MULTIVARIATE ANALYSIS OF CHILLI
(*Capsicum frutescens* L.)

G. M. RUNA LAILA

DEPARTMENT OF GENETICS AND PLANT BREEDING
SHER-E-BANGLA AGRICULTURAL UNIVERSITY
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MULTIVARIATE ANALYSIS OF CHILLI
(*Capsicum frutescens* L.)

BY

G. M. RUNA LAILA

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Approved by:

(Dr. Md. Abdur Rahim)
Associate Professor
Supervisor

(Dr. Mohammad Saiful Islam)
Professor
Co-supervisor

(Prof. Dr. Md. Sarowar Hossain)
Chairman
Examination Committee

Dr. Md. Abdur Rahim
Associate Professor
Department of Genetics Plant Breeding
Sher-e-Bangla Agricultural University
Sher-e -Bangla Nagar, Dhaka-1207
Email : rahimgepb@sau.edu.bd

CERTIFICATE

*This is to certify that the thesis entitled, “**MULTIVARIATE ANALYSIS OF CHILLI (Capsicum frutescens L.)**” 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 bona fide research work carried out by **G. M. Runa Laila**, Registration No. **09-03602** 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.

Dated: December, 2015
Place: Dhaka, Bangladesh

……………………………………………
(Dr. Md. Abdur Rahim)
Supervisor

LIST OF ABBREVIATED TERMS

Full word	**Abbreviation**
Agro-Ecological Zone	AEZ
Agriculture	*Agric.*
Agricultural	*Agril.*
Agronomy	*Agron.*
And others	*et al.*
Applied	*Appl.*
Bangladesh	BD
Bangladesh Bureau of Statistics	BSS
Bangabandhu Sheikh Mujibur Rahman Agricultural University	BSMARU
Bioavailability	*Bioavial.*
Biodiversity	*Biod.*
Biological	*Biol.*
Biotechnology	*Biotech.*
Breeding	*Breed.*
Centimeter	cm
Ecology	*Ecol.*
Environment	*Env.*
Environmental variance	σ^2_e
Etcetera	etc.
Food and Agricultural Organization	FAO
Genetic Advance	GA
Genetic Advance in Percentage of Mean	GAPM
Genetics	*Genet.*
Genotypic variance	σ^2_g
Genotypic coefficient of variation	GCV
Gram	gm
Horticulture	*Hort.*
Heritability in broad sense	h^2_b
International	*Int.*
Journal	*J.*
Kilogram	kg
Meter	m
Ministry of Agriculture	MOA
Murate of Potash	MP
Nitrozen	N
Negative Logarithm of Hydrogen Ion	P^H
Percent	%

(***Continued…***)

Full word	**Abbreviation**
Phosphorus	P
Phenotypic variance	σ^2_p
Phenotypic coefficient of variation	PCV
Potassium	K
Production	*Prod.*
Randomized Complete Block Design	RCBD
Research	*Res.*
Science	*Sci.*
Sher-e-Bangla Agricultural University	SAU
Square Meter	m^2
Sulfur	S
Sustainable	*Sustain.*
Technology	*Tech.*
Tropical	*Trop.*
United Kingdom	UK

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December, 2015
SAU, Dhaka *The Author*

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MULTIVARIATE ANALYSIS OF CHILLI
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BY

G. M. RUNA LAILA

Abstract

An investigation was carried out during kharif 2014-15 at experimental field of Sher-e-Bangla Agricultural University, Dhaka, with 13 genotypes of chilli (*Capsicum frutescens* L.) in a randomized block design with three replications. The study revealed significant differences among genotypes for different characters studied. The GCV for all the characters studied were lesser than the PCV indicating the masking effect of the environment. High heritability coupled with high genetic advance as percent of mean was observed for fruit length, fruit circumference, individual fruit weight and yield per plant indicating the predominance of additive gene action suggesting, direct phenotypic selection may be useful with respect to these traits. Correlation and path analysis revealed that number of primary brunches per plant, fruit length and individual fruit weight had positive significant association and positive direct effects on yield per plant indicating the use of these attributes in selection to evolve high yielding varieties of chilli. The results of multivariate analysis indicated the presence of considerable genetic divergence among the genotypes. Principal component analysis identified two principal components, which contributed 91.26% of cumulative variance. The 13 genotypes were grouped into 3 clusters. The highest inter-cluster distance was observed between cluster I and II (607.55), Therefore, considering the magnitude of genetic distance, contribution of character towards divergence, magnitude of cluster mean and agronomic performance the genotype G10 (GPB0010/14) from cluster I, G6 (GPB0006/14), G7 (GPB0007/14) and G12 (GPB0012/14) from cluster II should be used for the development of heterotic hybrids in future breeding programmes.

CHAPTER I

INTRODUCTION

Chilli (*Capsicum frutescens* L.) is one of the major spice crops in Bangladesh that belongs to the genus *Capsicum* and is a member of the Solanaceae family which also includes tomato, potato, tobacco and eggplant. It is a native crop of tropical areas of Central America and West Indies, but quickly spread throughout the world including the tropics, subtropics and also temperate region (Pickersgill, 1997). Chilli was introduced in this sub-continent by the Portuguese from Brazil in the middle of 17th century (Maradana, 2013). India, China, Ethiopia, Myanmar, Mexico, Vietnam, Peru, Pakistan, Ghana and Bangladesh are the top ten chilli producing countries in the world (Huq and Arshad, 2010).

The genus *Capsicum* has twenty-five wild species and only five of which are domesticated (Bosland and Votava, 2000). The domesticated species are *Capsicum frutescens*, *C. annuum*, *C. chinense*, *C. pubescens* and *C. baccatum*. There are differences among these species. Chillies are usually classified based on fruit characteristics including pungency, color, shape, flavor, size and use (Bosland, 1992). *C. frutescens* is a member of nightshade family and pungent in taste.

Chilli has high demand among the consumers due to its diversified use. It is used as spice, condiment, vegetable, culinary supplement, medicine and as ornamental plant (Berke and Shieh, 2001). It is rich in vitamin A, C and E also contains capsaicin (8-methyl-N-vanillyl-6-nonenamide), a lipophilic chemical that is responsible for pungent taste. It is also a good source of oleoresin which has varied uses in processed food and beverage industries and got high export potential, thus the second largest commodity after black pepper (*Piper nigrum* L.) in the international spice trade. Medically, extract from chilli is used to produce pain relief products (Berke and Shieh, 2001). It can also be used for cosmetic production. It is one of the most important ingredients used in culinary preparation in Bangladesh. Among spices and condiments, chilli is the central and most extensively grown spices crop in Bangladesh. Without chilli, daily diet chart is uncompleted.

Chilli is widely grown in all parts of Bangladesh in both summer and winter season. It is widely cultivated in Comilla, Noakhali, Faridpur, Barisal, Patuakhali and Bogra. But the average yield is very low compared to other important chilli producing countries of the world (FAO, 2007). Due to the low yield its annual production cannot meet the total requirement of the country. Despite continuous efforts by the researchers and other stake holders of the crop at various levels, the productivity of the crop has not gained momentum, considering its potential. The major constraints are unavailability of suitable cultivars, biotic and abiotic stresses, severe incidence of insect pests (thrips, mites and borers) and diseases (anthracnose, leaf spots and viral diseases). Further, the high variability present in the crop has so far not been fully exploited in the crop improvement programme. For the purpose of intensive cultivation and increased production of chilli, improved varieties or lines with desirable traits need to be identified.

