

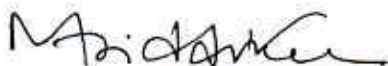
**MORPHOGENETIC DIVERSITY IN NATURAL
POPULATION OF CHILI
(*Capsicum spp*)**

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REG NO. 08-3055**

*A Thesis
submitted to the Faculty of Agriculture
Sher-E-Bangla Agricultural University, Dhaka
In partial fulfillment of the requirement for the degree of*

**MASTERS OF SCIENCE
IN
GENETICS AND PLANT BREEDING**

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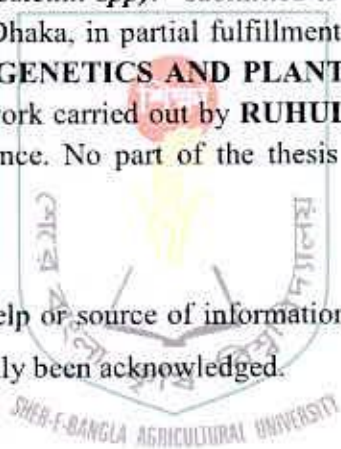
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CERTIFICATE

This is to certify that thesis entitled, “**MORPHOGENETIC DIVERSITY IN NATURAL POPULATION OF CHILI (*Capsicum spp.*)**.” submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of **MASTER OF SCIENCE** in **GENETICS AND PLANT BREEDING**, embodies the result of a piece of *bonafide* research work carried out by **RUHUL AMIN**, Registration No. **08-3055** under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.

I further certify that such help or source of information, as has been availed of during the course of this investigation has duly been acknowledged.



Semester: January-June, 2014

Place: Dhaka, Bangladesh

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**DEDICATED TO
MY BELOVED
PARENTS**

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CONTENTS

CHAPTER	TITLE	PAGE NO.
	ACKNOWLEDGEMENTS	IV
	CONTENTS	VI
	LIST OF TABLES	VIII
	LIST OF FIGURES	IX
	LIST OF APPENDICES	IX
	LIST OF SYMBOLS AND ABBREVIATIONS	X
	ABSTRACT	XIII
CHAPTER 1	INTRODUCTION	01
CHAPTER 2	REVIEW OF LITERATURE	04
	2.1 Variability among chili genotypes	05
	2.2 Genetic diversity of chili genotypes	09
	2.3 Relationship between genetic and geographic diversity in chili	15
	2.4 Techniques of multivariate analysis	17
CHAPTER 3	MATERIALS AND METHODS	21
	3.1 Experimental Site	21
	3.2 Soil and Climate	21
	3.3 Genetic materials used for the experiment	21
	3.4 Experimental design	21
	3.5 Preparation of the experimental field	21
	3.6 Fertilizer application	23

CHAPTER	TITLE	PAGE NO.
	3.7 Transplanting of seedling	24
	3.8 Intercultural operations	24
	3.9 Top dressing	24
	3.10 Plant protection measures	24
	3.11 Data collection	25
	3.12 Statistical analyses of data	26-30
CHAPTER 4	RESULTS AND DISCUSSIONS	31
	4.1 Variability of chili genotypes on the basis of yield and yield Contributing characters	32-39
	4.2 Heritability and genetic advance in genotypes	40-42
	4.3 Correlation coefficients among yield and yield contributing Characters	43-44
	4.4 Diversity of the chili genotypes	44-55
CHAPTER 5	SUMMARY AND CONCLUSION	56-61
CHAPTER 6	REFERENCES	62-70

LIST OF TABLE

TABLE NO.	TITLE OF TABLES	PAGE NO.
3.1	List of fifteen chili genotypes	14
3.2	List of fertilizers with doses and application procedures	15
4.1	Analysis of variance (mean squares) for different characters of fifteen genotypes of chili	33
4.2	Average performance for eight characters of 15 chili genotypes	34
4.3	Estimation of some genetic parameters	39
4.4	Genotypic (G) and phenotypic (P) correlation coefficients	42
4.5	Distribution of 15 chili genotypes in different clusters	46
4.6	Average intra (bold) and inter-cluster distances for 15 chili genotypes.	49
4.7	Relative contribution of eight individual characters (%) towards the total divergence	52
4.8	Cluster means with inter-cluster CV (%)	54



LIST OF FIGURES

FIGURE NO	TITLE	PAGE NO
4.1	Distribution of 15 chili genotypes in two-dimensional scatter diagram based on PCA scores superimposed with clusters	47
4.2	Cluster diagram showing the average inter and intra-cluster distance (D-values) of 15 chili genotypes	50

LIST OF APPENDICES

APPENDIX	TITLE	PAGE NO.
I	Morphological, physical and chemical characteristics of initial soil in experimental site	69
II	Monthly average temperature, number of rainy days, Relative humidity and total rainfall of the experiment site during the period from October, 2013 to April, 2014	69

LIST OF SYMBOLS AND ABBREVIATIONS

FULL WORDS	ABBREVIATION
Percentage	%
Exempli gratia (by way of example)	e.g.
and others (<i>et al.</i>)	<i>et al.</i>
Food and Agricultural Organization	FAO
Centimeter	cm
Bangladesh Agriculture Research Institute	BARI
Sher-e-Bangla Agricultural University	SAU
Journal	<i>J.</i>
Number	No.
Variety	var.
Namely	viz.
Degrees of freedom	df.
Triple Super Phosphate	TSP
Muriate of Potash	MP
Emulsifiable concentrate	EC
At the rate of	@
Milliliter	ml

Randomized Complete Block Design	RCBD
Gram	gm
Bangladesh Bureau of Statistics	BBS
Analysis of variances	ANOVA
Kilogram	Kg
Error mean sum of square	EMS
North	N
East	E
Negative logarithm of hydrogen ion concentration (-log [H ⁺])	pH
High yielding varieties	HYV

MORPHOGENETIC DIVERSITY IN NATURAL POPULATION OF CHILI

BY
Ruhul Amin

ABSTRACT

To study the degree of diversity in chili, an experiment was conducted in the growing season 2013-14 at the field Sher-e-Bangla Agricultural University, Dhaka. Genetic divergence, heritability and genetic advance for 8 characters in 15 genotypes of chili (*Capsicum spp* L.) were studied. Based on D^2 values, the genotypes were grouped into 4 clusters. Grouping of genotypes in different clusters was not related to their geographical origin. Considerable amount of genotypic and phenotypic coefficients of variation was observed for plant height, no. of fruits per plant, fruit weight, and total yield, indicating existence of greater diversity for these characters. High heritability coupled with high genetic advance as percentage of mean and genetic coefficients of variation was observed in respect of plant height (98.5%), days to first flowering (95.68%), no of fruits per plant (99.79%), fruit weight (72.62%), fruit circumference (97.24%), fruit length (98.92%) etc. indicating that these characters are under control of additive gene or non-environmental effects and could be dependable for yield improvement in chilies. The maximum inter cluster distances was observed between cluster I and IV (76.42) followed by the distances between cluster II and IV. Therefore the genotypes from cluster II along with cluster III and cluster IV should be prioritized in future breeding program for having higher fruit yield.

INTRODUCTION



CHAPTER I

INTRODUCTION

Chili (*Capsicum annuum* L.) is grown worldwide both as a spice and as a vegetable crop and world's second most important solanaceous vegetable after tomato. Landraces are variable plant populations adapted to local agro climatic conditions, which are locally named, selected and maintained by the traditional farmers to meet their social, economic, cultural and ecological needs (Teshome *et al* 1997). Over 100 species have been named under the genus *Capsicum*, but most worker recognize only two species, *Capsicum annuum* L and *Capsicum frutescens* L. (Purseglove 1968, Cobbey 1967, Berrie 1977). There is a distinct difference between the sweet pepper, *Capsicum annuum* and the hot chili or cayenne pepper named *Capsicum frutescens* a wild, taller and with a more woody stock than *Capsicum annuum*, is generally cultivated in warm regions of both hemispheres. It is now cultivated in every tropical country and provides the chief species of the warmer parts of the world. Chili is one of the most important ingredients used in the everyday diet of the people of south and south-east Asia. The capsicums are the native of Central America and West Indies, but they quickly spread throughout the tropical world after the discovery of America and West Indies. Chili has high demand among the consumers due to its diversified uses. For the intensive cultivation and increased production of chili, improved varieties/lines with desirable traits need to be identified throughout the world.

It is an important spice crop in Bangladesh. It is also a cash crop of the country (Ahmed and Haque 1980). It is cultivated on small family-owned farms where sale of its produce serves as a ready source of cash income throughout the year. A large no. of cultivars or landraces is under cultivation in different parts of the country. At present, the total cultivated area under spices and condiments is 793 thousand acres (BBS, 2006). Depending on yield preference, a numbers of chili varieties are cultivated in our country. Winter chili contributes about 90% of its total production (Anonymous, 1987). The actual area under chili cultivation in Bangladesh is not available due to its nature of cultivation. Total area covered by chili is about 352 thousand acres from (BBS, 2006) and production of chili is about 155 thousands M. tons (BBS, 2006). In Bangladesh the harvest price of chili is about 56100 taka per M. tons (BBS, 2006). A wide range of genetic diversity is found here due to the availability of different land races and their wild relatives. In spite of its importance no major breakthrough has been made and limited number of

improved varieties is being grown in the country. Under this situation, new avenues for crop improvement required to be exploited. For achieving a substantial genetic improvement, a huge knowledge of genetic diversity and variability is essential to improve new varieties of chili in the country. Selection of better plant type either from local or exotic genotypes can be of immense value to the breeder. Keeping this view in mind, 15 germplasms of chili from local origin were collected and their genetic diversity was assessed in this study.

Chilies are widely used throughout the tropics and are major ingredients of curry powder in the culinary preparations. They extensively used in Central America as constituents of dishes such as tamales and "chili con carne". Extracts of chilies are used in the production of ginger beer and other beverages. *Capsicum frutescens* is used in medicine as carminatives internally, besides being in external counter irritant. The green chilies are rich in routine which is of immense pharmaceutical need (Purseglove, 1977)

It is quite rich in nutritive value and supposed to contain certain medicinal properties.(Chawdhury,1976).Commercial cayenne pepper is the preparation of dried, finally grounded, mature of various highly pungent or "hot" forms of *Capsicum frutescens*. These pungent are used in the manufacture of sauces and curry powders and in the preparations of pickles. The chief constituent of chili (*Capsicum frutescens*) pericarp is crystalline colorless pungent principle known as capsaicin or capsicutin ($C_{18}H_{27}NO_3$) a condensation product of 3-hydroxy-4-methoxy benzylamine and declyninc acid which produces a highly irritating vapor in heating (Anon,1952).Green chili are rich in vitamin A and C and the seed contains a trace of starch (Saimbhi *et al*,1977 ; Sayed and bagavandas,1980).the fruits also contain a fixed oil, red coloring matter which is non-pungent and yield 20-25% alcoholic extract, dry matter-22.025, ascorbic acid 131.06 mg/100g (fresh weight), oleoresin 66.53 ASTA units, coloring matter 67.38 ASTA unit s, capsaicin 0.34% (dry weight), crude fiber 26.75% and total ash 6.69% (Bajaj *et al* (1980).

Genetic diversity is one of the most important criteria for parent selection. Genetic diversity is the prerequisite for an efficient plant breeding program. The availability of transegressive sergeants in any breeding program depends upon the diversity of involving parents. The divergence analysis has a definite role to play in an efficient choice of divergent parents for hybridization to exploit maximum heterosis such as produce cultivar with increasing yields, wider adaptation,

desirable quality, and pest and disease resistance. The importance of genetic diversity in the improvement of crop has been stressed in both self and cross pollinated crops (Griffin and Lindtorm, 1954; Murty and Anand, 1966; Gaur *et al* 1998). The quantification of genetic diversity through biometrical procedure (Anderson, 1957; Rao, 1952) has made it possible to choose genetically diverse parents for a successful hybridization program. Genetic diversity is important to know the source of genes for a particular trait within the available Germplasm. In order to increase the frequency of desired genotypes in breeding progenies; superior parents with high breeding values are needed.

Variability and diversity is the fundamental law of plant breeding which is major tool being used in parent selection for efficient hybridization program (Bhatt, 1973). Knowledge of the interrelationship between yield and yield components is desirable to know the magnitude and direction of changes expected during selection. More diverse the parents greater are the chances of the obtaining high heterotic F1 and broad spectrum variability in segregating generation (Arunachalam, 1991). The supreme parents having desirable characters could be identified through divergence analysis. Several statistical methods are known for discriminating purposes viz, Mahalonobis's generalized distance (Mahalonobis, 1936), Fisher's discriminate analysis (Fisher, 1936). Inspection of biometric data and total of grouped data (Whitehead, 1954), the algorithm methods of Williams and lamberts (1960) and Copers's statistical D²-statistics based on multivariate analysis appears to be good index. This technique has been followed by many researchers on wide ranges of crops. Based on the above information, the present experiment was conducted to study the available variation, genetic nature and genetic diversity of 15 chili cultivars of local origin. The specific objectives of the present study were as follows:

1. To estimate the genetic variability for different quantitative characters of 15 chili cultivars
2. To assess the genetic diversity among 15 chili materials
3. To characterize and study interrelationship among the genotypes on the basis of yield and yield contributing traits.
4. To select suitable diverse parents for the utilization in future hybridization program.

