), Ajjappalavara *et al.* (2005), Rao *et al.* (2006), Khader and Mini (2006), Ahmed *et al.* (2006), Reddy *et al.* (2008), Hosamani and Shivakumar (2008), Sharma *et al.* (2010), Singh and Singh (2011), Berhanu *et al.* (2011b), Kumar *et al.* (2012) and Satish *et al.* (2015).

Table 4.5 : Phenotypic (above diagonal) and genotypic (below diagonal) correlation coefficients among quantitative characters in paprika (*Capsicum annuum* L.)

Character	PH	PS	NPBP	DFF	DM	NFP	FL	FD	FPL	NSF	WSF	1000SW	DFYP
PH	1.0000	0.5853**	0.5515**	-0.0113	0.1392	-0.0321	0.0047	0.2308*	0.1596	0.3307**	0.3115**	-0.0295	-0.1532
PS	0.4851**	1.0000	0.6573**	-0.1263	-0.0498	0.1589	0.1511	0.0233	0.2523*	0.1431	0.0529	-0.2234*	0.1208
NPBP	0.6215**	0.7757**	1.0000	-0.0539	0.1409	0.1617	0.1803	0.0055	0.1709	0.0294	-0.0155	-0.2361*	0.0990
DFF	0.0112	-0.2227*	-0.1083	1.0000	0.3665**	-0.1050	0.0458	0.0564	0.0531	-0.0461	-0.0048	-0.0296	-0.0260
DM	0.1439	-0.0730	0.1275	0.6156**	1.0000	0.3289**	0.0430	0.1180	0.1833	-0.0930	-0.0439	-0.3542**	0.1912
NFP	0.0290	0.2726*	0.2609*	-0.1210	0.3884**	1.0000	0.4736**	-0.1719	0.3884**	-0.3844**	-0.3622**	-0.4885**	0.6149**
FL	0.0541	0.3145*	0.2367*	0.0155	0.1050	0.5385**	1.0000	-0.2036	0.7011**	-0.2697*	-0.2700*	-0.3877**	0.4723**
FD	0.4234**	0.0036	-0.0204	0.1058	0.1549	-0.1914	-0.2521*	1.0000	-0.0024	0.6307**	0.6158**	0.3440**	0.0486
FPL	0.2748**	0.5152**	0.3423**	0.0091	0.3574**	0.4355**	0.7364**	-0.0355	1.0000	-0.0468	-0.1891	-0.5176**	0.4307**
NSF	0.5477**	0.2499*	-0.0031	-0.0382	-0.1045	-0.4405**	-0.3407**	0.7131**	-0.1027	1.0000	0.8672*	0.3871**	-0.1211
WSF	0.4517**	0.0663	-0.0667	0.0610	-0.1062	-0.3894**	-0.3063**	0.6824**	-0.2269*	0.9566**	1.0000	0.4976**	-0.1780
1000 SW	-0.1285	-0.3623**	-0.4293**	0.0014	-0.4534**	-0.5327**	-0.4140**	0.3883**	-0.6327**	0.4268**	0.5315**	1.0000	-0.4433**
DFYP	-0.0438	0.2923**	0.2296*	-0.1012	0.2772**	0.6957**	0.5269**	0.0812	0.5908**	-0.1245	-0.2013	-0.4765**	1.0000

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

Note :

PH – Plant height (cm), PS-Plant spread (cm), NPBP – Number of primary branches per plant, DFF – Days to 50 per cent flowering , DM- Days to maturity, NFP – Number of fruits per plant, FL – Fruit length (cm), FD – Fruit diameter (cm), FPL- Fruit pedicel length (cm), NSF – Number of seeds per fruit, WSF- Weight of seeds per fruit (g), 1000 SW- 1000 seed weight (g), DFYP – Dry fruit yield per plant (g).

Table 4.6 : Phenotypic (above diagonal) and genotypic (below diagonal) correlation coefficients among qualitative characters and yield per plant in paprika (*Capsicum annuum* L.)

Character	Ascorbic acid (mg /100g)	Oleoresin content (%)	Capsaicin content (SHU)	Total extractable colour (ASTA Units)	Red carotenoids (%)	Yellow carotenoids (%)	Total carotenoids (%)	Dry fruit yield Per plant (g)
Ascorbic acid (mg /100g)	1.0000	0.0505	-0.0575	-0.3234**	0.2261*	0.0231	0.2065	-0.3482**
Oleoresin content (%)	0.0361	1.0000	-0.1764	0.0338	-0.2308*	0.0591	-0.1599	-0.1793
Capsaicin content (SHU)	-0.0705	-0.1913	1.0000	-0.1621	-0.0039	-0.1024	-0.0682	-0.1720
Total extractable colour (ASTA Units)	-0.3656**	0.0442	-0.2010	1.0000	0.0005	0.0139	0.0105	-0.0752
Red carotenoids (%)	0.2227*	-0.2477*	-0.0093	-0.0120	1.0000	-0.1023	0.7753**	-0.2066
Yellow carotenoids (%)	0.0254	0.0368	-0.1257	-0.0064	-0.1221	1.0000	0.5484**	-0.1879
Total carotenoids (%)	0.2091	-0.1950	-0.0866	-0.0110	0.7835**	0.5211**	1.0000	-0.2956**
Dry fruit yield Per plant (g)	-0.3953**	-0.2040	-0.1800	-0.1101	-0.2383*	-0.2235*	-0.3469**	1.0000

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

4.4.1.2 Plant spread (cm)

Plant spread showed significant and positive correlation with plant height (0.5853** and 0.4851**), primary branches per plant (0.6573** and 0.7757**), fruit pedicel length (0.2523** and 0.5152**) at both phenotypic and genotypic levels, where increase in one character will lead to increase in second and *vice versa* indicating possibility of simultaneous selection for these traits. At both phenotypic and genotypic levels plant spread showed significant and negative association with 1000 seed weight (-0.2234** and -0.3623**) indicating that simultaneous selection for these traits is not possible. This trait showed significant and positive association with number of fruits per plant (0.2726*), fruit length (0.3145*) and dry fruit yield per plant (0.2923*) at genotypic level indicating that there is strong association between these traits with plant spread genetically, where the phenotypic value is lessened by significant interaction of environment. Significant and negative association with days to 50% flowering (-0.2227*) at genotypic level was observed indicating that there is strong association between these two traits genetically while the phenotypic value is lessened by significant interaction of environment. Similar results were earlier reported by Chatterjee *et al.* (2007).

4.4.1.3 Number of primary branches per plant

At both phenotypic and genotypic levels this trait showed significant and positive association with plant height (0.5515** and 0.6215**), plant spread (0.6573** and 0.7757**) indicating simultaneous selection for these traits. At genotypic level this trait showed positive and significant association with number fruits per plant (0.2609*), fruit length (0.2367*), fruit pedicel length (0.3423*) and yield per plant (0.2296*) indicating strong association of these traits with number of primary branches per plant genetically while the phenotypic value is lessened by significant interaction of environment. At both phenotypic and genotypic levels number of primary branches per plant showed significant and negative association with 1000 seed weight (-0.2361** and -0.4293**) indicating simultaneous selection

for these traits is not possible. Similar results were also reported by Acharya and Rajput (2003), Reddy *et al.* (2008) and Rohini and Lakshmanan (2015).

4.4.1.4 Days to 50 per cent flowering

At both phenotypic and genotypic levels this trait showed positive and significant association with days to maturity (0.3665** and 0.6156**) indicating that simultaneous selection of these traits is possible. These findings are in conformity with the previous reports of Kumar *et al.* (2014), Vikram *et al.* (2014) and Satish *et al.* (2015). This trait showed significant and negative association with plant spread (-0.2227*) at genotypic level indicating that there is strong association between these two traits genetically, where the phenotypic value is lessened by significant interaction of environment. At both phenotypic and genotypic levels this trait showed negative and non-significant association with yield per plant (-0.0260 and -0.1012) clearly indicating the independent nature of these two characters and selection for dry fruit yield based on days to 50% flowering is not reliable. These findings are in agreement with those reported by Acharya and Rajput (2003), Choudary and Samadia (2004), Ahmed *et al.* (2006), Farhad *et al.* (2008), Reddy *et al.* (2008), Hasanuzzaman and Faruq (2011) and Kumar *et al.* (2012).

4.4.1.5 Days to maturity

Days to maturity recorded positive and significant association at both phenotypic and genotypic levels with days to 50% flowering (0.3665** and 0.6156**) and number of fruits per plant (0.3289** and 0.3884**) indicating that simultaneous selection of these traits is possible. At both phenotypic and genotypic levels this trait showed significant and negative association with 1000 seed weight (-0.3542** and -0.4534**) indicating simultaneous selection for these traits is not possible. This trait showed significant and positive association with fruit pedicel length (0.3574**) and dry fruit yield per plant (0.2772**) at genotypic level indicating that there is strong association between these traits genetically, where the

phenotypic value is lessened by significant interaction of environment. These findings are in agreement with Berhanu *et al.* (2011b).

4.4.1.6 Number of fruits per plant

This trait showed significant and positive association with days to maturity (0.3289** and 0.3884**), fruit length (0.4736** and 0.5385**), fruit pedicel length (0.3884** and 0.4355**) and dry fruit yield per plant (0.6149 ** and 0.6957**) at both phenotypic and genotypic levels indicating that simultaneous improvement of these traits is possible. The fruit number had significant and positive association with plant spread (0.2726**), number of primary branches per plant (0.2609**) at genotypic level indicating that there is strong association between these traits genetically and can be influenced by interaction of environment. At both phenotypic and genotypic levels this trait showed significant and negative association with number of seeds per fruit (-0.3844** and -0.4405**), weight of seeds per fruit (-0.3622** and -0.3894**) and 1000 seed weight (-0.4885** and -0.5327**) indicating that simultaneous selection for fruit number, number of seeds per fruit, weight of seeds per fruit and 1000 seed weight is not possible.

Similar association of these characters with yield were noticed by Begum (2002), Choudary and Samadia (2004), Krishna *et al.* (2007 b), Singh *et al.* (2007), Farhad *et al.* (2008), Reddy *et al.* (2008), Tembhurne *et al.* (2008), Gupta *et al.* (2009), Jabeen *et al.* (2009), Patel *et al.* (2009), Singh *et al.* (2009), Arup *et al.* (2011), Hasanuzzaman and Faruq (2011), Singh and Singh (2011), Kumar *et al.* (2012), Lahbib *et al.* (2012), Srividhya and Ponnuswamy (2012), Mahantesh *et al.* (2013b), Vijaya *et al.* (2014), Rohini and Lakshmanan (2015), Satish *et al.* (2015), Rinchan *et al.* (2015), Hasan *et al.* (2016) and Priyanka and Mishra (2016).

4.5.1.7 Fruit length (cm)

Positive fruit length associated with number of fruit per plant (0.4736** and 0.5385**), fruit pedicel length (0.7011** and 0.7364**) and dry fruit yield per plant

(0.4723** and 0.5269**) at both phenotypic and genotypic levels indicating that simultaneous improvement of these traits is possible. At both phenotypic and genotypic levels this trait showed significant and negative association with number of seeds per fruit (-0.2697** and -0.3407**), weight of seeds per fruit (-0.2700** and -0.3063**) and 1000 seed weight (-0.3877** and -0.4140**) indicating that simultaneous selection for fruit length, number of seeds per fruit, weight of seeds per fruit and 1000 seed weight is not possible. The fruit length had significant positive association with plant spread (0.3145*) and number of primary branches per plant (0.2367*) and significant negative association with fruit diameter (-0.2521*) at genotypic level indicating strong association between these characters with fruit length genetically.

Similar association of these characters with yield were noticed by Begum (2002), Ajjappalavara *et al.* (2005), Ahmed *et al.* (2006), Khader and Mini (2006), Jayashree *et al.* (2007), Krishna *et al.* (2007b), Singh *et al.* (2007), Vani *et al.* (2007a), Gupta *et al.* (2009), Patel *et al.* (2009), Sharma *et al.* (2010), Hasanuzzaman and Faruq (2011), Singh and Singh (2011), Berhanu *et al.* (2011b), Kumar *et al.* (2012), Srividhya and ponnuswamy (2012), Mahantesh *et al.* (2013), Vikram *et al.* (2014), Kumar *et al.* (2014), Vijaya *et al.* (2014), Rohini and Lakshmanan (2015), Satish *et al.* (2015) and Priyanka and Mishra (2016).

4.4.1.8 Fruit diameter (cm)

At both phenotypic and genotypic levels fruit diameter was recorded significant and positive association with plant height (0.2308* and 0.4234*), number of seeds per fruit (0.6307** and 0.7131**), weight of seeds per fruit (0.6158** and 0.6824**) and 1000 seed weight (0.3440** and 0.3883**) indicating that simultaneous selection of these traits is possible. Significant negative association with fruit length (-0.2521*) at genotypic level indicated strong association between these two characters genetically, but the phenotypic value was lessened by significant interaction of environment. At both phenotypic and

genotypic levels this trait showed positive and non-significant association with yield per plant (0.0486 and 0.0812) clearly indicating the independent nature of these two characters and hence selection for dry fruit yield based on fruit diameter is not reliable. These results are in accordance with the findings of Begum (2002), Acharya and Rajput (2003), Ajjappalavara *et al.* (2005), Rao *et al.* (2006) and Lahbib *et al.* (2012).

4.4.1.9 Fruit pedicel length (cm)

At both phenotypic and genotypic levels this trait showed significant and positive association with plant spread (0.2523* and 0.5152*), number of fruits per fruit (0.3884** and 0.4355**), fruit length (0.7011** and 0.7364**) and dry fruit yield per plant (0.4307** and 0.5908**) indicating that simultaneous selection of these traits is possible. At both phenotypic and genotypic levels this trait showed significant and negative association with 1000 seed weight (-0.5176** and -0.6327**) indicating that simultaneous selection for fruit pedicel length, 1000 seed weight is not possible. Significant positive association of pedicel length with plant height (0.2748**), number of primary branches per plant (0.3423**) and days to maturity (0.3574**) and significant negative association with weight of seeds per fruit (-0.2269*) at genotypic level indicated strong association between these characters with fruit pedicel length genetically, but the phenotypic value was lessened by significant interaction of environment. These results are in accordance with the findings of Pandit *et al.* (2009) and Hasan *et al.* (2016).

4.4.1.10 Number of seeds per fruit

At both phenotypic and genotypic levels this trait showed significant and positive association with plant height (0.3307** and 0.5477**), fruit diameter (0.6307** and 0.7131**), weight of seeds per fruit (0.8672** and 0.9566**) and 1000 seed weight (0.3871** and 0.4268**) indicating possibility of simultaneous selection of these traits. The no. of seeds per fruit showed significant and negative association with number of fruits per plant (-0.3844* and -0.4405*) and fruit length

(-0.2697** and -0.3407**) at both phenotypic and genotypic levels indicating that simultaneous selection of these traits is not possible. At genotypic level, this trait showed significant and positive association with plant spread (0.2499**) indicating strong association between these characters with fruit pedicel length genetically, but the phenotypic value is lessened by significant interaction of environment. At both phenotypic and genotypic levels this trait showed negative and non-significant association with yield per plant (-0.1211 and -0.1245) clearly indicating the independent nature of these two characters and selection for dry fruit yield based on number of seeds per fruit is not reliable. These results corroborate with the findings of Begum (2002), Khurana *et al.* (2003), Ajjappalavara *et al.* (2005), Arup *et al.* (2011), Hasanuzzaman and Faruq (2011) and Rohini and Lakshmanan (2015).

4.4.1.11 Weight of seeds per fruit (g)

At both phenotypic and genotypic levels this trait showed significant and positive association with plant height (0.3115** and 0.4517**), fruit diameter (0.6158** and 0.6824**), number of seeds per fruit (0.8672** and 0.9566**) and 1000 seed weight (0.4976** and 0.5315**) indicating that simultaneous selection of these traits is possible. At both phenotypic and genotypic levels this trait showed significant and negative association with number of fruits per plant (-0.3622** and -0.3894**) and fruit length (-0.2700** and -0.3063**) indicating that simultaneous selection of these traits is not possible. At genotypic level, seed weight had significant negative association with fruit pedicel length (-0.2269*) indicating strong association between these characters with fruit pedicel length genetically, but the phenotypic value is lessened by significant interaction of environment. At both phenotypic and genotypic levels this trait showed negative and non-significant association with yield per plant (-0.1780 and -0.2013) clearly indicating the independent nature of these two characters and selection for dry fruit yield based on number of seeds per fruit is not reliable. These findings are in conformity with the previous reports of Shiva *et al.* (2015).

4.4.1.12 1000 seed weight (g)

At both phenotypic and genotypic levels this trait showed significant and positive association with fruit diameter (0.3440** and 0.3883**), number of seeds per fruit (0.3871** and 0.4268**) and weight of seeds per fruit (0.4976** and 0.5315**) indicating possibility of simultaneous selection of these traits. At both phenotypic and genotypic levels seed weight showed significant and negative association with plant spread (-0.2234** and -0.3623**), number of primary branches per plant (-0.2361* and -0.4293**), days to maturity (-0.3542** and -0.4534**), number of fruits per plant (-0.4885** and -0.5327**), fruit length (-0.3877** and -0.4140**) fruit pedicel length (-0.5176** and -0.6327**) and dry fruit yield per plant (-0.4433** and -0.4765**) indicating that simultaneous selection of these traits is not possible. These findings are in conformity with the previous reports of Gogoi and Gautam (2003), Hari *et al.* (2005), Chatterjee *et al.* (2007) and Kumar *et al.* (2014).

4.4.1.13 Dry fruit yield per plant (g)

This trait showed significant and positive association with number of fruits per plant (0.6149** and 0.6957**), fruit length (0.4723** and 0.5269**), fruit pedicel length (0.4307** and 0.5908**) at both phenotypic and genotypic levels. Since most of the important morphological parameters are showing strong significant positive association with dry fruit yield per plant rational improvement in yield is possible through simultaneous selection for these component characters. The yield per plant had significant positive association with plant spread (0.2923**), number of primary branches per plant (0.2296**) and days to maturity (0.2772**) at genotypic level indicating strong association between these characters with yield per plant genetically while the phenotypic value is lessened by significant interaction of environment. At both phenotypic and genotypic levels this trait showed significant and negative association with 1000 seed weight (-0.4433** and -0.4765**) indicating that simultaneous selection of these traits is not possible.

These results are in accordance with earlier observations of Farhad *et al.* (2008), Reddy *et al.* (2008), Gupta *et al.* (2009), Jabeen *et al.* (2009), Patel *et al.* (2009), Singh *et al.* (2009), Padhar and Zaveri (2010), Arup *et al.* (2011), Hasanuzzaman and Faruq (2011), Singh and Singh (2011), Kumar *et al.* (2012), Lahbib *et al.* (2012), Tasso *et al.* (2014), Kumar *et al.* (2014), Vikram *et al.* (2014), Rohini and Lakshmanan (2015) and Priyanka and Mishra (2016).

4.4.2 Character association analysis among six qualitative characters and yield per plant

4.4.2.1 Ascorbic acid (mg/100g)

At both phenotypic and genotypic levels this trait showed significant and positive association with red carotenoids (0.2261* and 0.2227**) which suggested that selection for red carotenoids based on ascorbic acid is beneficial. At both phenotypic and genotypic levels this trait showed significant and negative association with total extractable colour (-0.3234** and -0.3656**) and dry fruit yield per plant (-0.3482** and -0.3953**) indicating that simultaneous selection of these traits is not possible. These findings are in conformity with the previous report of Farhad *et al.* (2008).

4.4.2.2 Oleoresin content (%)

At both phenotypic and genotypic levels this trait showed significant and negative association with red carotenoids (-0.2308* and -0.2477**) indicating that simultaneous selection of these traits is not possible. This trait showed non-significant and positive association with ascorbic acid (0.0505 and 0.0361), total extractable colour (0.0338 and 0.0442) and yellow carotenoids (0.0591 and 0.0368) at both phenotypic and genotypic levels. At both phenotypic and genotypic levels this trait showed non-significant and negative association with yield per plant (-0.1793 and -0.2040). This clearly indicated the independent nature of these two characters and selection for dry fruit yield based on oleoresin content is not reliable.

These results are in line with earlier findings of Gupta *et al.* (2009) and Arup *et al.* (2011).

4.4.2.3 Capsaicin content (SHU)

Capsaicin content had negative association with yield per plant (-0.1720 and -0.1800) both at phenotypic and genotypic levels which was not significant. This clearly indicated the independent nature of these two characters and selection for dry fruit yield based on capsaicin content is not reliable. These results are similar to the earlier observations of Arup *et al.* (2011) and Shiva *et al.* (2015).

4.4.2.4 Total extractable colour (ASTA units)

At both phenotypic and genotypic levels, this trait showed significant and negative association with ascorbic acid (-0.3234** and -0.3656**) indicating that simultaneous selection of these traits is not possible. Further, at phenotypic and genotypic levels this trait showed negative association with dry fruit yield per plant (-0.0752 and -0.1101) which was not significant. This clearly indicated the independent nature of these two characters and selection for dry fruit yield based on total extractable colour is not reliable. At both phenotypic and genotypic levels this trait showed non-significant and positive association with oleoresin content (0.0338 and 0.0442). These results are in accordance with earlier observations of Gupta *et al.* (2009) and Shiva *et al.* (2015).

4.4.2.5 Red carotenoids (%)

Both at phenotypic and genotypic levels, this trait showed significant and positive association with ascorbic acid (0.2261** and 0.2227**) and total carotenoids (0.7753** and 0.7835**) indicating that simultaneous selection of these traits is possible. At both phenotypic and genotypic levels this trait showed significant and negative association with oleoresin content (-0.2308** and -0.2477**) indicating that simultaneous selection of these traits is not possible. At genotypic level this trait showed significant and negative association with yield per

plant (-0.2383*) indicating strong association between these characters with red carotenoids genetically. These results are in accordance with earlier observations of Naresh *et al.* (2013).

4.4.2.6 Yellow carotenoids (%)

At both phenotypic and genotypic levels, yellow carotenoids showed significant and positive association with total carotenoids (0.5484** and 0.5211**) indicating that simultaneous selection of these traits is possible. At genotypic level this trait showed significant negative association with dry fruit yield per plant (-0.2235*) indicating strong association between these characters with yellow carotenoids genetically, but the phenotypic value is lessened by significant interaction of environment. These results are in accordance with earlier observations of Naresh *et al.* (2013)

4.4.2.7 Total carotenoids (%)

At both phenotypic and genotypic levels, total carotenoids showed significant and positive association with red carotenoids (0.7753** and 0.7835**) and yellow carotenoids (0.5484** and 0.5211**) indicating that simultaneous selection of these traits is possible. Total carotenoids showed significant and negative association with dry fruit yield per plant (-0.2956** and -0.3469**) both at phenotypic and genotypic levels indicating that simultaneous selection of these traits is not possible. . These results are in accordance with earlier observations of Naresh *et al.* (2013)

4.4.2.8 Dry fruit yield per plant (g)

The per plant yield showed significant negative association with ascorbic acid (-0.3482** and -0.3953**) and total carotenoids (-0.2956** and -0.3469**) at both phenotypic and genotypic levels indicating that simultaneous selection of these traits is not possible. This trait showed significant and negative association with red carotenoids (-0.2383**) and yellow carotenoids (-0.2235*) at genotypic level indicating that there is strong association between these two characters genetically,

where the phenotypic value is lessened by significant interaction of environment. These results are in accordance with previous reports of Farhad *et al.* (2008).

From the study it was observed that in general, genotypic correlation coefficients were of higher magnitude than the phenotypic correlation coefficients. The correlation study indicated that number of fruits per plant, fruit length and fruit pedicel length had positive significant association with yield per plant at both phenotypic and genotypic levels indicating the importance of these traits in selection for yield and are identified as yield attributing characters on which selection can be relied upon for the genetic improvement of yield in paprika

4.5 PATH COEFFICIENT ANALYSIS

Upon assessment of apparent relationship between yield and yield components, it is necessary to partition the direct and indirect effects of each character on yield to understand the nature of association at genotypic and phenotypic level.

As a guideline for interpretation of the results of path analysis, the following broad points as suggested by Singh and Chaudhary, 1977 are considered. If the correlation coefficient between a causal factor and the effect is almost equal to its direct effect, then correlation explains the true relationship and a direct selection through this trait will be effective. If the correlation coefficient is positive, but the direct effect is negative or negligible, the indirect effects seem to be the cause of positive correlation. In such situations, the indirect causal factors are to be considered simultaneously for selection. Under the circumstances where correlation coefficient may be negative but the direct effect is positive and high, a restricted simultaneous selection model is to be followed *i.e.*, restrictions are to be imposed to nullify the undesirable indirect effects in order to make use of the direct effect. In case correlation coefficient as well as direct effect are negative, the selection based on that character has to be dropped.

Thus, the direct and indirect effects of different quantitative and qualitative traits on dry fruit yield per plant were estimated through path analysis at phenotypic and genotypic levels and are presented in Table 4.7, 4.8, 4.9 and 4.10 (Fig 4.11, 4.12, 4.13 and 4.14).

4.5.1 Direct and indirect effects of quantitative characters on yield per plant

4.5.1.1 Plant height (cm)

This trait showed high and negative direct effect on yield per plant at phenotypic level (-0.3160) and moderate and negative direct effect at genotypic level (-0.1512).

At phenotypic level, this trait exhibited negligible positive indirect effect on yield per plant via plant spread (0.0503), number of primary branches per plant (0.0210), fruit length (0.0011), fruit diameter (0.0575), number of seeds per fruit (0.0671) and 1000 seed weight (0.0080) and negligible and negative indirect effect via days to 50 per cent flowering (-0.0003), days to maturity (-0.0061), number of fruits per plant (-0.0151), fruit pedicel length (-0.0051) and weight of seeds per fruit (-0.0156).

At genotypic level, this trait showed negligible and positive indirect effect on yield per plant through days to maturity (0.0373), number of fruits per plant (0.0007), fruit length (0.0045), fruit pedicel length (0.0320) and 1000 seed weight (0.0512) ; high and positive indirect effect through plant spread (0.4117) and weight of seeds per fruit (0.6189) and high and negative indirect effect through primary branches per plant (-0.3378) and number of seeds per fruit (-0.9888) and moderate and positive indirect effect through fruit diameter (0.2817) and negligible and negative indirect effect via days to 50 per cent flowering (-0.0039).