To develop new high yielding cultivar, it is necessary to identify the best germplasm. Genetic variability analysis among existing germplasm and identification of best genotype by field experiment is the best method. It is very important to acquire adequate knowledge on variability, genetic divergence, character association and the extent of contribution of each character to fruit yield to plan appropriate breeding programme. To develop such breeding programmes, the breeders need to evaluate the available germplasm for variability and divergence and to understand the performance of genotypes in terms of yield and yield attributing characters. The best genotype could be used in hybridization program and the new variety which will be developed may show better yield than previous one.

Heritability is the portion of phenotypic variation that is transmitted from parent to progeny. It is possible to fixing the characters by selection methods if the heritable variation is higher. Therefore, heritability studies are of foremost important to judge whether the observed variation for a particular character is due to the influence of genotype or environment. Correlation and path coefficient analysis furnishes information regarding the nature and magnitude of various associations and help in the measurement of direct influence of one variable on other. Correlation coefficient analysis measures the mutual relationship between various plant characters and determines the component characters on which selection can be based for improvement in yield.

Long term sustainable yield and buffering capacity of a crop species depends on the infield, genetic divergence of the various cultivars. Genetic divergence is existing in the population that helps in the selection of suitable parents for utilization in any crop breeding program leading to reduction in the number of crosses (Guerra *et al.*, 1999). The information on the nature and degree of genetic divergence is essential for the breeder to choose genetically diverse parents for purposeful hybridization in heterosis breeding (Farhad *et al.*, 2010; Khodadabi *et al.*, 2011). In order to benefit transgressive segregation, the knowledge of genetic distance between parents is necessary (Khodadabi *et al*., 2011). Various statistical analyses are available to select suitable parents. Among them Mahalanobis's D^2-statistics based on multivariate analysis appears to be a good index.

A good number of landraces of chilli are present in Bangladesh. Systematic research was not made in the past to evaluate the potentialities of the available genotype. By considering this matter the present study was undertaken with following objectives:

1. To assess the genetic diversity among chilli materials,
2. To characterize and interrelationship among the genotypes on the basis of yield and yield contributing traits and
3. To screen genetically diverse parents for the utilization in future hybridization program.

CHAPTER II

REVIEW OF LITERATURE

Chilli (*Capsicum frutescens* L.) is an economically important spice crop in Bangladesh, but a very few works had been done for the betterment of this crop in Bangladesh as well as the other countries in the world. It is very important to understand the genetic architecture of the various quantitative and qualitative characters and interrelationship among them for breeding purpose. An attempt has been made to gather available relevant information in chilli to study genetic variability, heritability, genetic advance, character association, path coefficient analysis and genetic divergence and a brief review of available literature pertaining to the investigation is presented in this chapter.

2.1. Genetic variability, heritability and genetic advance

2.2. Path coefficient analysis

2.3. Genetic divergence

2.1. Genetic variability, heritability and genetic advance

The analysis of presence of genetic variability is a pre-requisite for initiating appropriate breeding programs. The possibility of improvement in any crop is proportional to the magnitude of its genetic variability present in the germplasm. It explained greater the variability in a population, greater the chance for effective selection for desirable characters (Vavilov, 1951). However, estimation of heritability accompanied with genetic advance is useful in prediction of the resultant effect for selecting the best genotypes (Johnson *et al.*, 1955). Therefore, a character having high heritability may have very less phenotypic variation thus leading to low genetic advances. But, in the presence of additive gene effects high genetic advances can be expected (Maradana, 2013).

Paul *et al.* (2013); carried out an experiment for collection of wild, semi-wild, and domesticated genotypes of Chilli from West Bengal, India. The collection was carried out from 2009 to 2012. They collected a total 88 accessions from 17 districts of West Bengal on the basis of their shape, size, color and pungency. They reported that the diversity could mainly be attributed to diverse agro climatic conditions in West Bengal. This diversity is a valuable source of research for further crop improvement through characterization and evaluation. They also established a Seed Gene bank to store natural orthodox seeds in low temperature and low humidity condition.

Twenty-five diverse chilli (*Capsicum annum* L.) genotypes were evaluated by Kadwey *et al.* (2016) in a field study to assess genetic variability, heritability and genetic advance. The highest phenotypic coefficient of variation (PCV) along with genotypic coefficient of variation (GCV) were recorded for number of fruits/plant, dry fruit yield/plant, seed yield/plant and fruit weight of dry chilli. Number of primary branches/plant at 30 DAT and fruit width showed high PCV that indicated effects of environment on these traits. The value of heritability was found to be very high for fruit yield/plant, seed yield/plant, dry fruit yield/plant, days to first picking, fruit length, fruit weight of green chilli, fruit yield/plot, fruit yield/ha and fruit width. The highest estimates of genetic advance as percentage of mean was recorded for number of fruits/plant, fruit weight of dry chilli, fruit width, dry fruit yield/plant, seeds yield/plant, fruit weight of green chilli, fruit yield/plant and fruit length, imply the potential for crop improvement in chilli through selection.

A field experiment was conducted by Aklilu *et al*. (2016) to evaluated plant morphology and yield contributing characters of 49 capsicum (*Capsicum annum* L.) genotypes. They found higher phenotypic coefficient of variation (PCV) than genotypic coefficient of variation (GCV) for most characters except pericarp thickness and leaf area index. Higher value of GCV was observed in leaf area index followed by pericarp thickness, number of branches, internode length and plant height. They also recorded close estimation of GCV and PCV for fruit and internode length, pericarp thickness and fruiting period. Very high PCV and very low GCV were obtained from fruit weight and no. of fruits, fruit yield, plant height and canopy width. They also found higher broad sense heritability for fruiting date, fruit length, plant height, internode length and fruit diameter. However, they recorded high to moderate genetic advance as percent of the mean (GAM) for length and no. of internodes, no. of branches, fruit diameter and weight, pericarp thickness and leaf area index.

Twenty-six inbred lines and three local accessions from North-West Spain were evaluated for their performance and genetic diversity by Rivera *et al.* (2016) on the basis of twenty-seven morphological traits and twenty microsatellite markers. They found phenotypic variability for all the studied traits among accessions, which were influenced by the location, except for the yield. They divided the landraces in well-defined groups using principal component analysis, with some degree of overlapping in some genotypes. Fruit weight, pericarp thickness and fruit shape and color featured the greater part of the variance. They observed a high level of genetic diversity within the accessions through molecular analyses and the presence of specific alleles, which were not previously detected in other Spanish pepper landraces. Multivariate and Bayesian clustering showed that landraces were primarily grouped according to their geographical origin and secondarily in agreement with the characteristics of their fruits. Finally, they identified six groups of landraces, with a great genetic variation.

Janaki *et al.* (2015); conducted an experiment with sixty three accessions of chilli (*Capsicum annum* L.) to evaluate the genetic variability, heritability and genetic advance for 10 quantitative traits. They reported significant differences among the accessions for all the traits studied. The PCV was higher than GCV and the difference between PCV and GCV was narrow for most of the characters revealing little influence of the environment in the expression of these traits. Higher value of PCV and GCV were observed for percent fruit set, number of fruits/plant, fruit diameter, average dry fruit weight, number of seed/fruit and yield/plant that indicated the existence of wide range of genetic variability in the germplasm for these traits. High heritability coupled with high genetic advance as percent of mean was observed for all the characters except days to 50% flowering indicating the predominance of additive gene action making the simple selection more effective.