REVIEW OF LITERATURE



CHAPTER II

REVIEW OF LITERATURE

Variability and genetic diversity is the fundamental law of plant breeding which is a major tool being used in parent selection for efficient hybridization program (Bhatt, 1973). It is a prerequisite for effective parent selection. The quantification of genetic diversity through biometrical procedures such as Mahalanobis's D^2 -statistics and canonical variate analysis (CAV) has possible to choose genetically diverged parents. Recent work indicates that the Mahalanobis's generalized distance (D^2 statistics) may be an efficient tool to exploit maximum heterosis in terms of the diverse goals such as producing cultivars with increased yield, wider adaptation, desirable quality, disease and insect resistance. More diverse the parents exhibit higher in heterotic F1 and broad spectrum variability in segregating generation (Arunachalam, 1991).

Therefore, relevant information available in the literature pertaining to the characterization, variability and diversity of the chili and some other crops of the same family were reviewed in this section. Moreover literature related to the efficient multivariate techniques for diversity analysis was also reviewed in the following headings.

2.1 Variability in fifteen chili cultivars

2.1 Genetic diversity of chili (*Capsicum spp*)

2.3 Relationship between genetic diversity and geographical distribution

2.4 Techniques of multivariate analysis

2.1 Variability of fifteen chili genotypes

Genetic variability, heritability, genetic advance and genetic advance in percent of mean for 12 characters were assessed by field evaluation of 80 chili accessions by Krishna *et al.* (2007) at Kittur Rani Channamma of Horticulture, Arabhabhi (karnataka), India during 2002. High degree of variation was observed for all characters. The difference between phenotypic coefficient of variation were found to be narrow for most of the traits except primary and secondary branches, tertiary branches, fifty percent flowering, early and late fruit yield per plant. Most of these characters also had moderate to high estimates of genetic advances as a percent over mean except days to first flowering.

Forty diverse chili genotypes were cultivated by Smitha and Basvaraja (2007) to study the extent of variability present in the genotypes for 32 characters studied which was confirmed by analysis of variance as indicated by high GCV and PCV values. Selection strategy for yield improvement should rely on number of fruits per plant, fruit weight, no of primary branches, fruit length, fruit diameter, plant height during selection process, because these characters are going to contribute directly towards the yield.

Arya *et al.* (1977) conducted an experiment on variability; correlation and path analysis among different characters of thirteen sweet pepper genotypes. They observed a wide genetic variation among the genotypes for fruit yield per plant, number of flowers per plant and individual fruit weight. They reported that genotypic and phenotypic coefficients revealed that the major portion of the phenotypic variance was genetic in nature. They estimated heritability along with high genetic gain were observed for individual fruit weight, fruit diameter, days to 50% flowering as well as number of flowers per plant. They also reported that number of flowers per plant exhibited significant positive correlations with plant height at final harvest both at phenotypic and genotypic levels. On the basis of the estimates of path analysis it has revealed that the number of fruits per plant and fruit length is the important component of fruit yield.

Sing *et al.* (2005) conducted an experiment on 15 advance generation breeding lines of tomato, including 4 control cultivars to study the variation and heritability of quality characters in tomato raised under normal and high temperature conditions. Data were recorded for total soluble solids (TSS), pericarp thickness, fruit firmness, acidity, lycopene

content and dry matter content. There were significant differences among the genotypes under normal conditions, whereas differences were not significant under high temperature conditions. In general, the phenotypic coefficients of variation were higher than genotypic coefficients of variation indicating that the genotypic effect is less under the influence of the given environment. Heritability estimates (in broad sense) were high for all the characters for November planting except for lycopene content. Rikovski *et al* (1956) studied variability and path-coefficient analysis in chili with 40 strains of chili grown in Pune, Maharashtra, India, during kharif season. The observed days to flowering, maturity, number of primary and secondary branches, plant height & spread, fruit length and girth, seeds per fruit, number of fruits per plant, fresh fruit weight per plant, dry fruit weight per plant. They revealed correlation (genotypic and phenotypic) among these characters and path analysis (direct and indirect effects) for fresh fruit weight and number of fruits per plant as the most important and reliable yield indicators in chili. They demonstrated the interrelationships that tall and spreading plants with higher number of secondary branches early maturity would be high-yielding types.

Prabhakaran *et al.* (2004) conducted an experiment to study genetic variability, heritability and genetic advance for 18 characters in chili (*Capsicum annum*) in Coimbatore, Tamil Nadu, and India with 97 genotypes of chili. They recorded high genotypic co-efficient of variation for plant spread, number of fruits per plant, yield per plant, fruit length, mean fruit weight, placenta length and and capsaicin. They observed that the heritability estimates were high for most of the characters. They found that the genetic advance as percentage of mean was high for yield per plant, mean fruit weight, placenta length and capsaicin. High heritability estimates coupled with high genetic advance as percentage of mean were recorded by them for yield per plant, mean fruit weight, placenta length and capsaicin.

Wasule *et al.* (2004) carried out variability in 17 newly developed genotypes of chili (*Capsicum annum* L) in Akola, Maharashtra, India and revealed that there were a wide range of variability among the genotypes for all the characters. They recorded variability for days to 50% flowering, plant height, no of primary branches per plant, number of fruits per plant, fruit length, fruit girth, 1000-seed weight, seed percentage and yield of red chilies per plant. They noted high genotype co-efficient of variation, number of fruits pr plant, Z They estimated heritability ranged from 27.60 to 92.70% and 9 characters showed high heritability (>70%). The described the expected genetic advance ranged from 3.73 to 74.90. They observed high heritability (92.70%) was accompanied b high genetic advance (70%) in respect of

number of fruits per plant, indicating prevalence of additive gene action which offers good scope for further improvement.

Das *et al* (2004) evaluated the performance of 25 chili genotypes during summer season at Sabour, Bihar, India. They recorded the data for plant height, number of branches per plant, days to 50% flowering, days to 50% fruit set, fruit length, fruit diameter, number of fruits per plant, weight of 10 fruit yield per plant and yield per hectare. They observed the genotype 94-3 showed the highest fruit yield of 110.82 q/ha with a fruit weight of 20.31g and fruit length of 5.90cm followed by Pant-C1 and 85-2 which gave high yield (106.82 and 102.43 q/ha) and oppositely genotype 95-1 performed the lowest yield of 31.66q/ha.

Sreelathakumary *et al.* (2004) evaluated 35 genotypes of chili genotypes (*Capsicum annum*) to assess genetic variability, heritability and genetic advance during 1997-98 at Vellayani, Kerala, India. They recorded high genotypic and phenotypic coefficient of variation for leaf area, fruits per plant, fruit weight, fruit length, fruit girth and yield per plant. The observed high heritability coupled with high genetic advance for these characters imply the potential for crop improvement through selection.

Zewdie Yayeh Zeven A C (1997) made a trial to studied variation in Yugoslavian hot pepper (*Capsicum annum* L). He evaluated 67 accessions of hot pepper based on 35 morphological and physiological characters and recorded highly significant differences among the genotypes were observed in a number of characters. He grouped the accessions into six clusters and mainly based on fruit weight, 1000 seed weight, and fruits number per plant and yield per plant showed wide genetic diversity among the genotypes.

Plant and fruit characteristics of eleven cultivars of chili were studied by Padda *et al.* (1970) under the environmental conditions of the vegetable farm of Punjab Agricultural University, India during the year 1968. They found that the cultivar differences in plant height were statistically significant and ranged from 54.4 to 102.4 cm. The plants of the cultivar Gurdaspur Black (102.4cm) and Long Red (101.2 cm) were tall while those of cultivar N.P. (54.4cm) were dwarf. They stated that the data of the number of fruits per plant also showed highly significant differences among the cultivars and on an average ranged from 82.0 to 532.2. They also observed that the fruit length varied from 2.0 to 8.6 cm and breadth from 0.6 to 1.5 cm. The yield of fruits per plant was found to vary 113.7 to 399.8 gm. The yield of red fruits per hectare varied from 4544.0 to 16004.2 kg. They found significant cultivar

differences at both green and red of fruit maturity and the contents of vitamin C ranged from 75.7 to 220.0 mg/100g in green chili while 68.7 to 250.3 g in red fruits.

Pruthi (1976) noted that chili was a variable annual sub shrub to which the flowers were born singly and there were usually pendent varying in size, shape and color of fruits. Heiser and Smith (1953) noted that the high nutritional value in chili lay in the vitamin c content; the ripe fruit had 150-180 mg /100g green weight which was higher than that found in tomatoes (20-25mg). They also stated that fruit size, shape and color were extremely variable and the fruits varied from 4.0 to 30.0 in length and other vegetative characters also varied greatly.

In the Punjab of India, Nandpuri *et al.* (1971) carried out an extensive investigation on 25 strains of chili and studied on yield, seed weight, fruit size, number of fruits and branches, plant height, days for flowering and maturity. They found the cultivar Fazilaka, Rujpura, Long red, T23-2/2 and 72-2/1 was to be the best in performance for all the traits. In India, in a close similar, Sharma (1975) made a trial on the plant and fruit characters, yield and capsaicin content of 16 chili cultivars. From all selections he found that there were no relationship between capsaicin content and color, size, shape and no of the fruits per plant.

In a taxonomic and genetic studies on the cultivated chili, Smith and Heiser (1951) observed that plants under cultivation attained a height of 30.5 to 76.2 cm and fruit were extremely variable sizes, generally, over 0.8 cm wide and 0.8 to 25.0 cm long whereas fruit length was found by Standely (1931) from 0.8 to 25.0 cm having a wide range in width. While under the climatic conditions of Ludhiana, India, Singh and Singh (1970) conducted an experiment on chili and concluded that yield was significantly correlated with fruit number, length, width and weight. Whereas Chua and Tech (1974) observed that yield per plant of chili was 400.8 to 501.2 g.

Information of genetic variation, heritability and genetic advance was derived from data on 10 yield components in 16 tomato lines grown during the winter season of 1986 at Bhubaneswar reported by Sahu *et al* (1994). There were significant differences among the lines for all the characters studied. Yield per plant, number of fruits per plant, number of flower trusses per plant and fruit weight had high genotypic coefficient of variation with values for heritability and genetic advance.

Randhawa *et al.* (1933) studied 22 genotypes of brinjal on 24 quantitative characters for deriving information on yield correction and observed that fruits/plant and number of branches/plant had the highest direct effect on yield.

Vedivel and Bapu (1990) studied nineteen genotypes of eggplant which were grown in a Randomized Block Design for observation on growth and yield related traits. Plant height, fruit weight and fruits/plants exhibited high genotypic variance, high variability coupled high genetic gain from fruit yield /plant, fruit/plants and number of branches/plant had the highest direct effect on yield.

In Belgrade, Rikovski (1956) noted that ripening increased the vitamin c content and other morphological characters in some cultivars of chili. Misra and Khatai (1969) reported that higher vitamin c contents were found in red chili than in green one. They also stated that plant height, fruit size, shape and color were extremely variable.

Gopimony *et al.* (1984) studied the analysis of data on total fruit yield/plant and 11 related traits from 27 (*Solanum melongena*) varieties/lines revealed that the phenotypic coefficient of variation ranged being highest for yield and single fruit weight, heritability and genetic advance being highest for single fruit yield and overall mean. The association of high heritability and genetic advance shown by yield, single fruit weight and fruit diameter was taken as an indication of additive gene effects.

Shoemaker (1953) noted that chili plant grew 30.5 to 76.4 cm in height and that the roots occupied the soil around the plant to a depth of 25.4 to 35.6 cm. He also stated that failure of chili plants to set fruit properly was in certain areas. He further reported that low humidity and resulted in excessive transpiration of water in the plant and the abscission of buds, flowers and very small fruits. Low moisture supply in a soil also promoted blossom drop but with excessive transpiration a water deficit developed even when the soil was well supplied with water. Vitamin C ranged from 75.7 to 220.0 mg/100g in green chili while 68.7 to 250.3g in red fruits.

2.2 Genetic diversity of chili (*Capsicum frutescens* L.)

Morphological similarity, eco-geographic diversity were the few easier methods used to discriminate divergent populations which were reinstated by more scientific and advanced

biometrical techniques viz. multivariate analysis based on Mahalanobis's D^2 statistics. Nair Mukherjee (1960) estimated degree of divergence between biological populations and relevant contribution of different components to the total divergence by D^2 statistics as a measure of genetic divergence in the field of plant breeding. Comparative analysis of complex developmental pathway depends on the ability to solve function of members of gene families across taxonomic groups studied by Friedman *et al.* (2003).

Smitha *et al* (2006) conducted an experiment to observe genetic divergence in chili (*Capsicum annum* L.). Their analysis was carried out in 40 genotypes of Mahalanobis D^2 - statistic. They recorded the data for plant height (PH), days to 50% flowering (DAF), number of primary and secondary branches PB & SB, plant spread (PS), Number of fruits per plant (NF), fruit length, fruit weight (FW), fruit diameter (FD) and yield per plant (FY), seeds per fruit (S). They grouped the genotypes in 8 clusters (A-H). Cluster A included 10 genotypes 17, C 5, d 1, E 4, f 1, g 1 and H1. They observed that the maximum intra and inter-cluster distance for Cluster -A and between cluster E and H respectively, indicating their suitability in heterosis breeding with respect to few important characters. The maximum relative contribution to the total divergence was recorded for NF (28.08%), FY (21.15%), PB (15.00%) and SB (10.00%), PS (6.67%), FW (5.26%) and FL (3.44%), confirming the existence of ample amount of divergence genotypes with respect to the traits and hence the selection of best genotypes for such traits would be helpful in utilizing the maximum heterosis in the future breeding programs. They reported that PH (0.51%), FD (0.38%), DAF (0.13%) contributed lower, indicating that these traits will not help in yield improvement through hybridization until variability arte created in these traits. They also reported that the divergence analysis indicated that even though cluster H was agronomically superior, the other cluster were found to superior for one or another character.