Plant height showed non-significant and negative correlation with yield per plant (-0.1532 and -0.0438) at both phenotypic and genotypic levels. Negative direct

Table 4.7 : Phenotypic path analysis showing direct (diagonal) and indirect effects of quantitative characters on yield per plant in paprika (*Capsicum annuum* L.)

Character	PH	PS	NPBP	DFF	DM	NFP	FL	FD	FPL	NSF	WSF	1000SW
PH	-0.3160	-0.1849	-0.1743	0.0036	-0.0440	0.0102	-0.0015	-0.0729	-0.0504	-0.1045	-0.0984	0.0093
PS	0.0503	0.0860	0.0565	-0.0109	-0.0043	0.0137	0.0130	0.0020	0.0217	0.0123	0.0045	-0.0192
NPB	0.0210	0.0250	0.0381	-0.0021	0.0054	0.0062	0.0069	0.0002	0.0065	0.0011	-0.0006	-0.0090
DFF	-0.0003	-0.0033	-0.0014	0.0265	0.0097	-0.0028	0.0012	0.0015	0.0014	-0.0012	-0.0001	-0.0008
DM	-0.0061	0.0022	-0.0062	-0.0161	-0.0438	-0.0144	-0.0019	-0.0052	-0.0080	0.0041	0.0019	0.0155
NFP	-0.0151	0.0747	0.0761	-0.0494	0.1547	0.4704	0.2228	-0.0808	0.1827	-0.1808	-0.1704	-0.2298
FL	0.0011	0.0364	0.0434	0.0110	0.0104	0.1141	0.2409	-0.0490	0.1689	-0.0650	-0.0650	-0.0934
FD	0.0575	0.0058	0.0014	0.0141	0.0294	-0.0428	-0.0507	0.2492	-0.0006	0.1572	0.1535	0.0857
FPL	-0.0051	-0.0081	-0.0055	-0.0017	-0.0059	-0.0125	-0.0226	0.0001	-0.0322	0.0015	0.0061	0.0167
NSF	0.0671	0.0290	0.0060	-0.0094	-0.0189	-0.0780	-0.0547	0.1280	-0.0095	0.2030	0.1760	0.0786
WSF	-0.0156	-0.0027	0.0008	0.0002	0.0022	0.0182	0.0135	-0.0309	0.0095	-0.0435	-0.0501	-0.0249
1000 SW	0.0080	0.0608	0.0642	0.0081	0.0964	0.1329	0.1055	-0.0936	0.1408	-0.1053	-0.1354	-0.2720
'r' with DFYP	-0.1532	0.1208	0.0990	-0.0260	0.1912	0.6149**	0.4723**	0.0486	0.4307**	-0.1211	-0.1780	-0.4433**

r' – Correlation coefficient , *: Significant at 5 per cent level; **: Significant at 1 per cent level R SQUARE = 0.5597 RESIDUAL EFFECT = 0.663

Note :

PH – Plant height (cm), PS-Plant spread (cm), NPBP – Number of primary branches per plant, DFF – Days to 50 per cent flowering , DM- Days to maturity, NFP – Number of fruits per plant, FL – Fruit length (cm), FD – Fruit diameter (cm), FPL- Fruit pedicel length (cm), NSF – Number of seeds per fruit, WSF- Weight of seeds per fruit (g), 1000 SW- 1000 seed weight (g), DFYP – Dry fruit yield per plant (g).

Table 4.8 : Phenotypic path analysis showing direct (diagonal) and indirect effects of qualitative characters on yield per plant in paprika (*Capsicum annuum* L.)

Character	Ascorbic acid (mg /100g)	Oleoresin content (%)	Capsaicin content (SHU)	Total extractable colour (ASTA Units)	Red carotenoids (%)	Yellow carotenoids (%)	Total carotenoids (%)
Ascorbic acid (mg /100g)	-0.3660	-0.0185	0.0211	0.1184	-0.0827	-0.0085	-0.0756
Oleoresin content (%)	-0.0129	-0.2549	0.0450	-0.0086	0.0588	-0.0151	0.0408
Capsaicin content (SHU)	0.0171	0.0523	-0.2966	0.0481	0.0012	0.0304	0.0202
Total extractable colour (ASTA Units)	0.0727	-0.0076	0.0365	-0.2249	-0.0001	-0.0031	-0.0024
Red carotenoids (%)	0.7472	-0.7629	-0.0129	0.0018	3.3048	-0.3382	2.5622
Yellow carotenoids (%)	0.0564	0.1440	-0.2497	0.0338	-0.2495	2.4377	1.3369
Total carotenoids (%)	-0.8627	0.6682	0.2847	-0.0437	-3.2391	-2.2911	-4.1778
'r' with dry fruit yield Per plant (g)	-0.3482**	-0.1793	-0.1720	-0.0752	-0.2066	-0.1879	-0.2956**

R SQUARE = 0.3354 RESIDUAL EFFECT = 0.8152 *: Significant at 5 per cent level; **: Significant at 1 per cent level

Table 4.9 : Genotypic path analysis showing direct (diagonal) and indirect effects of quantitative characters on yield per plant in paprika (*Capsicum annuum* L.)

Character	PH	PS	NPBP	DFF	DM	NFP	FL	FD	FPL	NSF	WSF	1000SW
PH	-0.1512	-0.0733	-0.0940	-0.0017	-0.0218	-0.0044	-0.0082	-0.0640	-0.0416	-0.0828	-0.0683	0.0194
PS	0.4117	0.8486	0.6582	-0.1890	-0.0620	0.2313	0.2669	0.0031	0.4372	0.2120	0.0562	-0.3074
NPBP	-0.3378	-0.4216	-0.5436	0.0589	-0.0693	-0.1418	-0.1287	0.0111	-0.1861	0.0017	0.0362	0.2333
DFF	-0.0039	0.0781	0.0380	-0.3507	-0.2159	0.0424	-0.0054	-0.0371	-0.0032	0.0134	-0.0214	-0.0005
DM	0.0373	-0.0189	0.0330	0.1595	0.2591	0.1006	0.0272	0.0401	0.0926	-0.0271	-0.0275	-0.1175
NFP	0.0007	0.0069	0.0066	-0.0031	0.0098	0.0253	0.0136	-0.0048	0.0110	-0.0111	-0.0098	-0.0135
FL	0.0045	0.0261	0.0197	0.0013	0.0087	0.0448	0.0831	-0.0210	0.0612	-0.0283	-0.0255	-0.0344
FD	0.2817	0.0024	-0.0136	0.0704	0.1031	-0.1274	-0.1677	0.6654	-0.0237	0.4745	0.4541	0.2584
FPL	0.0320	0.0600	0.0398	0.0011	0.0416	0.0507	0.0857	-0.0041	0.1164	-0.0120	-0.0264	-0.0736
NSF	-0.9888	-0.4511	0.0056	0.0691	0.1886	0.7953	0.6151	-1.2875	0.1854	-1.8054	-1.7271	-0.7705
WSF	0.6189	0.0908	-0.0913	0.0836	-0.1455	-0.5335	-0.4197	0.9349	-0.3108	1.3106	1.3700	0.7282
1000 SW	0.0512	0.1444	0.1711	-0.0006	0.1807	0.2123	0.1650	-0.1547	0.2521	-0.1701	-0.2118	-0.3985
'r' 'DFYP	-0.0438	0.2923**	0.2296*	-0.1012	0.2772**	0.6957**	0.5269**	0.0812	0.5908**	-0.1245	-0.2013	-0.4765**

R SQUARE = 0.5603 RESIDUAL EFFECT = 0.6631

‘r’ – Correlation coefficient , *: Significant at 5 per cent level; **: Significant at 1 per cent level ,

Note :

PH – Plant height (cm), PS-Plant spread (cm), NPBP – Number of primary branches per plant, DFF – Days to 50 per cent flowering , DM- Days to maturity, NFP – Number of fruits per plant, FL – Fruit length (cm), FD – Fruit diameter (cm), FPL- Fruit pedicel length (cm), NSF – Number of seeds per fruit, WSF- Weight of seeds per fruit (g), 1000 SW- 1000 seed weight (g), DFYP – Dry fruit yield per plant (g).

Table 4.10 : Genotypic path analysis showing direct (diagonal) and indirect effects of qualitative characters on yield per plant in paprika (*Capsicum annuum* L.)

Character	Ascorbic acid (mg /100g)	Oleoresin content (%)	Capsaicin content (SHU)	Total extractable colour (ASTA Units)	Red carotenoids (%)	Yellow carotenoids (%)	Total carotenoids (%)
Ascorbic acid (mg /100g)	-0.5532	-0.0200	0.0390	0.2023	-0.1232	-0.0140	-0.1157
Oleoresin content (%)	-0.0069	-0.1920	0.0367	-0.0085	0.0476	-0.0071	0.0374
Capsaicin content (shu)	0.0271	0.0735	-0.3843	0.0772	0.0036	0.0483	0.0333
Total extractable colour (ASTA Units)	0.1622	-0.0196	0.0891	-0.4435	0.0053	0.0029	0.0049
Red carotenoids (%)	-3.3473	3.7233	0.1400	0.1810	-15.0307	1.8347	-11.7773
Yellow carotenoids (%)	-0.2811	-0.4074	1.3916	0.0712	1.3514	-11.0709	-5.7686
Total carotenoids (%)	3.6040	-3.3618	-1.4922	-0.1897	13.5077	8.9826	17.2391
' r ' dry fruit yield per plant (g)	-0.3953**	-0.2040	-0.1800	-0.1101	-0.2383*	-0.2235*	-0.3469**

‘r’ – Correlation coefficient , *: Significant at 5 per cent level; **: Significant at 1 per cent level

R SQUARE = 0.4528 RESIDUAL EFFECT = 0.7397

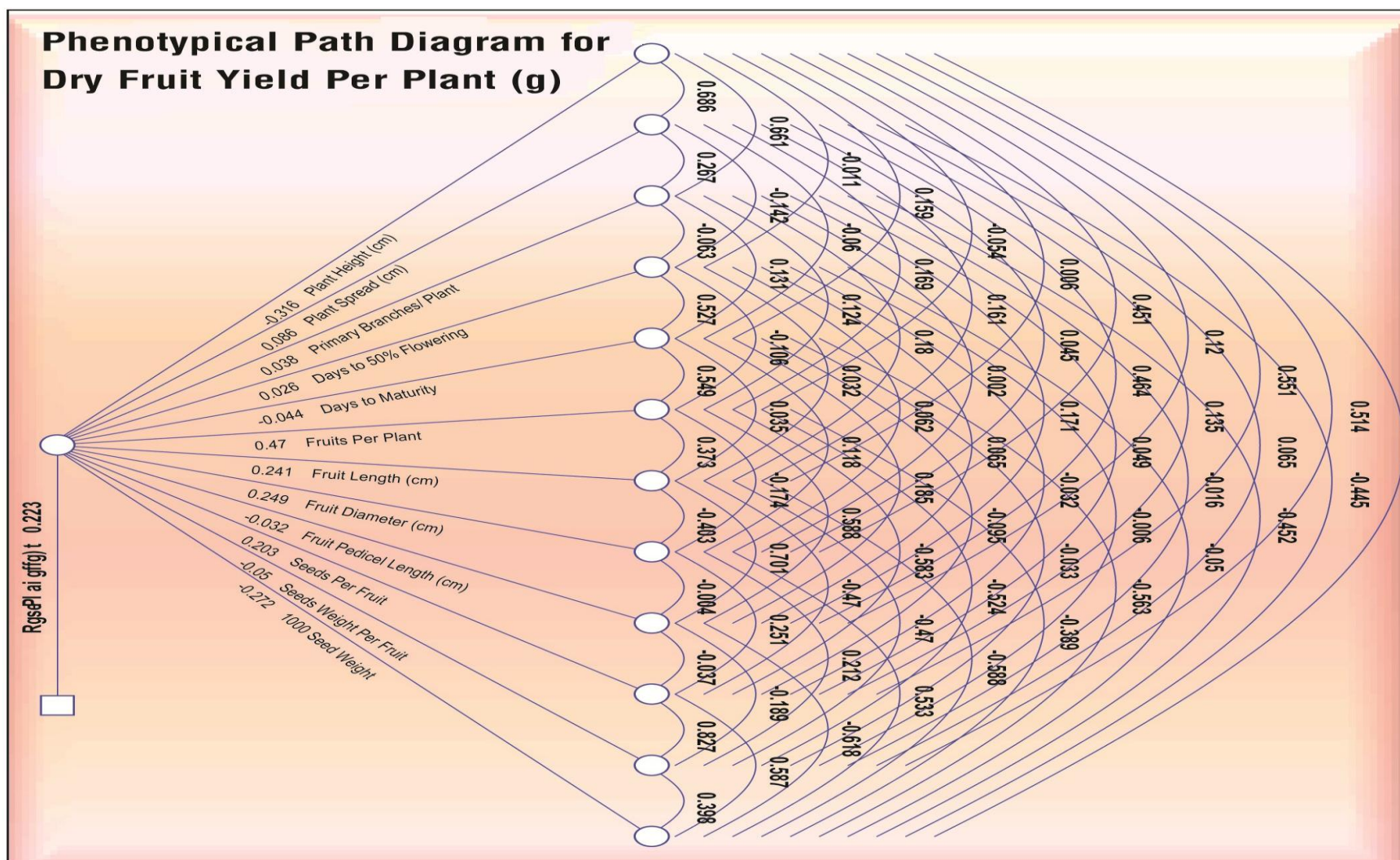


Fig.4.11: Phenotypic path diagram showing cause effect relationship of quantitative characters with yield per plant in paprika (*Capsicum annuum* L.).

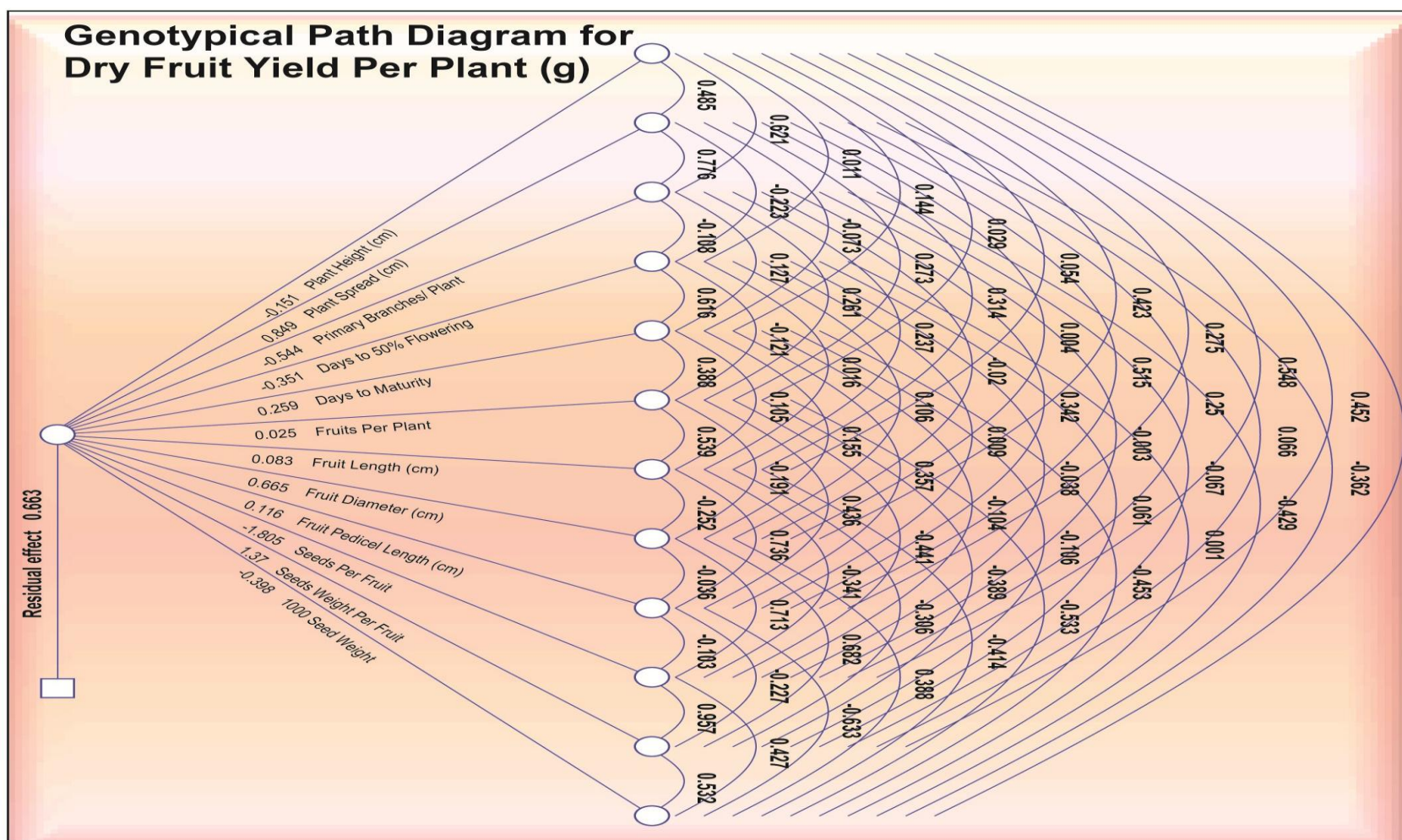


Fig.4.12: Genotypic path diagram showing cause effect relationship of quantitative characters with yield per plant in paprika (*Capsicum annuum* L.)

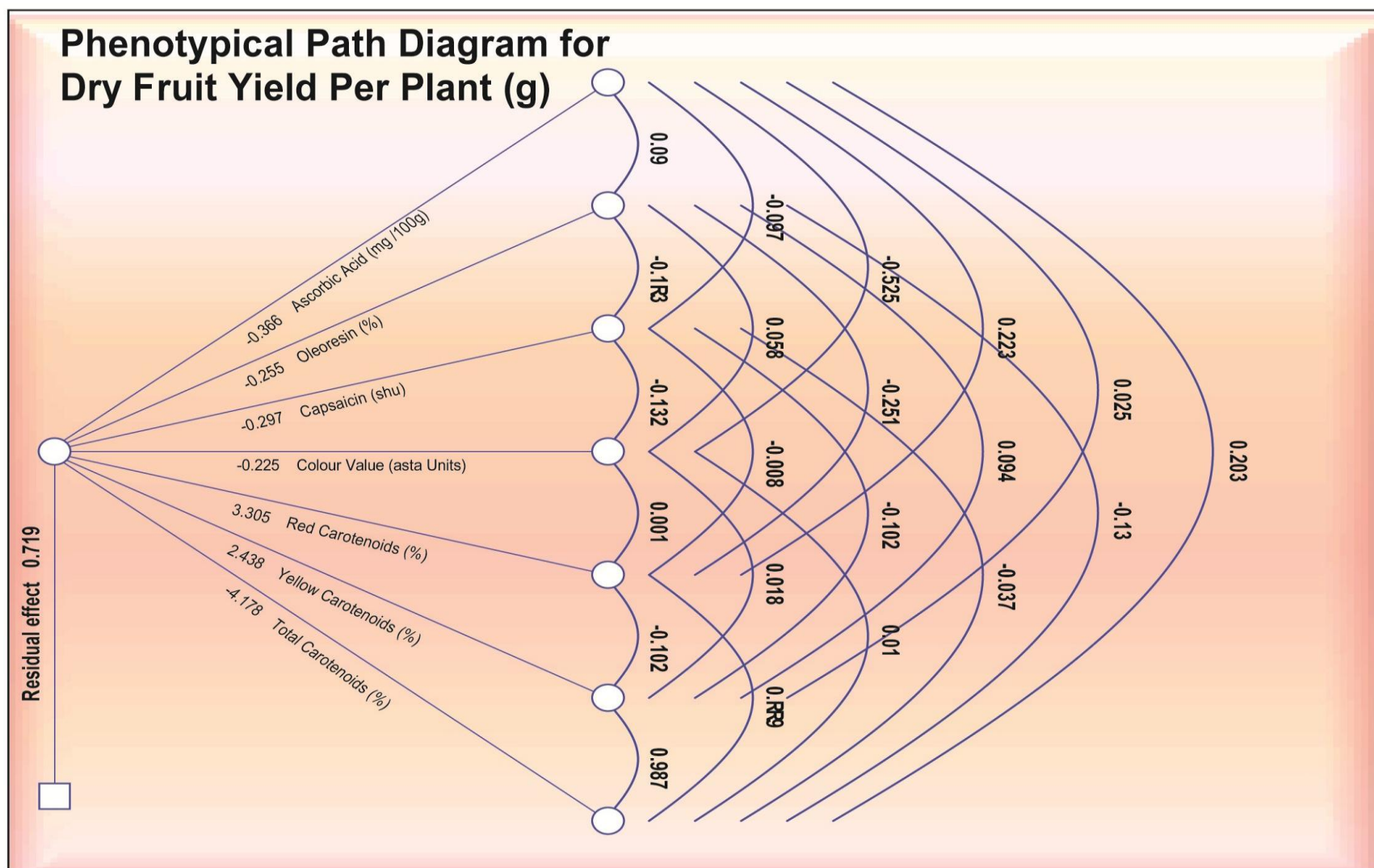


Fig.4.13: Phenotypic path diagram showing cause effect relationship of qualitative characters with yield per plant in paprika (*Capsicum annuum* L.)

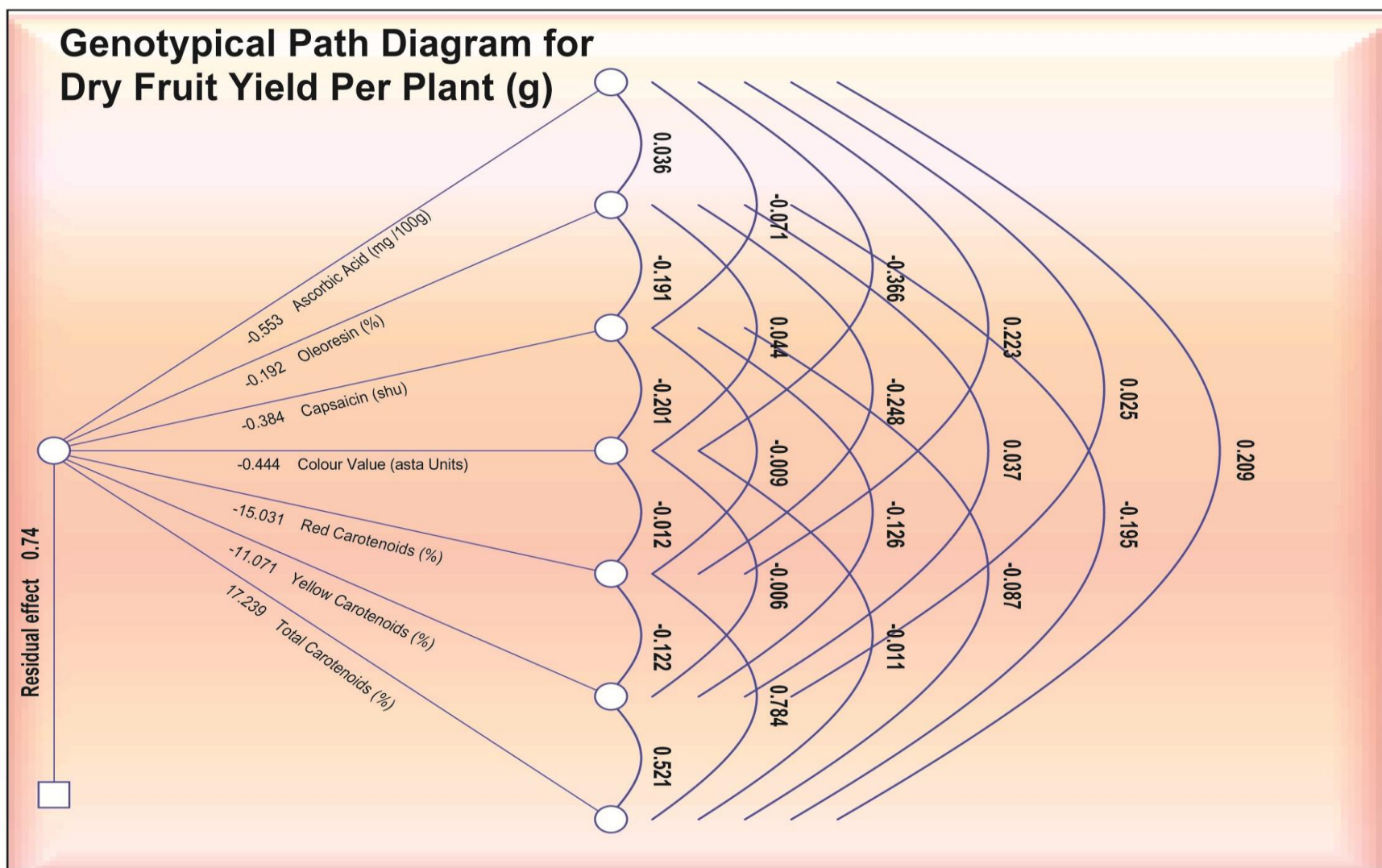


Fig.4.14: Genotypic path diagram showing cause effect relationship of qualitative characters with yield per plant in paprika (*Capsicum annum* L.)

effects and negative correlations indicated that direct selection for yield per plant through this trait will be not effective. These results are in agreement with the earlier reports of Rao (2005), Ahmed *et al.* (2006), Ajjappalavara *et al.* (2005), Farhad *et al.* (2008) and Rohini and Lakshmanan (2015).

4.5.1.2 Plant spread (cm)

Plant spread showed negligible and positive direct effect on yield per plant at phenotypic level (0.0860) and high and positive direct effect at genotypic level (0.8486).

At phenotypic level, this trait exhibited negligible and positive indirect effect on yield per plant via number of primary branches per plant (0.0250), days to maturity (0.0022), number of fruits per plant (0.0747), fruit length (0.0364), fruit diameter (0.0058), number of seeds per fruit (0.0290) and 1000 seed weight (0.0608) ; low and negative indirect effect through plant height (-0.1849) and negligible and negative indirect effect via days to 50 per cent flowering (-0.0033), fruit pedicel length (-0.0081) and weight of seeds per fruit(-0.0027).