Patel *et al.* (2015); carried out an experiment to study genetic variability, correlation and path coefficient analysis in 40 diverse genotypes of chilli. The analysis of variance revealed the significant differences among the genotypes for all the characters studied which indicating that presence of great deal of genetic variability for different traits. The high estimates of GCV and PCV were obtained for all of the traits except moisture content (%). They observed high genetic advance coupled with high heritability for the traits like days to flowering (days), plant height (cm), no. of primary branches/plant, no. of secondary branches/plant, no. of fruits/plant, average fruit length (cm), average fruit girth (cm), fruit-shape index, average fruit weight (g), green fruit yield/plant (g), chlorophyll content (mg/100g), ascorbic acid content (mg/100g) and capsaicin content (mg/g), indicating better scope for improvement of these traits by an effective selection programme.

Seventeen hot pepper genotypes were observed under greenhouse and field conditions by Rexford (2015) to evaluate variability on the basis of agro-morphological and fruit quality traits. He estimated genetic variance with high broad sense heritability in most of the traits under both environmental conditions. Genetic advance by percentage mean was high under both environments for all agro-morphological traits except antioxidant properties under field conditions. He found higher PCV than GCV in all the traits under both environments. Highly significant difference among most traits was observed for genotype, environment and genotype x environment interaction through combined analysis. He also reported that days to 50% fruiting and flowering had significant and positive associated with most of the traits.

An investigation was carried out by Yatung *et al.* (2015) with 30 accessions of chilli at Arunachal Pradesh, India during summer, 2011 to evaluate variability, correlation and path coefficient. They revealed significant differences among the accessions for all traits through analysis of variance. They observed high PCV and GCV, heritability, genetic advance for days to first flowering, plant height, no. of seeds/fruit, no. of fruits/plant, ascorbic acid content and fruit yield/plant.

Pandit and Adhikary (2014); studied variability and heritability among forty-one chilli strains in Bidhan Chandra Krishi Viswavidyalaya, India. They reported that GCV and PCV were closely related with all traits such as days to 50% flowering, fruit length, placenta length and 1000 seed weight except fruit width. They found the highest genetic advance as % of mean in fruit yield/plant and most of the traits showed moderately high genetic advance as % of mean. Finally, they made a decision that these traits were most likely governed by additive gene action thus would be used in further crop improvement.

Eight collecting trips were made to Northwestern Argentina by Occhiuto *et al.* (2014) to recover all the local landraces. They recovered five hundred new vegetable among which 32 belong to Capsicum which were further evaluated in field conditions. They observed 54 morphological and agronomical traits to conduct Multivariate analysis. They divided the accessions into three groups, where fruit characters were the most efficient for accession differentiation. They found high variability for fruit pungency and color. They also selected promising accessions for ex situ conservation and breeding programme.

Usman *et al.* (2014); conducted two experiments to study the genetic variability among chilli for heat tolerance and morph-physiological traits and to estimate heritability and genetic advance. They observed high significant variation among the accessions in response to high temperature (CMT), photosynthesis rate, plant height, disease incidence, fruit length, fruit weight, no. of fruits, and yield/plant. All the traits except plant height and disease incidence showed high genetic advance as percent of the mean (>20%) at 5% selection intensity. However they also observed high heritability (>60%) that indicated the substantial effect of additive gene more than the environmental effect. They reported strong to moderate positive correlations at phenotypic level with yield/plant while at genotypic level correlation coefficient ranged from 0.16 to 0.72 for the traits CMT, plant height, fruit length and no. of fruits.

Nsabiyera *et al.* (2013); conducted an experiment under screen-house conditions on 37 local and introduced genotypes of hot pepper (*Capsicum annum*) based on 20 quantitative and 28 qualitative traits. They found that exotic genotypes were superior compared to local genotypes. Local genotypes were identified by small fruits, late maturity and taller plants with wider canopies whereas introduced genotypes showed alternate characters. They observed highly significant differences for most of the traits except primary branches/plants and higher diversity for stem pubescence, leaf pubescence, anther color, calyx margin, fruit surface, and immature fruit color. They also accounted for the first and second principal components (PCs) for quantitative traits as 41.6% and 13.8% of the total variability, respectively where PC1 contained the characters fruit length, fruit weight and fruit wall thickness and PC2 contributed to days to flowering, fruiting, fruit maturity; stem diameter and height; plant height and width.

Ullah *et al.* (2011); carried out an experiment in twelve open pollinated chilli (*Capsicum frutescens* L.) genotypes at the Research and Development center (R&D) of Energypac Agro Ltd., Monipur, Gazipur, Bangladesh in 2009. They found significant variation among all the observed traits. The high GCV was found in some characters like fruit yield/plant followed by fruits/plant, average fruit weight and fruit length. All the traits except fruit diameter showed high heritability. They observed higher genetic advance in % of mean for the characters fruit yield/plant, fruits/plant, plant height and days to 50% flowering that explained involvement of additive gene to express these traits. However the major yield contributing characters were fruits/plant, fruit length and fruit diameter because these traits were significantly and positively associated with yield/plant.

Kumari *et al.* (2010); conducted an experiment on ninety four chilli (*Capsicum annum* L.) accessions to evaluate variability, heritability, genetic advance and genetic divergence on the basis of seventeen qualitative traits in Andhra Pradesh. They observed higher phenotypic and genotypic coefficient of variation (PCV and GCV) and heritability coupled with high genetic advance for number of fruits/plant, fresh and dry fruit yield/plant, 100 seeds weight, number of seeds/fruit and capsanthin, capsaicin and oleoresin contents. These indicated the higher magnitude of variability for these traits thus revealed more scope for their improvement through selection. However some traits like plant height, plant spread and fruit diameter exhibited moderate PCV and GCV estimates suggesting the possible role of environment in expression of these characters.

In order to estimate the nature and magnitude of variability among twenty Capsicum accessions Yadeta *et al.* (2011); conducted an experiment at Bako Agricultural Research Center, Ethiopia. All the traits studied showed significant genotypic variability among the tested materials. They noticed that the phenotypic coefficient of variation (PCV) was higher than that of genotypic coefficient of variation (GCV). The unmarketable fruit yield showed the highest PCV and GCV followed by single fruit weight. They observed highest broad sense heritability for pungency index and lowest for stem diameter.

Genetic variability as well as character association for 12 growth and fruit characters in 49 accessions of chilli was evaluated by Sarkar *et al.* (2009). They found significant variation among the genotypes. Fruit yield/plant, no. of fruits/plant, fruit length, placenta length, fruit weight, no. of seeds/fruit and plant height showed high values of GCV and PCV. High heritability in broad sense coupled with high genetic advance in % grand mean was recorded for fruit yield/plant, no. of fruits/plant, fruit length, days to 50% flowering and plant height indicating such characters were controlled by additive gene action. The phenotypic path-coefficient analysis revealed that no. of fruits/plant, fruit weight and 1000 seed weight had positive and high direct effect on fruit yield indicating their reliability as selection criteria to improve yield of chilli.

An experiment was designed by Sood *et al.* (2009); to assess genetic variation for marketable fruit yield and quality traits as fruits/plant, fruit weight, pericarp thickness, no. of lobes/fruit, TSS, ascorbic acid and capsaicin contents and to quantify the relationship among these traits in bell pepper (*Capsicum annum* L. var. *grossum*) germplasm. They observed significant difference among bell pepper genotypes. They found higher values of phenotypic coefficient of variation (PCV) than genotypic coefficient of variation (GCV) for all traits, indicating close association between phenotype and genotype. High heritability with high genetic advance was recorded for fruits per plant, marketable fruits/plant, pericarp thickness, and lobes/fruit, indicating the role of additive gene action for their inheritance. Besides high heritability with low genetic advance was estimated for days to 50% flowering, harvest duration, and ascorbic acid, indicating non-additive gene activity.