Sudre *et al* (2005) conducted an experiment to study the genetic divergence between chili and sweet pepper accessions using multivariate techniques. They used multivariate to evaluate the genetic divergence among 56 accessions of chili and sweet pepper (*Capsicum sp.*). They used Mahalanobis distance as dissimilarity measures. Canonical variate analysis, cluster analysis using Touchers method and distances in the plane were applied. The variables; Fruit length; fruit diameter, number of seed per fruit, fruit average wt., plant height, plant canopy width, 1000 seed wt., day to flowering, days to fruiting, fruits no per plant and fruit weight were evaluated there. They recorded that there were significant differences among accessions for all variable evaluated. They showed a general agreement among all multivariate techniques

used and it was possible to separate the accession in eight distinct groups, indicating that there is genetic variability for the evaluated traits. The highest generalized distance of mahalonobis's D^2 was 266.42. Hence; these accessions have the potential to be used as parents in artificial crosses to obtain progenies with higher heterosis. Through canonical variable analysis, we observed the crosses with the greatest heterotic potential were 56x43; 34x08 and 59x41.

Majnu *et al* (2004) studied genetic divergence in hot chili (*Capsicum chinensis*) for plant height, days to first flowering, pollen viability, fruits per plant, fruit weight, Seeds per fruits, no of harvests, ascorbic acid contents, mosaic incidents and yield per plant was assessed in 32 accessions of hot chili during 2000-01 in kerala, India. Analysis of variance showed significant differences among accessions for all characters studied. They reported that cluster analysis classified the accessions into 6 clusters. Cluster-1 was largest with 21 accessions, followed by cluster-2 with- 6 accessions and cluster-3 with 2 accessions. Cluster -4, 5 and 6 had one accessions each. They observed that cluster 1 had highest intra-cluster distance (229.93), followed by cluster 2 (217.55) and 3(188.74) They found maximum divergence was found between cluster 1 and 6 followed by cluster 1 and 5, as indicated by their high inter-cluster distances (1965.74 and 1640.10) respectively. Among the characters, fruits per plant and yield per plant contributed maximum divergence in *Capsicum chinenses*.

Khurana *et al.* (2003) observed genetic diversity for growth, yield and quality traits in chili (*Capsicum annum* L). They made a trial with 48 chili genotypes grown in Punjab, India, during 1994 and 1995. They observed a highly significant variation among the genotypes in terms of fruit yield, fruit length, fruit thickness, no of fruits per plant and peel: seed ratio. They recorded a high genetic coefficient of variation for number of fruits per plant, fruit yield, no of fruits per plant, fruit length, fruit diameter and number of seeds per fruit had high values of heritability. They also reported that fruit yield was positively correlated with number of fruits. Fruit length and diameter, peel: seed ratio, plant height, leaf area, capsaicin content and coloring matter, but was negatively correlated with number of days of flowering, number of days to fruit set, and wild and viral incidence. Fruit yield showed a significant phenotypic correlation with number of fruits per plant, fruit length, and peel: seed ratio, leaf area and capsaicin content. They investigated that the number of days to flowering fruit thickness and wilt & viral incidence had negative direct effects on fruit yield. They also reported that plant height had an indirect effect on fruit yield through number of fruits, plant height and fruit length.

Karad *et al.* (2002) studied genetic divergence in chili (*Capsicum annum* L) using Mahalonobis's D^2 - statistics among 40 genotypes of indigenous and exotic origin, collected from New Delhi, India, were evaluated to study the variability and genetic divergence. Diversity analysis revealed good amount of variation among the genotypes studied. D^2 values ranged between 0.1032 and 8.7702. They noted that the genotypes were grouped into eight clusters. Cluster 1 was the largest containing 23 genotypes, followed by cluster 2(4 genotypes), cluster 3(3), cluster 4(3), cluster 5(3), and cluster 6(2). Cluster 5 and 8 were mono genotypic. They showed the inter cluster distance (D^2) ranged 7.45 between (cluster 2 and 5) and 1.15 (cluster 3 and 7). They revealed that the variance of cluster means was fresh weight and fruits per plant had the highest contribution towards.

Rahman *et al* (2000) conducted an experiment on the genetic divergence among 22 genotypes of chili was estimated using Mahalonobis's D^2 and Rao's Canonical Variate Analysis. They grouped the genotypes into five clusters and the pattern of distribution of the genotypes into different clusters was random which indicated that the geographical isolation was not always related to genetic diversity. Days to first flower, plant height, number of fruits per plant, fruit length and diameter contributed maximum towards divergence. The genotype 3 (C-0004) individually formed a single cluster indicating its superiority in respect of primary branches per plant, fruits per plant, fruit diameter and yield potentiality than that of other clusters.

Singh *et al.* (2005) carried out research on thirty five genotypes of brinjal for genetic diversity in the rainy Season of 2003 in Punjab Agricultural University, Ludhiana. The genotypes were grouped into eleven clusters. The clustering was irrespective of geographical divergence. Therefore, for management of diversity in germplasm, the pattern obtained with cluster analysis may be single most effective one. These genotypes, viz. punjab Sodabahar, Punjab jamunigola and HP-14 exhibited maximum diversity from genotypes and thus could effectively be used as one of the parent in hybrid breeding program to exploit heterotic expressions for yield and other economic characters. Sundaram *et al.* (1980) conducted an experiment to study genetic divergence among 50 varieties of chili (*Capcicum frutescens* L). They reported that the D^2 analysis revealed no relationship between genetic and geographical diversity. They described that the number of branches and number of fruits per plant were the chief contributors towards genetic divergence.

Genetic diversity for the improvement of the crop has been stressed in both cross and self pollinated crops by (Gaur *et al.* 1978) and the quantification of genetic diversity through

biometrical procedures made it possible to assess genetic diverse parents for a successful hybridization program (Jain *et al*, 1975). Tomooka reported that evolution of genetic diversity is important to know the source of gene for a particular trait within the available Germplasm.

Mathew *et al*. (1986) studied on genetic distance among five botanical varieties of cucumber (*Cucumis melo*). The genetic distance was calculated for nodes to first female flower, fruit weight, seeds per fruit, and fruits per plant. Total D^2 was estimated according to Mahalanobis's (1936). The magnitude of D^2 indicated closeness among the varieties. The character fruit per plant contributed maximum to total divergence (80%). Seeds per fruit did not contribute to total divergence. Selection of divergence parents in any hybridization program.

Mishra *et al* (2000) conducted an experiment in Patnagar, Uttar Pradesh, India during 1999/2000 in rabi season to determine the genetic diversity among 38 potato genotypes. Based on the mean performance for various characters and genetic distance between genotype crosses, namely jp-100xKufri pukhraj, jp-100x jp-216 and jp-100xjx-371 were identified as promising and were likely result in progenies with heterotic performance for tuber yield and its components.

Genetic divergence among 20 cultivars of brinjal (*Solanum melongena*) was estimated by Mishra *et al* (1998) using D^2 statistics for eleven yield traits cultivars were grouped into 7 clusters. Maximum genetic distance was found between cluster 4 and 6 followed by that between cluster means and the genetic distances, the crosses of cultivar of cluster 6 (A-I) with the cultivars of clusters 1 and 4 were likely to recombine the genes for high yield.

An experiment was conducted by Gopal *et al* (1997) to study the effectiveness of genetic divergence for cross prediction in potato and progeny means, heterosis and specific combining ability effects were correlated with parental genetic distances (D^2 -values) estimated under six in vitro and four in vivo conditions for tuber yield in 72 crosses. Genetic distances under in vitro conditions had no relationship with the progeny means for tuber yield. The magnitudes of the significant correlation coefficients showed that genetic divergence could be used as an indirect parameter of moderate effectiveness in selecting parent to produce heterotic high yielding progenies.

Fifty two potato genotypes comprising *Solanum tuberosum* (35) were observed by Panday *et al* (1995). Indigena (4) and sub specific crosses (13) were compared for genetic divergence on the basis of 11 plants and tuber characters. The genotypes were grouped into 11 clusters. The genotypes with wild species in their pedigree had high genetic diversity and were distributed in almost all clusters. However genotypes with common species in their pedigree showed a low diversity. Genotypes developed from the same percentage at those or involving one common parent also had low genetic diversity.

It was revealed that by Ushakumary *et al.*(1991) through the evaluation of fifty four diverse genotypes of brinjal for 10 yield component that phenotypic co efficient of variation was higher than genotypic co-efficient of variation was higher than genotypic co-efficient of variation for all the characters since they showed high heritability values. They concluded that there was enough scope for improvement of quantitative characters in brinjal by selection. While Mandal and dana (1992) studied 20 genotypes of brinjal for the yield contributing characters and indicated that fruits/plant, secondary branches/plant and plant height were important traits for the selection of superior genotypes.

Information on genetic divergence of sweet potatoes (*Ipomoea batatas*) was reported by Naskar *et al.*(1996) from Meghalaya Pradesh ,India was derived from data on 8 quantitative characters if 18 genotypes each, cluster 4 had high genetic divergence for yield contributing characters in sweet potato(*Imopea batatus*)

Prasad *et al* (1993) evaluated 32 representative genotypes of cucumber (*Cucumis sativa*) for biological divergence by using Mahalonobis"s D^2 values. They found considerable diversity in material studied. The 32 populations were grouped into eight clusters. There was a considerable range in the magnitude of D^2 values which suggested the existence of appreciable genetic divergence in the population for the characters studied. Further the study inhibiting the pattern of distribution of genotypes from different regions into different clusters was at random, demonstrating that the geographical isolation may not be the only factor for causing biological or genetic diversity.

Hybrids from a diallel set of crosses between 11 varieties of tomato were evaluated by Sindhu *et al.* (1993) for field heterosis over the better parent in relation to the genetic distance between the parents. The genetic divergence between the parents was not clearly related to the performance of the hybrids with the highest heterosis were listed.

An investigation was carried out by Varalakshmi *et al.* (1991) on genetic divergence; heritability and genetic advance for 10 characters in 32 genotypes of chili (*Capcicum annum*) were studied. Based on D^2 values, the genotypes were cluster red in 11 gene constellations. Grouping of genotypes in different in different cluster were not related to their geographical origin. Considerable amount of genotypic and phenotypic coefficients of variation was observed for leaf area index, fruits per plant, fruit weight and total yield. High heritability coupled with high genetic advance as percentage of mean and genetic coefficients of variation was observed in respect of leaf area, fruit/plant, fruit wt., seeds/fruits, plant height and fruit length, indicating that these characters are under control of additive gene or no environmental effects and could be dependable for yield improvement in chilies.

Singh *et al.* (1963) studied genetic divergence through D^2 statistics with 40 potato genotypes growing in 12 environments based on 13 characters. They searched the clustering pattern and their intra-cluster distances taking 30 clusters using D^2 statistics. On the basis of stability, high yield and divergence among the genotypes the genotypes, nine crosses were recommended as suitable for using in breeding program.

2.3 Relationship between Genetic diversity and Geographical Distribution

Genetic divergence is not always related to geographical diversity. The genotypic divergence among different genotypes for several characters were studied by plant breeders using Mahalonobis;s D^2 statistic. They observed the characters namely yield contributed toward genetic divergence. They demonstrated that geographical isolation might not be the only factors causing genetic diversity, plant height, mature fruit, days to flowering, days to maturity, etc contributed much to the total divergence, several authors (Moll *et al.* 1962; Timothy, 1963; Murthy and arunacharam (1966) could not find any direct relationship between geographical distribution and genetic divergence in different crops.

Rahman *et al.* (2000) conducted an experiment on genetic divergence among 22 genotypes of chili was estimated using Mahalonobis,s D^2 statistic. Through the genotypes grouped into five clusters were random which indicated that the geographical isolation was not always related to genetic diversity.

Investigation of twenty potato genotypes (2 of sub sp. andigena and the rest of subsp. *Tuberosum*) were evaluated by Gopal *et al.* (1999) for ten morphological characters under four in vivo conditions. It appeared that genetic diversity was not related to geographical

diversity where distances higher between tuberosum and andigena species than within either tuberosum and andigena.

Yadav *et al.* (1996) tested genetic divergence using mahalonobis D^2 statistics in 40 diverse tope of brinjal. The genotypes differed significantly for 10 yield contributing characters and where grouped in 9 clusters. They observed that there was no correspondence between geographical distribution and genetic divergence.

Timber *et al.* (1993) studied the diversity using D^2 analysis among 25 diverse varieties/lines of brinjal. The 25 genotypes were grouped into 5 clusters with substantial genetic divergence between them. They reported that geographical distribution did not necessarily follow clustering pattern

Prashad *et al.* (1993) evaluated 32 repetitive genotypes of cucumber (*Cucumis sativus* L.) for biological divergence by using Mahalonobis; values. They found considerable diversity in the in the material studied. They also reported that the geographical isolation may not be the only factor only causing biological or genetic diversity

Pramanick *et al.* (1992) studied genetic diversity of 38 lines/varieties of egg plant for eighteen characters by using Mahalonobis, D^2 statistics. The 38 genotypes were grouped in nine clusters which were homogenous within and heterogenous between. The clustering pattern shower different behavior irrespective on their origin.

A close similarity was observed in an experiment of genetic diversity of bunch groundnut katule *et al.* (1992) reported there was no correlation between genetic diversity and geographic origin. Similar result was also observed by Reddy and Reddy (1933)

Golakiya and Makne (1992) found that the genotypes of common geographic origin or same location had a lack of relationship between genetic and geographic diversity.