At genotypic level, this trait showed negligible and positive indirect effect on yield per plant through days to 50 per cent flowering (0.0781), number of fruits per plant (0.0069), fruit length (0.0261), fruit diameter (0.0024), fruit pedicel length (0.0600) and weight of seeds per fruit (0.0908) ; low and positive indirect effect through 1000 seed weight (0.1444), high and negative indirect effect through primary branches per plant (-0.4216) and number of seeds per fruit(-0.4511) and negligible and negative indirect effect via plant height (-0.0733) and days to maturity (-0.0189).

Plant spread showed non-significant positive association and significant positive association with yield per plant (0.1208 and 0.2923**) at phenotypic level and genotypic levels respectively. Positive direct effects and positive correlations indicated that direct selection for yield per plant through this trait will be effective. This is in conformity with

earlier reports of Patil *et al.* (2004), Rao *et al.* (2006), Jabeen *et al.* (2009), Kumar *et al.* (2012) and Vijaya *et al.* (2014).

4.5.1.3 Number of primary branches per plant

This trait showed negligible and positive direct effect on yield per plant at phenotypic level (0.0381) and high and negative direct effect at genotypic level (-0.5436).

At phenotypic level, this trait exhibited negligible and positive indirect effect on yield per plant via plant spread (0.0565), number of fruits per plant (0.0761), fruit length (0.0434) and fruit diameter (0.0014), number of seeds per fruit (0.0060), weight of seeds per fruit (0.0008) and 1000 seed weight (0.0642); low and negative indirect effect through plant height (-0.1743) and negligible and negative indirect effect via days to 50 per cent flowering (-0.0014), days to maturity (-0.0062) and fruit pedicel length (-0.0055).

At genotypic level, the no. of primary branches showed negligible and positive indirect effect on yield per plant through days to 50 per cent flowering (0.0380), days to maturity (0.0330), number of fruits per plant (0.0066), fruit length (0.0197), fruit pedicel length (0.0398) and number of seeds per fruit (0.0056); high and positive indirect effect through plant spread (0.6582) and low and positive indirect effect through 1000 seed weight (0.1711) and negligible indirect effects via plant height (-0.0940), fruit diameter (-0.0136) and weight of seeds per fruit (-0.0913).

Number of primary branches per plant showed non-significant positive association and significant positive association with yield per plant (0.0990 and 0.2296*) at phenotypic level and genotypic levels respectively. Negligible and high direct effects and positive correlation were observed. In such situations, the indirect causal factors are also to be considered simultaneously for selection. These findings are in agreement with

observations of Rao (2005), Ahmed *et al.* (2006), Farhad *et al.* (2008), Kumar *et al.* (2012) and Dipak *et al.* (2017) in chilli.

4.5.1.4 Days to 50 per cent flowering

Days to 50 per cent flowering showed negligible and positive direct effect on yield per plant at phenotypic level (0.0265) and high and negative direct effect at genotypic level (-0.3507).

At phenotypic level, this trait showed negligible and positive indirect effect on yield per plant via plant height (0.0036), fruit length (0.0110) and fruit diameter (0.0141), weight of seeds per fruit (0.0002) and 1000 seed weight (0.0081), negligible and negative indirect effect via plant spread (-0.0109), number of primary branches per plant (-0.0021), days to maturity (-0.0161), number of fruits per plant (-0.0494), fruit pedicel length (-0.0017) and number of seeds per fruit (-0.0094).

At genotypic level, this trait showed negligible and positive indirect effect on yield per plant through number of primary branches per plant (0.0589), fruit length (0.0013), fruit diameter (0.0704), fruit pedicel length (0.0011), number of seeds per fruit (0.0691) and weight of seeds per fruit (0.0836); low and positive indirect effect through days to maturity (0.1595) and low negative indirect effect through plant spread (-0.1890) and negligible and negative indirect effect via plant height (-0.0017), number of fruits per plant (-0.0031) and 1000 seed weight (-0.0006).

At both phenotypic and genotypic levels this trait showed negative and non-significant association with yield per plant (-0.0260 and -0.1012). The present investigation showed negligible and high direct effects and negative correlation and such this traits. Similar observations of Rao (2005), Ahmed *et al.* (2006), Smitha and Basvaraja (2007), Farhad *et al.* (2008), Reddy *et al.* (2008) and Hasauzzaman and Faruq (2011) in chilli lend support to the findings of this investigation.

4.5.1.5 Days to maturity

Days to maturity showed negligible and negative direct effect on yield per plant at phenotypic level (-0.0438) and moderate and positive direct effect at genotypic level (0.2591).

At phenotypic level, this trait showed negligible and positive indirect effect on yield per plant via number of primary branches per plant (0.0054), days to 50 per cent flowering (0.0097), fruit length (0.0104), fruit diameter (0.0294), weight of seeds per fruit (0.0022) and 1000 seed weight (0.0964); low and positive indirect effect through number of fruits per plant (0.1547) and negligible and negative indirect effects via plant height (-0.0440), plant spread (-0.0043), fruit pedicel length (-0.0059) and number of seeds per fruit (-0.0189).

At genotypic level, the negligible and positive indirect effect on yield per plant due to this trait was through number of fruits per plant (0.0098), fruit length (0.0087) and fruit pedicel length (0.0416); low and positive indirect effect was through fruit diameter (0.1031), number of seeds per fruit (0.1886) and 1000 seed weight (0.1807) and moderate and negative indirect effect through days to 50 percent flowering (-0.2159) and low and negative indirect effect through weight of seeds per fruit (-0.1455); negligible and negative indirect effect via plant height (-0.0218), plant spread (-0.0620) and number of branches per plant (-0.0693).

Days to maturity showed non-significant positive association and significant positive association with yield per plant (0.1912 and 0.2772*) at phenotypic level and genotypic levels respectively. Negligible and moderate direct effects and positive correlation indicating the indirect effects seem to be the cause of positive correlation. In such situations, the indirect causal factors are to be considered simultaneously for selection as suggested by earlier worker viz., Gogoi and Gautam (2003) and Kumar *et al.* (2014).

4.5.1.6 Number of fruits per plant

Number of fruits per plant showed high and positive direct effect on yield per plant at phenotypic level (0.4704) and negligible and positive direct effect at genotypic level (0.0253).

At phenotypic level, this trait showed negligible and positive indirect effect on yield per plant via plant height (0.0102), plant spread (0.0137), number of primary branches per plant (0.0062) weight of seeds per fruit (0.0182); low and positive indirect effects through fruit length (0.1141), 1000 seed weight (0.1329) ; negligible and negative indirect effect via days to 50 per cent flowering (-0.0028), days to maturity (-0.0144), fruit diameter (-0.0428), fruit pedicel length (-0.0125) and number of seeds per fruit (-0.0780).

At genotypic level, this trait showed negligible and positive indirect effect on yield per plant through days to 50 per cent flowering (0.0424), fruit length (0.0448) and fruit pedicel length (0.0507) ; high and positive indirect effect through number of seeds per fruit (0.7953) and high and positive negative indirect effect through weight of seeds per fruit (-0.5335) and moderate and positive indirect effect through plant spread (0.2313) and 1000 seed weight (0.2123) and low and positive indirect effect through days to maturity (0.1006) and low and negative indirect effect through primary branches per plant (-0.1418) and fruit diameter (-0.1274) and negligible and negative indirect effects via plant height (-0.0044).

Significant and positive association with yield per plant (0.6149 ** and 0.6975**) at both phenotypic and genotypic levels was observed for this trait. The positive direct effects and positive correlations of this trait indicated that direct selection for yield per plant through this trait will be effective. These results are in conformity with the earlier

observations of Smitha and Basvaraja (2007), Vani *et al.* (2007a), Farhad *et al.* (2008), Reddy *et al.* (2008), Jabeen *et al.* (2009), Pandit *et al.* (2009), Sarkar *et al.* (2009), Datta and Jana (2010), Arup *et al.* (2011), Hasauzzaman and Faruq (2011), Misra *et al.* (2011), Kumar *et al.* (2012), Mahantesh *et al.* (2013b), Tasso *et al.* (2014), Kumar *et al.* (2014), Vikram *et al.* (2014), Patel *et al.* (2015), Rinchan *et al.* (2015), Rohini and Lakshmanan (2015) and Hasan *et al.* (2016). The results they indicated that the trait number of fruits per plant should be considered as one of the major selection criteria for high yield.

4.5.1.7 Fruit length (cm)

This trait showed moderate and positive direct effect on yield per plant at phenotypic level (0.2409) and negligible and positive direct effect at genotypic level (0.0831).

At phenotypic level, this trait showed negligible and positive indirect effect on yield per plant through plant spread (0.0130), number of primary branches per plant (0.0069), days to 50 per cent flowering (0.0012) and weight of seeds per fruit (0.0135); moderate and positive indirect effect through number of fruits per plant (0.2228) and low and positive indirect effect through 1000 seed weight (0.1055) and negligible and negative indirect effect via plant height (-0.0015), days to maturity (-0.0019), fruit diameter (-0.0507), fruit pedicel length (-0.0226) and number of seeds per fruit (-0.0547).

At genotypic level, this trait showed negligible and positive indirect effect on yield per plant through days to maturity (0.0272), number of fruits per fruit (0.0136) and fruit pedicel length (0.0857); high and positive indirect effect through number of seeds per fruit (0.6151) and high and negative indirect effect through weight of seeds per fruit (-0.4197) and moderate and positive indirect effect through plant spread (0.2669) and low and positive indirect effect through 1000 seed weight (0.1650) and low and negative indirect effect through primary branches per plant (-0.1287) and fruit diameter (-0.1677) and negligible and negative indirect effect through plant height (-0.0082) and days to 50 per cent flowering (-0.0054).

Fruit length showed significant and positive association with yield per plant (0.4723** and 0.5269**) at both phenotypic and genotypic levels. Positive direct effects and positive correlations indicated that direct selection for plant yield through fruit length will be rewarding. Positive direct effect of this trait was also reported by Gogoi and Gautam (2003), Khurana et al (2003), Verma *et al.* (2004), Ajjapplavara *et al.* (2005) and Singh *et al.* (2007). Krishna *et al.* (2007b), Smitha and Basvaraja (2007), Farhad *et al.* (2008), Reddy *et al.* (2008), Sarkar *et al.*(2009), Hasauzzaman and Faruq (2011), Kumar *et al.* (2012), Mahantesh *et al.* (2013b), Datta and jana (2013), Vikram *et al.* (2014), Rohini and Lakshmanan (2015), and Hasan *et al.* (2016). The findings thus suggest fruit length as one of the selection criteria for high yield in chilli.

4.5.1.8 Fruit diameter (cm)

Fruit diameter showed moderate and positive direct effect on yield per plant at phenotypic level (0.2492) and high and positive direct effect at genotypic level (0.6654).

At phenotypic level, this trait showed negligible and positive indirect effect on yield per plant via plant spread (0.0020), number of primary branches per plant (0.002), days to 50 per cent flowering (0.0015) and fruit pedicel length (0.0001) ; low and positive indirect effect through number of seeds per fruit (0.1280) and negligible and negative indirect effects via plant height (-0.0729), days to maturity (-0.0052), number of fruits per plant (-0.0808), fruit length (-0.0490), weight of seeds per fruit (-0.0309) and 1000 seed weight (-0.0936).

At genotypic level, this trait showed negligible and positive indirect effect on yield per plant through plant spread (0.0031), number of primary branches per plant (0.0031) and days to maturity (0.0401) ; high and positive indirect effect through weight of seeds per fruit (0.9349) and high and positive indirect effects through number of seeds per fruit (-1.2875) and low and positive indirect effect through 1000 seed weight (-0.1547) and negligible and negative indirect effect through plant height (-0.0640), days

to 50 per cent flowering (-0.0020), number fruits per plant (-0.0048), fruit length (-0.0210) and fruit pedicel length (-0.0041).

Non-significant and positive association of fruit diameter with yield per plant at phenotypic (0.0486) and genotypic levels (0.0812) was observed. The present investigation showed positive direct effects and positive correlation and hence selection based on this character may be rewarding. This is in agreement with the results of Munshi *et al.* (2000), Gogoi and Gautam (2003), Khurana *et al.* (2003), Karad *et al.* (2006), Verma *et al.* (2004), Ajjapplavara *et al.* (2005), Nazir *et al.* (2005), Smitha and Basvaraja (2007), Singh *et al.* (2007), Farhad *et al.* (2008), Sarkar *et al.* (2009), Kumar *et al.* (2012), Mahantesh *et al.* (2013b), Kumar *et al.* (2014), Vijaya *et al.* (2014) and Rohini and Lakshmanan (2015).

4.5.1.9 Fruit pedicel length (cm)

This trait showed negligible and negative direct effect on yield per plant at phenotypic level (-0.0322) and low and positive direct effect at genotypic level (0.1164).

At phenotypic level, this trait showed negligible and positive indirect effect on yield per plant through plant spread (0.0217), number of primary branches per plant (0.0065), days to 50 per cent flowering (0.0014) and weight of seeds per fruit (0.0095) ; low and positive indirect effect through number of fruits per plant (0.1827), fruit length (0.1687) and 1000 seed weight (0.1408) and negligible and negative indirect effect via plant height (-0.0504), days to maturity (-0.0080), fruit diameter (-0.0006) and number of seeds per fruit (-0.0095).

At genotypic level, this trait showed negligible and positive indirect effect on yield per plant through days to maturity (0.0926), number of fruits per fruit (0.0110) and fruit length (0.0612) ; high and positive indirect effect through plant spread (0.4372) and high and negative indirect effect through weight of seeds per fruit (-0.3108) and moderate and positive indirect effect through 1000 seed weight (0.2521). Similarly low

and positive indirect effect through number of seeds per fruit (0.1854) and low and negative indirect effect through number of primary branches per plant (-0.1861) and negligible and negative indirect effect through plant height (-0.0416) and days to 50 per cent flowering (-0.0032) and fruit diameter (-0.0237) were observed.

This trait showed significant and positive association with yield per plant (0.4307** and 0.5908**) at both phenotypic and genotypic levels. Negligible and low direct effects and positive correlations indicated that direct selection for yield per plant through this trait will be rewarding. This is in agreement with the results of Rohini and Lakshmanan (2015) and Hasan *et al.* (2016) who suggested pedicel length as one of the yield contributing characters.

4.5.1.10 Number of seeds per fruit

This trait showed moderate and positive direct effect on yield per plant at phenotypic level (0.2030) and very high and negative direct effect at genotypic level (-1.8054).

At phenotypic level, this trait showed negligible and positive indirect effect on yield per plant through plant spread (0.0123), number of primary branches per plant (0.0011), days to maturity (0.0041) and fruit pedicel length (0.0015); low and positive indirect effect through fruit diameter (0.1572); low and negative indirect effects through plant height (-0.1045), number of fruits per plant (-0.1808) and 1000 seed weight (-0.1053) and negligible and negative indirect effects via days to 50 per cent flowering (-0.0012), fruit length (-0.0650) and weight of seeds per fruit (-0.0435).

At genotypic level, this trait showed negligible and positive indirect effect on yield per plant through number of primary branches per plant (0.0017) and days to 50 per cent flowering (0.0134); high and positive indirect effect via weight of seeds per fruit (1.3106) and fruit diameter (0.4745) and moderate and positive indirect effect through plant spread (0.2120) and low and negative indirect effect through 1000 seed weight (-

0.1701) ; negligible and negative indirect effect through plant height (-0.0828), days to maturity (-0.0271), number of fruits per plant (-0.0111), fruit length (-0.0283) and fruit pedicel length (-0.0120).

At both phenotypic and genotypic levels this trait showed non- significant and negative association with yield per plant (-0.1211 and -0.1245). Thus moderate positive and high negative direct effects and positive correlations were observed and this findings are in agreement with the results of Kumar *et al.* (2014) and Dipak *et al.* (2017).

4.5.1.11 Weight of seeds per fruit (g)

Seed weight showed negligible and negative direct effect on yield per plant at phenotypic level (-0.0501) and very high and positive direct effect at genotypic level (1.3700).

At phenotypic level, it showed negligible and positive indirect effect on yield per plant through plant spread (0.0045), days to maturity (0.0019) and fruit pedicel length (0.0061) ; low and positive indirect effect through fruit diameter (0.1532) and number of seeds per fruit (0.1760) and low and negative indirect effects through number of fruits per plant (-0.1704) and 1000 seed weight (-0.1354) and negligible and negative indirect effects via plant height (-0.0984), number of primary branches per plant (-0.0006), days to 50 per cent flowering (-0.0001) and fruit length (-0.0650).

At genotypic level, this trait showed negligible and positive indirect effect on yield per plant through plant spread (0.0562) and number of primary branches per plant (0.0362); very high and negative indirect effect through number of seeds per fruit (-1.7271). High and positive indirect effect through fruit diameter (0.4541) and moderate and negative indirect effect through 1000 seed weight (-0.2118) ; negligible and negative indirect effect through plant height (-0.0683), days to 50 per cent flowering (-0.0214), days to maturity (-0.0275), number of fruits per plant (-0.0098), fruit length (-0.0255) and fruit pedicel length (-0.0264) were observed.

At both phenotypic and genotypic levels this trait showed non- significant and negative association with yield per plant (-0.1780 and -0.2013). Negligible negative and high positive direct effects and negative correlations. Under these circumstances, a restricted simultaneous selection model is to be followed i.e. restrictions to be imposed to nullify the undesirable indirect effects in order to make use of the direct effect.

4.5.1.12 1000 seed weight (g)

Seed weight showed moderate and negative direct effect on yield per plant at phenotypic level (-0.2720) and high and negative direct effect at genotypic level (-0.3985).

At phenotypic level, this trait showed negligible and positive indirect effect on yield per plant through plant height (0.0093), days to maturity (0.0155), fruit diameter (0.0857) and fruit pedicel length (0.0167) and number of seeds per fruit (0.0786) ; moderate and negative indirect effect through number of fruits per plant (-0.2298) ; negligible and negative indirect effect via plant spread (-0.0192), number of primary branches per plant (-0.0090), days to 50 per cent flowering (-0.0008), fruit length (-0.0934) and weight of seeds per fruit (-0.0249).

At genotypic level, negligible and positive indirect effect on yield per plant through plant height (0.0194); high and positive indirect effect through weight of seeds per fruit (0.7282) and high and negative indirect effect through plant spread (-0.3074) and number of seeds per fruit (-0.7705) were observed. Moderate and positive indirect effect through number of primary branches per plant (0.2333) and fruit diameter (0.2584) and low and negative indirect effect through days to maturity (-0.1175) ; negligible and negative indirect effect through days to 50 percent flowering (-0.0005), number of fruits per plant (-0.0135), fruit length (-0.0344) and fruit pedicel length (-0.0736) who also indicated from the results.

At both phenotypic and genotypic levels this trait showed significant and negative association with yield per plant (-0.4433** and -0.4765**). Negative direct effect and negative correlations and hence selection based on this character may not be rewarding. These findings are in agreement with the results of Sarkar *et al.* (2009) and Rohini and Lakshmanan (2015).

4.5.2 Direct and indirect effects of qualitative characters on yield per plant

4.5.2.1 Ascorbic acid (mg/100g)

At both phenotypic and genotypic levels, the direct contribution of this character on yield per plant was high and negative (-0.3660 and -0.5532).

At phenotypic level, this trait showed negligible and positive indirect effect on yield per plant through capsaicin content (0.0171), total extractable colour (0.0727) and yellow carotenoids (0.0564) ; high and positive indirect effect through red carotenoids (0.7472) and high and negative indirect effect through total carotenoids (-0.8627) and negligible and negative indirect effect through oleoresin content (-0.0129).

At genotypic level, ascorbic acid content showed negligible and positive indirect effect on yield per plant through capsaicin content (0.0271); low and positive indirect effect *via* total extractable colour (0.1622); negligible and negative indirect effect through oleoresin content (-0.0069) and very high and negative indirect effect *via* red carotenoids (-3.3473) and very high and positive indirect effect *via* total carotenoids (3.6040) and moderate and negative indirect effect *via* yellow carotenoids (-0.2811).

At both phenotypic and genotypic levels this trait showed significant and negative association with yield per plant (- 0.3482** and -0.3953**). Negative direct effects and negative correlations indicated that direct selection for yield per plant through this trait will be not effective.

4.5.2.2 Oleoresin content (%)

This trait showed moderate and negative direct effect on yield per plant at phenotypic level (-0.2549) and low and negative direct effect at genotypic level (-0.1920).

At phenotypic level, this trait showed negligible and positive indirect effect on yield per plant through capsaicin content (0.0523); low and positive indirect effect through yellow carotenoids (0.1440) and high and positive indirect effect through total carotenoids (0.6682) and high and negative indirect effect through red carotenoids (-0.7629); negligible and negative indirect effect through ascorbic acid (-0.0185) and total extractable colour (-0.0076).

At genotypic level, this trait showed negligible and positive indirect effect on yield per plant through capsaicin content (0.0735); very high and positive indirect effect through red carotenoids (3.7233); negligible and negative direct effect *via* ascorbic acid (-0.0200) and total extractable colour (-0.0196) and high and negative indirect effect through yellow carotenoids (-0.4074) and very high and negative indirect effect through total carotenoids (-3.3618).

This trait showed non-significant and negative association (-0.1793 and -0.2040) with yield per plant at genotypic and phenotypic levels respectively. Negative direct effects and negative correlations indicated that direct selection for yield per plant through this trait will be not effective. These results are supported by the earlier reports of Singh *et al.* (2007) and Arup *et al.* (2011) in chilli.

4.5.2.3 Capsaicin content (SHU)

Capsaicin content of fruits showed moderate and negative direct effect on yield per plant at phenotypic level (-0.2966) and high and negative direct effect at genotypic level (-0.3843).

At phenotypic level, this trait showed negligible and positive indirect effect on yield per plant through ascorbic acid (0.0211), oleoresin content (0.0450) and total

extractable colour (0.0365) and negligible and negative indirect effect through red carotenoids (-0.0129); moderate and negative indirect effect through yellow carotenoids (-0.2497) and moderate positive indirect effect through total carotenoids (0.2847)

At genotypic level, this trait showed negligible and positive indirect effect on yield per plant *via* ascorbic acid (0.0390), oleoresin content (0.0367) and total extractable colour (0.0891); low and positive indirect effect through red carotenoids (0.1400) and high and positive indirect effect through yellow carotenoids (1.3916) and high and negative indirect effect through total extractable colour (-1.4922).

At both phenotypic and genotypic levels, capsaicin content showed non-significant and negative association with yield per plant (-0.1720 and -0.1800). The results of present investigation revealed negative direct effect and negative correlation and hence selection based on this character may not be possible. These results are supported by the reports of Singh *et al.* (2009), Arup *et al.* (2011) and Vijaya *et al.* (2014).

4.5.2.4 Total extractable colour (ASTA units)

This trait showed moderate and negative direct effect on yield per plant at phenotypic level (-0.2249) and high and negative direct effect at genotypic level (-0.4435).

At phenotypic level, moderate and positive indirect effect on yield per plant through capsaicin content (0.0481), red carotenoids (0.0018) and yellow carotenoids (0.0338) and low and positive indirect effect through ascorbic acid (0.1184) and negligible and negative indirect effect through oleoresin content (-0.0086) and total carotenoids (-0.0437) were observed.

At genotypic level, this trait showed negligible and positive indirect effect on yield per plant *via* capsaicin content (0.0772), yellow carotenoids (0.0712), high and positive indirect effect *via* ascorbic acid (0.2023) and low and positive indirect effect through red

carotenoids (0.1810) and negligible and negative indirect effect oleoresin content (-0.0085) and low and negative indirect effect through total carotenoids (-0.1897).

At both phenotypic and genotypic levels total extractable colour was observed to be non-significant and thus was negative association with yield per plant (-0.0752 and -0.1101). The present investigation showed negative direct effect and negative correlation, so we have to drop the selection based on this character. However, contrary to the findings of the present investigation, Khurana *et al.* (2003) and Rinchan *et al.* (2015).

4.6.2.5 Red carotenoids (%)

Red carotenoids content showed very high and negative direct effect on yield per plant at phenotypic level (3.3048) and very high and negative direct effect at genotypic level (-15.0307).

At phenotypic level, this trait showed negligible and positive indirect effect on yield per plant via oleoresin content (0.0588) and capsaicin content (0.0012) and negligible and negative indirect effect via ascorbic acid (-0.0827) and total extractable colour (-0.0001) and low and negative indirect effect through yellow carotenoids (-0.2495) and very high and negative indirect effect through total carotenoids (-3.2391).

At genotypic level, this trait showed negligible and positive indirect effect on yield per plant via oleoresin content (0.0476) and capsaicin content (0.0036) and total extractable colour (0.0053) ; very high and positive indirect effect via yellow carotenoids (1.3514) and total carotenoids (13.5077) and low and negative indirect effect through ascorbic acid (-0.1232).

This trait showed non-significant and negative association and significant and negative association (-0.2066 and -0.2383*) with yield per plant at phenotypic and genotypic levels, respectively.

4.5.2.6 Yellow carotenoids (%)

Yellow carotenoids showed very high and positive direct effect on yield per plant at phenotypic level (2.4377) and very high and negative direct effect at genotypic level (-11.0709).

At phenotypic level, this trait showed negligible and positive indirect effect on yield per plant through capsaicin content (0.0304) and high and negative indirect effect through red carotenoids (-0.3382) and very high and negative indirect effect through total carotenoids (-2.2911) and negligible and negative indirect effect *via* ascorbic acid (-0.0085), oleoresin content (-0.0151) and total extractable colour (-0.0031).

At genotypic level, it showed negligible and positive indirect effect on yield per plant via capsaicin content (0.0483) and total extractable colour (0.0029) and high and positive indirect effect through red carotenoids (1.8347) and total carotenoids (8.9826) and negligible and negative indirect effect through ascorbic acid (-0.0140), and oleoresin content (-0.0071).

This trait showed non - significant and negative association and significant and negative association (-0.1879 and -0.2235*) with yield per plant at phenotypic and genotypic levels, respectively.