Fourteen quantitative traits of *Capsicum sp.* were analyzed by Farhad *et al.* (2008). They found significant variation among the genotypes for all the traits. The levels of phenotypic coefficient of variations (PCV) were higher than genotypic coefficients of variations (GCV) particularly for no. of secondary branches per plant, no. of primary branches per plant and yield of single plant. They also observed higher heritability for all the traits studied except days to 50% flowering and pedicel length.

Singh *et al.* (2009); reported that the potential for improvement in crops is proportional to the magnitude of genetic variability present in the germplasm. They conducted an experiment on thirty genotypes of chilli pepper (*Capsicum annum* L.) to evaluate the extent of genetic variability, determine the association between different characters, understand effects of component traits on fresh and dry yield, and identify desirable genotypes in Palampur, India. Sufficient variability was observed for all traits studied. On the basis of mean performance, the genotype Palam Yellow was found superior for marketable fresh yield; on the basis of dry yield, the genotype Surajmukhi was found to be promising. High PCV and GCV were observed for marketable fresh and dry yield per plant, numbers of marketable fruit, average fresh and dry fruit weight, fruit length and diameter, seed weight per fruit, number of primary structural branches per plant, and oleoresin and capsaicin content. Moderate PCV and GCV were recorded for numbers of secondary branches per plant, plant height, harvest duration, number of seeds per fruit, 100-seed weight, ascorbic acid and capsanthin. High heritability coupled with high genetic advance was noted for marketable fresh and dry yield per plant, average fruit weight, numbers of marketable fruit, fruit diameter, and oleoresin and capsaicin content, which indicated the role of additive gene action for the inheritance of these traits. These traits are likely to respond better to selection.

A field experiment was carried out by Meena *et al.* (2016); to find out the genetic variability, heritability and genetic advance in chilli (*Capsicum annum* L.) in Uttar Pradesh. They found the genotypes Azad mirch-1, Sel-16 and 7919 performed better in terms of leaf area had maximum value, succeeded by fruit yield per plant red ripe, fruit width, no. of branches/plant, days to 50% flowering, days to first harvest, pedicel length, fruit yield/plant, fruit length and plant height.

Stommel and Griesbach (2008); conducted an experiment using F_1, F_2, and backcross generations of Capsicum to observe inheritance patterns and relationships between foliar characters and traits related to fruit and plant habit. They reported that pepper fruit color, shape, and fruit/cluster were simply inherited with modifying gene action whereas leaf color, length, and plant height were quantitatively inherited. Broad-sense heritability was high for all the traits whereas almost all characters showed moderate to low narrow-sense heritability with the exception of leaf characters. High to moderate narrow-sense heritability for leaf characters and plant height denoted additive gene action for these traits. They also obtained new information on the genetic control of leaf characters and plant habit through the results of the analysis of segregating populations.

Chattopadhyay *et al.* (2011); noticed maximum diversity among the chilli landraces available in India with respect to shape, size, yield, quality, and other traits. They carried out an experiment on 34 landraces of chilli to identify the most promising varieties suited for green and dry fruit yield, to study the genetic variability for different traits and to assess the association of different yield attributing traits with the green and dry yield of chilli. They identified two genotypes, 'Chaitali Pointed' and 'BC CH Sel-4' as most promising with respect to green fruit yield and dry fruit yield. PCV and GCV values for green fruit weight, green fruit girth, weight of red ripe fruit, weight of dry fruit and number of fruits per plant were recorded to be high. Green fruit yield/plant, ascorbic acid content, and no. of fruits/plant also showed very high broad-sense heritability and genetic advance.

Sharma *et al.* (2010); investigated on twenty-three landraces of bell pepper (*Capsicum annum* L.) to evaluate genetic variability including mean, genotypic and phenotypic variances, coefficient of variation, heritability, and genetic advance. They observed significant differences among the genotypes for all the traits. They found some genotypes viz. PRC-1, SSP, Kandaghat Sel. and Ranichauri Sel-1 were outperformed for fruit yield/plant, average fruit weight, no. of fruits/plant and minimum days to 50% flowering on the basis of mean performance. The PCV and GCV were high for fruit yield/plant and ascorbic acid content. They reported high heritability along with high genetic advance for average fruit weight, fruit yield/plant, fruit diameter, no. of lobes/fruit, days to first harvest, leaf area and ascorbic acid content.

Fourteen quantitative and two qualitative traits of ripe fruits in sixty-nine *Capsicum* accessions were observed by do Rêgo *et al.* (2011). An analysis of variance was carried out using quantitative fruits data and the means were grouped by Scott-Knott test (p<0.01). They reported that all characteristics had significant effect of treatments (p<0.01) for all evaluated traits. The data showed high genetic variability for future use in a Capsicum breeding program. They found that the accessions 33, 44 and 41 showed major values for dry matter content and total soluble solids. However, the accession 48 showed major values for fresh weight, major fruit length and fruit width. Besides the accession 33, belonging to the *Capsicum frutescens* species, with high vitamin C content.

An experiment was conducted by Jabeen *et al.* (2009); in 2007-08 using twenty-five chilli genotypes. They found the genotypic coefficients were higher than the phenotypic coefficients that explained high heritability of the studied traits. They also found a highly significant correlation of fruits yield per plant with number of fruits per plant, number of branches per plant and plant height.

Adetula and Olakojo (2006); planned an experiment to observe the agronomic and genetic potential of 33 chilli accessions for breeding programmes in 1999 and 2000. They observed that growth habit of chilli plant as well as fruit characteristics (fruit length, width and weight) were highly significant (p<0.01).

Sreelathakumary and Rajamony (2004); reported higher GCV and PCV for leaf area, fruits/plant, fruit weight, fruit length, fruit girth and yield/plant while studying over thirty-five chilli (*Capsicum annum* L.) genotypes . They also observed high heritability with high genetic advance.

Choudhary and Samadia (2004); evaluated seventeen quantitative traits in thirty chilli genotypes to observe genetic variability, heritability, genetic advance as per cent of mean and correlation coefficients. The level of PCV and GCV were very high for yield/ plant, seed-weight/fruit, fruit weight and no. of fruits/plant. These traits were also highly heritable and genetically advanced.

Thirty-two genotypes of hot chilli (*Capsicum chinense Jacq*.) were evaluated by Manju and Sreelathakumary (2002); to estimate the variability, heritability and genetic advance in randomized block design with three replications. They observed higher phenotypic and genotypic coefficients of variation for fruits plant^{-1}, yield plant^{-1}, seeds fruit^{-1} and fruit weight. High estimates of heritability coupled with high genetic advance were also observed for these characters, indicating that they can be effectively improved through selection.

Quresh *et al.* (2015); carried over an experiment to evaluate ten accessions of *Capsicum annum* in the basis of thirty-five qualitative and eleven quantitative parameters in Islamabad. They observed wide variation among the genotypes for important characters pertaining to fruit and seed yield. Such genetic variability can be a valuable resource for genetic improvement including developing resistance against insect pests and diseases. They suggested more experiment to be undertaken on available accessions for further detail under Pakistani agro-climatic conditions to ascertain the statistical significance of variability, understand the genetic control and gene interactions involved.