Investigation on genetic diversity in 22 accessions f wild potato was done by Juned *et al.* (1988) from Paraguay and Argentina. They observed a close relationship between the geographical group using Principle Component Analysis (PCA), Cluster Analysis and genetic diversity Reddy *et al.* (1987) found no relationship of genetic diversity to geographical distribution of the varieties in a study of genetic diversity for pod yield/plant and 12 related traits of groundnut genotypes.

Golakia and Makne (1991) and Nadaf *et al* (1986) found that grouping of groundnut genotypes in to different clusters was not related to their geographical origin and that the geographical isolation might not be the only factor for genetic diversity.

In a two years study with 30 varieties of okra for genetic diversity using Mahalonobis's D^2 - statistics (Singh and Singh, 1979) indicated that varieties were grouped in eight clusters in both the year. They reported that the divergence between clusters did not follow their geographical distribution and was fairly at random. It has been also reported that no close correspondence is evident between geographical distributions to genetic divergence as estimated by D^2 statistics. They also observed that days to flower, Fruits per plant and fruit bearing branches contributed maximum towards total divergence and suggested to considerable weight on these characters to increase yield.

Arya and Saina (1977) in Haryana of India studied seven cultivars of chili on phenotypic and genotypic variation for 12 characters. They found that the green fruit yield per plant, Fruit size and fruit number per plant were found to be controlled genetically and less affected by environment.

Genetic divergence using Mahalonobis's D^2 statistics and Canonical Analysis among 25 varieties of tomatoes was studied by Peter and Rai (1976) found that genetic and geographical divergence was not related.

Tinder (1968) noted that chili had a shorter growing period and that flowering was adversely affected by heavy rainfall and more sensitive to excessive soil water. He explained that Plant attained a height of 30.5 to 91.4 cm, fruits were extremely variable in size and shape, 1.3 to 25.4 cm long, erect and pendulous, green or red and varied in degree of pungency, D^2 analysis original outline by Mahalonobis's (1936) and extended by Rao (1952) is one of the potential of a character however depends on the population and also the environmental conditions in which the population is grown (Akter, 1990).

2.4 Techniques of multivariate analysis

Selection of parent based on genetic divergence is a prerequisite in heterosis breeding program. Since hybrid vigor essentially depends on genetic divergence of parent, it is necessary to identify diverse parents for hybridization program. Genetic diversity analysis is mainly based on different multivariate techniques. Multivariate analysis by means of Mahalonobis's D^2 analysis has been widely used for assessing the genetic diversity in several

crops. It is a powerful tool in quantifying the degree of genetic divergence among parents (Joshi and Singh, 1979) Muppidathi *et al* 1995). During last decade different multivariate techniques have been developed which may be due to the improvement of computer. Multivariate statistical analysis in statistics describes a collection of procedures which involve observation and analysis of more than one statistical variable at a time. Sometimes a distinction is made between univariate (ANOVA, t-tests) and multivariate statistics Mardia *et al.* (1979). However related to efficient multivariate techniques for genetic diversity analysis are reviewed in the following paragraph.

Multivariate techniques were unused to evaluate the genetic divergence among 56 accessions of chili and sweet pepper (*Capsicum spp.*) By Amaral (2005) from the germplasm collection of Universidad Estadual do Notre Fluminense Eleven quantitative descriptors proposed by International Plant Genetic Resources Institute were utilized in a field experiment carried out in Campus dos Goytacazes, Rio de Jenerio State, Brazil. Generalized Mahalonobis's distance D^2 was used as dissimilarity measure. Canno variate analysis, Cluster analysis using Tochers optimization method and distances in the plan were applied. The variates fruit length; fruit diameter, no of seeds per fruit, plant height, plant canopy width,1000-seed weight, days to flowering, days to fruiting, fruit no. per plant and fruit weight per plant were evaluated. There were significant differences among accessions for all descriptors evaluated. General agreement among all multivariate techniques used was observed and it was possible to separate the accessions in 8 distinct groups, indicating that there is genetic variability for the evaluated traits.

An experiment was conducted by Mishra *et al.* (2004) to study the genetic diversity among 22 capsicum 22 capsicum genotypes, grown in the mid-hills of Uttaranchal, India, during Kharif 1998,was assessed based on 16 yield contributing Characters using Mahalonobis's D^2 -statics.The genotypes could be grouped into 4 clusters. The reported that clusters 1 was largest with 16 genotypes, followed by cluster-2 with 3 genotypes, cluster-3 with 2 genotypes and cluster-4 with only one genotypes. Based on genetic divergence (root-d2) Pepper Pepricax Sel. 1-2 are suggested as potential crosses to incorporate most of desirable traits in population through hybrid breeding in capsicum under rain fed condition in the mid hill of Uttaranchal.

The nature and magnitude of genetic divergence was assessed by Joshi *et al.* (2003) using non hierarchical Euclidean cluster analysis in 73 tomato (*Lycopersicon esculentum*) genotypes of

diverse origin for different quantitative and qualitative traits. Maximum value of co-efficient of variability (53.201) was recorded for shelf life of fruits while it was minimum (69.208) for days to first picking. The grouping of genotypes into 15 clusters indicated the presence of wide ranges of genetic diversity among the genotypes. The clustering pattern of tomato genotypes indicated non-parallelism between geographic and genetic diversity.

The hundred accessions of andigena of potato germplasms were evaluated by Sandhu *et al* (2001) for genetic divergence based on 8 distinct traits. Namely plant height, number of stems, number of nodes inters node length, leaflet index, tuber yield, tuber and average tuber weight. Principal Component Analysis (PCA) based on adjusted mean value yielded 8 each Eigen vectors and Eigen roots. Eight genetically diverse and ergonomically promising genetic stocks were identified which may be involved in crossing program. Thirty four genotypes of brinjal (*Solanum melongena*) of diverse origin were evaluated by Sharma *et al.* (2000) in plots of Jorhat. Analysis of data on yield and its component grouped the genotypes into 10 clusters using Mahalanobis's D²-statistics. Fruit circumference and average fruit weight were the main characters affecting grouping of genotypes. Eco-geographic diversity of the genotypes was not related to genetic diversity. Kumar and Kang (1998) conducted an investigation by using Multivariate analysis for genetic divergence among 30 andigena potato accessions by D²-statistics led to their grouping into 7 clusters. D²-estimates were based on 11 characters. The clustering pattern in pooled analysis was used for selecting parents. Cluster 7 and 4, 7 and 5, 7 and 6, 4 and 1, 4 and 3, 2 and 7 had high inter cluster distances. Cross involving pattern from these cluster combinations were recommended for an andigena breeding program.

Amaral *et al.* (1977) observed that the efficiency in predicting the behavior of tomato hybrid based on the parents and genetic divergence was evaluated via D²- analysis of data on 15 characteristics in 5 parents and their hybrids almost all correlation between D² and hybrid population means, heterosis and combining abilities were positive, indicating that genetic divergence was a high efficiency parameter for hybrid behavior prediction.

Thirty six genotypes of potato were grown in 16 environment during 1991-93 were evaluated by Desai *et al* (1997) for genetic divergence by Mahalanobis's D² statistics. Among nine clusters, 1, 3, 5, 6 and 7 showed larger genetic divergence. Genotypes in cluster 3 had the highest tuber yield and other characters like number of stems, number of leaves, maturity, shoot fresh weight, sugar content and harvest index. Cluster 1 contained genotypes with high dry matter and starch content, cluster 4 those with dwarf plant height and early maturity and

cluster 6 those with high protein content. The genotypes differed significantly for all characters, suggesting a good scope of selection.

An experiment was conducted by Naskar *et al.* (1995) and reported that cluster analysis was applied to 9 characters in 22 diverse Indian genotypes in 1981 and 1982, all genotypes were grouped into 9 clusters in both years although the clustering pattern was not consistent over the years. Genetically diverse (as estimated Mahalanobis's D^2 statistic) use in crosses to give promising segregants. High heterosis, it was suggested, could not be achieved by crosses between members of distance clusters.

In a close similar it was reported by dramatic *et al* that genetic diversity in a population of 402 tomato lines was assessed using multivariate analysis. In a population of 402 tomato lines was assessed using multivariate analysis, in a field experiment carried out in Dharwad, Karnataka, India, during 1994-1995. Observations were recorded for plant height, no of branches per plant, no of fruits per plant, yield per plant, incidence of tomato leaf curl virus (TLCV), and no of whiteflies per plant. The 402 lines were grouped into 4 clusters based on similarities of D^2 value. Considerable diversity within and between the clusters was noted, it was observed that the characters TLCV resistance. Therefore, selection of divergent parents based on these characters may be useful for heterosis breeding of summer tomato.

An experiment was conducted by Senapati *et al.* (2003) in order to estimate genetic divergence in chili by using Mahalanobis's D^2 -statistics was studied for 11 characters in a collection of 20 diverse chili genotypes. They reported that based on D^2 values, the genotypes were grouped into 6 clusters. Cluster 1 was largest with 13 genotypes, followed by cluster 3 and 4. Cluster 2, 5 and 6 each had single genotype. They observed that cluster 2 had maximum genetic distance from cluster 6, suggesting wide diversity between these groups. They suggested that four characters, namely fresh fruit weight, fruit girth, fruit length and fruit number per plant were the chief contributors toward genetic divergence.

**MATERIALS AND
METHODS**

CHAPTER III

MATERIALS AND METHOD

3.1 Experimental Site

The present research work was carried out in the experimental farm, Sher-e-Bangla Agricultural University (SAU), Dhaka during November 2013 - April 2014.

3.2 Soil and Climate

The soil of the experimental plots was clay loam, land was medium high to medium high fertility level. The site was situated in the subtropical climate zone, wet summer and dry winter is the general climatic feature of this region. The robi season is generally rainless with moderate temperature and short day length. Meteorological data on rainfall, temperature, relative humidity from December 2013 to February 2014 were obtained from the Department of Meteorological centre, Dhaka-1207, Bangladesh. The selected plot was a medium high land. The pH of soil 4.66 to 5.93 while the amount organic carbon content, total N, available P and available K were 0.82%, 0.12%, 21 ppm and 0.27 mg per 100 gm of soil respectively.

3.3 Genetic materials used for the experiment

The present study was performed with 15 genotypes of chili of different origin/source. Among them 6 genotypes were collected from Bangladesh Agricultural Research Institute (BARI), Gazipur. Other genotypes were collected from local market of Bogra, Chittagong, kushtia and Mymansingh. The materials used in that experiment is shown in Table 1.

3.4. Experimental design

The experiment was laid out in Randomized Complete Block Design (RCBD) further sub divided into 15 lines where genotypes were randomly assigned. The plot size was 3m with single line. Row to row distance were 50 cm. The genotypes were distributed to each line with each block randomly.

3.5 Preparation of the experimental field

The selected field for growing capsicum was first opened on 28-10-2013 with power tiller and was exposed to the sun for a week. Then the land was prepared to obtain good tilth by several ploughing, cross plugging and laddering. Other operations were

Table 3.1 List of chili genotypes used in experiment

Genotypes (Code)	Name of the genotypes/variety	Source of collection
V1	Bombae morich	Gene bank,BARI,Gazipur
V2	Oporajita morich	HRC, Savar
V3	Dhani morich	BADC Office,Muktagasa,Mymensingh
V4	Kamranga bombae morich	Gene bank,BARI,Gazipur
V5	kancha morich	BADC Office,Muktagasa,Mymensingh
V6	Akashi morich	Gene bank,BARI,Gazipur ,
V7	Kalo morich	Gene bank,BARI,Gazipur
V8	Roshni morich	BADC Office,Muktagasa,Mymensingh
V9	Baromashi kancha morich	BADC Office,Muktagasa,Mymensingh
V10	Lomba morich	Gene bank,BARI,Gazipur
V11	Sada morich	Bristi Nursery,Savar
V12	Joli lonka	Sohortoli seed market,Chittagong
V13	Capcicum morich	Gene bank,BARI,Gazipur
V14	khudi morich	Local market,Kushtia
V15	Bindu morich	Bristi Nursery,Savar

done with harrow, spade and hammer. Weeds and stubbles were removed; larger clods were broken into small particles and finally attained into a desirable tilth to ensure proper growing conditions. The plot was partitioned into the unit plots according to the experimental design as mentioned earlier. Recommended doses of well decomposed cow dung, manures and chemical fertilizers were applied and mixed well with the soil each plot. Irrigation and drainage channels were also prepared around the plots. Each unit plot was prepared keeping 5cm height from the drains. The bed soil was made friable and the surface of the bed was leveled.

3.6 Fertilizer application

Four days before planting of capsicum seedlings, the entire amount of well decomposed cow dung and TSP and other fertilizers were applied to the plots and well mixed with the bed soil. During final bed preparation, one fourth of both urea and MP were applied. The rest of the Urea and MP were top dressed in 3 equal installments, after 30, 45 and 60 days of planting (Table 3.1).

Table 3.2. List of fertilizers with doses and application procedures

SL. No.	Fertilizer	Doses	Application Procedure
1.	Urea	275 Kg/ha	50% basal and 50% at 30,45 and 60 DAP in 3 installment
2.	TSP	200 Kg/ha	as basal
3.	MP	200 Kg/ha	as basal
4.	Gypsum	20 Kg/ha	as basal
5.	Borax	10 Kg/ha	as basal
6.	ZnO	10Kg/ha	as basal
7.	Furadan	10Kg/ha	as basal

3.7 Transplanting of Capsicum seedlings

Thirty five day old seedlings were transplanted in the experimental plot on 05-12-2013 as per treatment. Planting was done at the afternoon. One seedling was planted in each pit. After planting, the bases of the seedling were covered with soil and then pressed by hand.