4.5.2.7 Total carotenoids (%)

This trait showed very high and negative direct effect on yield per plant at phenotypic level (-4.1778) and very high and positive direct effect at genotypic level (17.2391).

At phenotypic level, total carotenoids showed negligible and positive indirect effect on yield per plant through oleoresin content (0.0408) and capsaicin content (0.0202) and very high and positive indirect through red carotenoids (2.5622) and

yellow carotenoids (1.3369) and negligible and negative indirect effect via ascorbic acid (-0.0756), and total extractable colour (-0.0024).

At genotypic level, this trait showed negligible and positive indirect effect on yield per plant via oleoresin content (0.0374), capsaicin content (0.0333) and total extractable colour (0.0049) and very high and negative indirect effect through red carotenoids (-11.7773) and total carotenoids (-5.7686) and low and negative indirect effect through ascorbic acid (-0.1157).

This trait showed significant and negative association (-0.2956** and -0.3469**) with yield per plant at phenotypic and genotypic levels, respectively.

The present investigation revealed high direct effect and negative correlation of the red/yellow or total carotenoids with yield suggesting a restricted simultaneous selection *i.e.*, restrictions are to be imposed to nullify the undesirable indirect effects in order to make use of the direct effect.

The path analysis in general has revealed that number of fruits per plant, fruit length, fruit pedicel length had positive direct effect on yield per plant indicating that direct selection based on these traits may be more helpful in evolving high yielding varieties of paprika.

Further, based on the results of correlation and path analysis, the present study revealed that major emphasis should be laid on selection process with number of fruits per plant and fruit length and there should be economic balance among these traits to get higher fruit yield per plant.

4.6 GENETIC DIVERGENCE

Genetic divergence plays a key role in analyzing the general distance among the genotypes selected as parents. Within a certain limit, hybridization of more divergent

parents is expected to enhance the level of heterosis and generate wide range of variability in segregating generations.

Generally, geographical diversity was considered as a measure of genetic diversity when no scientific tools were available. But geographical distribution of genotypes is not the only factor that causes genetic diversity. This may be due to exchange of breeding material over the locations and further selections at different locations which could result in genetic drift. So, selection of parents for hybridization programme should be based on genetic diversity rather than geographical diversity as there is no parallelism between genetic divergence and geographical divergence of genotypes.

The data collected on 20 yield and quality contributing characters from 44 genotypes of paprika were subjected to multivariate analysis like Mahalanobis' D^2 statistic, principal component and cluster analysis. The magnitude of values suggested that there was considerable variability in the material studied, which led to genetic diversity.

4.6.1 Mahalanobis' D^2 analysis

4.6.1.1 Test with *Wilk's* criterion ' $\wedge$ '

Significant differences among the genotypes for individual characters were first determined and later the statistically significant differences between the genotypes based on the pooled effects of all the characters were carried out using the Wilk's criterion ' $\wedge$ '. The Wilk's criterion thus obtained was used in calculations of ' V ' statistic. The statistic was highly significant indicating that genotypes differed significantly when all the characters were considered simultaneously. The value of ' V ' statistic was 2167.81 in the present investigation.

4.6.1.2 Mahalanobis' D^2 values

To estimate the D^2 values, correlated mean of characters were transformed into standardized uncorrelated characters by using pivotal condensation method. It measures the degree of diversification and determines the relative proportion of each component character to total divergence. The statistical differences (D^2) between pairs of genotypes was obtained as the sum of squares of the differences between the pairs of corresponding uncorrelated values of any two genotypes considered at a time.

4.6.1.3 Relative contribution of different characters towards genetic divergence

The per cent contribution towards genetic divergence by all the 20 contributing characters is presented in Table 4.11 (Fig 4.15). The maximum contribution towards genetic divergence was by total extractable colour (21.56%) followed by red carotenoids (19.87%), yellow carotenoids (13.95%), ascorbic acid (7.29%) and dry fruit yield per plant (7.29%), oleoresin content (6.98%), capsaicin content (6.87%), weight of seeds per fruit (5.92%), 1000 seed weight (4.33%), fruit diameter (2.96%), number of fruits per plant and fruit length (1.06%), number of seeds per fruit (0.42%), fruit pedicel length (0.21%), days to 50 per cent flowering and total carotenoids (0.11%), plant height, plant spread, number of primary branches per plant and days to maturity (0.01%). Hence, selection for divergent parents based on these characters will be useful for heterosis breeding in paprika

4.6.1.4 Grouping of genotypes into various clusters

The 44 genotypes were grouped into six clusters using the Tocher's method (Table 4.12) with the criterion that the intra-cluster average D^2 values should be less than the inter-cluster D^2 values.

Table 4.11 : Relative contribution of different characters towards genetic divergence in paprika (*Capsicum annuum* L.)

S.No.	Source	Times ranked 1 st	Contribution %
1	Plant height (cm)	0	0.01
2	Plant spread (cm)	0	0.01
3	Number of primary branches per plant	0	0.01
4	Days to 50 per cent flowering	1	0.11
5	Days to maturity	0	0.01
6	Number of fruits per plant	10	1.06
7	Fruit length (cm)	10	1.06
8	Fruit diameter (cm)	28	2.96
9	Fruit pedicel length (cm)	2	0.21
10	Number of seeds per fruit	4	0.42
11	Weight of seeds per fruit (g)	56	5.92
12	1000 seed weight (g)	41	4.33
13	Ascorbic acid (mg /100g)	69	7.29
14	Oleoresin content (%)	66	6.98
15	Capsaicin content (SHU)	65	6.87
16	Total extractable colour (ASTA units)	204	21.56
17	Red carotenoids (%)	188	19.87
18	Yellow carotenoids (%)	132	13.95
19	Total carotenoids (%)	1	0.11
20	Dry fruit yield per plant (g)	69	7.29

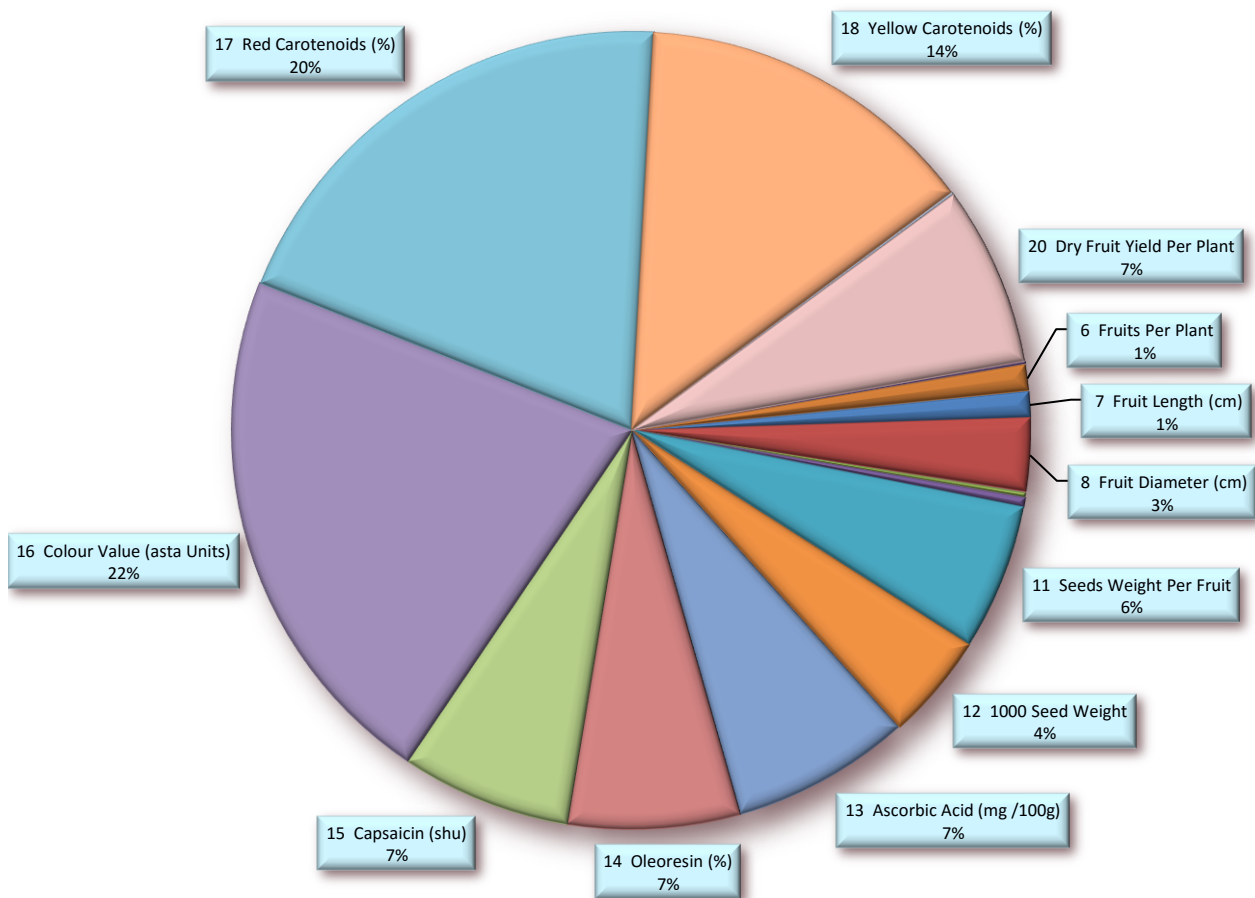


Fig 4.15: Relative contribution of different characters towards genetic divergence in paprika.

Table 4.12 : Clustering of 44 paprika (*Capsicum annuum* L.) genotypes by Tocher's method

Cluster No.	No. of genotypes	Name of genotypes
I	9	LCA 445, LCA 472, LCA 442, LCA 470, LCA 503, LCA 430, LCA 499, LCA 457, LCA 425.
II	15	LCA 488, LCA 501, LCA 447, LCA 504, LCA 506, LCA 441, LCA 439, LCA 437, LCA 475, LCA 465, LCA 466, LCA513, LCA 482, Byadagi dabbi, LCA 450
III	17	LCA 511, Warngal chappatta single patti, LCA 512, LCA 498, LCA 440, LCA 510, LCA 510, LCA 476, Kt-1 , LCA 436, LCA 446, LCA 490, LCA 453, LCA 443, Jangareddy gudem local, LCA 424, LCA 436
IV	1	LCA 480
V	1	Byadagi kaddi
VI	1	Warangal chappatta double patti

The distribution of 44 genotypes into 6 clusters was at random with maximum number of genotypes in cluster III (17 genotypes) from different locations. Cluster II was the second largest with 15 genotypes followed by cluster I with 9 genotypes. The clusters IV, V and VI were solitary clusters with zero intra-cluster D^2 values. The formation of distinct solitary clusters may be due to the fact that geographic barriers preventing gene flow or intensive natural and human selection for diverse and adoptable gene complexes must be responsible for this genetic diversity.

This pattern of grouping has indicated that the diversity need not be necessarily related to geographical diversity and it may be the outcome of several other factors like natural selection, exchange of breeding material, genetic drift and environmental variation. Therefore, selection of varieties for hybridization programme should be based on genetic diversity rather than geographical diversity.

The tree like structure called dendrogram was constructed based on clustering by Tocher's method (Fig 4.16). The mutual relationships between the clusters were presented diagrammatically by taking average intra and inter-cluster D^2 values (Fig 4.17).

4.6.1.5 Average intra and inter- cluster D^2 values

The average intra and inter-cluster D^2 values estimated as per the procedure given by Singh and Chowdhary (1977) are presented in the Table 4.13. The proximity and divergence among six clusters are indicated in Table 4.14.

The mean intra-cluster D^2 values ranged from 0.00 to 275.34, where the maximum intra-cluster distance was 275.34 in cluster III and 179.33 in cluster II and 102.55 in cluster I, while it was zero for clusters IV, V and VI.

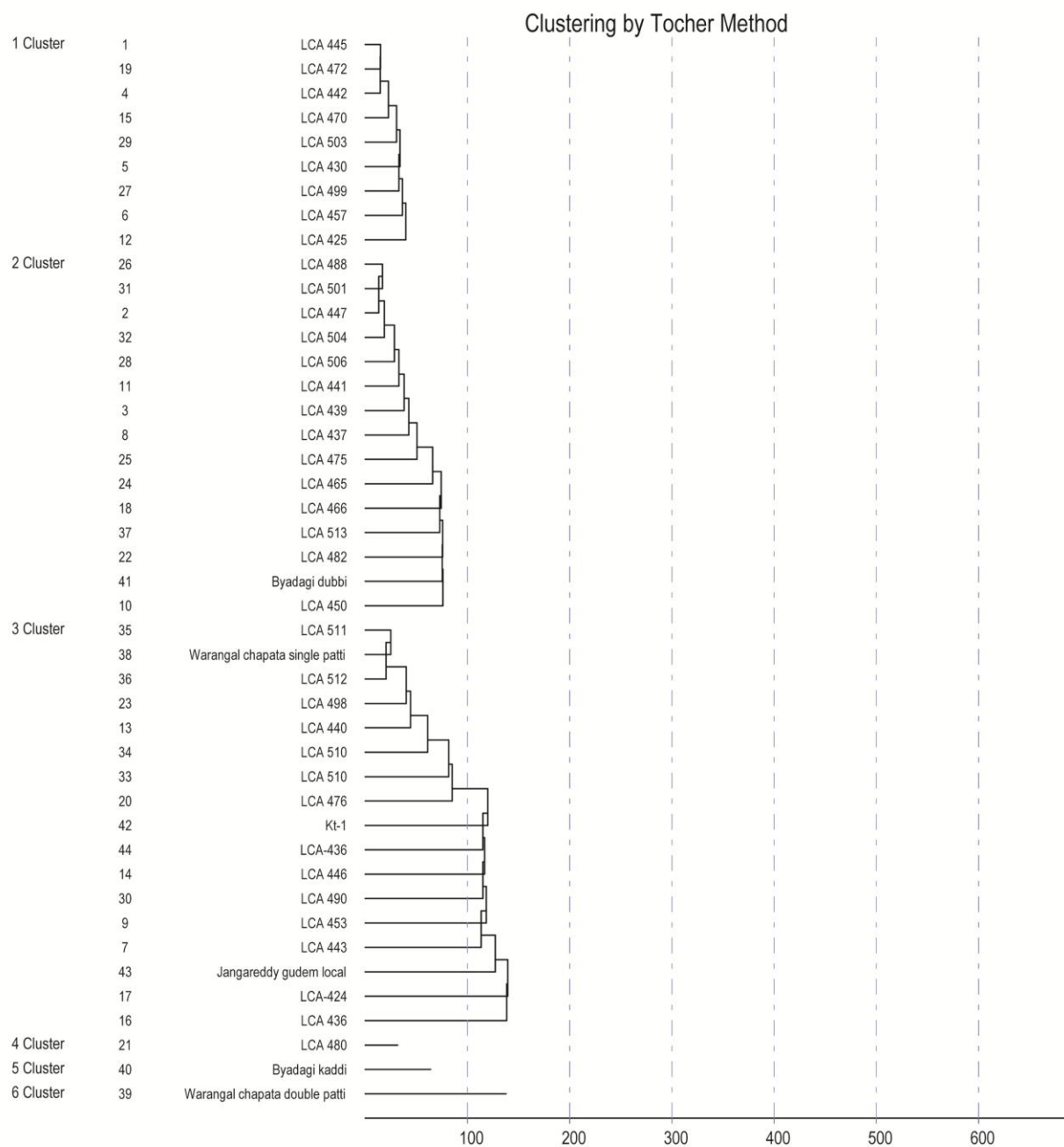
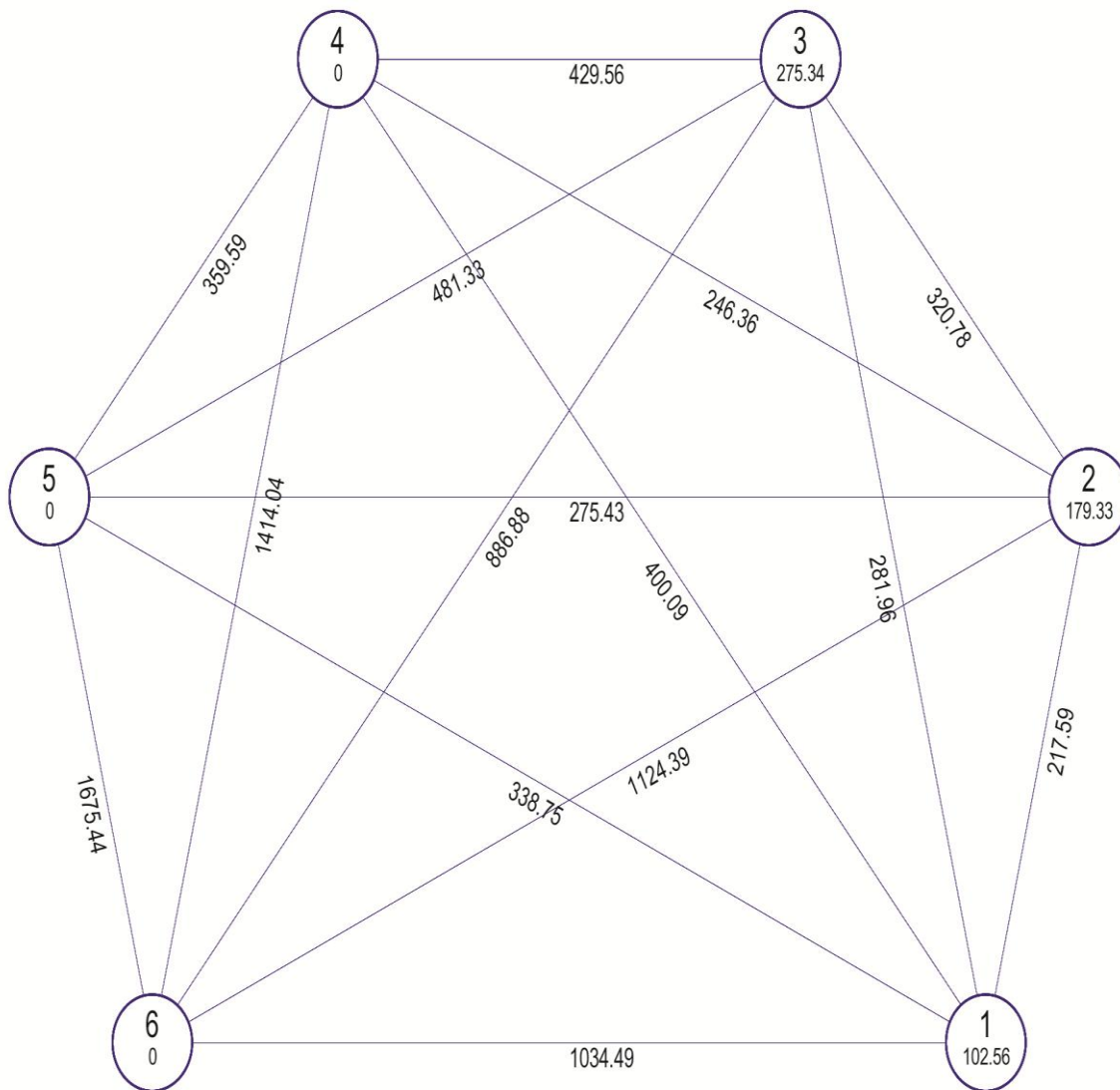


Fig.4.16 Dendrogram showing clustering pattern of 44 paprika (*Capsicum annuum* L.) genotypes (Tocher' s method).

Tocher Method



Mahalanobis Euclidean Distance (Not to the Scale)

Fig 4.17: Average intra and inter cluster D^2 values of six clusters in paprika (*Capsicum annuum* L.)

Table 4.13 : Average intra (bold) and inter cluster D² values of six clusters in paprika (*Capsicum annuum* L.)

Cluster	1 Cluster	2 Cluster	3 Cluster	4 Cluster	5 Cluster	6 Cluster
I	102.55	217.58	281.96	400.09	338.74	1034.49
II		179.33	320.78	246.35	275.43	1124.39
III			275.34	429.56	481.32	886.88
IV				0.00	359.58	1414.04
V					0.00	1675.44
VI						0.00

*Bold and diagonal values indicate intra cluster distance

Table 4.14 : Nearest and farthest clusters from each cluster based on D² values using Tocher's method in paprika (*Capsicum annuum* L.)

Cluster No.	Nearest cluster with D² Values	Farthest cluster with D² values
I	II (217.58)	VI (1034.49)
II	I (217.58)	VI (1124.39)
III	I (281.96)	VI (886.88)
IV	II (246.35)	VI (1414.04)
V	II (275.43)	VI (1675.44)
VI	III (886.88)	V (1675.44)

The inter- cluster D^2 values varied from 217.58 to 1675.44 and maximum genetic divergence existed between cluster V and VI (1675.44) followed by cluster IV and VI (1414.04) indicating wider genetic diversity among the genotypes included in these groups. The minimum genetic divergence was registered between cluster I and II (217.58) preceded by clusters II and IV (246.35).

Cluster I comprised of 9 genotypes. It was nearest to cluster II (217.58) preceded by cluster III (281.96) and farthest from cluster VI (1034.49) followed by cluster IV (400.09).

Cluster II comprised of 15 genotypes. It was nearest to cluster I (217.58) preceded by cluster IV (246.35) and farthest from cluster VI (1124.39) followed by cluster III (320.78).

Cluster III comprising of 17 genotypes was the largest of all clusters. It was closest to cluster I (281.96) preceded by cluster II (320.78) and farthest from cluster VI (886.88) followed by cluster V (481.32).

Cluster IV was mono genotypic (LCA 480). It was closest to the cluster II (246.35) preceded by cluster V (359.58) and farthest from cluster VI (1414.04) followed by cluster III (429.56).

Cluster V comprised of one genotype (Byadagi kaddi). It was nearest to cluster II (275.43) preceded by cluster I (338.74) and farthest from cluster VI (1675.44) followed by cluster IV (481.32).

Cluster VI was mono genotypic (Warangal Chapatta double patti). It was nearest to the cluster III (886.88) preceded by cluster I (1034.49) and farthest from cluster V (1675.44) followed by cluster IV (1414.04).

The intra and inter-cluster distances revealed that inter-cluster distance values were greater than intra-cluster distance values. Maximum intra-cluster D^2 distance was recorded by cluster III (275.34) followed by cluster II (179.33) and cluster I (102.55). The high intra-cluster distance in cluster III indicates the presence of wide genetic diversity among the genotypes present within this cluster.

The maximum inter-cluster distance was observed between cluster V and VI (1675.44) followed by cluster IV and VI (1414.04) and cluster II and VI (1124.39) and cluster I and VI (1034.49) and cluster III and VI (886.88). This suggested wide genetic diversity between these clusters. Based on these studies, crosses can be made between genotypes of these clusters to obtain heterotic hybrids and desirable segregants.

Genotypes grouped into the same cluster presumably differ little from one another as the aggregate of characters measured. General notion exists that the larger is the divergence between the genotypes, the higher will be the heterosis (Falconer, 1964). Therefore, it would be desirable to attempt crosses between genotypes belonging to distant clusters for getting highly heterotic crosses which are likely to yield a wide range of segregants on which selection can be practiced.

The minimum inter-cluster distance was observed between cluster I and II (217.58) preceded by cluster II and IV (246.35), cluster II and V (275.43) and cluster I and III (281.96). The lowest inter-cluster distance between these cluster pairs suggested that the genetic constitution of these genotypes in one cluster were in close proximity with the genotypes in other cluster of the pair.

Choice of the particular cluster and selection of particular genotype from selected cluster are the two important points to be considered before initiating the crossing programme. The hybrids between genotypes of different clusters will express high heterosis and throw more useful segregants. Further, one or two varieties from different clusters may be chosen for further genetic studies either by diallel or line x tester analysis.

4.6.1.6 Cluster Mean Values

Cluster means indicate average performance of all varieties clubbed in a cluster. The relative importance of yield components contributing towards divergence can be judged by comparing the group means of 20 characters. The clusters mean values for all the 20 characters are presented in Table 4.15.

The maximum plant height was observed in cluster III (92.17) followed by cluster VI (91.80) while minimum plant height was recorded in cluster IV (83.10) preceded by cluster V (83.30).

The maximum plant spread was observed in cluster V (141.10) followed by cluster I (132.77) while minimum in cluster VI (117.80) preceded by cluster II (124.57).

The number of primary branches per plant exhibited maximum mean value in cluster IV and V (4.00) followed by cluster I (3.64) while minimum mean value was recorded in cluster VI (3.40) closely preceded by cluster II (3.44).

Days to 50 per cent flowering showed highest mean in cluster II (61.73) followed by cluster I (61.33) and lowest mean value observed in cluster V (52.50) preceded by cluster III (58.14).

Days to maturity showed highest mean in cluster IV (138.00) followed by cluster II (137.56) and lowest mean value observed in cluster V (97.50) preceded by cluster VI (112.00).

The maximum number of fruits per plant was observed in cluster VI (197.10) followed by cluster II (168.43) and cluster I (165.21) while minimum mean value observed in cluster V (118.70) preceded by cluster VI (120.50).