Bozokalfa *et al.* (2009); carried out a research to assess phenotypic diversity on the basis of sixty-seven quantitative and qualitative agro-morphological traits in pepper (*Capsicum annum* L.) accessions from different areas of Turkey. They evaluated principal components analysis followed by hierarchical agglomerative clustering. They grouped the accessions into 7 clusters based on morphological and agronomic properties. The first six principal components axes accounted for 54.29% of the variance among the 48 accessions. The traits like fruit diameter, fruit weight, volume, fruit wall thickness, fruit productivity, and fruit soluble solid & dry matter content showed maximum part of the variance.

2.2. Correlation and path analysis

The correlation coefficient analysis explains the mutual relationship between various traits and it also indicates the component traits on which selection can be made upon to improve the yield (Johnson *et al*., 1955). The path analysis is a standardized partial regression coefficient as it indicates the direct influence of one variable upon other and separates direct and indirect effects of various characters, which is not possible through correlation coefficient. In 1921 Wright developed the concept of path analysis, but the technique was first applied for plant selection by Dewey and Lu (1959). Basically the technique aims to improve a dependent character such as yield while the independent characters have a significant relation in desirable direction. The use of this technique requires cause and effect situation among the variables (Singh and Choudhary, 1979). Some research works were carried out to evaluate correlation coefficient and path coefficient in chilli which were reviewed.

Usman *et al.* (2016); conducted an experiment to measure genotypic and phenotypic correlations coefficient among twenty six genotypes of chilli. They found that individual plant yield showed positive and highly significant correlations with almost all traits. On the other hand days to flowering showed a significant negative association with yield. They also found that fruit weight and number of fruits per plant had a positive direct effect but fruit length showed a low negative direct effect on yield. Both of the traits showed a positive and significant correlation with yield per plant.

Yield and important yield contributing traits were studied by Rokib *et al.* (2016); at the experimental field of Regional Spices Research Centre, BARI, Gazipur with thirty chilli (*Capsicum annum* L.) accessions to evaluate genetic association and selection indices. They reported significant and positive correlation of yield/plant with fruit length, fruit weight, 100 seeds weight and fruits/plant. They observed that fruits/plant had highest positive direct effect followed by fruits/plant; fruit weight, fruit length and number of primary branches/plant on yield in path coefficient analysis. They suggested selecting high yielding chilli genotypes on the basis of higher fruit weight, fruits/plant and yield/plant for breeding purpose.

Plant morphology and yield contributing characters were evaluated and analyzed by Aklilu *et al.* (2016); in forty-nine capsicum (*Capsicum annum* L.) genotypes. They observed that, fruit yield/plant showed high positive significant genotypic correlation value with pericarp thickness and number of fruits/plant whereas significant negative correlation were observed with days to flowering and 50% fruiting period. The phenotypic correlation coefficient of most characters with yield was not significant except for flowering period, fruit length and number of fruits/plant. The path coefficient analysis revealed that pericarp thickness, fruit diameter, number of fruits per plant, number of branches and flowering period had the highest direct positive effect on yield. On the other hand, fruit weight, number of internodes, leaf area index and plant height had a high negative direct effect on yield.

Six parents and their thirty hybrids of chilli were observed by Rohini and Lakshmanan (2015); to evaluate correlation and cause effect analysis for fruit yield and its contributing traits. All the traits studied showed significant variation among tested materials. They observed significant and positive association of yield with no. of fruits/plant, fruit length, individual fruit weight, fruit girth, plant height and seeds/fruit. The result of path analysis revealed highest contribution of fresh fruits yield/plant to dry pod yield which was followed by individual dry pod weight, no. of fruits/plant, no. of harvest, days to 50% flowering, pedicle length and no. of branches/plant through higher direct effect. They reported that a chilli hybrid should have higher no. of fruits/plant, coupled with large fruit length, high fruit girth and high average fruit weight to increase fruit yield/plant.

Patel *et al.* (2015); reported that, genotypic correlation coefficients were higher in magnitude than their corresponding phenotypic correlation coefficients for all the traits in chilli. They observed high, significant and positive association of green fruit yield/plant with no. of fruits/plant, average fruit weight, moisture content and chlorophyll content at both genotypic and phenotypic levels which indicating that these traits were main yield attributing traits. Path analysis indicated that characters like no. of secondary branches/plant, number of fruits/plant and average fruit weight had high and positive direct effects on green fruit yield.

Correlation and path analysis were studied by Yatung *et al.* (2015); in thirty diverse genotypes of chilli at Arunachal Pradesh, India during kharif, 2011. They reported positive and significant correlation on fruit yield/plant with no. of branch/plant, no. of fruit/plant and chlorophyll content. However they found negative and significant association on fruit yield/plant with ascorbic acid content. Path coefficient analyses revealed that maximum positive direct effect on fruit yield/plant was imposed by fruit weight, number of fruit per plant, number of seed per fruit and capsaicin content.

Fifteen qualitative and quantitative traits of sixteen accessions of chilli (*Capsicum annum* L) were observed by Bijalwan and Mishra (2016). They reported that fruit yield per plant was positively and significantly correlated with fruit weight at edible maturity, no. of fruits/plant, fruit length, no. of branches/plant and ascorbic acid content whereas negative and significant association was found with days to 50% flowering. Path coefficient analysis indicated that the highest positive direct effect on fruit yield/plant was observed by fruit weight at edible maturity followed by number of fruits per plant and fruit length. On the other hand, highest negative direct effect on fruit yield/plant was exerted by no. of branches per plant and pedicel length.

A wide range of variability was observed by Joshi *et al.* (2013); in capsicum (*Capsicum annum* L.). for different traits like plant height, number of fruits/plant, fruit weight, fruit yield/plant, number of seeds/fruit, speed of germination, standard germination, seedling length and vigor index-II. The plant height showed significant positive correlation with pedicle length (0.467) at genotypic level, while its relation with fruit weight was significantly positive both at genotypic and phenotypic levels (0.661 and 0.503 respectively). They noticed that the genotype PRC-1001 showed good performance in mid hill conditions for the different seed quality and field parameters.

Maga *et al.* (2013); conducted two field evaluations to study the pattern of genetic variability and character association in yellow pepper (*Capsicum annum* L.) in Nigeria during 2009 and 2010. They sorted 49 promising genotypes from all the genotypes that were evaluated in 2009 season in progeny rows and studied in 2010. They reported a considerable variability in the genotypes through the descriptive analysis. In 2009, the correlation analysis revealed that number of fruits/plant had significant correlation while other traits showed positive but non-significant correlation with fruit yield. In 2010, correlation analysis showed that no. of leaves/plant, fruit girth, single fruit weight and no. of fruits/plant were highly correlated with fruit yield, while plant height and fruit girth had positive but non-significant correlation with fruit yield. The path coefficient analyses revealed that the no. of fruits/plant for exerting the highest direct effects on fruit yield, followed by single fruit weight in both years. Thus they reported that the no. of fruits/plant and fruit weight could be the most important traits that improved yield through selection.

A correlation analysis was carried out with four sets of crosses and their parents of paprika by Srividhya and Ponnuswamy (2012). They reported positive association of all the traits except percent disease index with dry fruit yield/plant that indicated least incidence of anthracnose would result in more dry fruit yield/plant. They reported a strong negative association of total phenol content with disease incidence in the crosses that suggested total phenol played a significant role in reducing disease incidence. However ascorbic acid, total extractable color content and oleoresin were positively associated with total phenol content.