3.8 Intercultural operations

The growing seedlings were always kept under careful observation. After planting the seedlings, the following intercultural operations were accomplished for their better growth and development. Intercultural operations, such as weeding, thinning, irrigation, pest management, etc. were done uniformly in all the plots. One post sowing irrigation was given by sprinkler after sowing of seeds to bring proper moisture condition of the soil to ensure uniform germination of the seeds. A good drainage system was maintained for immediate release of rainwater from the experimental plot during the growing period. The first weeding was done after 15 days of sowing. During the same time, thinning was done for maintaining a distance of 10 cm from plant to plant in rows of 30 cm apart. Second weeding was done after 35 days of sowing. The crop was protected from the attack of aphids by spraying Malathion-57 EC@ 2 ml/liter of water. The genotypes differed widely for days to flowering. The insecticide was applied for the first time approximately before one week of flower initiation and it was applied for another two times at an interval of 15 days. To protect the crop from the Alternaria leaf spot, Rovral-50 WP was sprayed at the rate of 2g/l at 50% flowering stage for the first time and it was again applied for two times at an interval of 15 days. Both the insecticide and fungicide were applied in the evening.

3.8.1 Irrigation

Immediately after transplanting the experimental plot were semi-flooded by irrigation. The crop was irrigated as and when needed depending on the moisture status of the soil and requirement of the plants.

3.8.2 Gap filling

Plots with transplanted seedling were regularly observed to find out any damage dead seedlings for its replacement. Gap filling was done and when required.

3.8.3 Weeding and mulching

Weeding and mulching were necessary to keep the plots free from weeds, easy aeration and for conserving soil moisture. When the plants were established, the soil around the base of plants was pulverized.

3.9 Top dressing

The remaining doses of Urea and MP were applied as top dressing in each plot by 3 equal installments.

3.10. Plant protection measures

The chili plants are affected by aphids. Diazinon 60 EC (15cc/10 liter) was applied against aphids and other insects. To prevent chili plants from anthracnose and die back Cupravit (3g/l) at 15 days interval was sprayed. Few plants found to be infected by bacterial wilt were uprooted.

Harvesting

Harvesting of fruits was started 75 DAP and continued up to 125 DAP with an interval of 25 days. Harvesting was done usually by hand.

3.11 Data collection

In order to study the genetic divergence among the genotypes, the data were collected in respect of 8 parameters, plant height, days to first flower, no of primary branches per plant, Fruit length, Fruit circumferences, fruit weight, no of fruits per plant and fruit yield per plant during the growth of plant at the harvesting of the crop. During the plant growth, 10 plants were selected randomly from each unit plot for data collection. The sampling was done in such a way that the border effects were completely avoided. For this purpose, the outer two lines and the extreme end of the middle row were excluded.

a. Plant height

The height of plant was taken in centimeter (cm) from ground level to tip of the longest main stem of the plant. It was recorded at 25, 50, 75, 100, and 125 DAP

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12.10.15

b. Days to first flowering:

Days to first flowering were recorded from transplanting date to the date to first flowering of every plant of every genotype.

c. No of primary branches:

No of primary branches were recorded from the selected plant at final harvest It was considered only main lateral shoot with main shoot.

d. Fruit length (cm)

The length of the fruits was recorded with a measuring tape in cm from the neck of the fruit to the bottom of the fruit. Ten selected fruit from each plant were measured and their average was taken as the length of the fruit.

e. Fruit circumference (cm)

Circumferences of the fruit were recorded by measuring tape at the middle portion of 10 selected fruits from each plant in cm and their average was taken as the circumference of the fruits.

f. Individual Fruit weight:

Weight of individual fruits from sample fruits were measured in gram at each harvest and the mean was recorded.

g. No of fruits per plant

Fruits were collected in different dates from the selected plants and the average was taken as the no of fruits per plant.

h. Fruit yield per plant

Total weight (Kg or gm) of all fruits per plant harvested at different periods was recorded by electric balance.

3.12 Statistical Analysis of Data:

The data were analyzed for variance, different components of phenotypic and genotypic variance, heritability and genetic advance, correlation co-efficient and then the genetic diversity. According to Singh and Chaudury (1985), one way ANOVA (RCBD) was done with the mean data of the replications subjected. Duncan's New Multiple Range Test (DMRT) was performed to test the differences between genotypes, following the method of Steel and Torrie (1960).

Genetic diversity was subjected to both univariate and multivariate analysis using MSTAT and GENSTAT 5.13 Software program. Genetic diversity analysis involves several steps, i.e. estimation of distance between genotypes, clustering and analysis of inter-cluster distance between genotypes, clustering and inter cluster distance.

Therefore, more than one technique will be required to represent the result more clearly and it obvious from the result of many researchers (Uddin, 2001); Juned *et al.*, 1998 and Balasch *et al.* (1984)

The data were analyzed for variance, different components of phenotypic and genotypic variance, heritability and genetic advance, correlation, coefficient and the genetic divergence. According to Singh and Chaudhury (1985), One-way ANOVA (Completely randomized Design) was done with the mean data of all the replication subjected. Duncan's New Multiple Range Test (DMRT) was performed to test the differences between genotypes, following the method of Stel and Torrie (1960).

Collection of data

For studying different genetic parameters and inter-relationships the ten characters were taken into consideration.

i) Estimation of genotypic and phenotypic variances: Genotypic and phenotypic variances were estimated according to the formula of Johnson *et al.* (1955).

a. Genotypic variance, $\delta^2 g = \frac{MSG - MSE}{r}$

Where, MSG = Mean sum of square for genotypes

MSE= Mean sum of square for error, and

r = Number of replication

b. Phenotypic variance, $\delta^2 p = \delta^2 g + \delta^2 e$

Where, $\delta^2 g$ = Genotypic variance,

$\delta^2 e$ = Environmental variance = Mean square of error

ii) Estimation of Genotypic and Phenotypic Co-efficient of variation: Genotypic and phenotypic co-efficient of variation were calculated by the following formula (Burton 1952).

$$GCV = \frac{\delta g \times 100}{\bar{x}}$$

$$PCV = \frac{\delta p \times 100}{\bar{x}}$$

Where, GCV= Genotypic co-efficient of variation

PCV = Phenotypic co-efficient of variation

δg = Genotypic standard deviation

δp = Phenotypic standard deviation

\bar{x} = Population mean

iii) Estimation of heritability: Broad sense heritability was estimated by the formula suggested by Singh and Chaudhary (1985).

$$h^2b (\%) = \frac{\delta^2 g}{\delta^2 p} \times 100$$

Where, h^2b = Heritability in broad sense.

$\delta^2 g$ = Genotypic variance

$\delta^2 p$ = Phenotypic variance

iv) **Estimation of Genetic Advance:** The following formula was used to estimate the expected genetic advance for different characters under selection as suggested by Allard (1960).

$$GA = \frac{\delta^2g}{\delta^2p} \cdot K \cdot \delta p$$

Where, GA = Genetic advance

δ^2g = Genotypic variance

δ^2p = Phenotypic variance

δp = Phenotypic standard deviation

K = Selection differential which is equal to 2.06 at 5% selection intensity



v) **Estimation of Genetic Advance in percentage of mean:** Genetic advance in percentage of mean was calculated by the following formula given by Comstock and Robinson (1952).

$$\text{Genetic Advance in percentage of mean} = \frac{\text{Genetic advance}}{X} \times 100$$

vi) **Estimation of simple correlation co-efficient:** Simple correlation co-efficients (r) was estimated with the following formula (Clarke, 1973; Singh and Chaudhary, 1985).

$$r = \frac{\sum xy - \frac{\sum x \sum y}{N}}{\sqrt{[\{\sum x^2 - \frac{(\sum x)^2}{N}\} \{ \sum y^2 - \frac{(\sum y)^2}{N} \}]}}$$

Where, \sum = Summation

x and y are the two variables correlated

N = Number of observations

RESULT AND DISCUSSIONS

Chapter 4

RESULT AND DISCUSSION

For selection of better chili genotypes the knowledge of genetic diversity is essential. So to generate information of the degree of diversity among chili genotypes an experiment was conducted in the robi season 2013-14 at the field Sher-e-Bangla Agricultural University, Dhaka. Data on plant height, days to 1st flowering, and primary branches per plant, fruit length, fruit circumference, fruit weight, no of fruit per plant and fruit yield were recorded, analyzed and presented in this chapter. Performance of 15 genotypes of chili was investigated in winter season and the findings have been discussed under different morphological characters. The results of the study showed marked variation in different characters and the variation of different characters are presented in the following tables, figures and plates. The data pertaining to 8 characters were commuted and statistically analyzed and the result obtained is described below.

4.1 Variability among 15 chili cultivars

4.2 Heritability, genetic advance and genetic advances in percentage of mean

4.3 Correlation coefficient among 8 yields contributing characters

4.4 Genetic diversity for 15 genotypes of chili

4.1 Variability among 15 chili genotypes

Mean square (MS) from analysis of variance for different characters is presented in (Table 4.1). The mean values of all characters for all the genotypes along with the least significant difference (LSD) are shown in (Table 4.2). The estimate of genotypic variance, phenotypic variance, and genetic co efficient of variation is summarized in (Table 4.3).

4.1.1 Plant height

Significant differences were observed for plant height among the genotypes under study (Table 4.1). The significant varietal differences indicated that there was a wide range of variation among the genotypes for plant height with the mean values ranging from 83.93 cm to 20.1 cm (Table 4.2). The highest plant height 83.93 was recorded in lomba morich (V-10) which was significantly different from all other genotypes. The smallest mean value for plant height was 20.1 cm. in khudi morich (V-14). Padda *et al.* (1970) found that the cultivar differences in plant height were statistically significant and ranged from 54.4 to 102.4 cm. They also reported that the plants of the cultivar Gurdaspur Black (102.4 cm.) and Long Red (101.2 cm.) were tall while those of cultivar N.P. (54.4cm.) were dwarf. Tinder (1968) noted that plants attained a height of 30.5 to 91.4 cm. Smith and Heiser (1951) observed that plants under cultivation attained a height of 30.5 to 76.2 cm. Majnu *et al.* (2004) and Rahman *et al.* (2000) reported that analysis of variance showed significant differences among the accessions for plant height. Shoemaker (1953) noted that chili plant grew 30.5 to 76.4 cm. in height. The genotypic variance was (254.65) considerably lower than the phenotypic variance (258.33) for plant height in chill genotypes suggesting moderate influence of environment of this trait. Genotypic co-efficient of variation (26.74) was also lower than the phenotypic co-efficient of variation (26.93). The wide range of variation between genotypic and phenotypic variance for plant height indicated that the genotypes represented differently even when grown under the same environment.



Table 4.1 Analysis of variance (mean squares) for different characters of 15 genotypes of chili

Source of variation	df	Plant height (cm)	Days to 1st flowering	Primary branches per plant	Fruit length (cm)	Fruit circumference	Fruit weight (g)	Fruit no./plant	Fruit yield per plant (kg)
Replication	2	2.889	3.385	0.107	0.009	0.028	0.011	0.426	0.001
Genotypes	14	767.632**	137.434**	3.512**	6.905**	1.491**	3.469**	5412.338**	0.068**
Error	28	3.682	2.036	0.069	0.025	0.014	0.010	3.717	0.001

** = Significant at 1% level of probability

Table 4.2: Average performances of 15 genotypes of chili for 8 characters

Name of The Genotypes	Plant Height (cm)	Days to 1st Flowering	Primary Branches Per Plant	Fruit Length	Fruit circumference (cm)	Fruit weight (g)	Fruit no./plant	Fruit Yield Per Plant (g)
v-1	78.8	52.08	8.23	3.5	3	3.4	26	81.4
v-2	74	58	6	4.11	3.26	2.74	51.33	112.17
v-3	52.63	47.7	7	3.79	2.92	2.12	81.33	170.52
v-4	65.25	56.08	7	4.5	3.85	4.23	40	160.25
v-5	56.17	47.57	7	7.4	3.31	3.28	70.33	270.8
v-6	51.03	51.03	5	6.63	2.43	3.31	82.66	250.56
v-7	66.3	61.8	6	7.14	4.05	4.61	53	210.32
v-8	62	41.5	7	5.83	1.97	1.86	79	130.89
v-9	51.98	60	6	5.5	2.4	3.1	79	230.56
v-10	83.93	47.3	7	4.47	3	3.77	197.6	680.25
v-11	45.98	45.9	6	3.5	2	1.87	57.33	77.67
v-12	77.56	55.73	7	5.02	3.02	2.87	101	280
v-13	58.2	52.02	8	3.75	4.25	5	29.67	150.5
v-14	20.1	40.3	4.08	1.92	3.13	1.38	22.33	65.75
v-15	51.25	42.08	6	4.1	2.2	1.95	63	120.25

4.1.2 Days to first flowering

The analysis of variance for days to first flowering showed highly significant variation among the genotypes (Table 4.1). Sudre *et al.* (2005), Raikar *et al.* (2005), Majnu *et al.* (2004), Rahman *et al.* (2000) also reported significant differences among different genotypes of tomato for its traits. The maximum days 61.80 required for first flowering was recorded in kalo morich (V-7) followed by 60 in (V-9). On the other hand variety (V-14) required the minimum no of days to first flowering (40.30).

Phenotypic variance (47.17) was slightly higher than genotypic variance (45.13) and phenotypic co-efficient of variation (13.57) also slightly higher than genotypic co-efficient of variation (13.28). From the result it is revealed that environmental effect for this trait was low.