**Table 4.15 : Mean performance of yield per plant and its component characters in various clusters of paprika
(Tocher' s method)**

Cluster No.	PH	PS	NPBP	DFP	DM	NFP	FL	FD	FPL	NSP	WSP	1000 SW	AA	OC	CC	TEC	RC	YC	TC	DFYP
I	89.10	132.77	3.64	61.33	135.77	165.21	13.17	4.66	4.05	71.62	0.49	3.80	55.74	6.95	6959.77	134.25	0.22	0.13	0.36	150.88
II	85.80	124.57	3.44	61.73	137.56	168.43	12.06	4.20	3.55	57.81	0.38	5.65	94.80	8.21	8544.80	99.05	0.14	0.26	0.41	130.53
III	92.17	130.38	3.62	58.14	130.20	141.38	10.42	4.80	3.34	76.48	0.55	6.59	103.11	9.72	11810.79	105.71	0.22	0.17	0.40	118.79
IV	83.10	132.40	4.00	61.00	138.00	197.10	11.55	4.85	3.90	53.90	0.32	2.59	167.31	11.50	4552.00	61.81	0.06	0.13	0.19	144.00
V	83.30	141.10	4.00	52.50	97.50	118.70	16.80	2.55	3.70	45.40	0.25	8.40	181.40	11.35	6052.50	115.00	0.16	0.26	0.42	82.00
VI	91.80	117.80	3.40	59.00	112.00	120.50	8.30	9.70	2.40	154.00	1.35	18.10	72.93	14.55	5463.00	147.35	0.16	0.25	0.41	95.00

*Bold values indicate maximum and minimum mean performance

Note :

PH - Plant height (cm), PS-Plant spread (cm), NPBP – Number of primary branches per plant, DFP – Days to 50 per cent flowering, DM –Days to maturity, NFP – Number of fruits per Plant, FL – Fruit length (cm), FD – Fruit diameter (cm), FPL- Fruit pedicel length (cm), NSF – Number of seeds per fruit, WSF- Weight of seeds per fruit (g), 1000 SW- 1000 seed weight (g), AA-Ascorbic acid(mg/100mg), O- Oleoresin content (%), CC- Capsaicin content (SHU), TEV- Total extractable colour (ASTA units), RC- Red carotenoids (%), YC- Yellow carotenoids (%), DFYP – Dry fruit yield per plant (g),

The fruit length exhibited maximum mean value in cluster V (16.80) followed by cluster I (13.17) while minimum mean value was recorded in cluster VI (8.30) preceded by cluster III (10.42).

The fruit diameter showed highest mean in cluster VI (9.70) and lowest mean in cluster IV (2.55). The fruit pedicel length exhibited maximum mean value in cluster I (4.05) followed by cluster IV (3.90). The minimum mean value for this trait was observed in cluster VI (2.40) preceded by cluster III (3.34).

The number of seeds per fruit exhibited maximum mean value in cluster VI (154.00) while minimum mean value in cluster IV (45.40).

The weight of seeds per fruit exhibited maximum mean value in cluster VI (1.35) while minimum mean value in cluster V (0.25). The 1000 seed weight exhibited maximum mean value in cluster VI (18.10) while minimum mean value in cluster IV (2.59).

The ascorbic acid exhibited maximum mean value in cluster V (181.40) followed by cluster IV (167.31) while minimum mean value in cluster I (55.74) preceded by cluster VI (72.93).

The oleoresin content recorded maximum mean value in cluster VI (14.55) followed by cluster IV (11.50) while the minimum mean value in cluster I (6.95).

The capsaicin content showed highest mean in cluster III (11810.79) and lowest mean in cluster IV (4552.00) preceded by cluster VI (5463.00).

The total extractable colour showed highest mean in cluster VI (147.35) followed by cluster I (134.25) and lowest mean in cluster IV (61.81).

Red carotenoids recorded highest mean in cluster I and cluster III (0.22) followed by cluster V and cluster VI (0.16) and lowest mean in cluster IV (0.06).

Yellow carotenoids recorded highest mean in cluster II and cluster V (0.26) followed by cluster VI (0.25) and lowest mean in cluster IV (0.13) and cluster I (0.13).

Total carotenoids recorded highest mean in cluster V (0.42) followed by cluster II (0.41) and cluster VI (0.41) and lowest mean in cluster IV (0.19).

The dry fruit yield per plant exhibited maximum mean value in cluster I (150.88) followed by cluster IV (144.00) while minimum mean value in cluster V (82.00) preceded by cluster VI (95.00).

The clusters V, VI, IV, I and II were found superior for one or more characters. Therefore, it is proposed to arrange a multiple crossing programme involving genotypes from these clusters to isolate superior segregants in advanced generations with high genetic yield potential and other desirable characters in paprika.

The success and usefulness of Mahalanobis' D^2 analysis in quantifying genetic divergence has been studied by Prabhudeva (2003), Senapati *et al.* (2003), Gogate *et al.* (2006), Vani *et al.* (2007b), Dutonde *et al.* (2008), Ajjapplavara (2009), Thul *et al.* (2009), Farhad *et al.* (2010), Finger *et al.* (2010), Kumar *et al.* (2010), Kumari *et al.* (2010), Pandit *et al.* (2010), Singh and Singh (2010), Misra *et al.* (2011), Datta and Das (2013), Hasan *et al.* (2015), Rana *et al.* (2015), Janaki *et al.* (2015b) and Razzaq *et al.* (2016)

4.6.2 Principal component analysis (PCA) in genetic divergence

Principal component analysis or canonical (vector) analysis is a sort of multivariate analysis where canonical vectors or roots representing different axes of differentiation and amount of variation accounted by each of such axes, respectively are derived (Rao, 1952).

Results obtained from PCA on the correlation matrix of the traits reduce the dimensionality of the data set by creating eight significant

principal components having eigen value more than one. The PCA scores for individual genotypes were used for clustering the genotypes as suggested by Anderberg (1993). Results of PCA and cluster analysis are discussed here under.

Principal components (eigen value greater than one), eigen values (Latent Root), per cent variability, cumulative per cent variability and component loading of different characters are presented in Table 4.16.

In the present study, the eight principal components with eigen values more than one contributed 83.62 per cent towards the total variability. The principal component with eigen values less than one were considered as non-significant. It was therefore inferred that the essential features of data set had been represented in the first eight principal components.

The first principal component (PC_1) contributed maximum towards the total variability (25.18%). The characters viz., weight of seeds per fruit (0.38), fruit diameter (0.37), number of seeds per fruit (0.35), 1000 seed weight (0.31), capsaicin content (0.18), dry fruit yield per plant (0.16), fruit pedicel length (0.15), days to 50 per cent flowering(0.09), plant height (0.09), red carotenoids (0.09) were positively loaded. Number of fruits per plant (-0.28), fruit length (-0.28), total extractable colour (-0.25), yellow carotenoids (-0.22), plant spread (-0.18), total carotenoids (-0.17) number of primary branches per plant (-0.14), ascorbic acid (-0.10), days to maturity (-0.03), oleoresin content (-0.03) were negatively loaded.

The second principal component (PC_2) was characterized by 15.02 per cent contribution towards the total variability. The characters viz., total carotenoids (0.40), total extractable colour (0.37), dry fruit yield per plant (0.26), plant height (0.24), plant spread (0.24), number of seeds per fruit (0.17), capsaicin content (0.17), oleoresin content (0.16), fruit pedicel length (0.15), number of primary branches per plant (0.12), red carotenoids (0.11), fruit length (0.10), weight of seeds per fruit (0.085), number of fruits

Table 4.16 : Eigen values, proportion of the total variance, cumulative per cent variance and component loading of different characters in paprika (*Capsicum annuum* L.).

	PC ₁	PC ₂	PC ₃	PC ₄	PC ₅	PC ₆	PC ₇	PC ₈
Eigene Value (Root)	5.03	3.00	2.46	1.75	1.42	1.16	1.00	0.86
% Var. Exp.	25.18	15.02	12.33	8.79	7.12	5.84	5.00	4.31
Cum. Var. Exp.	25.18	40.20	52.54	61.33	68.45	74.30	79.30	83.62
Plant Height (cm)	0.09	0.24	0.15	0.15	0.18	0.24	0.17	0.52
Plant Spread (cm)	-0.18	0.24	-0.02	0.06	0.19	0.28	-0.46	-0.45
Number of Primary Branches Per Plant	-0.14	0.12	0.003	0.33	0.10	0.57	0.19	0.12
Days to 50% Flowering	0.09	-0.30	0.24	0.34	-0.03	-0.12	-0.25	0.25
Days to Maturity	-0.03	-0.07	0.35	0.47	-0.02	-0.26	-0.09	0.00002
Number of Fruits Per Plant	-0.28	0.06	0.37	-0.05	0.15	0.02	0.21	-0.16
Fruit Length (cm)	-0.28	0.10	0.36	-0.07	-0.01	0.03	-0.17	-0.03
Fruit Diameter (cm)	0.37	0.05	0.12	0.03	0.19	-0.13	0.09	0.03
Fruit Pedicel Length (cm)	0.15	0.15	-0.31	0.40	-0.17	-0.11	-0.33	-0.05
Number of Seeds Per Fruit	0.35	0.17	0.06	-0.01	0.20	0.05	-0.34	-0.03
Weight of seeds Per Fruit (g)	0.38	0.08	0.09	-0.13	0.20	0.11	-0.18	0.02
1000 Seed Weight (g)	0.31	-0.16	0.01	-0.35	0.07	0.01	0.06	-0.05
Ascorbic Acid (mg /100g)	-0.10	-0.33	-0.34	0.18	-0.06	0.25	-0.01	-0.05
Oleoresin content (%)	-0.03	0.16	-0.29	0.08	0.54	-0.12	0.17	-0.12
Capsaicin content (SHU)	0.18	0.17	-	0.10	-0.44	-0.02	0.29	-0.32
Total extractable colour (ASTA Units)	-0.25	0.37	-0.01	-0.15	-0.01	-0.24	-0.20	0.21
Red Carotenoids (%)	0.09	0.11	0.13	-0.25	-0.43	0.39	-0.22	0.14
Yellow Carotenoids (%)	-0.22	-0.31	0.14	-0.16	0.14	-0.08	-0.1	-0.05
Total Carotenoids (%)	-0.17	0.40	-0.18	-0.06	-0.15	-0.28	0.01	0.24
Dry Fruit Yield Per Plant (g)	0.16	0.26	0.33	0.14	-0.08	-0.03	0.22	-0.38

per plant (0.06) and fruit diameter (0.05) were positively loaded. Ascorbic acid (-0.33), days to 50 per cent flowering (-0.30), yellow carotenoids (-0.31), 1000 seed weight (-0.16), days to maturity (-0.07), were negatively loaded.

The third principal component (PC₃) was characterized by 12.33 per cent contribution towards the total variability. The characters viz., number of fruits per plant (0.37), fruit length (0.36), days to maturity (0.35), dry fruit yield per plant (0.33), days to 50 per cent flowering (0.24), plant height (0.15), Yellow carotenoids (0.14), red carotenoids (0.13), fruit diameter (0.12), weight of seeds per fruit (0.09), number of seeds per fruit (0.06), 1000 seed weight (0.01) and number of primary branches per plant (-0.003) yellow carotenoids (-0.51) were positively loaded. Capsaicin content (-0.009), total extractable colour (-0.29), number of primary branches per plant (-0.24), ascorbic acid (-0.34), fruit pedicel length (-0.31) and oleoresin content (-0.29), total carotenoids (-0.18), plant spread (-0.02), were negatively loaded.

The fourth principal component (PC₄) was characterized by 8.79 per cent contribution towards the total variability. The characters viz., fruit pedicel length (0.40), days to maturity (0.47), days to 50 per cent flowering (0.34), number of primary branches per plant (0.33), ascorbic acid (0.18), plant height (0.15), dry fruit yield per plant (0.14), capsaicin content (0.10), oleoresin content (0.08), plant spread (0.06), fruit diameter (0.03) were positively loaded. 1000 seed weight (-0.35), red carotenoids (-0.25), yellow carotenoids (-0.16), total extractable colour (-0.15), weight of seeds per fruit (-0.13), fruit length (-0.07), total carotenoids (-0.06), number of fruits per plant (-0.05) and number of seeds per fruit (-0.01) were negatively loaded.

The fifth principal component (PC₅) was characterized by 7.12 per cent contribution towards the total variability. The characters viz., oleoresin content (0.54), number of seeds per fruit (0.20), weight of seeds per fruit (0.20), plant spread (0.19), fruit diameter (0.19), plant height (0.18), number of fruits per plant (0.15), yellow carotenoids (0.14), number of primary branches per plant (0.10) and 1000 seed weight

(0.07) were positively loaded. Capsaicin content (-0.44), red carotenoids (-0.43), fruit pedicel length (-0.17), total carotenoids (-0.15), dry fruit yield per plant (-0.08), ascorbic acid (-0.06), days to 50 per cent flowering (-0.03), days to maturity (-0.02), fruit length (-0.01) and total extractable colour (-0.01) were negatively loaded.

The sixth principal component (PC₆) was characterized by 5.84 per cent contribution towards the total variability. The characters viz., number of primary branches per plant (0.57), red carotenoids (0.39), plant spread (0.28), ascorbic acid (0.25), plant height (0.24), weight of seeds per fruit (0.11), number of seeds per fruit (0.05), fruit length (0.03), number of fruits per plant (0.02) and 1000 seed weight (0.01) were positively loaded. Total carotenoids (-0.28), days to maturity (-0.26), total extractable colour (-0.24), fruit diameter (-0.13), days to 50 per cent flowering (-0.12), oleoresin content (-0.12), fruit pedicel length (-0.11), yellow carotenoids (-0.08), dry fruit yield per plant (-0.03) and capsaicin content (-0.02) were negatively loaded.

The seventh principal component (PC₇) was characterized by 5.00 per cent contribution towards the total variability. The characters viz., capsaicin content (0.29), dry fruit yield per plant (0.22), number of fruits per plant (0.21), number of primary branches per plant (0.19), plant height (0.17), oleoresin content (0.17), fruit diameter (0.09), 1000 seed weight (0.06) and total carotenoids (0.01) were positively loaded. Plant spread (-0.46), number of seeds per fruit (-0.34), fruit pedicel length (-0.33), days to 50 per cent flowering (-0.25), red carotenoids (-0.22), total extractable colour (-0.20), weight of seeds per fruit (-0.18), yellow carotenoids (-0.17), fruit length (-0.17), days to maturity (-0.09) and ascorbic acid (-0.01) were negatively loaded.

The eighth principal component (PC₈) was contributed 4.31 per cent towards the total variability. The characters viz., plant height (0.52), days to 50 per cent flowering (0.25), total carotenoids (0.24), total extractable colour (0.21), red carotenoids (0.14), number of primary branches per plant (0.12), fruit diameter (0.03), weight of seeds per fruit (0.02) and days to maturity (0.00002) were positively loaded. Plant spread (-0.46),

dry fruit yield per plant (-0.38), capsaicin content (-0.32), number of fruits per plant (-0.16), oleoresin content (-0.12), yellow carotenoids (-0.05), fruit pedicel length (-0.05), ascorbic acid (-0.05), 1000 seed weight (-0.05), number of seeds per fruit (-0.03) and fruit length (-0.03) were negatively loaded.

The characters viz., weight of seeds per fruit, fruit diameter, number of seeds per fruit, 1000 seed weight, number of fruits per plant and fruit length significantly loaded in PC₁ and contributed more towards variability. It is important for studying the variance as the relative contributions are more important than the signs (indicative of direction) in principal component analysis.

The PCA scores for 44 paprika genotypes in the first three principal components were computed. Principal component I, II and III were considered as three axes as X, Y and Z and squared distance of each genotype from these three axes were calculated and presented in Table 4.17. These PCA scores for 44 paprika genotypes were plotted on graph to get two dimensional and three dimensional scattered diagrams (Fig.4.18 and Fig.4.19) to reveal diversity between the genotypes. These genotypes may be used in crop improvement programmes for generating transgressive segregants.

Thul *et al.* (2009), Kadri *et al.* (2009), Farhad *et al.* (2010), Sudre *et al.* (2010), Misra *et al.* (2011), Lahbib *et al.* (2012) and Janaki *et al.* (2015b), studied the utilization of principal component analysis in genetic divergence studies in chilli.

4.6.3 Cluster analysis

To group the 44 genotypes into clusters, agglomerative hierarchical cluster analysis was followed. Principal component scores for genotypes were used as an input for clustering using Ward's minimum variance method. The tree like structure called dendrogram (Fig 4.20) was constructed based on Euclidean ² distance computed from PCA scores of genotypes.

Table 4.17 : PCA scores of 44 genotypes of paprika (*Capsicum annuum* L.)

Genotype	PCA I X VECTOR	PCA II Y VECTOR	PCA III Z VECTOR
LCA 445	4.385	5.411	29.589
LCA 447	-0.694	-1.524	31.827
LCA 439	-6.157	-0.404	30.998
LCA 442	2.442	5.506	28.320
LCA 430	-3.019	4.836	28.320
LCA 457	2.046	1.693	26.030
LCA 443	12.442	8.235	27.238
LCA 437	-3.498	1.424	22.507
LCA 453	10.142	7.998	29.007
LCA 450	0.432	-0.054	25.557
LCA 441	-0.962	-0.858	23.675
LCA 425	-4.436	5.808	25.420
LCA 440	6.080	1.808	26.976
LCA 446	2.773	8.083	28.348
LCA 470	-0.988	6.394	28.493
LCA 436-1	-1.946	8.116	32.249
LCA 466	0.013	-5.673	23.365
LCA 472	2.678	4.827	21.014
LCA 476	1.553	-8.735	29.119
LCA 480	-3.824	-4.883	29.848
LCA 482	2.553	-4.077	22.738
LCA 498	6.464	-0.186	25.620
LCA 465	-4.731	-0.412	29.210
LCA 475	0.338	-3.214	26.078
LCA 488	-3.088	-3.824	28.656
LCA 499	-1.449	4.998	29.617
LCA 506	3.050	0.282	26.614
LCA 503	-0.586	6.125	28.849
LCA 490	0.949	4.763	28.558
LCA 501	-1.450	-1.799	23.493
LCA 504	-5.068	0.147	30.387
LCA 510	-0.984	-7.279	22.147
LCA 510-1	6.235	-2.907	23.505
LCA 511	12.076	0.286	27.898
LCA 512	14.401	0.434	27.965
LCA 513	2.009	-6.155	20.367

Warangal chappatta single patti	12.883	-3.640	26.848
Warangal chappatta double patti	27.883	2.594	31.100
Byadagi kaddi	-8.077	-2.147	19.554
Byadagi dabbi	2.344	-3.950	21.586
Kt-1	0.387	2.028	16.065
Jangareddy gudem Local	7.435	-3.241	16.153
LCA 436	-0.426	8.134	23.272
LCA 424	-2.795	10.203	24.913

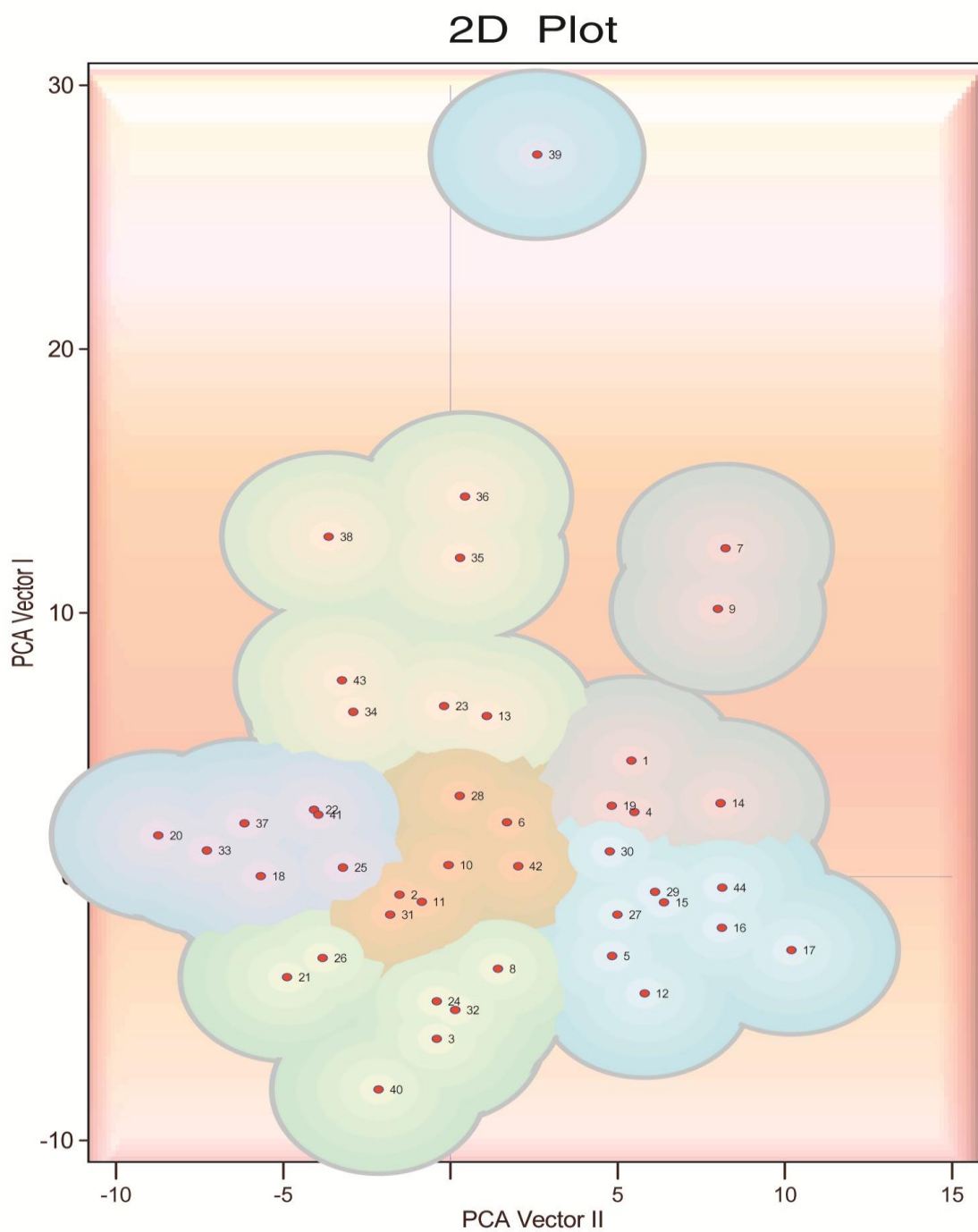


Fig 4.18: Two dimensional graph showing relative position of 44 paprika (*Capsicum annuum* L.) genotypes based on PCA scores

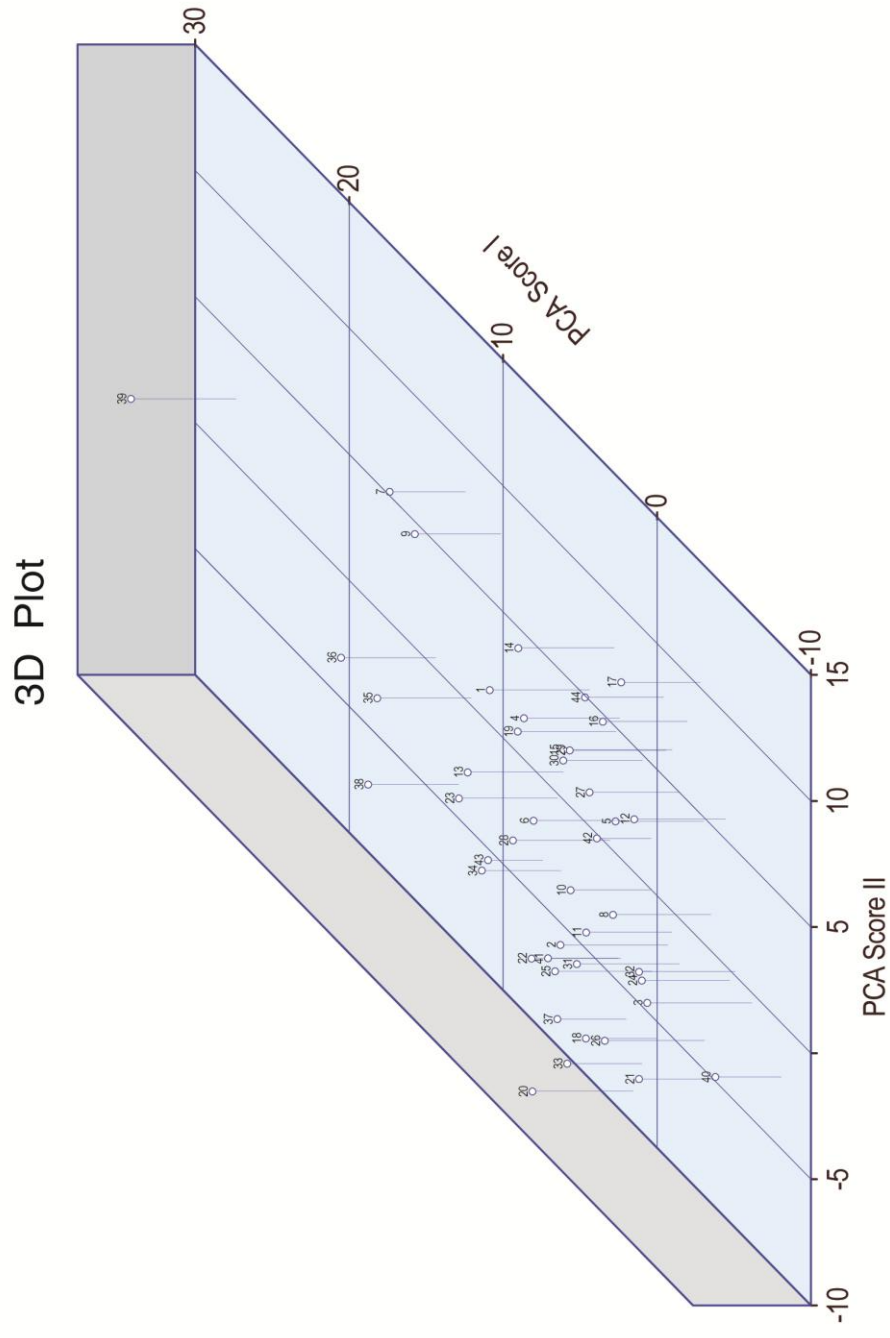


Fig 4.19: Three dimensional graph showing relative position of 44 paprika (Capsicum annuum L.) genotypes based on PCA scores.