Ullah *et al.* (2011); observed highest contribution of fruits/plant to yield/plant in path analysis. They also found a higher direct effect of average fruit weight, days to first flowering and fruit length on yield/plant.

An investigation was carried out by Kumari *et al.* (2011); to evaluate correlation and path coefficient in ninety four genotypes of paprika (*Capsicum annum*) at Lam (Andhra Pradesh). They reported significant and positive association of dry fruit yield/plant with plant height, plant spread, no. of fruits/plant, fruit girth, seeds/fruit and capsanthin content. Path coefficient studies indicated that number of fruits/plant had the highest positive direct effect on dry fruit yield/plant followed by no. of fruits/plant,

plant height, plant spread, no. of seeds/fruit, days to maturity and capsanthin content respectively.

Chattopadhyay *et al.* (2011); carried out correlation and path coefficient analyses while conducting an experiment on 34 genotypes of chilli. They found the no. of fruits/plant, green fruit length for green chilli and weight of dry fruit as the most important selection indices.

Sharma *et al.* (2010); reported the traits fruit length, fruit diameter and number of fruits/plant revealed significant positive correlation with fruit yield per plant while conducting an experiment on 23 landraces of bell pepper (*Capsicum annum* L.). They also observed that no. of fruits/plant exhibited the highest positive direct effect followed by average fruit weight, number of branches per plant, pedicel length and harvest duration at genotypic level.

Sood *et al.* (2009); planned an experiment to evaluate correlation coefficients for marketable fruit yield and quality traits. They reported higher genotypic correlations than the corresponding phenotypic correlations, indicating inherent associations among traits. The maximum direct effect on fruit yield per plant was exhibited by fruit/plant followed by harvest duration, average fruit weight and pericarp thickness while marketable fruits per plant and days to 50% flowering had negative direct effects. They recommended a selection procedure based on higher fruits/plant, harvest duration and average fruit weight might be effective in improving fruit yield.

Farhad *et al.* (2008); reported that fruit yield has significant positive correlation with different yield contributing traits such as no. of secondary branches per plant, fruit girth, fruit weight and no. of fruits per plant. They also revealed that yield per plant and fruit weight showed maximum positive direct effect at genotypic and phenotypic levels.

Singh *et al.* (2009); reported that correlation and path analysis studies indicated the contribution of average fruit weight, numbers of total and marketable fruits per plant, and fruit length to marketable fresh yield. Average dry fruit weight, numbers of total and marketable fruits per plant, seed weight per fruit, and harvest duration played a predominant role for predicting dry yield. Among quality traits, capsanthin was significantly and positively correlated with yield. Ascorbic acid and capsaicin content were positively associated with total soluble solids at green and red stage, respectively.

Jabeen *et al*. (2009); evaluated the performance of twenty five chilli accessions. According to them no. of fruit per plant, no. of branches per plant and plant spread had the highest direct effect whereas fruit length, fruit breadth, average fruit weight and plant height had the highest indirect effect on fruit yield per plant.

Ajjappalavara *et al.* (2005); studied the correlation and path coeffiicient analysis in thirty-six genotypes in chilli for eighteen different quantitative characters. They observed significant and desirable correlation between dry fruit yield per plant with all other characters except no. of primary and secondary branches, fruit diameter, fruit volume, powdery mildew disease incidence and leaf curl complex incidence. They reported that fruit weight and fruits per plant were the traits that should be considered during selection.

Choudhary and Samadia (2004); found that red fruit yield had a significant positive correlation with green fruit yield/plant, fruit weight, fruit diameter, no. of seeds/fruit and weight of seeds/fruit. They also reported these traits as important yield contributing characters. Path analysis revealed that red ripe fruit weight followed by green fruit yield/plant, weight of seeds/fruit and no. of branches/plant had maximum direct effects on red ripe fruit yield.

A research was conducted by Cankaya *et al.* (2010); to estimate canonical correlation between plant characters and yield components in fifty-six red peppers (*Capsicum annum* L.) in the Black Sea Region of Turkey. They observed the plant characters like fruit length (FL), fruit width (FW), fruit wall thickness (FWT), placenta length, stem thickness, plant height (PH), leaf length, leaf width, flowering time (50%), and time to maturity as set-X and yield components like total fruit weight per plant (FW/P), average fruit weight and number of fruits per plant (FN/P) as set-Y. They found significant correlation coefficients between all the pairs of canonical variables. The findings showed that FN/P had the largest contribution on yield, FL and PH had largest contribution on plant characters and PH, FWT and FW should be used with the aim of increasing yield per plant in red pepper genotypes.

Thirteen F_1 hybids and its sixteen parents of pepper (*Capsicum annum* L.) were observed by Ming (1988); to conduct phenotypic correlation analysis and path analysis based on total yield along with other 15 characters. The study showed significant positive correlations between total yield and early yield, total yield and placenta width of fruit, fruit weight and placenta width , single fruit weight and fruit wall thickness, plant height and days to 50% flowering, Vitamin C content and fruit length. However, significant negative correlations were found between total yield and dry matter content of fruit, fruit weight and fruit number per plant. They found the greatest direct effect of fruit number/plant on total yield whereas width and early yield showed direct effect on total yield, while other characters had only a limited direct effect on total yield.

2.3. Genetic diversity

The magnitude of divergence between two groups under consideration is provided by D^2 statistic developed by Mahalanobis (1936). D^2 analysis can be applied to the situations where overlapping species need to be discriminated and also when the discrimination at subspecies level is needed (Murthy and Pavate, 1962). Now this technique is used in different vegetable crops.

Srinivas *et al.* (2015); conducted an experiment to observe genetic diversity in chilli (*Capsicum frutescens* L.) using Mahalanobis D^2 statistics among seventy eight accessions in Kerala. They observed fifteen quantitative and one qualitative trait. They divided the accessions into 9 clusters on the basis of relative magnitude of D^2 values using Euclidean^2 method. The highest no. of accessions (24) were accommodated with cluster II, whereas lowest (1 accession) with cluster III. The inter-cluster distances (D values) ranged between 3.90 to 12.68. Cluster II and IV showed lowest inter-cluster distance (3.90) and highest inter-cluster distance was observed between cluster VII and VIII (12.68). The intra-cluster divergence varied from 3.32 to 5.45. The highest intra-cluster divergence was observed in cluster VIII (5.45) and lowest in cluster V (3.32). Cluster III was showed zero intra-cluster distance as it contains only one accession. The maximum relative contribution to the total divergence was made by fruit yield/plant (61.07 %) and cluster VIII and cluster IX may be taken into consideration as better parents for an efficient hybridization programme of chilli.

The performance of thirty chilli (*Capsicum annum* L.) genotypes on twelve quantitative traits were observed by Matin *et al.* (2016); to screen out suitable parents for hybridization programme. Genetic diversity was estimated using Mahalanobis's D^2-statistic. The genotypes were grouped into six different clusters. The cluster I accommodated the maximum number of genotypes (9) and minimum number in Cluster V that was only one genotype. The maximum inter-cluster distance was obtained between cluster II and V (532.214) and the minimum inter-cluster distance was obtained between the cluster I and IV (91.948). The results indicated that fruit diameter (16%) contributed maximum to the total divergence followed by plant height (14.5%) and fruits/plant (12.5%). Cluster VI produced highest mean for fruit diameter (14.04), fruits/plant (219), whereas cluster V produced highest mean for fruit length (8.15) and yield/plant (617.13). They also found six different homozygous divergent parents which were selected from six different clusters. A Genotype by trait (GT) biplot analysis was done to show the six potential parents from six different clusters along with their suitable characters in one frame.