4.1.3 Number of primary branches per plant

The mean square due to know of primary branches per plant was found significant at 0.1% including highly significant variation among the genotypes selected for the study.(Table 4.1).The mean value for this traits ranged between 4.08 and 8.23. The highest no of primary branches per plant 8.23 was observed in bombae morich (V-1) followed by (V-13) capsicum morich. The least branch 4.08 genotype was (V-14) khudi morich. similar significant differences were reported for this trait by Raikar *et al.* (2005),Smitha *et al.* (2006), Rahman *et al.* (2000).

Phenotypic variance (1.22) was slightly higher than genotypic variance (1.15) and phenotypic co-efficient of variation (16.88) also slightly higher than genotypic co-efficient of variation (16.40). From the result it is revealed that environmental effect for this trait was low.

4.1.4 Fruit Length

Highly significant variation for the fruit length was observed among the genotypes (table 4.1). The genotypes (V-5) gave highest mean value of fruit length 7.40cm which was significantly superior to all other varieties (table 4.2). The lowest fruit length was observed in (V-14) 1.92 cm that was statistically different from all other lines or varieties (Table 4.2). The average mean value for fruit length ranged 1.92 cm to 7.40 cm (table 4.2). Padda *et al.* (1970) reported that the fruit length varied from 2.0 to 8.6 cm. Tinder (1968) noted that fruits were extremely variable in length and ranged from 1.3 to 25.4 cm long whereas fruit length was found by Standely (1931) from 0.8 to 25.0cm. Smith and Heiser (1951) observed that fruits were extremely variable sizes and 0.8 to 25.cm long. Senapoti *et al.* (2003) suggested that fruit length were the chief contributors toward genetic divergence.

Phenotypic variance (2.32) was slightly higher than genotypic variance (2.29). Phenotypic coefficient of variation (32.08) was also slightly higher than genotypic co-efficient of variation (31.91) indicating a moderate influence of environment of expression of this characters. Sreelanthakumary *et al.* (2004) recorded high genotypic and phenotypic coefficient of variation for fruit length. Khurara *et al.* (2003) and Rahman *et al.* (2000) observed a highly significant variation among the genotypes in terms of fruit length and recorded a high genetic co-efficient of variation for fruit length and had high values of heritability. Prabhakaran *et al.* (2004) recorded high genotypic co-efficient of variation for fruit length.

4.1.5 Fruit circumference

The analysis of variance for fruit circumference showed highly significant variation among the genotypes. The maximum fruit circumference 4.25 was recorded in (V-13) morich which was significantly different from all others genotypes. The smallest mean value for fruit circumference 1.97 cm was observed in (V-8) which is statistically identical with (V-11) 2.00 cm, (V-15) 2.2cm and (V-9) 2.4cm. Padda *et al.* (1970) reported that fruit breadth ranged from 0.6 to 1.5 cm. Smith and Heiser (1951) reported that fruit circumference generally over 0.8 cm wide.

The genotypic variance (0.492) was slightly lower than phenotypic variance (0.506) for fruit circumference in chili genotypes. Sreelanthakumary *et al.* (2004) recorded high genotypic and phenotypic coefficient of variation for fruit girth. Rahman *et al.* (2000) indicating superiority

in respect of fruit diameter potentially than that of others. Khurana *et al.* (2003) and Rahman *et al.* (2000) observed a highly significant variation among fruit diameter and recorded a high genetic co-efficient of variation and high values of heritability.

4.1.6 Individual Fruit Weight

The analysis of variance for this character showed highly significant differences among the genotypes (table.4.1) Majnu *et al* (2004) recorded that there were significant differences among the lines for fruit weight and had high genotypic coefficient of variation. The genotype (V-13) gave the highest mean value of individual fruit weight 5.0 which was significantly superior to all other varieties/lines (Table-4.2). The lowest mean value for individual fruit weight 1.38 was observed in (V-14) which is statistically different from all other varieties/lines (Table-4.2). Average fruit weight ranged from 5.0 to 1.38 reported that a wide range of variation was observed for individual fruit weight.

Phenotypic variance (1.16) and genotypic variance (1.15) were for this trait with little differences in genotypic co-efficient of variation (35.40) and phenotypic co-efficient of variation (35.56) indicating negligible environmental effect (Table 4.3). Karad *et al.* (2002), Senapoti *et al.*(2003), Sreelanthakumary *et al.*(2004), Sudre *et al.*(2005), Smitha *et al.* (2006), Abdullah *et al.* (2006) also recorded high genotypic co-efficient of variation for mean fruit weight.

4.1.7 Number of fruits per plant

Highly significant variation for the number of fruits/plant was observed among the genotypes (Table 4.1). Padda *et al* . (1970), Rahman *et al.* (2000), Karad *et al.* (2002), Senapoti *et al.*(2003) , Abdullah *et al.*(2006) reported that the number of fruits per plant showed highly significant differences among the cultivars and on an average ranged from 82.0 to 532.2. The genotype (V-10), produces highest number of fruits per plant 197.6 followed by (V-12). The genotype (V-14) bears lowest number of fruits per plant 22.33. Similarly the genotypes which also produces a lower no of fruits per plant were V-1 (26), V-4 (40). Number of fruits per

plant showed a wide range from 22.33 to 197.6 .Senapoti *et al.* (2003) suggested fruit number per plant were the chief contributors towards genetic divergence.

The environmental influence was considerable for these traits, which could not be realized from the difference between genotypic variance (1806.87) and phenotypic variance (1806.59). and also the difference between genotypic coefficient of variation (61.68) and phenotypic coefficient of variation (61.68) (Table 4.3). Sreelanthakumary *et al.* (2004) recorded high genetic coefficient of variation for number of fruits per plant, had high values of heritability.

4.1.8 Yield per plant

Highly significant differences were observed among the varieties for yield per plant.(Table 4.1) From the mean values it was found that the maximum yield per plant 0.680 gm was produced by genotype (V-).The range of yield per plant was from 0.680 kg to 0.066 kg. Padda *et al.* (1970) reported that the yield of fruit per plant was found to vary 113.7gm to 399.8 gm . Chua and Tech (1974) observed that the yield per plant of chili was 400.8 to 501.2 gm. Das et al.(2004) reported that the genotype 94-3 showed the highest fruit yield of 110.82 q/ha, with a fruit weight of 20.31 gm and fruit length of 5.90cm followed by pant-c1 and 85-2 whivh give high yield (106.82 and 102.43 q/ha) and oppositely genotype 95-1 performed the lowest yield of 31.66 q/ha.

The phenotypic variance (0.023) was slightly higher than genotypic variance (0.022) indicating negligible environmental influence on this traits (Table 4.3) and genotypic coefficient of variation (74.72) to that of phenotypic coefficient of variation (76.38) was considerable which indicated environmental influence on yield per plant.(Table 4.

Table 4.3: Estimation of genetic parameters of 15 genotypes of chili

Characters	Range	Mean±SE	Genotypic variance	Phenotypic variance	GCV (%)	PCV (%)	Heritability (%)	GA	GA (%)
Plant height (cm)	20.10 83.93	59.68 ± 4.13	254.65	258.33	26.74	26.93	98.57	32.64	54.69
Days to 1 st flowering	40.30 61.80	50.61±1.75	45.13	47.17	13.28	13.57	95.68	13.54	26.75
Primary branches per plant	4.08 8.23	6.53±0.279	1.15	1.22	16.40	16.88	94.33	2.14	32.80
Fruit length (cm)	1.92 7.40	4.74±0.391	2.29	2.32	31.91	32.08	98.92	3.10	65.38
Fruit circumference	1.97 4.25	2.99±0.182	0.492	0.506	23.50	23.83	97.24	1.43	47.73
Fruit weight (g)	1.38 5.00	3.03±0.278	1.15	1.16	35.40	35.56	99.14	2.20	72.62
Fruit no./plant	22.33 197.60	68.91±10.97	1802.87	1806.59	61.62	61.68	99.79	87.38	126.81
Fruit yield per plant (kg)	0.066 0.680	0.199±0.039	0.022	0.023	74.72	76.38	95.71	0.301	150.59

4.2 Heritability and genetic advance in percentages of mean

The estimation of heritability, genetic advance in percentage of mean are presented in Table 4.3

4.2.1 Plant height

Plant height exhibited heritability estimates (98.57%) along with value of genetic advance in percentage of mean (54.69) that indicated a high degree of genetic variability for these characters, so there is a good scope of isolating some good genotypes.

4.2.2 Days to first flowering

Days to first flowering exhibited high heritability (95.68%) in broad sense (h^2_b) coupled with moderate genetic advance in percentage of mean (26.75) (table) indicated possibility of additive gene action for expression of character. Therefore, selection would be effective for producing varieties with reduced day to first flowering from the genotypes under study.

4.2.3 No of primary branches per plant

The magnitude of heritability (94.33) in broad sense (h^2_b) for no of primary branches per plant was high with considerably moderate genetic advance in percentage of mean (32.80) which indicated high degree of genetic variability for this character i.e., there is a good scopes for isolating some superior genotypes.

4.2.4 Fruit length

Fruit length exhibited high heritability (98.92%) in broad sense (h^2_b) coupled with low genetic advance (3.10) in percentage of mean (65.38%) indicated the possibility of additive gene action for the expression of this character. Therefore, selection would be effective and there is a good scope of isolating some good genotypes on the basis of this trait.

4.2.5 Fruit circumference

The magnitude of heritability (97.24%) in broad sense for fruit circumference was high with considerably moderate genetic advance in percentage of mean (47.73 %) which indicated a high degree of genetic variability for this character i.e., there is good scope of isolating some superior genotypes.

4.2.6 Individual fruit weight

Individual fruit weight showed high heritability (99.14%) coupled with low genetic advance (72.62%) and moderate genetic advance in percentage of mean. The results of individual fruits weight through selection would be effective.

4.2.7 Number of fruits per plant:

The estimates of heritability and genetic advance in percentage of mean were (99.79%) and 112.08 (High) respectively indicating high degree of genetic variability for this character. Therefore, there is good scope of isolating some good genotypes on the basis of these traits.

4.2.8 Yield per plant

High heritability (95.71%) along with high genetic advance and high genetic advance in percentage of mean (150.59) were obtained for yield per plant. The scope of selection on the basis of this parameter would be good of its high heritability, high genetic advance in percentage of mean.



Table 4.4 : Genotypic (G) and phenotypic (P) correlation coefficients among eight yield contributing characters for 15 chili genotypes

Characters		Days to 1st flowering	Primary branches per plant	Fruit length (cm)	Fruit circumference (cm)	Fruit weight (g)	Fruit no./plant	Fruit yield per plant (g)
Plant height (cm)	G	0.474**	0.682**	0.271**	0.223 **	0.506**	0.441**	0.478**
	P	0.479**	0.686**	0.274**	0.227 **	0.508 **	0.442 **	0.481 **
Days to 1st flowering	G		0.162*	0.364**	0.490**	0.656***	-0.075	0.081
	P		0.171 **	0.369**	0.497 **	0.659*	-0.073	0.089
Primary branches per plant	G			0.041 ns	0.280	0.465**	0.097	0.152**
	P			0.045 ns	0.288 **	0.469**	0.099	0.159**
Fruit length (cm)	G				0.032 ns	0.377**	0.257 **	0.317**
	P				0.036 ns	0.379 **	0.258**	0.319**
Fruit circumference	G					0.754**	-0.262 ns	0.069
	P					0.756**	-0.260 ns	0.074
Fruit weight (g)	G						0.031 ns	0.344**
	P						0.032 ns	0.347 **
Fruit no./plant	G							0.918**
	P							0.917**

4.3 Correlation coefficient among eight yield contributing characters

Estimation of simple genotypic and phenotypic correlation co-efficient was made among yield and eight yield contributing characters of the 15 chili varieties in all possible one way paired combinations. Correlation co-efficient (Table 4.5). Genotypic correlation co-efficient were higher than phenotypic correlation coefficient in almost of cases were suggested that character association had not been largely influenced by environment in this cases.

4.3.1 Plant height

Interrelationships among the yield contributing characters showed that plant height had highly significant and positive correlated with days to first flowering (G-0.474,P-0.479),Primary branches per plant (G-0.682,P-0.686), fruit weight(G-0.506,P-0.508),fruits number per plant(G-0.441,P-0.442) and also frits yield per plant(G-0.478,0.481) while plant height showed no significant positive correlation with fruit length (G-0.271,P-0.274) and fruit circumference(G-0.223,P-0.227) .This result also indicated that taller plants enhanced more vegetative growth liked by more primary branches per plant and ultimately produced more fruits resulting increased yield.

4.3.2 days to first flowering

Days to first flowering exhibited highly significant and positive association, fruit length (G-0.364, P-0.369), and fruit circumference (G-0.490, P-0.497), while Fruits no per plant (G- -0.075, P- -0.073) showed considerable non significant negative correlation with days to first flowering. This result indicated that late flowering plants enhanced more vegetative growth and produced more branches per plant bearing large number of fruits resulting more yield.

4.3.3 Primary branches per plant

Correlation coefficient revealed that primary branches per plant were significant and positively correlative with fruit weight (G-0.465, P-0.469), But non significant positive co relation with fruit circumference (G-0.280, P-0.288), fruit yield per plant (G-0.152, P-0.169) was observed for this traits. The result indicated more primary branches per plant enhanced more vegetative growth and produced more fruit yield.

4.3.4 Fruit length

Highly significant and positive correlation was observed between fruit length with fruit weight (G-0.377, P-0.379) and fruit yield (G-0.317, P-0.319) while it showed no significant positive association with fruit no (G-0.257, P-0.258) and fruit circumference (G-0.032,P-0.036).So, fruit length promoted fruit weight resulting increased fruit yield.