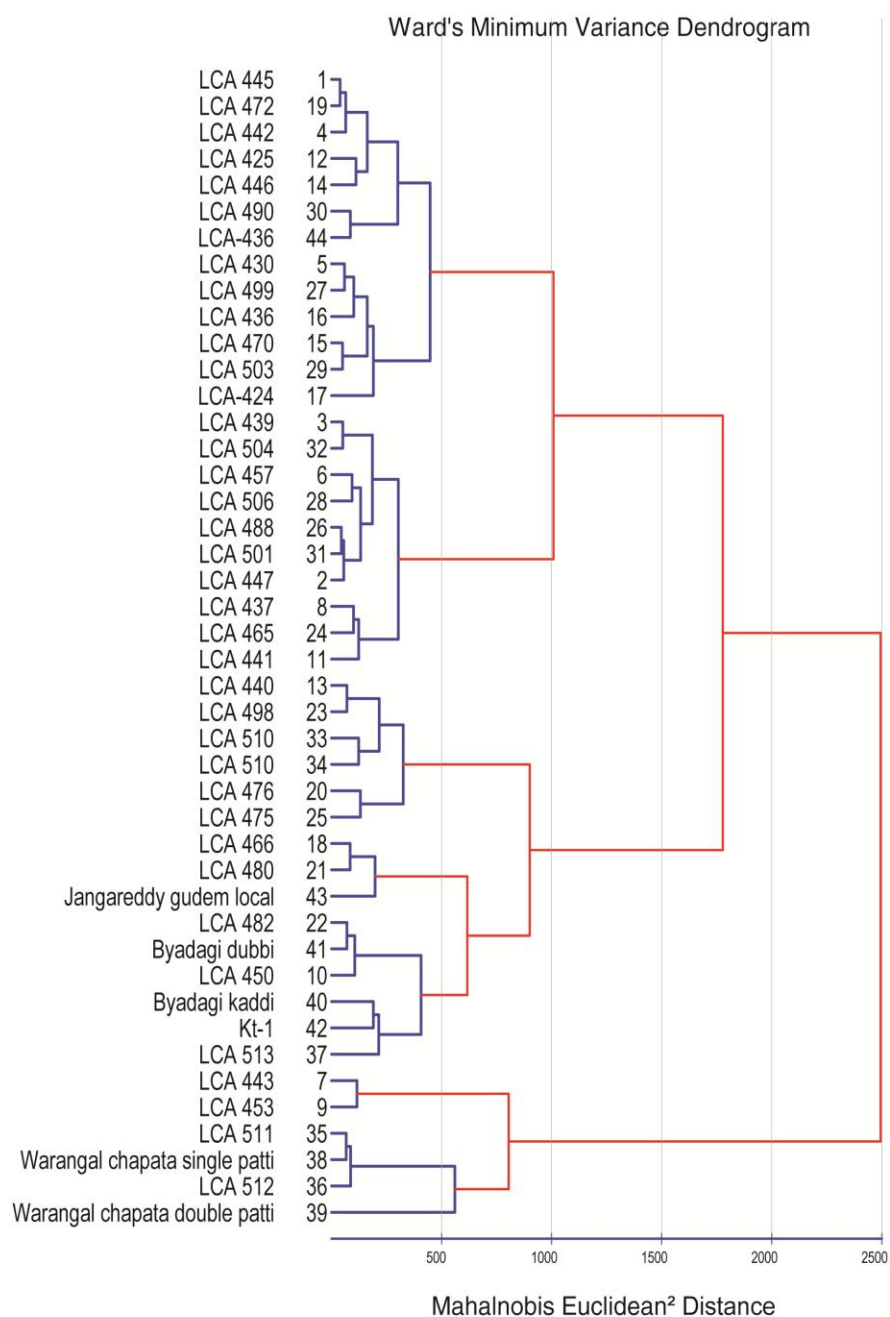


Fig.4.20 : Dendrogram showing clustering pattern of 44 paprika (*Capsicum annuum* L.)

The 44 genotypes of paprika were grouped into seven clusters. The distribution of genotypes into 7 clusters is presented in Table 4.18. Among all the clusters, cluster I was the largest containing 13 genotypes followed by cluster II with 10 genotypes, cluster III and cluster V with 6 genotypes, cluster VII with 4 genotypes, cluster IV with 3 genotypes, cluster VI with 2 genotypes. The random distribution of genotypes indicated absence of parallelism between geographical and genetic diversity. The mutual relationship between clusters is represented diagrammatically (Fig. 4.21) by taking average intra and inter-cluster Euclidean² distances.

4.6.3.1 Average intra and inter- cluster Euclidean² distance values

The average intra and inter-cluster Euclidean² distance were estimated based on Ward's minimum variance and are presented in Table 4.19. The proximity and divergence among seven clusters are indicated in Table 4.20.

By Ward's method, the 44 genotypes were grouped into 7 clusters. Of the 7 clusters formed, the mean intra-cluster D² values ranged from 231.65 to 475.42 where cluster VI had minimum intra-cluster Euclidean² distance value of 231.65 preceded by cluster II (242.37), cluster IV (282.82), cluster I (296.69), cluster III (347.26), cluster V (395.51) and cluster VII (475.42).

The inter-cluster Euclidean² distances varied from 424.39 (between cluster I and cluster II) to 1217.10 (cluster IV and VII).

Cluster I comprising of 13 genotypes was the largest of all clusters. It was closest to cluster II (424.39) preceded by cluster V (571.97) and farthest from cluster VII (1105.19) followed by cluster IV (838.02).

Cluster II consisted of 10 genotypes. It was nearest to cluster I (424.39) preceded by cluster V (482.89) and farthest from cluster VII (1105.94) followed by cluster VI (939.10).

**Table 4.18 : Clustering of 44 paprika genotypes (*Capsicum annuum* L.) by
Ward's minimum variance method**

Cluster No.	No. of genotypes	Name of genotypes
I	13	LCA 445, LCA 472,LCA 442, LCA 425, LCA 446, LCA 490, LCA 436, LCA 430, LCA 499,LCA 436, LCA 470, LCA 503, LCA 424
II	10	LCA 439, LCA 504, LCA 457, LCA 506,LCA 488, LCA 501, LCA 447, LCA 437, LCA 465, LCA 441
III	6	LCA 440, LCA 498, LCA 510, LCA 510, LCA 476, LCA 475
IV	3	LCA 466, LCA 480, Jangareddy gudem local
V	6	LCA 482, Byadagi dabbi, LCA 450, Byadagi kaddi, Kt-1, LCA 513
VI	2	LCA 443, LCA 453
VII	4	LCA 511, Warangal chappatta single patti, LCA 512, Warngal chappatta double patti

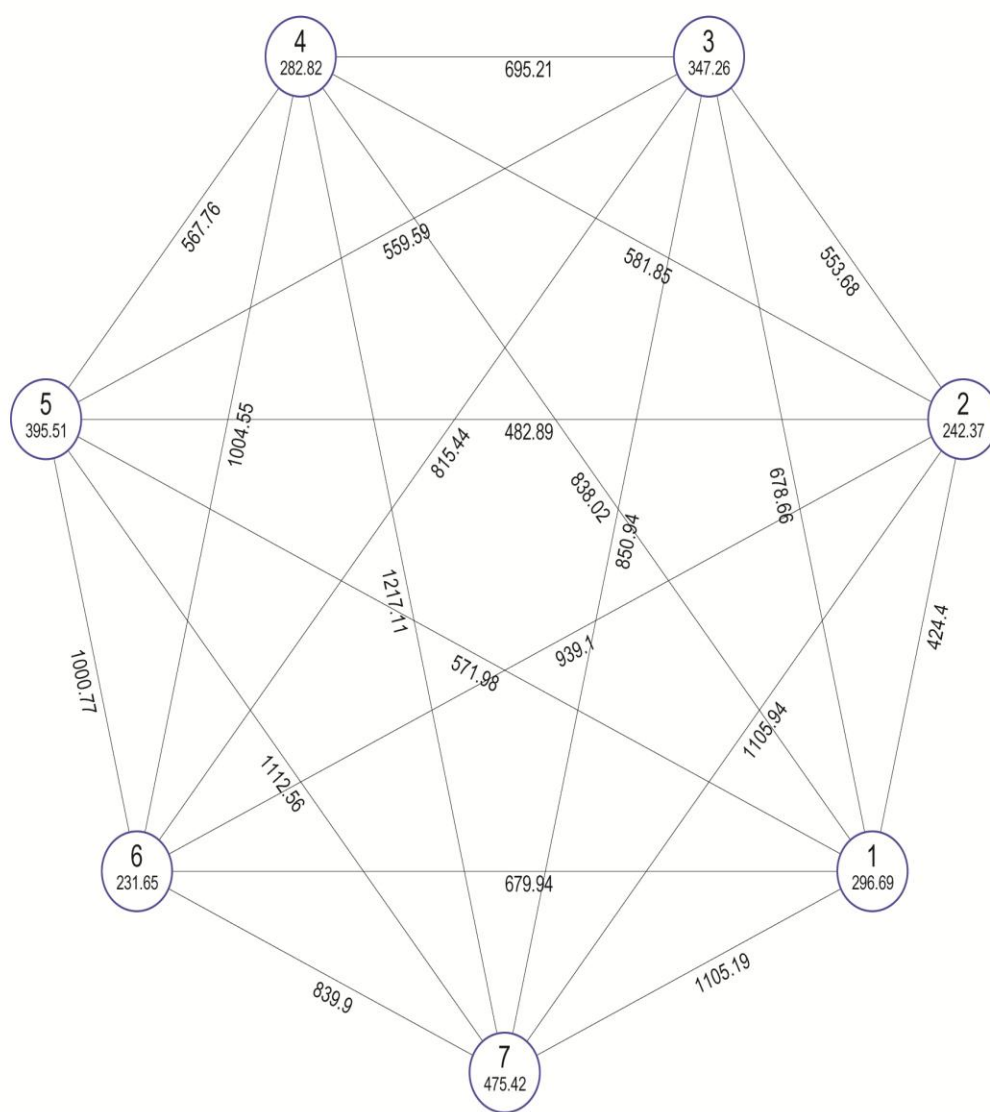
Table 4.19 : Average intra (bold) and inter cluster Euclidean² values of seven clusters in paprika (*Capsicum annuum* L.)

Cluster	1 Cluster	2 Cluster	3 Cluster	4 Cluster	5 Cluster	6 Cluster	7 Cluster
I	296.69	424.39	678.65	838.02	571.97	679.94	1105.19
II		242.37	553.68	581.84	482.89	939.10	1105.94
III			347.26	695.20	559.59	815.43	850.93
IV				282.82	567.75	1004.54	1217.10
V					395.51	1000.77	1112.55
VI						231.65	839.90
VII							475.42

*Bold and diagonal values indicate intra cluster distance

Table 4.20 : Nearest and farthest clusters from each cluster based on Euclidean² values in paprika (*Capsicum annuum* L.)

Cluster No.	Nearest cluster	Farthest cluster
I	II (424.39)	VII (1105.19)
II	I (424.39)	VII (1105.94)
III	II (553.68)	VII (850.93)
IV	V (567.75)	VII (1217.10)
V	II (482.89)	VII (1112.55)
VI	I (679.94)	IV (1004.54)
VII	VI (839.90)	IV (1217.10)



Euclidean² Distance (Not to the Scale)

Fig 4.21: Average intra and inter cluster Euclidean values of seven clusters in paprika (*Capsicum annuum* L.)

Cluster III consisted of 6 genotypes. It was closest to cluster II (553.68) preceded by cluster V (559.59) and farthest from cluster VII (850.93) followed by cluster VI (815.43).

Cluster IV consisted of 3 genotypes. It was nearest to cluster V (567.75) preceded by cluster II (581.84) and farthest from cluster VII (1217.10) followed by cluster VI (1004.54).

Cluster V comprised of 6 genotypes. It was nearest to cluster II (482.89) preceded by cluster III (559.59) and farthest from cluster VII (1112.55) followed by cluster VI (1000.77).

Cluster VI comprised 2 genotypes. It was nearest to cluster I (679.94) preceded by cluster III (815.43) and farthest from cluster IV (1004.54) followed by cluster V (1000.77).

Cluster VII comprised 4 genotypes. It was closest to cluster VI (839.90) preceded by cluster III (850.93) and farthest from cluster IV (1217.10) followed by cluster V (1112.55).

Of the seven clusters formed, maximum intra-cluster Euclidean² distance was recorded by cluster VII (475.42) followed by cluster V (395.51) and cluster III (342.26) and cluster I (296.69). The high intra-cluster distance in cluster VII indicates the presence of wide genetic diversity among the genotypes present within this cluster.

The maximum inter-cluster distance was observed between cluster IV and cluster VII (1217.10) followed by cluster V and cluster VII (1112.55) and cluster II and cluster VII (1105.94), cluster I and cluster VII (1105.19), cluster IV and cluster VI (1004.54) and cluster V and cluster VI (1000.77). This suggested that there was wide genetic diversity between these clusters. Based on these studies, crosses can be made between genotypes of these clusters to obtain heterotic hybrids and desirable segregants. The minimum inter-

cluster distance was observed between cluster I and cluster II (424.49) followed by cluster II and cluster V (482.89), cluster II and cluster III (553.68), cluster III and cluster V (559.59) and cluster II and cluster IV (581.84). The lowest inter-cluster distance between these cluster pairs suggested that the genetic constitution of the genotypes in one cluster was in close proximity with those of genotypes in other cluster of the pair.

Results of cluster analysis based on PCA scores were compared with the results of the principal component analysis on a visual aid in desecrating clusters in the 2 D and 3 D scattered diagrams. The genotypes falling in same cluster were present closer to each other in scattered diagram.

4.6.3.2 Cluster means

The cluster mean values for all the 20 characters studied on pooled basis are presented in Table 4.21.

The maximum plant height was observed for cluster VII (98.70) followed by cluster VI (93.55) while the minimum plant height for cluster V (79.98) preceded by cluster III (82.81).

The maximum plant spread was observed for cluster I (138.00) followed by cluster IV (130.03) while the minimum plant height for cluster III (120.15) preceded by cluster V (121.26).

The number of primary branches per plant exhibited maximum mean value for cluster I (3.70) and cluster IV (3.70) while minimum mean value for cluster V (3.40) preceded by cluster VII (3.45).

Days to 50 per cent flowering showed highest mean for cluster II (62.10) followed by cluster III (62.00) and lowest mean for cluster I (56.92) preceded by cluster V (59.33).

Table 4.21 : Mean performance of yield per plant and its component characters in various clusters of paprika (Ward's minimum variance method)

*Bold values indicate maximum and minimum mean performance

Cluster No.	PH	PS	NPBP	DFF	DM	NFP	FL	FD	FPL	NSP	WSP	1000 SW	AA	OC	CC	TEC	RC	YC	TC	DFYP
I	89.86	138.00	3.70	56.92	129.96	167.19	12.79	4.75	3.92	73.48	0.49	3.78	62.08	8.64	7764.11	132.71	0.20	0.14	0.34	154.30
II	92.29	129.50	3.56	62.10	144.95	187.50	12.90	4.29	3.78	57.74	0.40	5.37	66.68	8.82	9132.95	98.36	0.09	0.26	0.35	141.15
III	82.81	120.15	3.56	62.00	143.66	164.29	10.77	4.20	3.10	50.55	0.41	6.82	137.51	6.88	14640.91	64.54	0.30	0.16	0.46	124.33
IV	88.1	130.03	3.70	61.00	127.66	143.70	8.60	4.61	3.00	64.36	0.39	5.34	171.15	11.26	6983.50	91.37	0.08	0.22	0.30	114.33
V	79.98	121.26	3.40	59.33	111.41	119.70	11.36	3.51	3.28	59.66	0.38	7.10	139.69	8.78	5772.00	116.58	0.27	0.24	0.51	92.75
VI	93.55	123.15	3.50	60.50	153.25	112.75	8.42	6.00	3.97	92.70	0.53	5.76	29.85	8.22	19381.00	151.76	0.11	0.16	0.28	96.75
VII	98.70	124.35	3.45	61.50	121.87	111.05	10.67	6.77	3.12	123.20	1.03	11.53	97.02	10.93	8302.00	110.49	0.20	0.25	0.45	100.00

Note :

PH – Plant height (cm), PS-Plant spread (cm), NPBP – Number of primary branches per plant, DFF – Days to 50 per cent flowering, DM –Days to maturity, NFP – Number of fruits per Plant, FL – Fruit length (cm), FD – Fruit diameter (cm), FPL- Fruit pedicel length (cm), NSF – Number of seeds per fruit, WSF- Weight of seeds per fruit (g), 1000 SW- 1000 seed weight (g), AA-Ascorbic acid(mg/100mg), O- Oleoresin content (%), CC- Capsaicin content (SHU), TEV- Total extractable colour (ASTA units), RC- Red carotenoids (%), YC- Yellow carotenoids (%), DFYP – Dry fruit yield per plant (g),

Days to maturity showed highest mean for cluster VI (153.25) followed by cluster II (144.95) and lowest mean for cluster V (111.41) preceded by cluster VII (121.87).

The number of fruits per plant exhibited maximum mean value for cluster II (187.50) followed by cluster I (167.19) while minimum for cluster VII (111.05) preceded by cluster VI (112.75).

The fruit length exhibited maximum mean value for cluster II (12.90) followed by cluster I (12.79) while minimum for cluster VI (8.42) preceded by cluster IV (8.60).

The fruit diameter showed highest mean for cluster VII (6.77) followed by cluster VI (6.00) and lowest mean for cluster V (3.51).

The fruit pedicel length exhibited maximum mean value for cluster VI (3.97) followed by cluster I (3.92) while minimum for cluster IV (3.00) preceded by cluster III (3.10) and cluster VII (3.12).

The number of seeds per fruit exhibited maximum mean value for cluster VII (123.20) while minimum mean value for cluster III (50.55).

The weight of seeds per fruit exhibited maximum mean value for cluster VII (1.03) while minimum mean value for cluster V (0.38) preceded by cluster IV (0.39).

The 1000 seed weight exhibited maximum mean value for cluster VII (11.53) while minimum mean value for cluster I (3.78).

The ascorbic acid exhibited maximum mean value for cluster IV (171.15) while minimum mean value for cluster VI (29.85).

The oleoresin content recorded maximum mean value for cluster IV (11.26) followed by cluster VII (10.93) while minimum mean value for cluster III (6.88).

The capsaicin content showed highest mean for cluster VI (19381.00) followed by cluster III (14640.91) while lowest mean for cluster V (5772.00) preceded by cluster IV (6983.50)

The total extractable colour showed highest mean for cluster VI (151.76) followed by cluster I (132.71) while lowest mean for cluster III (64.54).

Red carotenoids recorded highest mean for cluster III (0.30) followed by cluster V (0.27) and lowest mean for cluster IV (0.08) preceded by cluster II (0.09).

Yellow carotenoids recorded highest mean for cluster II (0.26) followed by cluster VII (0.25) and lowest mean for cluster I (0.14) preceded by cluster III (0.165).

Total carotenoids recorded highest mean for cluster III (0.51) followed by cluster III (0.46) and lowest mean for cluster VI (0.28) preceded by cluster IV (0.30).

The yield per plant exhibited maximum mean value for cluster I (154.30) followed by cluster II (141.15) while minimum mean value for cluster V (92.75) preceded by cluster VI (96.75).

In general, the clusters V, I, III, VI, VII, IV and II were found superior for one or more characters. Therefore, it is proposed to arrange a multiple crossing programme involving genotypes from these clusters to isolate superior segregants in advanced generations with high genetic yield potential and other desirable characters in chilli.

Pandey *et al.* (2008), Kadri *et al.* (2009), and Sudre *et al.* (2010), Tasso *et al.* (2014), Srinivas *et al.* (2015) Janaki *et al.* (2016) were earlier studied the utilization of Ward's minimum variance method in genetic divergence studies in chilli.

Comparative study of D^2 analysis, principal component analysis and cluster analysis

The grouping of clustering pattern using D^2 analysis, principal component analysis and cluster analysis were compared and their implications are discussed here under.

All the three methods of grouping revealed a single concept of non correspondence of genetic divergence and geographical diversity. In D^2 analysis, the intra-and inter-cluster distances were low compared to the cluster analysis. This is same with the utilization of correlation matrix in principal component analysis derived from covariance matrix. The standardization made the principal component analysis to support the cluster analysis.

Mahalanobis' D^2 statistic and Jackson's principal component analysis both are the tools for analyzing multivariate data. PCA confirms the group constellations obtained by D^2 analysis. It determines the effective number of axes of differentiation primary and secondary or based on number of canonical vectors. The advantage of PCA over D^2 analysis is that it reduces the dimensionality of the data set by creating significant principal components which contributed towards maximum variability of the genotypes. The largest element (absolute value) in each vector constitute the greatest contributor for divergence. In PCA, standardization of data made attributes to contribute equally towards the divergence studies irrespective of the units taken.

The principal component analysis sorted only significant principal components out of the total 20 attributes. The contribution of the main characters for variance easily identified by the characters loaded on the PC_1 with high loading values. PCA facilitates in depth analysis for genetic diversity. In D^2 analysis, total extractable colour value followed by red carotenoids and yellow carotenoids contributed maximum for the divergence, while in PCA the characters viz., weight of seeds per fruit, fruit diameter, number of seeds per fruit, 1000 seed weight, number of fruits per plant, fruit length significantly loaded in PC_1 and contributed more towards variability.

Both cluster analysis and PCA grouped the 44 paprika genotypes into seven clusters and in D^2 analysis six clusters. In D^2 analysis, cluster III had the largest with 17 genotypes followed by cluster II (15 genotypes), cluster I (9 genotypes). As per Ward's method, the cluster I was the largest comprising of 13 genotypes followed by cluster II (10 genotypes), cluster III and cluster V (6 genotypes), cluster VII (4 genotypes) and cluster VI (2 genotypes).

The pattern of distribution of genotypes into different clusters was at random. Furthermore, the two clustering methods grouped the genotypes differently and clustering pattern for genotypes were not same. There was no solitary cluster formed in Ward's minimum variance method, whereas in case of D^2 analysis, cluster IV, V and cluster VI represented solitary clusters. Genetic diversity was the outcome of several factors along with geographic diversity. Hence, the selection for hybridization should be based on genetic diversity rather than geographic diversity.

Ward's minimum variance dendrogram (cluster analysis) created sub group within a cluster. Hence relative position of the genotypes within the clusters can be examined by seeing the dendrogram distance. In case of D^2 analysis, one can only know the intra-cluster distance but not the genotypes relative position in the respective cluster.

Chapter V

Summary and Conclusions

Chapter V

SUMMARY AND CONCLUSIONS

The present investigation was carried out during *kharif* 2016-17 at Horticultural Research Station, Lam Farm, Guntur with 44 genotypes of paprika (*Capsicum annuum* L.).

The mean, genetic variability, heritability, genetic advance as per cent mean, genetic divergence, character association and the magnitude of direct and indirect effects of yield component traits on dry fruit yield per plant were studied for 20 characters viz., plant height, plant spread, number of primary branches per plant, days to 50 per cent flowering, days to maturity, number of fruits per plant, fruit length, fruit diameter, fruit pedicel length, number of seeds per fruit, weight of seeds per fruit, 1000 seed weight, ascorbic acid, oleoresin content, capsaicin content, total extractable colour, red carotenoids, yellow carotenoids, total carotenoids and dry fruit yield per plant.

The analysis of variance revealed significant differences among the genotypes for all the characters studied indicating the presence of variability in the experimental material.

The genotypic coefficients of variation for all the characters studied were lesser than the phenotypic coefficients of variation indicating the interaction of genotypes with environment. High magnitude of PCV and GCV were observed for number of fruits per plant, fruit diameter, number of seeds per fruit, weight of seeds per fruit, 1000 seed weight, ascorbic acid, oleoresin content, capsaicin content, total extractable colour, red carotenoids, yellow carotenoids, total carotenoids and dry fruit yield per plant indicating the existence of wide range of genetic variability in the germplasm for these traits. This also indicated 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 selection.

High heritability coupled with high genetic advance as per cent of mean was observed for days to maturity, number of fruits per plant, fruit diameter, fruit length, fruit pedicel length, number of seeds per fruit, weight of seeds per fruit, 1000 seed weight, ascorbic acid, oleoresin content, capsaicin content, total extractable colour, red carotenoids, yellow carotenoids, total carotenoids and dry fruit yield per plant indicating the predominance of additive gene action and hence direct phenotypic selection is useful with respect to these traits.

High heritability coupled with moderate genetic advance as per cent of mean was observed for days to 50 per cent flowering indicating the role of additive and non additive gene action and further improvement of this character would be easier through mass selection, progeny selection or any modified selection procedure aiming to exploit the additive gene effects rather than simple selection.

Studies on character association indicated that number of fruits per plant, fruit length and fruit pedicel length had positive significant association with yield per plant indicating the importance of these traits in selection for yield and were identified as yield attributing characters on which selection can be relied upon for the genetic improvement of yield in paprika.

The path analysis revealed that plant spread, number of fruits per plant, fruit length, fruit diameter had positive direct effect on yield per plant indicating that direct selection based on these traits may be helpful in evolving high yielding varieties of paprika.

From the results of multivariate analysis, the presence of considerable genetic divergence among the 44 genotypes was revealed. The 44 genotypes were grouped into 6

clusters in D^2 analysis and 7 clusters in Ward's minimum variance method and clearly indicated that the genetic diversity and geographical diversity were not related.

By Mahalanobis' D^2 statistic, it could be inferred that total extractable colour followed by red carotenoids and yellow carotenoids contributed maximum towards genetic divergence. Based on intra and inter-cluster distance, it is suggested to make crosses between the genotypes of cluster III (LCA 511, Warngal chappatta single patti, LCA 512, LCA 498, LCA 440, LCA 510, LCA 510, LCA 476, Kt-1, LCA 436, LCA 446, LCA 490, LCA 453, LCA 443, Jangareddy gudem local, LCA 424, LCA 436), cluster V (Byadagi kaddi) and the cluster VI (Warangal chappatta double patti) after confirming their general combining ability.

Principal component analysis identified eight principal components (PCs), which contributed 83.62 per cent of cumulative variance. The significant factors loaded in PC_1 towards maximum genetic divergence were ., weight of seeds per fruit, fruit diameter, number of seeds per fruit, 1000 seed weight, number of fruits per plant, fruit length. 2D and 3D graphs showed wide divergence between Warangal chappatta double patti and Byadagi kaddi, which are also distantly placed with LCA-512, Warangal chappatta single patti and LCA 511 signifying their usefulness in paprika breeding to develop high heterotic hybrids.

Agglomerative cluster analysis revealed wide genetic distance between the genotypes of cluster VII (LCA 511, Warangal chappatta single patti, LCA 512, Warngal chappatta double patti) and cluster IV (LCA 466, LCA 480, Jangareddy gudem local).