Sixteen quantitative traits were observed by Saleh *et al.* (2016); to evaluate the diversity and structure of sixty pepper (*Capsicum* spp.) genotypes grown in Eritrean. They observed the results of Principal Component Analysis, Hierarchal clustering with Euclidean distance and Analysis of variance. Cluster analysis of the combined data grouped the 60 genotypes into five clusters and 10 sub-clusters. Finally they reported at least four promising genotypes (HD0134, HD0031 and NRSG21 and NRSAF06) that should be used in breeding programme. They also found higher diversity within the evaluated pepper genotypes.

An investigation was carried out by Hasan *et al.* (2015); to estimate the genetic diversity in thirteen genotypes of chilli (*Capsicum annum* L.) on the basis of 6 yield contributing characters using Mahalanobis's D^2 statistics. They divided the genotypes into five different clusters by non-hierarchical clustering. The cluster I had the maximum number (5) of genotypes while cluster IV and V each contained only one genotype. The highest inter-cluster distance was observed between cluster I and IV (24.483) and the lowest was observed between the clusters II and V (11.633). The results revealed that fruits/plant (35.8%) contributed maximum to the total divergence followed by fruit length (21.6%) and yield/plant (21.1%). They observed that cluster IV showed highest mean for fruit weight (4.48), fruits/plant (149.90) and yield/plant (676.03) whereas cluster V showed highest mean for fruit length (10.23), pedicel length (4.94) and fruit diameter (10.36). However, cluster I and III produced maximum lowest mean for almost all characters. Therefore, accessions belongs to the cluster IV and V may be used as potential parents for future hybridization programme.

Yatung *et al.* (2014); studied genetic diversity in thirty chilli (*Capsicum annum* L.) accessions at the research farm of Central Agricultural University, Arunachal Pradesh, India during March-October 2011. They considered twelve quantitative traits viz. plant height (cm), number of primary branch/plant, days to first flowering, fruit length (cm), fruit diameter (cm), number of fruit/plant, average fruit weight (g), green fruit yield/plant (g), number of seeds/fruit, ascorbic acid (mg/100g), capsaicin content (%) and chlorophyll content (mg/g). They revealed considerable variability among the accessions through analysis of variance. They grouped 30 chilli genotypes into six clusters using cluster analysis. Cluster III accommodated the maximum (14) and cluster IV and V accommodated only one genotype that was the minimum. The highest (459.81) inter cluster distance was recorded between cluster II and IV and the lowest (36.04) between cluster I and IV. Cluster III (D^2= 67.66) have exhibited highest intra cluster distance and the lowest was observed in cluster II (D^2=11.19). They recommended the genotypes CHFC-7 from cluster VI, genotype CHFC-27 from cluster II and CHFC-15 from cluster III as better parents for an efficient hybridization programme of chilli.

Fifty four genotypes of chilli (*Capsicum annum* L.) were investigated by Hasan *et al.* (2014); to understand the extent of genetic diversity among twelve yield attributing characters through Mohalanobis's D^2 and principal component analysis. The selected traits were plant height, no. of secondary branch/plant, canopy breadth, days to first flowering, days to 50% flowering, fruits/plant, fruits weight, fruit length, fruit diameter, seeds/fruit, 1000 seed weight and yield/plant. They found that the traits yield/plant, canopy breadth, secondary branches/plant, plant height and seeds/fruit contributed most for divergence in the studied genotypes. Using Cluster analysis, they grouped the 54 chilli genotypes into seven clusters. Cluster II accommodated the maximum (13) and cluster III accommodated only one genotype that was the minimum. They estimated highest inter-cluster distance between cluster I and III and the lowest between cluster II and VII. Finally they suggested to use inter genotypic crosses between cluster I and cluster III, cluster III and cluster VI, cluster II and cluster III and cluster III and cluster VII for future hybridization program, considering group distance, mean performance and variability among the groups.

Usman *et al.* (2014); conducted two experiments on chilli based on heat tolerance and morph-physiological traits. They divided the chilli accessions into eight groups using Cluster analysis. Group VIII recorded the highest response to high temperature (CMT) and yield. Group IV accommodated 13 genotypes while Groups II, VII, and VIII recorded one each. The results showed that the availability of genetic variance could be useful for exploitation through selection for further crop improvement.

Seven morphological characters were observed by Lahbib *et al.* (2013); in eleven genotypes of *Capsicum annum* species to estimate phenotypic divergence using multivariate analysis technique. They applied canonical discriminant analysis combined with cluster analysis using generalized Malahanobis distance D^2 method to measure dissimilarity. They found significant canonical variates for first two genotypes that was 84.524% of the total variability. They arranged 11 genotypes into 3 clusters using generalized Mahalanobis's distances. The genetic stocks within cluster had smaller D^2 values among themselves than those belonging to different clusters. They found distinct identity in accessions FTC-6 and FTC-11 (clusters II and III, respectively). Phenotypic divergence in accessions were reported for no. of fruits/plant, fruit diameter, placenta weight and fruit length into similar groups.

Nsabiyera *et al.* (2013); reported higher cluster analyses while conducting an experiment under screen-house conditions on thirty-seven genotypes of hot pepper (*Capsicum annum*) based on 20 quantitative and 28 qualitative traits. It showed diversity among the genotypes at phenotypic level but with some level of genotypic relatedness and closeness. On the basis of Euclidean distance in cluster analysis dendrograms, introduced genotypes grouped more with local genotypes in qualitative compared with quantitative traits.

Divergence among twenty landraces of chilli was observed by Hasanuzzaman and Golam (2011). They grouped the accessions into six clusters. Maximum number of genetic stocks were accommodated in Cluster V (seven genotype) while cluster I consisted of minimum (only one) genotype. The maximum intra-cluster divergence (1.7153) was reported for cluster VI. However the minimum and maximum inter-cluster divergences were observed between cluster III & cluster VI (3.247) and clusters I & V (12.677), respectively. They identified four differentiating characters viz. yield/plant, plant height, days to 50% flowering and fruits/plant. They found that the clustering pattern did not follow their geo-climatic zonal distribution and taxonomic labels which explained present of other factors rather than regional boundaries and taxonomic characters for divergence. They selected a genotype from each groups as a group representative (CCA 2, CCA 5, BARI Morich 1, CCA 11, CCA 15 and CCA 19 respectively) and estimated the divergence by developing dendogram using 11 different characters. The lowest similarity was 17.52% among accession CCA 5 and CCA 11 and highest similarity was less than 50% among accession BARI Morich 1 and CCA 19 indicating the adequate divergence. They reported genotypes significant difference for all the traits and considerable amount of variation in selected six parents.

Kumari *et al.* (2010); reported considerable genetic diversity in ninety-four chilli (*Capsicum annum* L.) accessions. This was observed by Cluster analysis through

Mahalanobis D^2 analysis. Based on D^2 values, the 94 genotypes were grouped into 10 clusters. The largest was cluster I which comprised of 24 genotypes. The cluster distances ranged from 15789.6 (between cluster II and cluster X) to 856.7 (between cluster 1 and cluster II).