4.3.5 Fruit circumference

Fruit circumference exhibited highly significant and positive association with fruit weight (G-0.754, P-0.756) ,but non significant positive correlation with fruit yield per plant (G-0.069, P-0.074).On the other hand, non-significant and negative correlation between fruit circumference and fruits number (G- -0.262,P- -0.260) were observed. The result indicated that fruits circumference promoted fruit weight and increased fruit yield.

4.3.6 Fruit weight

Interrelationship among the yield contributing traits showed that fruit weight had highly significant and positive correlation with fruits yield per plant (G-0.344, P-0.347) and non significant positive correlation with fruit no per plant (G-0.031, P-0.032). The correlation showed fruit weight increased fruit yield.

4.3.7 Number of fruits per plant

Number of fruits per plant showed a highly significant and positive correlation with fruit yield (G-0.918, P-0.917) .Similarly, significant and positive was observed between no of fruits per plant and plant height, fruit weight and primary branches per plant. All the correlation showed that fruits number highly increased fruit length.

4.4 Study of genetic divergence among the genotypes of chili

The genetic diversity of 15 genotypes of chili carried out based on 8 characters. Genetic divergence among the varieties/lines was assessed on multivariate scale by using Mahalonobis's D₂ statistics. Based on this variation D₂ estimates were predicted accurately.

The Mahalanobis's D₂ value Of 1485 combination were estimated as Rao's (1952) method Singh and Chaudhury (1985)

4.4.1 Nature and magnitude of genetic diversity

The genotypes were grouped into distinct clusters by using Mahalanobis's d₂ statistics. Based on D₂ value the genotypes were grouped into 4 distinct clusters. The genotypes belonging to the same clusters had smaller D₂ value than those belonging to different cluster. The principle component analysis (PCA) showed that the first component s accounted for more than 80% of total variation and a two dimensional scatter diagram was constructed using 1 as X axis and 2 as Y axis, reflecting the relative position of the genotypes. The 15 chili genotypes were apparently distributed into 4 groups according to the scattered diagram. The 15 genotypes were also constellated into 4 cluster comparing D₂ valued for all possible pairs of populations. The clustering pattern reflected by principal component analysis has been confirmed by D₂ analysis. Same trend was reported by masud *et al.*(1995). Among 4 clusters ,cluster 1 contained the highest no of 14 genotypes while group II had only 2 genotypes. The other two cluster viz. clusters III contained 6 and cluster IV contained 8 genotypes respectively. The average intra and inter cluster distances, D-values and D₂ values are presented in table. From table it could be revealed that the inter cluster distances, reflecting wider diversity among the genotypes of different groups. The results are agreed with Rahman *et al.* (1998). In respect of inter cluster distances, the maximum inter cluster distance was observed between genotypes of cluster I and II followed by clusters I and cluster IV and clusters II and III, suggesting wider diversity between them and the genotypes in these clusters could be used as parent in hybridization program for getting transgressive sergeants. Buu and Tuan (1989) also suggested that use of diverse genotypes in the hybridization program for getting transegressive sergeant in Rice.

On the other hand, the minimum inter cluster distance was found between the genotype of cluster III and IV followed by I and III, which showed low divergence. The intra cluster distance of cluster I, II, III, and IV were 15.15, 20.40 and 19.28 respectively. The mutual relationship among the 4 cluster was presented in fig. 4.2. The average intra and inter cluster distance was maximum in cluster 1 (76.42) and minimum in cluster II, indicating the genotype in cluster I were the most heterogenous and those in cluster II were comparatively homogenous.

Table 4.5 Distribution of 15 chili genotypes in different clusters

Cluster no	Variety no.	No of genotypes	Name of genotypes
I	V ₁ ,V ₄ ,V ₁₃	3	Bombae morich, Kmranga bombae moricha, Capcicum morich
II	V ₂ ,V ₅ ,V ₆ ,V ₇ , V ₉ , V ₁₂	6	Oporajita morich, kancha morich, Akashi morich, Kalo morich, Baromashi kancha morich, Joli lonka
III	V ₃ ,V ₈ ,V ₁₁ ,V ₁₄ , V ₁₅	5	Dhani morich, Roshni morich, Sada morich, khudi morich, Bindu morich
IV	V ₁₀	1	Lomba morich

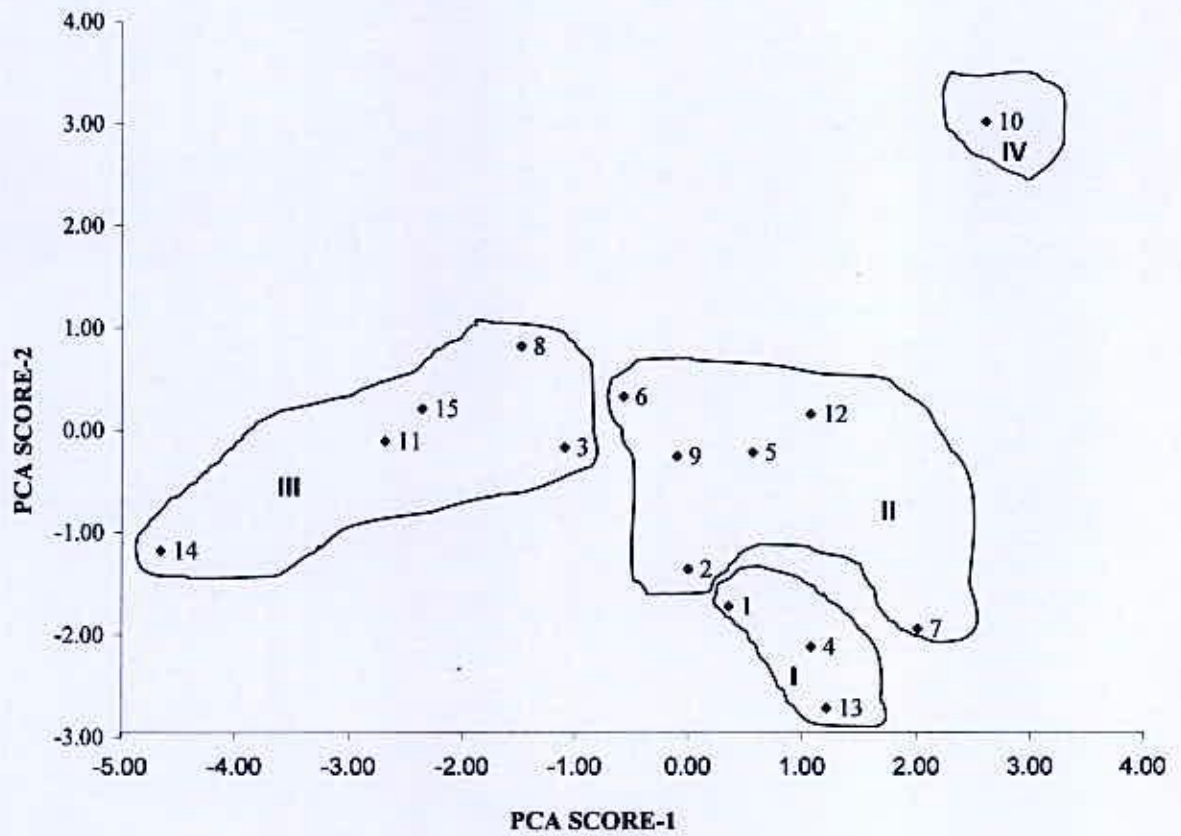


Fig.4.1: Distribution of 15 chili genotypes in two-dimensional scatter diagram based on PCA scores superimposed with clusters

Therefore, the genotypes of the widely divergent cluster I with high yield potential would likely to produce heterotic combination and wide variability in segregating generation.

Senapati *et al.* (2003) conducted an experiment in order to estimate genetic divergence in chili by using Mahalanobis's D^2 statistic was studied for 11 characters in a collection of 20 diverse chili genotypes and were grouped into 6 clusters. Karad *et al.* (2002) studied genetic divergence in chili (*Capsicum annum* L) using Mahalanobis's D^2 statistics among 40 genotypes and noted that the genotypes were grouped into 8 clusters. Sudre *et al.* (2005) evaluated genetic divergence and reported eight distinct groups between 56 chili and sweet pepper accessions by using multivariate technique. They used Mahalanobis's distance (D^2) as dissimilarity measures. Canonical variate analysis using Tocher's method and distances in the plane were applied to assess genetic diversity. They also reported that the magnitude of intra cluster distance was cooperatively lower than that of inter cluster-distances which supports the findings of the present study. Mishra *et al.* (2004) while evaluating 22 capsicum genotypes to assess the genetic diversity can group into 4 clusters by using Mahalanobis's D^2 statistics for 16 yield and yield contributing characters. Smitha *et al.* (2006) reported the presence of high degree of genetic divergence in 40 genotypes of chili (*Capsicum annum* L) consisting 8 characters.

Table 4.6: Average intra (bold) and inter-cluster distances for 15 chilli genotypes

Clusters	I	II	III	IV
I	15.15	30.63	32.01	76.42
II		20.40	19.68	53.68
III			19.28	53.07
IV				0.00

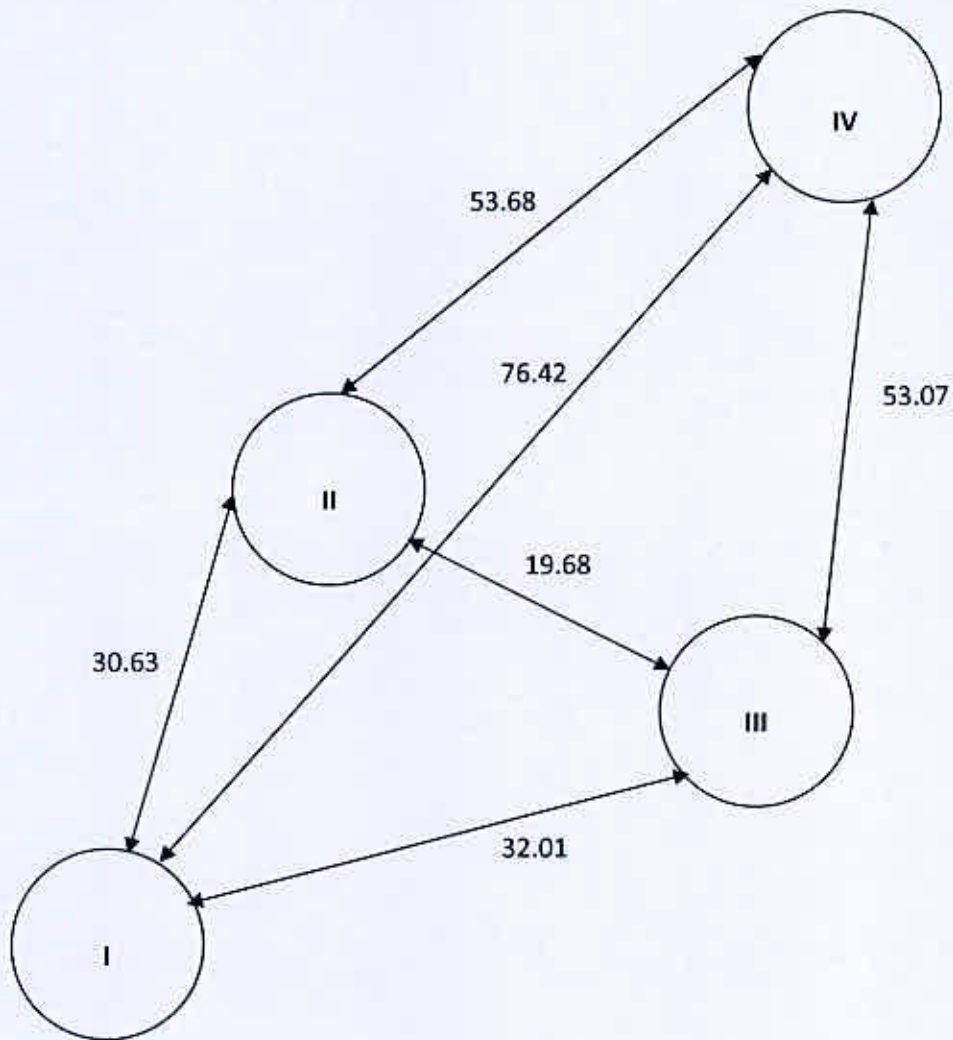


Fig. 4.2: Cluster diagram showing the average inter and intra-cluster distance (D-values) of 15 chilli genotypes. The values along the lines represents inter cluster distances and the values within the circle indicate intra cluster distances.

4.4.2 Relative contribution of individual character towards divergence

The present study was carried out on 8 characters viz plant height, days to first flowering, primary branches per plant, fruit length, fruit circumference, fruit weight, no of fruits per plant and fruit yield per plant were used to estimate genetic divergence. The number of fruit per plant contributed maximum (33.33%) to the total diversity. Fruit weight contributed (21.90%), Plant height (14.29%), days to first flowering (13.33%), Fruit length (8.57%), Fruit circumference (4.76%), Primary branches per plant (2.86%) and Yield per plant (0.95%) to the total diversity. So, on the basis of the priority in contribution the order of the characters were as the number of fruit per plant, Fruit weight, Plant height, days to first flowering, Fruit length, Fruit circumference, Primary branches per plant, and Yield per plant. Senapati *et al* (2003) suggested that four characters, namely fresh fruit weight, fruit girth, fruit length, and fruit no per plant were the chief contributors toward genetic divergence. Karad *et al* (2002) revealed that the variance of cluster means was fresh fruit weight and fruits per plant had the highest contribution towards diversity. Smitha *et al* (2006) recorded the maximum relative contribution to the total divergence was for NF (28.08%), FY (21.15%), PB (15.0%) and SB (10%), S(10.0%) confirming the existence of ample amount of divergence genotypes with respective to the traits and hence the selection of best genotypes for such traits would be helpful in utilizing the maximum heterosis in the future breeding programs. They also suggested that PH(0.51%),FD(0.38%), DAF(0.13%), DAF (0.13%), and AAC (0.38%) contributed lower, indicating that these traits will not help in yield improvement through hybridization until variability are created in these traits. Chowdury *et al.* (1994) reported that plant height, days to maturity and pods per plant had maximum contribution towards divergence in groundnut. Hossainand Alam(1989) and Bhagat *et al.*(1986) also reported same results.