The genotypes Warangal chappatta double patti, Warangal chappatta single patti, LCA-511 and LCA-512 showed maximum inter-cluster distance in Mahalanobis' D^2 analysis, principal component analysis and cluster analysis. So they can be exploited for the development of heterotic hybrids in future breeding programmes.

FUTURE LINE OF WORK

- In the present study, high heritability coupled with high genetic advance as per cent of mean was observed for all the characters studied except for plant height, plant spread, number of primary branches per plant and days to 50 per cent flowering and positive significant correlation along with positive direct effects were observed for number of fruits per plant and fruit length, these findings need to be validated in the subsequent generations for the improvement of these traits through direct selection.
- Number of fruits per plant showed high heritability, high genetic advance as per cent of mean with positive significant correlation and high positive direct effect on yield. Therefore, this character shall be given prime importance for further improvement in yield in future breeding programme.
- The superior accessions over checks need to be evaluated in comparison with checks under multilocal trials to know the stable expression of the characters and for their use in future hybridization programme.
- Genotypes of clusters IV and V which showed better performance for quality traits can be used in breeding programme for introgression of their desired genes into the high yielding varieties.
- The genetically divergent genotypes may be used as mapping populations to detect diversity at molecular level and also to identify molecular markers linked to desirable traits for marker assisted selection (MAS).

Literature Cited

LITERATURE CITED

- Acharya, P. and Rajput, C.B.S. 2003. Variability and correlation studies for different traits in *Capsicum* with respect to leaf curl complex. *Indian Journal of Horticulture*. 60 (4): 381-87.
- Ahmed, N, Bhat, M.A, Tanki, M.I. and Singh, A.K. 2006. Correlation and path coefficient analysis in (*Capsicum annuum* L.). *Indian Journal of Horticulture*. 63 (1): 92-95.
- Ahmed, N, Bhat, M.A, Tanki, M.I. and Singh, A.K. 2007. Correlation and path coefficient analysis in paprika (*Capsicum* var. *grossum* L.). *Indian Journal of Horticulture*. 63 (1): 92-95.
- Ajit, P.M. and Manju, P. 2006. Genetic variation for yield and anthracnose resistance in chilli (*Capsicum annuum* L.). *Indian Journal of Genetics*. 66 (2): 161-162.
- Ajith, P.M. and Manju, P. 2015. Genetic parameters and character association for yield and anthracnose resistance in chilli (*Capsicum annuum*). *International Journal of Agriculture Innovations and Research*. 4(1):121-123.
- Ajjappalavara, P.S, Patil, S.S, Hosmani, R.M, Patil, A.A. and Gangaprasad, S. 2005. Correlation and path coefficient analysis in chilli. *Karnataka Journal of Agricultural Sciences*. 18 (3): 748-751.
- Ajjapplavara, P.S. 2009. Genetic diversity in chilli (*Capsicum annuum* L.). *Asian Journal of Horticulture*. 4(1): 29-31.
- Allard, R.W. 1960. Principles of plant breeding. *John Wiley and Sons*. Landon. pp: 83-88.

- Alpatev, A.V. and Khernova. V.V. 1970. Heterosis in sweet pepper. *Gribov, Ovoshsh, Selektivs, St. 1*: 130-136.
- Amit, K, Ahad, I, Kumar, V. and Thakur, S. 2014. Genetic variability and correlation studies for growth and yield characters in chilli (*Capsicum annuum* L.). *Journal of Spices and Aromatic Crops*. 23 (2) : 170–177.
- Anderberg, M.R. 1993. Cluster Analysis for Application. *Academic Press*. New York.
- Arup, C, Amit, B.S, Dai, N. and Dutta, S. 2011. Diversity of genetic resources and genetic association analyses of green and dry chillies of eastern India. *Chilean Journal of Agricultural Research*. 71 (3): 350-356.
- Ashish, K.M, Kushwaha, M.L. and Singh, B.K. 2015. Genetic studies in chilli (*Capsicum annuum* L.). *The International Journal of Science & Technology*. 3(8): 289-291.
- Ashok kumar, G. V, Ponnuswami, V, Savitha, B.K. and S.T. Bini Sundar, S.T.2010. Correlation Analysis in Paprika (*Capsicum annuum* var. *Longum*) cv. KtPl- 19 and Bydagi Kaddi. *Madras Agricultural Journal*. 97 (10-12): 332-333.
- ASTA. 1986. Official analytical methods of the American spice trade association. 2nd edition, ASTA, Englewood Cliffs, New Jersey.
- Balasubramanian, T, Raj, D, Kasthuri, R. and Rangaswami, P. 1982. Capsaicin and plant characters in chillies. *Indian Journal of Horticulture*. 39: 239-242.
- Banfield, C.F. 1978. Principal component analysis for genstat. *Journal of Statistics and Computer Simulation*. 6: 211-222.
- Begum, M.S. 2002. Evaluation of chilli germplasm for productivity, its component traits and resistance to some biotic stresses. *M.Sc. (Agri.) Thesis*, University of Agricultural Sciences, Dharwad.

- Bendale, V.W, Palsuledesai, M.R, Bhawe, S.G, Sawat, S.S. and Desai, S.S. 2006. Genetic evaluation of some economic traits in chilli (*Capsicum annuum* L.) in Konkan region of Maharashtra. *Crop Research*. 31 (3): 401-403.
- Berhanu, Y, Derbew, B, Wosene, G. and Fekadu, M. 2011a. Variability, heritability and genetic advance in hot pepper (*Capsicum annuum* L.) genotypes in West Shoa, Ethiopia. *American –Eurasian journal of Agriculture and Environmental Science*. 10(4): 587- 592.
- Berhanu, Y, Derbew, B, Wosene, G. and Fekadu, M. 2011b. Genetic association among some attributes of hot pepper (*Capsicum annuum* L.) genotypes in West Shoa, Ethiopia. *Middle –East journal of Scientific Research*. 7(4): 567-573.
- Betlach, J. 1967. Some results of heterosis breeding of sweet pepper (*Capsicum annuum* L.). *Genetica*. 3: 239-252.
- Bhalekar, M.N, Warded, S.D. and Gupta, N.S. 2002. Path coefficient analysis in chilli. National Seminar on opportunity and potential of spices for crop diversification held at JNKVV, Jabalpur during January 2002. pp : 265-266.
- Bharadwaj, D.N, Singh, H. and Yadav, R.K. 2007. Genetic variability and association of component characters for yield in chilli (*Capsicum annuum* L.). *Progressive Agriculture*. 7(1/2): 72-74.
- Boronat, M, Madrid, R, Egea, C. and Collados, I. 1999. Fruit colour development of red pepper cultivars. *ITEA Production Vegetable*. 95 (2): 125-135.
- Burton, G.W. and Devane, E.H. 1953. Estimating the heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agronomy Journal*. 45: 478-481.
- Burton, G.W. 1952. Quantitative inheritance in grasses. *Proceedings of 6th International Grassland Congress*. 1: 277-283.

- Cankaya, S, Balkaya, A. and Karaagac, O. 2010. Canonical correlation analysis for the determination of relationships between plant characters and yield components in red pepper [*Capsicum annuum* L. var. *conoides* (Mill.) Irish] genotypes. *Spanish Journal of Agricultural Research*. 8(1): 67-73.
- Chadha, M.L. and Sindhu, A.S. 1983. Variability and correlation studies in brinjal (*Solanum melongena* L.). *Indian Journal of Horticulture*. 40: 60-64.
- Chaim, A.B. and Paran, I. 2000. Genetic analysis of quantitative traits in pepper (*Capsicum annuum*). *Journal of American Society for Horticultural Science*. 125(1): 66–70.
- Chatterjee, B, Chenga Reddy, V, Satish Babu, J, Ramana, J. V. and Pandurranga, R. C. 2006. Application of principal component and cluster analyses in chilli (*Capsicum annuum*.L). *The Andhra Agricultural Journal*. 53 (3&4): 141-146.
- Chatterjee, B, Chenga Reddy, V, Ramana, J. V, Ravi, Sankar, C. and Panduranga, R. C. 2007. Correlation and path analysis in chilli (*Capsicum annuum*.L). *The Andhra Agricultural Journal*. 54 (1&2) : 36-39.
- Chatterjee, B. 2006. Character association and genetic divergence in chilli (*Capsicum annuum*.L). M.Sc. (Ag). Thesis Acharya N. G. Ranga Agricultural University, Hyderabad.
- Cheema, S.K. and Pant, M.R. 2011. Estimation of vitamin C in seven cultivated varieties of *Capsicum annuum* L. *International Journal of Pharmaceutical Sciences*. 3(2): 1397-1401.
- Cherian, E.V, Indira, P. and Rajan, S. 2003. Variability, heritability and genetic advance for yield, quality and bacterial wilt incidence in *Capsicum chinense* Jacq. *Capsicum and Eggplant Newsletter*. 22: 47-50.

- Choudhary, B.S. and Samadia, D.K. 2004. Variability and character association in chilli land races and genotypes under arid environment. *Indian Journal of Horticulture*. 61 (2): 132-136.
- Dabrowska, B, Suchorska, K. and Capecka, E. 2000. Value of matri conditioned seed of pepper. *Horticultura*. 8: 369-375.
- Datta, S. and Das, L. 2013. Characterization and genetic variability analysis in *capsicum annum* l. germplasm. *SAARC Journal of Agriculture*. 11(1): 91-103.
- Datta, S. and Jana, J.C. 2010. Genetic variability, heritability and correlation in chilli genotypes under Terai zone of West Bengal. *Journal of Agriculture*. 8 (1): 33-45.
- Derrera, N. F. 2000. Condiment paprika – A potential new crop. *Agric. Ssi.*, 1 : 24-27.
- Dewey, D.R. and Lu, K.H. 1959. A correlation and path analysis of components of crested wheat grass seed production. *Agronomy Journal*. 51: 515-518.
- Dipak, K. M, Hore, J.K. and Hazra, P. 2014. Genetic variability for yield components of Chilli. 2nd International Conference on Agricultural & Horticultural Sciences.2(4):44.
- Dipak, K. M, Bimal, D, Rakesh, Y. and Ratul, B. 2017. Assessment of genetic variability, character association and path coefficient of some quantitative traits of chilli. *International Journal of Current Microbiology Applied Science*. 6(3): 2002-2012.
- Dutonde, S.N, Bhalekar, M.N, Patil, B.T, Kshirsagar, D.B. and Dhumal, S.S. 2008. Genetic diversity in chilli (*Capsicum annum* L.). *Agricultural Science Digest*. 28 (1): 45-47.
- Dutonde, S.N, Bhalekar, M.N, Warade, S.D, Gupta, N.S. and Nagatale, P.V. 2006. Genetic variability and heritability in chilli (*Capsicum annum* L.). *Agricultural Science Digest*. 23 (3): 162-166.

- East, E.M.1916. Studies on size inheritance in *Nicotiana*. *Genetics*. 1: 164-176.
- Ehrenberg, A.S.C. 1985. *Data reduction analysis and interpreting statistical data*. John Wiley and Sons Inc., New York.
- Everitt, B.S. 1974. *Cluster Analysis*. John Wiley and Sons Inc., New York. 1-117.
- Falconer, D.S. 1964. An introduction to quantitative genetics. Second Edition. *Oliver and Boyd Ltd*. Edinburgh. pp 312-324.
- Farhad, M, Hasanuzzaman, M, Biswas, B.K, Azad A.K. and Arifuzzaman, M. 2008. Reliability of yield contributing characters for improving yield potential in chilli (*Capsicum annuum*). *International Journal of Sustainable Crop Production*. 3(3):30-38.
- Farhad, M, Hasanuzzaman, M, Biswas, B.K, Arifuzzaman, M. and Islam, M.M. 2010. Genetic divergence in chilli (*Capsicum annuum L.*). *Bangladesh Research Publications Journal*. 3(3): 1045-1051.
- Finger, F.L, Lannes, S.D, Schuelter, A.R, Doege, J, Comerlato, A, Goncalves, L.S.A, Ferreira, F.R.A, Clovis, L.R. and Scapim, C.A. 2010. Genetic diversity of *Capsicum chinensis* (Solanaceae) accessions based on molecular markers and morphological and agronomic traits. *Genetics and Molecular Research*. 9(3): 1852-1864.
- Fisher, R.A. and Yates, F. 1963. Statistical tables for biological, agricultural and medical research. *Oliver and Boyd*. Landan pp: 46-63.
- Gadaginmath, N.B. 1992. Studies related to genetics economic and quality traits and exploitation of heterosis in chilli (*Capsicum annuum L.*) *Ph.D, Thesis*, University of Agricultural Sciences, Dharwad.

- Gagala, N, Ahmed, N, Hussain, K, Qadir, R. and Das, Z.A. 2007. Seed yield and its correlation studies in bell pepper (*Capsicum annuum* Var. *grosum* L.). *The Asian Journal of Horticulture*. 2 (2): 181-183.
- Gobinath, P, Zachariah, T.J, Shiva, K.N, Leela, N.K, Jayarajan, K. and Kiptoo, G.2014.Cluster analysis based on biochemical constituents in paprika like chillies (*Capsicum annuum* L.). *Journal of Spices and Aromatic Crops*.23 (2) : 164–169.
- Gogate, S.M, Patel, R.K, Patel, M.J. and Patel, J.A. 2006. Genetic divergence in chilli (*Capsicum annuum* var. *longum* (D.C.) Sendt.). *Vegetable Science*. 33 (1): 21-25.
- Gogoi, D. and Gautam, B. P. 2003. Correlation and path coefficient analysis in chilli (*Capsicum annuum* L.). *Agricultural Science Digest*. 23 (3) : 162-166.
- Gogoi, D. and Gautam, B.P. 2002. Variability, heritability and genetic advance in chilli. (*Capsicum* spp. L.) *Agricultural Science Digest*. 22(2): 102-104.
- Gupta, A.M, Singh, D. and Kumar, A. 2009. Genetic variability, genetic advance and correlation in chilli (*Capsicum annuum*). *Indian Journal of Agricultural Sciences*. 79(3): 221-223.
- Hanson, C.H, Robinson, H.R. and Comstock, R.S.1956. Biometrical studies of yield in segregating populations of Korea, Lesedezo. *Agronomy Journal*. 48: 268-272.
- Hari, G.S, Rao, P.V. and Reddy, Y. N. 2005. Correlation studies in paprika (*Capsicum annuum* L.). *Crop Research*. 29 (3) : 495-498.
- Harland, S.C. 1939. The genetics of Cotton. Jonathan Cope London.
- Hasan, M.J, Kulsum, M.U, Ullah, M.Z, Manzur Hossain, M. and Eleyash Mahmud, M. 2014. Genetic diversity of some chili (*Capsicum annuum* l.) genotypes. *International Journal of Agricultural Research, Innovation and Technology*. 4 (1): 32-35.

- Hasan, R, Mahmudul, H.A.K.M, Kamal, H. M. and Nazmul, A. 2015. Assessment of genetic divergence in chilli (*Capsicum annuum* L.) genotypes. *Plant Gene and Trait*. 6(3): 1-5.
- Hasan, R, Akand, M, Alam, N, Bashar, A. and Huque, M. 2016. Genetic association analysis and selection indices for yield attributing traits in available chilli (*Capsicum annuum* L.) Genotypes. *Molecular Plant Breeding*. 7(19): 1-9.
- Hasanuzzaman, M. and Faruq, G. 2011. Selection of traits for yield improvement in chilli (*Capsicum annuum* L.). *Journal of Innovation and Development Strategy*. 5(1):78-87.
- Havaladar, M.H.K. and Hossain, T. 1997. Biochemical changes in chilli fruit at different stage of fruit development. *Annals of Bangladesh Agriculture*. 6 (2): 145-149.
- Hornero-Mendez, D. and Minguez-Mosquera, I.M. 2001. Rapid spectrophotometric determination of red and yellow isochromic carotenoid fractions in paprika and red pepper oleoresins. *Journal of Agricultural Food Chemistry*. 49: 3584-3588.
- Hosamani, R.M. and Shivkumar. 2008. Correlation and path coefficient analysis in chilli. *Indian Journal of Horticulture*. 65 (3): 349-352.
- Hosmani, M.M. 1993. Chilli crop (*Capsicum annuum*). *Bharat Photo Offset Works*. Dharwad.
- <http://www.spicesboard.in/tis/statearea/areaproduct.php>: Spice Board of India, 2015, IISR, Calicut.
- Ibrahim, M, Ganigar, V.M. and Yenjerappa, S.T. 2001. Genetic variability, heritability, genetic advance and correlation studies in chilli. *Karnataka Journal of Agricultural Sciences*. 14: 784-878.

- Jabeen, N, Sofi, P.A. and Wani, S.A. 2009. Character association in chilli (*Capsicum annuum* L.). *Revista Cientifica UDO Agricola*. 9(3): 487-490.
- Jackson, J.E. 1991. *A user's guide to principal components*. John Wiley and Sons Inc., New York.
- Janaki, M, Naram, N.L, Venkata, R.C. and Paratpara, R. M. 2015a. Assessment of genetic variability, heritability and genetic advance for quantitative traits in chilli (*Capsicum annuum* L.). *Supplement on Genetics and Plant Breeding*. 10(2): 729-733.
- Janaki, M, Naram, N.L, Venkata, R.C. and Paratpara, R.M. 2015d. Selection of promising genotypes for qualitative traits in chilli (*capsicum annuum* l.) *Plant Archives*. 15(1) : 441-446.
- Janaki, M, Naram, N.L, Venkata, R.C. and Paratpara, R. M. 2016. Genetic divergence among chilli (*Capsicum annuum* L.) genotypes based on quantitative and qualitative traits. *International Journal of Science and Nature*. 7 (1) : 181-189.
- Janaki, M, Venkata, R.C, Naram, N.L. and Paratpara, R. M. 2015b. Assessment of genetic divergence through multivariate analysis in chilli (*Capsicum annuum* L.). *Electronic Journal of Plant Breeding*. 6(4): 981-991.
- Janaki, M, Venkata, R.C, Naram, N.L. and Paratpara, R. M. 2015c. Performance of chilli (*capsicum annuum* l.) genotypes for yield and yield attributing traits. *Plant Archives*. 15(2) : 661-666.
- Jayashree, W, Potdukhe, N.R, Deshmukh, D. and Dheva, N. 2007. Path analysis in chilli. *Annals of Plant Physiology*. 21(1): 130-131.

- Jha, A.K, Ali, M.M. and Dograj, V.V. 2001. Changes in ascorbic acid content and capsaicin in developing fruits of chilli. *Indian Journal of Plant Physiology*. 6 (3): 320-322.
- Johannsen, W.1909. *Elements der exateten exhibich keitslehra jena : Gustan Fisher*. pp.20.
- Johnson, H.W, Robinson, H.F. and Comstock, R.E. 1955. Estimation of genetic and environmental variability in soybean. *Agronomy Journal*. 47: 477-483.
- Joshi, S, Verma, T.S. and Thakur, P.C. 1995. Performance of paprika genotypes for export. In Proceedings of National Symposium on Advances in Research and Development in Horticulture for Export, CCSHAU, Hisar, P: 45.
- Jyothi, K.U, Kumari, S.S, Reddy, K.V.S, Vijayalakshmi, T. and Reddy, P.V. 2008. Biochemical evaluation of chilli (*Capsicum annuum* L) cultivars suitable for export. *Journal of Spices and Aromatic Crops*. 17(2): 209-211.
- Jyothi, K.U, Kumari, S.S. and Ramana, C.V. 2011. Variability studies in chilli (*Capsicum annuum* L.) with reference to yield attributes *Journal of Horticultural Science*. 6(2):133-135.
- Kadri, M.B, Eşiyok, D. and Turhan, K. 2009. Patterns of phenotypic variation in a germplasm collection of pepper (*Capsicum annuum* L.) from Turkey. *Spanish Journal of Agricultural Research*. 7(1): 83-95.
- Kannan, D, Singh, D.K, Singh, S.K. and Palanisamy, A. 2016. Genetic variability and agronomic performance studies in chilli (*Capsicum annuum* L.) *SAARC Journal of Agriculture*, 14(2): 56-62 (2016).

- Kannan, K, Jawaharlal, M. and Prabhu, M. 2009. Correlation studies in paprika (*Capsicum annuum* var Longum) cv. KTPL-19. *Agricultural Science Digest*. 29 (3) : 186-189..
- Karad, S.R, Navale, P. and Kadam, D. E. 2006. Variability and path-coefficient analysis in chilli (*Capsicum annuum* L.). *International Journal of Agricultural Science*. 2 (1) : 90-92.
- Karad, S.R, Raikar, G.R. and Navale, P.A. 2002. Genetic divergence in chilli (*Capsicum annuum* L.). *Journal of Maharashtra Agricultural Universities*. 27(2): 143-145.
- Kashinath, C.B. 2003. Evaluation and genetic variability studies in chilli genotypes (*Capsicum annuum* L.). *M.Sc. (Agri.). Thesis*, University of Agricultural Sciences, Dharwad.
- Kaur, B. and Singh, D. 2007. Correlation and path coefficient analysis in chilli for yield and quality parameters. *Indian Journal of Horticulture*. 66(4): 534-537.
- Kaur, B. and Singh, D. 2009. Evaluation of hot pepper (*Capsicum annuum* L.) germplasm of diverse origin for various horticultural characters. *Indian Journal of Plant Genetic Resource*. 22 (1): 41-45.
- Khader, K.M.A. and Mini, S. 2006. Correlation and path coefficient analysis in wax type chilli (*Capsicum annuum* L.). *Research on Crops*. 7(2): 522-525.
- Khurana, D.S, Singh, P. and Hundal, J.S. 2003. Studies on genetic diversity for growth, yield and quality traits in chilli (*Capsicum annuum* L.). *Indian Journal of Horticulture*. 60 (3): 277-282.
- Kranthi, R. G, Naram, N. L, Venkata, R. C, Umajyothi, K, Paratpararao, M. and Sasikala, K. 2016. Variability, heritability and genetic advance in chilli. *Journal of Plant Development Sciences*. 8 (2) : 51-55.

- Krishna, U. 2002. Genetic variability studies in chilli (*Capsicum annuum* L.). *M.Sc. (Olericulture) Thesis*, University of Agricultural Sciences, Dharwad.
- Krishna, U.C, Madalageri, M.B, Patil, M.P, Ravindra, M. and Kotlkal, Y.K. 2007a. Variability studies in green chilli (*Capsicum annuum* L.). *Karnataka Journal of Agricultural Sciences*. 20(1): 102 – 104.
- Krishna, U.C, Patil, M.P, Madalageri, M.B, Ravindra, M. and Jagadeesh, R.C. 2007b. Character association and path analysis studies in green chilli for yield and yield attributes (*Capsicum annuum* L.). *Karnataka Journal of Agricultural Science*. 20 (1): 99-101.
- Kumar, B.K, Munshi, A.D, Joshi, S. and Kaur, C. 2003. Correlation and path coefficient analysis for yield and biochemical characters in chilli (*Capsicum annuum* L.). *Capsicum and Eggplant Newsletter*. 22: 67-70.
- Kumar, D, Bahadur, V, Rangare S.B. and Singh, D. 2012. Genetic variability, heritability and correlation studies in chilli (*Capsicum annuum* L.). *Hort Flora Research Spectrum*. 1(3): 248-252.
- Kumar, S, Rattan, P, Sharma, J.P. and Gupta, R.K. 2010a. Genetic variation and inter-relationship studies in chilli (*Capsicum annuum* L.). *Journal of Research*. 9(1): 132-136
- Kumar, D.B.M, Anand, K. and Mallikarjunaiah, H. 2010b. Genetic divergence in chilli accessions. *Electronic Journal of Plant Breeding*. 1(5): 1363-1366.
- Kumar, M.N.H. 2008. Genetic variability studies for growth, yield and quality traits in chilli (*Capsicum annuum* L.) germplasm. *M.Sc. (Agri.) Thesis*, University of Agricultural Sciences, Dharwad.

- Kumar, P.S, Kumar, A. and Ishtiyaq, A. 2014. Correlation and path coefficient analysis in yield contributing characters in chilli, *Capsicum annuum* L *International Journal of Farm Sciences*. 4(4) : 104-111, 2014.
- Kumari, S.S, Srihari, D, Ravi shankar, C, Chenga Reddy, V. and siva sanker, A. 2014. Genetic divergence and combining ability studies for exploitation of heterosis in paprika (*Capsicum annuum*). *International Journal of Agricultural Science and Research (IJASR)*. 4 (2) : 59-66.
- Kumari, S.S, Jyothi, K.U, Srihari, D, Sankar, A.S. and Sankar, C.R. 2010. Variability and genetic divergence in paprika (*Capsicum annuum* L.). *Journal of Spices and Aromatic Crops*. 19 (1 & 2): 71–75.
- Lahbib, K, Bnejdi, F. and Mohamed, E.L.G. 2012. Genetic diversity evaluation of pepper (*Capsicum annuum* L.) in Tunisia based on morphologic characters. *African Journal of Agricultural Research*. 7(23): 3413-3417.
- Lakshmi, R. and Padma, V. 2012. Studies on performance, genetic variability, heritability and genetic advances in chilli (*Capsicum annuum* L.) varieties in high altitude and tribal zone of Srikakulam district of Andhra Pradesh, India. *Plant Archives*. 12(2): 717-720.
- Leaya, J. and Khader, K.M.A. 2002. Correlation and path coefficient analysis in chilli (*Capsicum annuum* L.). *Capsicum and Eggplant Newsletter*. 21: 56 – 59.
- Leeladhar, S, Jitendra, T. and Dhananjay, S. 2016. Genetic variability, heritability and divergence analysis in chilli (*Capsicum annuum* L.). *Plant Archives*. 16(1) : 445-448.
- Lekshmi, S. L. and Sreelathakumary, I. 2016. Evaluation of paprika (*Capsicum annuum* L.) accessions for capsaicin content and pungency. *Imperial Journal of Interdisciplinary Research (IJIR)*. 2(4): 2454-1362.

- Lush, J.L. 1949. Heritability of quantitative characters in farm animals. *Proceedings of 85th Congress on Genetic Heriditas* (Suppl.). 356-375.
- Mahalanobis, P.C. 1936. On the generalized distance in statistics. *Proceedings of National Academic Science*. 2: 55-79.
- Mahantesh, Y, Jogi, M, Madalageri, V.M, Ganiger, G, Bhuvaneswari, H.B, Patil. and Kotikal, Y.K. 2013a. Genetic variability studies in chilli (*Capsicum annuum* L.) *International Journal of Plant Sciences*. 8 (2) : 241-248.
- Mahantesh, Y, Jogi, M.B, Madalageri, V.M, Ganiger, G, Bhuvaneswari, H.B, Patil. and Kotikal, Y.K. 2013b. Character association and path analysis studies in green chilli (*Capsicum annuum* L.). *International Journal of Agricultural Sciences*. 9 (2) : 547-550.
- Mallikarjun, C. G, Manjunath, A, Nehru, S. D. and Kulkarni, R. S. 2003b. Genetic variability and correlations in chilli (*Capsicum annuum* L.) with special reference to quality characters. *Mysore Journal of Agricultural Science* .37 (4) : 325-331.
- Mallikarjun, C. G, Manjunath, A, Nehru, S. D. and Rudresh, N. S. 2003a. A study on association of fruit colour with other traits in chilli (*Capsicum annuum* L.). *Indian Journal of Genetics and Plant Breeding*. 63 (2): 183- 184.
- Mallikarjun, C.G. 2001. Genetic variability, association of characters and formulation of selection indices with special emphasis on quality characters in chilli (*Capsicum annuum* L.). *M.sc. Thesis*, University of Agricultural Sciences, Bangalore.
- Manju, P. R. and Sreelathakumary, I. 2004. Genetic divergence in hot chilli (*Capsicum chinease* Jacq.). *Capsicum and Eggplant Newsletter*. 23 : 69-72

- Manju, P.R. and Sreelathakumary, I. 2002. Genetic variability, heritability and genetic advance in hot chilli (*Capsicum chinense* jacq.). *Journal of Tropical Agriculture*. 40: 4-6.
- Mathur, R, Dangi, R.S, Dass, S.C. and Malhotra, R.C. 2000. The hottest chilli varieties in India. *Current Science*. 79 (3): 287-288.
- Meena, M.L, Kumar, N, Meena, J.K. and Rai, T. 2016. Genetic variability, heritability and genetic advances in chilli (*Capsicum annuum*). *Bioscience Biotechnology Research Communications*. 9(2): 258-262.
- Minguez-Mosquera, M.I. and Perez-Galvez, A. 1998. A colour quality in paprika oleoresins. *Journal of Agricultural Food Chemistry*. 46: 5124-5127.
- Mini, C. and Vahab, M.A. 2002. Correlation and path analyses for oleoresin in chilli (*Capsicum* spp.). *Journal of Applied Horticulture*. 4(1): 33-34.
- Mini, S. and Khader, K.M.A. 2004. Variability, heritability and genetic advance in wax type chilli (*Capsicum annuum* L.). *Capsicum & Eggplant Newsletter*. 23: 49-52.
- Mishra, A, Sahu, G. S. and Mishra, P. K. 2001 Variability in fruit characters of chilli (*Capsicum annuum* L.). *Orissa Journal of Horticulture*. 29 (2) : 107-109.
- Mishra, A.C, Singh, R.V. and Ram, H.H. 2005. Studies on genetic variability in capsicum (*Capsicum annuum* L.) under mid hills of Uttaranchal. *Indian Journal of Horticulture*. 62(3): 248-252.
- Misra, S, Lal, R.K, Darokar, M.P. and Khanuja, S.P.S. 2011. Genetic variability in germplasm accessions of *Capsicum annuum* L. *American Journal of Plant Sciences*. 2(5): 629-635.

- Misra, S, Lal, R.K, Darokar, M.P. and Khanuja, S.P.S. 2010. Genetic associations and path-coefficient analysis of the economic traits in the chili (*Capsicum annuum* L.). *Electronic Journal of Plant Breeding*, 1(3): 346-350.
- Munshi, A.D, Behra, T.K. and Singh, G. 2000. Correlation and path coefficient analysis in chilli. *Indian Journal of Horticulture*. 57(2): 157-159.
- Munshi, A.D, Kumar, B.K, Sureja, A.K. and Joshi, S. 2010. Genetic variability, heritability and genetic advance for growth, yield and quality traits in chilli. *Indian Journal of Horticulture*. 67 (1): 114-116.
- Munshi, A.D. and Behera, T.K. 2000. Genetic variability, heritability and genetic advance for some traits in chillies (*Capsicum annuum* L.). *Vegetable Science*. 27(1): 39-41.
- Murthy, G.S. and Pavate, M.Y. 1962. Studies on qualitative inheritance in *Nicotiana tobaccum* L. I. Varietal classification and selection by multivariate analysis. *Indian Journal of Genetics and Plant Breeding*. 22: 68.
- Murthy, N.S.R. and Murthy, B.S. 1962. Proliferation of the central axis in *Capsicum* – a fruit abnormality in *Capsicum* var. *grossum*. *Andhra Agricultural Journal*. 9: 348-350.
- Nair, K.R. and Mukharji, H.K. 1960. Classification of natural and plantation teak (*Tectona grandis*) grown at different localities of India, Burma with respect to its physiological and mechanical properties. *Sankhya*. 22: 1-20.
- Nandadevi, R. and Hosamani, R.M. 2003. Variability, correlation and path analysis in *Kharif* chilli genotypes for different characters. *Capsicum and Egg Plant Newsletter*. 22: 43-46.

- Naresh, P, Madhavi, R.K, Shivashankara, K.S. and Christopher, G.M. 2013. Genotypic variation for biochemical compounds in capsicum. *Indian Journal of Horticulture*. 70 (1): 43-47.
- National Horticulture Board, 2015. Data base of horticultural crops. Gurgaon, New Delhi.
- Nawalagatti, C.M, Chetti, M.B. and Hiremath, S.M. 1999. Evaluation of chilli (*Capsicum annuum* L.) genotypes for quality parameters. *Crop Research*. 18(2): 218-221.
- Nazir, G, Narayan, R, Hussain, K, Ahmed, H. and Bhat, K. 2005. Correlation and path coefficient analysis in sweet pepper (*Capsicum annuum* var. *grossum* L.). *Vegetable Science*. 32 (1): 88-89.
- Nehru, S.D, Manjunath, A. and Rangaiah. 2003. Genetic variability and stability for fruit yield and other characters in chilli (*Capsicum annuum* L.). *Karnataka Journal of Agricultural Sciences*. 16(1): 44-47.
- Nehru, S.D, Thimmegowda, M.N. and Gowda, M. 2012. Growth, yield, genetic variability and correlation studies in chilli (*Capsicum annuum* L.). *Research Journal of Agricultural Sciences*. 3 (2): 517-519.
- Nelson-Ehle, H. 1909. *Kreuzung, untersuchungen an Hafer and Weizenjunds*, Univ. Asserter, N. F. *Afala*. 2: 1-22.
- Padhar, P.R. and Zaveri, P.P. 2010. Genetic studies in relation to selection criteria in chilli. *Research on Crops*. 11(3): 722-727.
- Pandey, J, Singh, J, Verma, A, Singh, A.K, Mathura, R. and Kumar, S. 2008. Evaluation of chilli (*Capsicum annuum* L) genotypes for some quality traits. *Journal of Food Science and Technology*. 45(5): 463-465.

- Pandit, M.K, Muthukumar, P. and Mukhopadhyay, T.P. 2010. Study of genetic divergence through multivariate analysis in chilli (*Capsicum annuum* L.) germplasms. *Journal of Interacademia* . 14 (3): 298-301.
- Pandit, M.K, Muthukumar, P. and Mukhopadhyay, T.P. 2009. Genetic variability, character association and path analysis in chilli (*Capsicum annuum* L.) genotypes. ICH pp 41.
- Pandit, M.K. and Adhikary, S. 2014. Variability and heritability estimates in some reproductive characters and yield in chilli (*Capsicum annuum* L.). *International Journal of Plant & Soil Science*. 3 (7): 845-853.
- Panse, V.G. 1957. Genetics of quantitative characters in relation to plant breeding. *Indian Journal of Genetics*. 17: 318-328.
- Panse, V.G. and Sukhatme, P.V. 1985. Statistical methods for agricultural workers. *Indian Council of Agricultural Research*. New Delhi.
- Patel, D. K. Patel, B.R. Patel, J.R, and Gopal, V.K. 2015. Genetic variability and character association studies for green fruit yield and quality component traits in chilli (*Capsicum annuum* var. *longum* (dc.) sendt.) *Electronic Journal of Plant Breeding*, 6(2): 472-478.
- Patel, P.N, Fougat, R.S. and Sasidharan, N. 2009. Studies on genetic variability, correlation and path analysis in chillies (*Capsicum annuum* L.). *Research on Crops*. 10(3): 626-631.
- Patil, B.R, Kulkarni, R.S, Chavan, M.L. and Adiga, J.D. 2004. Character association and path analysis for dry fruit yield and capsaicin content in chillies (*Capsicum annuum* L.). *Karnataka Journal of Horticulture*. 1(1): 6-10.

- Patil, S.D., Bidari, B.I., Shashidhara, G.B. and Hegde, N.K. 2008. Genetic variability in chilli (*Capsicum annuum* L.) genotypes. *Asian Journal of Horticulture*. 3(2): 310-312.
- Prabhakaran, T.S, Natarajan, S. and Veeraragavatham, D. 2004. Studies on genetic variability, heritability and genetic advance in chilli (*Capsicum annuum* L.). *South Indian Horticulture*. 52(1/6): 70-72.
- Prabhudeva, S.A. 2003. Variability, genetic diversity and heterosis study in chilli (*Capsicum annuum* L.). *M. Sc. Thesis*, University of Agricultural Sciences, Dharwad.
- Prasanth, D., Ponnuswami, V. and Muralidharan, V. 2007. Evaluation of chilli (*Capsicum* spp.) germplasm for extractable colour and pungency. *Indian Journal of Genetics and Plant Breeding*. 67(1): 97-98.
- Priyanka, B. and Mishra, A.C. 2016. Correlation and path coefficient analysis in chilli (*Capsicum annuum* L.) for yield and yield attributing traits. *International Journal of Science and Research (IJSR)*. 5(3) : 1589-1591.
- Priyanka, B. and Madhvi, N. 2016. Genetic variability, heritability and genetic advance of growth and yield components of chilli (*Capsicum annuum* L.) genotypes. *International Journal of Science and Research (IJSR)*. 5(7): 1305-1307.
- Rajya, L. and Vijaya, P. 2011. Correlation and path analysis studies in chilli in high altitude and tribal zone of Srikakulam district of Andhra Pradesh. *Research on Crops*, 12 (2): 548-550.
- Rana, M, Sharma, R, Sharma, P, Bhardwaj, S.V, Sandeep Kumar, Navjot Singh, B. Sharma, M. and Rajesh, D. 2015. Studies on genetic variability and divergence in capsicum for fruit yield and quality traits in North- Western Himalayas. *Ecology Environment and Conservation*. 21: 415-421

- Ranganna, S. 1986. Handbook of analysis and quality control for fruits and vegetable products. 2nd edition. pp: 259.
- Rao, C.R. 1952. *Advanced statistical methods in biometrical research*. John Wiley and Sons Inc., New York. 236-272.
- Rao, N.S.B. 2005. Heterosis and combining ability in chilli (*Capsicum annuum* L.). M.Sc. (Agri.) Thesis, Acharya N. G. Ranga Agricultural University, Hyderabad.
- Rao, S. B, Chenga Reddy, V, Razia Sultana, Srinivasa Rao, V. and Satish Babu, J. 2006. Correlation and path analyses for qualitative and quantitative traits in inter-varietal crosses of chilli (*Capsicum annuum*.L.). *The Andhra Agricultural Journal*. 53 (3&4) : 133-135.
- Rathod, R.P, Deshmukh, D.T, Ghode, P.B. and Gonge, V.S. 2002. Correlation and path analysis studies in chilli (*Capsicum annuum* L.). *Haryana Journal of Horticultural Sciences*. 31 (1/2): 141 – 143.
- Razzaq, A, Tariq, M.K, Asif, S, Sohail, K. and Alam, Z.2016. Genetic diversity and association analysis for different morphological traits in *Capsicum annuum* L. *International Journal of Biomolecules and Biomedicine (IJBB)*. 5 (1) : 20-28.
- Reddy, M.G, Kumar, H.D.M. and Salimath, P.M. 2008. Correlation and path coefficient analysis in chilli (*Capsicum annuum*, L.). *Karnataka Journal of Agricultural Sciences*. 21(2): 259-261.
- Reves, M.J. 1987. Re-evaluation of *capsicum* color data. *Journal of Food Science*. 52: 1047-1049.
- Rinchan, D, Madalageri, M.B. and Manjunath, G. 2015. Correlation and path analysis for growth, earliness, yield and quality parameters in chilli (*Capsicum annuum* L.). *Hort Flora Research Spectrum*, 4(3): 268-272.

- Rohini, N. and Lakshmanan, V. 2015. Correlation and path coefficient analysis in chilli for yield and yield attributing traits IASET: *Journal of Applied and Natural Sciences* (JANS). 4(1) : 25-32.
- Rosmaina, Syafrudin, Hasrol, Yanti, Juliyanti and Zulfahmi. 2016. Estimation of variability, heritability and genetic advance among local chili pepper genotypes cultivated in peat lands. *Bulgarian Journal of Agricultural Science*, 22 (3): 431–436.
- Sadasivam, S. and Balasubramanian, T. 1987. Practical manual in biochemistry. TNAU, Coimbatore. pp:14.
- Sandeep, D, Patil, B.I, Bidari, Shashidhara, G.B. and Hegde, N.K. 2008. Genetic variability in chilli (*Capsicum annuum* L.) genotypes. *The Asian Journal .of Horticulture*.3(2): 310-312.
- Sarkar, S, Murmu, D, Chattopadhyay, A. and Hazra, P.2009. Genetic variability, correlation and path analysis of some morphological characters in chilli. *Journal of Crop and Weed*, 5(1):157-161.
- Satish, K, Ashwini, D, Sunil, P. and Ravi, K. 2015. Correlation and path co-efficient analysis of quantitative and qualitative traits in chilli (*Capsicum annuum* L.,) *Supplement on Genetics and Plant Breeding* 10(4): 1909-1914.
- Satish, K, Ashwini, D. and Sunil, P. 2016. Genotypes performance and genetic variability studies in hot chilli (*Capsicum annuum* L.). *Indian Journal of Agriculture Research*. 50 (1) 2016: 56-60
- Senapati, B.K, Sahu, P.K. and Sarkar, G. 2003. Genetic divergence in chilli. *Crop Research*. 26 (2): 314-317.

- Sharma, A. and Sharma, S. 2006. Variation studies for bell pepper (*Capsicum annuum*) improvement under cold desert conditions of North-Western Himalayas. *Indian Journal of Genetics and Plant Breeding*. 66 (4) : 357 -358.
- Sharma, S, Swati, B, Sengupta, S.K. Verma, B.K. and Tarun, J. 2014. Genetic variability, heritability and genetic advance in chilli *Capsicum annuum* L. *International Journal of Farm Sciences*. 4(4) : 112-116, 2014.
- Sharma, V.K, Semwal, C.S. and Uniyal, S.P.2010. Genetic variability and character association analysis in bell pepper (*Capsicum annuum* L.). *Journal of Horticulture and Forestry*.2(3) : 058-065.
- Shimeles, A, Bekele, A, Dagne, W. and Adeferis, T.W. 2016. genetic variability and association of characters in ethiopian hot pepper (*capsicum annuum* l.) landraces. *Journal of Agricultural Sciences*. 6(1) : 119-36.
- Shirshat, S.S, Giritammannavar, V.A. and Patil, S.J. 2007. Analysis of genetic variability for quantitative traits in chilli. *Karnataka Journal of Agricultural Sciences*. 20(1): 29 -32.
- Shiva, K.N, Zachariah, T.J, Leela, N.K. and Mathew, P.A. 2013. Performance of paprika and paprika alike chillies (*Capsicum annuum* L.). *Journal of Spices and Aromatic Crops*, 22 (2) : 222–227.
- Shiva, K.N, Gobinath, P, Zachariah T.J. and Leela, N.K. 2014. Variability in quality attributes of paprika and paprika alike chillies (*Capsicum annuum* L.). *Journal of Spices and Aromatic Crops*. 23 (1) : 17–25.
- Shiva, K.N, Prasath, D, Gobinath, P, Leela, N.K. and Zachariah, T.J.2015. Variability and character association in paprika and paprika alike chillies *Journal of Spices and Aromatic Crops*. 24 (1) : 61–65.

- Shiva, K.N, Prasath, D, Zachariah, T.J. and Parthasarathy, V.A. 2006. Chilli and Paprika. In: Parthasarathy V. A. & Rajeev P. (Eds.) Major Spices - Production and Processing, *Indian Institute of Spices Research, Kozhikode, Kerala*, 228-272.
- Singh, D.K. and Singh, A. 2011. Assessment of variability parameters and character association for quantitative traits in chilli (*Capsicum annuum* L.). *Progressive Agriculture*. 11(1): 113-116.
- Singh, M.D, Laisharam, J.M. and Bhagirath, T. 2005. Genetic variability in local chillies (*Capsicum annuum* L.) of Manipur. *Indian Journal of Horticulture*. 62(2): 203-205.
- Singh, M.D. and Singh, N.G. 2004. Correlation and path analysis studies in selected local chillies (*Capsicum annuum* L.). *Environment and Ecology*. 22(4): 672-675.
- Singh, N.B. and Singh, B. 2001. Correlation and genetic advance in yield and other characters in chillies (*Capsicum annuum* L.). *Madras Agriculture Journal*. 57: 369-373.
- Singh, P, Singh, D. and Kumar. A. 2007. Genetic variability, heritability and genetic advances in chilli (*Capsicum annuum* L.). *Indian Journal of Agricultural Sciences*. 77(7): 459-461.
- Singh, R, Hundal, J.S. and Chawla, N. 2003. Evaluation of chilli (*Capsicum annuum*) genotypes for quality components. *Indian Journal of Agricultural Sciences*. 73(1): 51-53.
- Singh, R.K. and Chaudhary, B.D. 1977. Biometrical methods in quantitative genetic analysis. *Kalyani Publishers*. New Delhi. pp 215-218.

- Singh, R.K. and Chaudhary, B.D. 1979. Biometrical methods in quantitative genetic analysis. *Kalyani Publishers*. Ludhiana. Pp75-78.
- Singh, R.K. and Singh, D.B. 2010. Genetic divergence and selection of genotypes in chilli (*Capsicum annuum* L.). *Green Farming*. 3(2): 116-118.
- Singh, V.K. and Singh, S.N. 1994. Genetic variability in brinjal (*Solanum melongena* L.). *Journal of Applied Biology*. 4: 16-18.
- Singh, Y, Sharma, M. and Sharma, A. 2009. Genetic variation, association of characters, and their direct and indirect contributions for improvement in chilli peppers. *International Journal of Vegetable Science*. 15(4): 340-368.
- Sivasubramanian, S. and Menon, P.M. 1973. Genotypic and phenotypic variability in rice. *Madras Agricultural Journal*. 60: 1093-1096.
- Smitha, R. P. and Basavaraja, N. 2006b. Genetic divergence studies in chilli (*Capsicum annuum*.L). *Karnataka Journal of Agricultural Sciences*.19 (4) : 975-977
- Smitha, R.P. and Basvaraja, N. 2007. Variability and selection strategy for yield improvement in chilli. *Karnataka Journal of Agricultural Sciences*. 20(1): 109 – 111.
- Smitha, R.P. and Basavaraja, N. 2006a. Variability and correlation studies in chilli (*Capsicum annuum*.L) *Karnataka Journal of Agricultural Sciences*. 19 (4) : 888-891
- Sood, S, Bindal, A.K. and Sharma, A. 2006. Genetic variability, heritability and genetic advance of various polygenic traits in Capsicum (*Capsicum annuum* L.). *Scientific Horticulture*. 10: 201-207.

- Sood, S, Sood, R, Sagar, V. and Sharma, K.C. 2009. Genetic variation and association analysis for fruit yield, agronomic and quality characters in bell pepper. *International Journal of Vegetable science*. 15 (3): 272-284.
- Sorenson, T.A. 1948. A method of establishing groups of equal amplitude in plant sociology based on similarity of species content and its application to analysis of the vegetation on Danish Commons. *Biologiske Skrifter*. 5: 1-34.
- Spice India. 2015. All time record spices export cross US \$ 500 million mark 19 (17): 20-25
- Sreelathakumary, I. and Rajamony, L. 2002. Variability, heritability and correlation studies in chilli under shade (*Capsicum* spp.) under shade. *Indian Journal of Horticulture*. 59: 493-494.
- Sreelathakumary, I. and Rajamony, L. 2004. Variability, heritability and genetic advance in chilli (*Capsicum annuum* L.). *Journal of Tropical Agriculture*. 42 (1-2): 35-37.
- Srinivas, B, Thomas, B. and Gogineni, S. 2015. Genetic divergence for yield and its component traits in chilli (*Capsicum frutescens* L) accessions of Kerala. *International Journal of Science and Research (IJSR)*. 4 (4) : 442-446.
- Srividhya, S. and Ponnuswamy, V. 2012 Correlation analysis in hybrid population of paprika (*Capsicum annuum* var. longum). *Crop Research*. 44 (1 & 2) : 129-134.
- Sudre, C.P, Goncalves, L.S.A, Rodrigues, R, Amaral Junior, A.T, Riva-Souza, E.M. and Bento, C. S. 2010. Genetic variability in domesticated *Capsicum* spp as assessed by morphological and agronomic data in mixed statistical analysis. *Genetics and Molecular Research*. 9 (1): 283-294.

- Tasso, Y, Rakesh, K, Dubey, Vikas, S. and Garima, U. 2014. Genetic diversity of chilli (*Capsicum annuum* L.) genotypes of India based on morpho-chemical traits. *Australian Journal of Crop Science* (AJCS). 8(1):97-102
- Tembhurne, B.V, Revanappa, R. and Kuchanur, P.H. 2008. Varietal performance, genetic variability and correlation studies in chilli (*Capsicum annuum* L.). *Karnataka Journal of Agricultural Science*. 21(4): 541-543.
- Thul, S.T, Lal, R.K, Shasany, A.K, Darokar, M.P, Gupta, A.K, Gupta, M.M, Verma, R.K. and Khanuja, S.P.S. 2009. Estimation of phenotypic divergence in a collection of *Capsicum* species for yield-related traits. *Euphytica*.
- Ukkund, C, Krishna, M.B, Madalageri, M.P, Patil, R. and Kotikol, Y.K. 2007. Variability studies in green chilli (*Capsicum annuum* L.). *Karnataka Journal of Agriculture. Science*. 20 (1): 102-104.
- Ullah, M.Z, Hasan, M.J, Saki, A.I, Rahman, A.H.M.A. and Biswas, P.L. 2011. Association of correlation and cause-effect analysis among morphological traits in chilli (*Capsicum frutescens* L.). *International Journal of Biological Research*. 10 (6): 19-24.
- Vani, S.K, Sridevi, O. and Salimath, P.M. 2007b. Genetic divergence in chilli (*Capsicum annuum* L.). *Annals of Biology*. 23(2): 123-128.
- Vani, S.K, Sridevi, O. and Salimath, P.M. 2007a. Studies on genetic variability, correlation and path analysis in chilli (*Capsicum annuum* L.). *Annals of Biology*. 23(2): 117-121.
- Varkey, J, Saiyed, M.P, Patel, J.S. and Patel, D.B. 2005. Genetic variability and heritability in chilli. *Journal of Maharashtra Agricultural Universities*. 30 (3): 346-347.

- Vavilov, N.I. 1951. The origin, variation, immunity and breeding of cultivated plants. *Chronica Botanica*, Waltham, Mass, USA.
- Verma, S.K, Singh, R.L. and Arya, R.R. 2004. Genetic variability and correlation studies in chillies. *Progressive Horticulture*. 36(1): 113-117.
- Vijaya, H.M, Mallikarjuna, A.P, Gowda. and Nehru, S.D. 2014. Genetic variability, correlation coefficient and path analysis in chilli (*Capsicum annuum* L.,) genotypes. *Research in Environment and Life Science*.7(3) : 175- 178.
- Vikram, A, Warshamana, I.K. and Meenu, G.2014. Genetic correlation and path coefficient studies on yield and biochemical traits in chilli (*Capsicum annuum* L.). *International Journal of Farm Sciences*. 4(2): 70-75.
- Wasule, J.H, Paramar, I.N, Potdukhe, N.K. and Deshmuh, D.T. 2004. Variability studies in chilli. *Annals of Plant Physiology*. 18 (2): 187-191
- Wilson, D. and Philip, 2009. Genetic variability and genetic divergence in paprika (*Capsicum annuum* L.). ICH pp 16.
- Wright, S. 1921. Correlation and causation. *Journal of Agricultural Research*. 20: 557-585.

Appendices



APPENDIX I

Season and Crop condition at Horticultural Research Station, Lam during the crop season 2016-17

The weather conditions prevailed during the season under report and their impact on paprika crop growth and yield are as detailed below

Meteorological data: AICCIP Main centre, RARS, Lam during 2016-2017

Month & year	Rainfall (mm)	No. of rainy days	Mean temperature (°C)		Relative humidity (%)		Sun shine (hrs)	Wind speed (km/hr)
			Max.	Min.	I	II		
Aug., 16	11.7	1	36.4	25.2	55.4	55.4	8.6	6.7
Sep.,16	33.9	2.8	32.6	24	82.9	71.6	5.4	3.2
Oct.,16	38.6	1.5	34	20.9	80.3	66	3.7	4
Nov.,16	0	0	33.7	18.2	79.8	59.5	3.5	4.2
Dec.,16	1.8	0.2	31.9	15.8	79	56.8	3.5	3.5
Jan., 17	0	0	31.7	15.9	77.2	54.9	3.6	3.7
Fab., 17	0	0	34.5	17.1	75	41.4	5.4	4.8
Mar., 17	2.1	0.3	36.3	21.4	78.1	58.6	8.2	5.3
Total/Mean	88.1	5.8	271.1	158.5	607.7	464.2	41.9	35.4