Table 4.7: Relative contribution of eight individual characters (%) towards the total divergence

No. of characters	Characters	Percent contribution towards genetic divergence
01	Plant height (cm)	14.29
02	Days to 1st flowering	13.33
03	Primary branches per plant	2.86
04	Fruit length (cm)	8.57
05	Fruit circumference	4.76
06	Fruit weight (g)	21.90
07	Fruit no./plant	33.33
08	Fruit yield per plant (kg)	0.95

The relative contributions of different characters among 4 clusters towards divergence are demonstrated by co-efficient of variation (CV %) - values at inter cluster level (Sharma, 1998). In the present study, fruit yield per plant (CV=9.53%), Primary branches per plant (CV=4.02%), Fruit circumference (CV=3.99%), Fruit weight (CV= 3.37%), Fruit length (CV= 3.30%), Plant height (CV= 3.22%), Days to 1st flowering (CV= 2.82%) and Fruit no./plant(CV= 2.82%) are potential contributors to genetic divergence in the genotypes (Table 4.8). The highest intra-cluster mean was in cluster I for fruit yield.

4.4.3 Characterization of individual clusters

The cluster means of 8 characters for 30 genotypes of chili are given in table 4.8. There was a wide range of variation in the cluster mean values for all the characters. From the range and mean values of all cluster for the respective character were categorized into low (L), intermediate (I) and High (H) classes. To facilitate the characterization of each cluster in relation of these characters regards to plant height cluster IV and I showed high value. Cluster II showed intermediate value and cluster III showed low values. For days to first flowering cluster I and cluster II showed high values whereas cluster III and IV showed low values. With regard to primary branches per plant cluster IV and I showed high values whereas other showed intermediate values. For Fruit length cluster II showed high and rest showed intermediate values. With regards to fruit circumference, cluster I, II and IV showed high values and Cluster III showed intermediate values. For fruit weight cluster I and IV showed high values and rest of the clusters showed lower values. For no of fruits per plant cluster IV and II showed high values whereas rest of the cluster showed intermediate values. And for fruit yield per plant cluster IV and II showed high values whereas rest of the cluster showed intermediate values. Masud *et. al.* (1995) found a single genotype in cluster II having highest cluster mean for fruit weight, sex ratio, seeds per fruit, dry weight in pumpkin. Sumabae *et al.* (1987) reported significant variation among varieties for days to flowering, plant height and fruit length in chili.

Table 4.8: Cluster means with inter-cluster CV (%) for eight characters in 15 genotypes of chilli

Characters	No. of clusters				CV (%)
	I	II	III	IV	
Plant height (cm)	67.4167	62.84	46.392	83.93	3.22
Days to 1st flowering	53.39	55.68	43.49	47.30	2.82
Primary branches per plant	7.81	6.18	6.07	7.11	4.02
Fruit length (cm)	3.92	5.97	3.83	4.47	3.30
Fruit circumference	3.70	3.08	2.44	3.00	3.99
Fruit weight (g)	4.21	3.32	1.84	3.77	3.37
Fruit no./plant	31.89	72.89	60.60	197.60	2.80
Fruit yield per plant (kg)	0.130	0.226	0.113	0.680	9.53

4.4.5 Proposed to selection of genotypes for future hybridization program

Multivariate analysis is a useful tool to quantify the degree of divergence among biological populations at genotypic level and in assessing relative contribution of different components to the total divergence both at intra and inter cluster levels (Sudre *et al.*,2005;Majnu *et al.*,2004;Senapoti *et al.*,2003; Karad *et al.*, 2002;Jatasra and Paroda,1983);Sachan and Sharma,1971).Based on the study of genetic diversity) of chili, the genotypes having the different performance and located in the distant clusters could be utilized for hybridization program to develop desired high yielding varieties. Clusters by D2 statistics are useful in the matter. The genotypes grouped together are less divergent than the ones which into different clusters. Three important points are considered while selecting the genotypes-1) Choice of the particular cluster from which genotypes are to be used as parents; 2) Selection of particular genotype from the selected cluster and 3) Relative contribution of characters to total divergence (Singh and Chawdhury, 1985). Contribution of individual characters towards divergence was also observed in this study. In respect of cluster mean performance of different cluster revealed that cluster IV and cluster II can be selected for fruit yield, fruits no per plant, plant height, primary branches per plant and fruit length, cluster III are important for days to first flowering and cluster I are superior for fruit weight and fruit circumference in while lowest value of fruit yield, fruits no per plant etc. Finally findings of genetic parameters and cluster analysis revealed that the characters no of fruits per plant and fruit yield along with plant height, primary branches per plant and fruit length in cluster II found most important for genotypic coefficient of variance, heritability, genetic advance and maximum contribution toward genetic divergence in respect chili genotypes. Therefore, considering the magnitude of genetic distance and agronomic performance, the genotypes from cluster II along with cluster IV and cluster III should be prioritized in future breeding program for having higher fruit yield. The greater genetic distance among the genotypes due to these characters in such clusters would also offer prime score for the development of high yielding chili varieties.

SUMMARY AND CONCLUSION

CHAPTER 5

SUMMARY AND CONCLUSION

In order to evaluate the variability and genetic diversity of chili, the present experiment was carried out during the period of 1st November, 2013 to 15th April, 2014 at the experimental farm of Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka. It was involved with 15 varieties/lines of chili of different origin/source. The experiment was conducted to study the genetic divergence considering eight important yield and yield contributing characters, viz plant height, days to first flowering, number of primary branches per plant, fruit length, fruit circumference, number of fruits per plant, fruit weight, fruit yield per plant. The experiment was laid out in randomized Complete Block Design (RCBD) with 3 replications and seeds of the different genotypes were sown in separate seedbeds and thirty five days seedlings were transplanted in the main field. The result of the study is summarized as follows:

Analysis of variance revealed highly significant differences among the accessions for all the characters. Characters like plant height, days to first flowering, number of primary branches per plant, fruit length, fruit circumference, number of fruits per plant, fruit weight, and fruit yield per plant exhibited high genotypic and phenotypic co-efficient of variation. The phenotypic co-efficient of variation was higher than the Genotypic co-efficient of variation for all the characters. The phenotypic variance was higher than the corresponding genotypic variance for all the characters indicating greater influence of environment for the expression of these characters. The phenotypic co-efficient of variation was higher than the genotypic co-efficient of variation for all the characters. The maximum differences between phenotypic and genotypic co-efficient of variation were 74.72 and 76.38 respectively which indicated that fruit yield per plant was mostly dependent on the environmental condition. Amongst the characters, the highest genotypic co-efficient of variation was recorded for fruit yield per plant (74.72) followed by fruit no per plant (61.62), fruit wt. (35.40), and fruit circumference (23.50). The maximum genotypic and phenotypic variations were 1802.87 and 1806.59 respectively in fruit yield per plant.









The highest estimated heritability amongst eight characters of chili was 99.79% for number of fruits per plant and the lowest for 94.33% for primary branches per plant. The highest genetic advance amongst all the characters was found in fruit number per plant 87.38 and the lowest genetic advance was carried out in fruit yield per plant (0.301). The maximum genetic advance











in percent of mean was observed for fruit yield per plant (150.59), followed by fruit number per plant (126.81), fruit weight (72.62) and fruit length (65.38). Whereas the lowest was for days to first flowering (26.75) followed by primary branches per plant (32.80). The high heritability with low genetic advance in percent of mean indicated non-additive gene action for expression of the characters. Again, considering both genotypic and phenotypic correlation coefficient among 8 yield contributing characters of 15 chili genotypes, fruit yield was positively and significantly correlated with plant height, days to first flowering, no of primary branches per plant, fruit length, fruit weight and fruits number per plant.











To estimate genetic diversity, multivariate analysis was performed through principal component analysis, principal coordinate analysis, cluster analysis and canonical variate analysis. The first two principal component characters with average values were greater than unity contributed a total of 70% variation toward divergence. As per principal component analysis, (PCA), D^2 and cluster analysis, the genotypes were grouped into four different clusters. These clusters were found from a scatter diagram formed by Z-1 and Z-2 values obtained from PCA group-2 indicated highest no of 6 genotypes viz V-2, V-5, V-6, V-7, V-9 and V-12. On the other hand group 4 contained lowest no only 1 genotype that is V-10. Group 1 contained 3 genotypes viz V-1, V-4 and V-13. And group 3 contained 5 genotypes viz V-3, V-8, V-11, V-14 and V-15 respectively. The clustering pattern of the accessions under this study revealed that the genotypes collected from the same area were grouped into different clusters.

The clustering pattern of the accessions under study revealed that genotypes collected from the same area were grouped into different cluster. The maximum inter cluster divergence was observed between cluster I and IV (76.42) followed by the distances between cluster II and IV and cluster III and IV. It was found that the genotypes of the cluster -II had usually higher intra cluster distance than the genotypes of other groups. It is suggested that the genotypes selected from the more diversified cluster-II. And cluster III and I could be used as parents for future breeding programs. On the other hand, the minimum inter-cluster divergence was observed between cluster II and cluster III (19.68). The maximum intra-cluster distance was carried in cluster II (20.40) and this cluster had 6 accessions. While the minimum intra cluster distance was in cluster IV (0.00) and it had only 2 genotypes. Contribution of individual characters towards divergence was also observed in the study.

In respect of cluster mean performances of different cluster revealed that cluster-II can be selected for fruit yield, fruit no per plant, plant height, primary branches per plant and fruit length in while lowest value of fruit yield, fruits number per plant, plant height, primary branches per plant, fruit length and fruit weight in cluster-II indicated the maximum contribution of these characters toward divergence between cluster I and cluster II. Finally findings of genetic parameters and cluster analysis revealed that the characters number of fruits per plant and fruit yield along with plant height, primary branches per plant and fruit length in cluster-I found most important for genotypic co-efficient of variance, phenotypic co-efficient of variance, heritability, genetic advance and maximum contribution towards genetic divergence in the respective chili genotypes. Therefore considering the magnitude of genetic distance and agronomic performances, the genotypes from cluster-II along with cluster-III and cluster-IV should be prioritized in future breeding program for having higher fruit yield. It is suggested that selection of genotypes from these more diversified groups would give better segregation when they are crossed. The greater genetic distance among the genotypes due to these characters in cluster would also offer prime scope for the development of high yielding chili variety.

	<p>CLUSTER 3 V-8</p>	
	<p>CLUSTER 3 V-11</p>	
	<p>CLUSTER 3 V-14</p>	
	<p>CLUSTER 3 V-15</p>	
	<p>CLUSTER 4 V-10</p>	

	<p>CLUSTER 2 V-6</p>	
	<p>CLUSTER 2 V-7</p>	
	<p>CLUSTER 2 V-9</p>	
	<p>CLUSTER 2 V-12</p>	
	<p>CLUSTER 3 V-3</p>	

	<p>CLUSTER 1 V-1</p>	
	<p>CLUSTER 1 V-4</p>	
	<p>CLUSTER 1 V-13</p>	
	<p>CLUSTER 2 V-2</p>	
	<p>CLUSTER 2 V-5</p>	



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APPENDIX

Appendix I. Morphological, physical and chemical characteristics of Initial soil (0-15 cm depth) of the experimental site

A. Physical composition of the soil

Soil separates	%	Methods employed
Sand	36.90	Hydrometer method (Day, 1915)
Silt	26.40	Do
Clay	36.66	Do
Texture class	Clay loam	Do

B. Chemical composition of the soil

Sl. No.	Soil characteristics	Analytical data	Methods employed
1	Organic carbon (%)	0.82	Walkley and Black, 1947
2	Total N (kg/ha)	1790.00	Bremner and Mulvaney, 1965
3	Total S (ppm)	225.00	Bardsley and Lanester, 1965
4	Total P (ppm)	840.00	Olsen and Sommers, 1982
5	Available N (kg/ha)	54.00	Bremner, 1965
6	Available P (kg/ha)	69.00	Olsen and Dean, 1965
7	Exchangeable K (kg/ha)	89.50	Pratt, 1965
8	Available S (ppm)	16.00	Hunter, 1984
9	pH (1 : 2.5 soil to water)	5.55	Jackson, 1958
10	CEC	11.23	Chapman, 1965

Source: Soil Resource and Development Institute (SRDI), Dhaka

Appendix II. Monthly average Temperature, Relative Humidity and Total Rainfall of the experimental site during the period from October, 2013 to April, 2014

Month	Air temperature (°c)		Relative humidity (%)	Rainfall (mm) (total)	Sunshine (hr)
	Maximum	Minimum			
October, 2013	34.8	18.0	77	227	5.8
November, 2013	32.3	16.3	69	0	7.9
December, 2013	29.0	13.0	79	0	3.9
January, 2014	28.1	11.1	72	1	5.7
February, 2014	33.9	12.2	55	1	8.7
March, 2014	34.6	16.5	67	45	7.3
April, 2014	35.8	20.3	65	88	8.3

Source: Bangladesh Metrological Department (Climate division), Agargaon, Dhaka-1212.

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