Based on the degree of divergence on thirty-two accessions of chilli, Moreno-Pérez *et al.* (2011); conducted an experiment, quantitative and qualitative characters were suggested by IPGRI and analyzed by primary components (PC) and hierarchical clustering (HC). They managed the crop in padded black with silver colored plastic and a fertigation system. They reported that 58% of the total quantitative variation was observed in first three principle components. The largest contribution to this variation was the characteristics associated with leaf and flower morphology structure (length and width of mature leaf, petiole length, corolla length and width) and number of days fruiting fruits per plant, in addition to phenological variables. However on the basis of qualitative variables, three PC explained 76% of the variation; density of branch and leaf, tillering, shape of the corolla, fruit color , fruit and termination of the tip contributed more to explaining the variation detected Among accessions. They divided the accessions into five groups and eight groups in the dendrogram of quantitative and qualitative variables respectively through the HC.

Fonseca *et al.* (2008); carried out an experiment to observe genetic diversity of thirty eight genotypes of the genus Capsicum based on 51 morphological characters whereas similarity of the genotypes was calculated based on 17 essential characters and on the general similarity coefficient of Gower. Grouping analyses and a dispersion diagram of the genotypes were established based on the similarity coefficients using, respectively, the UPGMA method and the principal coordinate analysis (PCO) as criterion of grouping and dispersion. Great variations among classes were identified in the fruit trait: nine colors, four shapes and a great range of variation in fruit size and weight. They found only three genotypes that were not pungent.

Sudré *et al.* (2005); used multivariate techniques to estimate genetic divergence among 56 accessions of chilli and sweet pepper based on eleven quantitative traits proposed by International Plant Genetic Resources Institute in Brazil. They applied Canonical variated analysis, cluster analysis using Tocher's optimization method and Generalized Mahalanobis's D^2 method to measure dissimilarity. They found significant difference among accessions for all the traits. They observed general agreement among all multivariate techniques and classified the accessions in eight distinct groups. The highest generalized distance of Mahalanobis's D^2 method was 266.42, indicating promising genotypes to be used in artificial crosses to obtain infor-progenies with higher heterosis. They observed que crosses with the greatest heterotic potential had Been 56x43; 34x08, and 59x41 through Canonical variable analysis.

CHAPTER III

MATERIALS AND METHODS

The investigation was undertaken on chilli (*Capsicum frutescens* L.) at the experimental field of Sher-e-Bangla Agricultural University, Dhaka, Bangladesh during the period from December, 2014 to June, 2015 to study the genetic variability, heritability, genetic advance, character association, path coefficient analysis and genetic divergence. Details pertaining to materials used and methodology employed in the investigation are presented in this chapter.

3.1. Location of experimental site

The experiment was conducted at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka-1207, that was located at 23°74'N latitude and 90°35'E longitude and at an altitude of 8.6 meter above the sea level (Anon, 2004). The experimental field belongs to the Agro-ecological zone of The Modhupur Tract, AEZ-28. The experimental site was shown in the map of AEZ of Bangladesh in Appendix I.

3.2. Characteristics of soil

The soil of the experimental site was clay loam in texture and belongs to Tejgaon soil series characterized by shallow red brown terrace Soils. Soil p^H ranged from 5.47 to 5.63 whereas organic matter was 0.82%. Experimental area was flat having available irrigation and drainage system and above flood level. Soil samples from 0-15 cm depths were collected from experimental field and analyzed. The analyses were done by Soil Resource and Development Institute (SRDI) Dhaka. Physicochemical properties of the soil were presented in Appendix II.

3.3. Climate

The experimental site is situated in subtropical climatic region, that is characterized by high temperature along with high relative humidity and heavy rainfall in Kharif (April-September) season and scanty rainfall accompanied by moderately low temperature and short sunshine hours during the Rabi (October-March) season. This experiment was conducted from December, 2014 to June, 2015. A detail of the meteorological information regarding temperature, relative humidity, rainfall and sunshine hours prevailed at the experimental site during the study period were collected from Abhawa Bhaban (Bangladesh Metrological Department), Agargaon, Dhaka and presented in Appendix III.

3.4. Genetic materials used in the experiment

Thirteen local genotypes of chilli (*Capsicum frutescens* L.) were collected from the different sources. Among them 4 genotypes were collected from Rajshahi and Rangpur, 3 from Siddik Bazar, Gulistan, Dhaka and 2 from Naogaon. Thirty germplasm were also collected from Plant Genetic Resources Centre (PGRC) of Bangladesh Agricultural Research Institute (BARI), Gazipur which were unfortunately unviable. The name and origin of these genotypes are presented in (Table I).

3.5. Design and layout of the experiment

The thirteen germplasm of chilli was laid out in a Randomized Complete Block Design (RCBD) with three replications (Figure 3). Twelve plants of each genotype were transplanted in each replication in two rows. The layout of the experiment was described below:

Design : Randomized Complete Block Design (RCBD)

No. of genotypes : 13

Replications : 3

Plot size : 14 m x 11 m

Block size : 13 m x 3 m

Spacing per plant : 50 cm x 50 cm

No. of plants per row : 6

No. of rows per block : 26

Block to block distance: 50 cm

3.6. Seed treatment

Seed treatment was done to facilitate the germination. Seeds were soaked 18 hours with water and then were tied with cloth and kept under moderate warm condition with adequate moisture for three days. It was checked twice daily. After three days it showed the symptoms of germination. It was then sown to seedbed.

Table 1. Sources of thirteen chilli genotypes

Genotypes	Designation	Source	Year
G1	GPB0001/14	Bagmara, Rajshahi.	2014
G2	GPB0002/14	Bagmara, Rajshahi.	2014
G3	GPB0003/14	Bagmara, Rajshahi.	2014
G4	GPB0004/14	Manda, Naogaon.	2014
G5	GPB0005/14	Bagmara, Rajshahi.	2014
G6	GPB0006/14	Siddik bazar, Gulistan, Dhaka	2014
G7	GPB0007/14	Rangpur sadar, Rangpur.	2014
G8	GPB0008/14	Rangpur sadar, Rangpur.	2014
G9	GPB0009/14	Manda, Naogaon.	2014
G10	GPB0010/14	Siddik bazar, Gulistan, Dhaka.	2014
G11	GPB0011/14	Rangpur sadar, Rangpur.	2014
G12	GPB0012/14	Siddik bazar, Gulistan, Dhaka	2014
G13	GPB0013/14	Rangpur sadar, Rangpur.	2014

3.7. Seedling raising in seedbed

Seedbeds of 3 m x 1 m size were prepared and leveled. Treated seeds of 13 genotypes were sown in lines at 5cm spacing on 8 December, 2014. As a precaution against fungal diseases of the seedlings, the seeds were mixed with Bavistin 50 DF before sowing. Sevin dust was spread over seedbed to protect the seeds from the attack of soil inhibiting insects like ant. However urea fertilizer was applied to ensure the optimum growth of seedling after 20 days after sowing and light irrigation was done when required.

3.8. Preparation of the experimental field

The experimental field was first opened in the 20 December, 2014 with a power tiller, and was left exposed to the sun for a week. Three more times cross ploughing were done subsequently to make the land suitable for transplanting the seedlings. All weeds, stubbles and residues were eliminated from the field. Finally, a good tilth was achieved. Well decomposed cow dung, manure and chemical fertilizers were applied and mixed properly with the soil as per recommendation during final land preparation. Then blocks were made with proper irrigation and drainage channels according to the experimental site layout and were leveled the surface of blocks by harrowing.

3.9. Application of manure and fertilizers

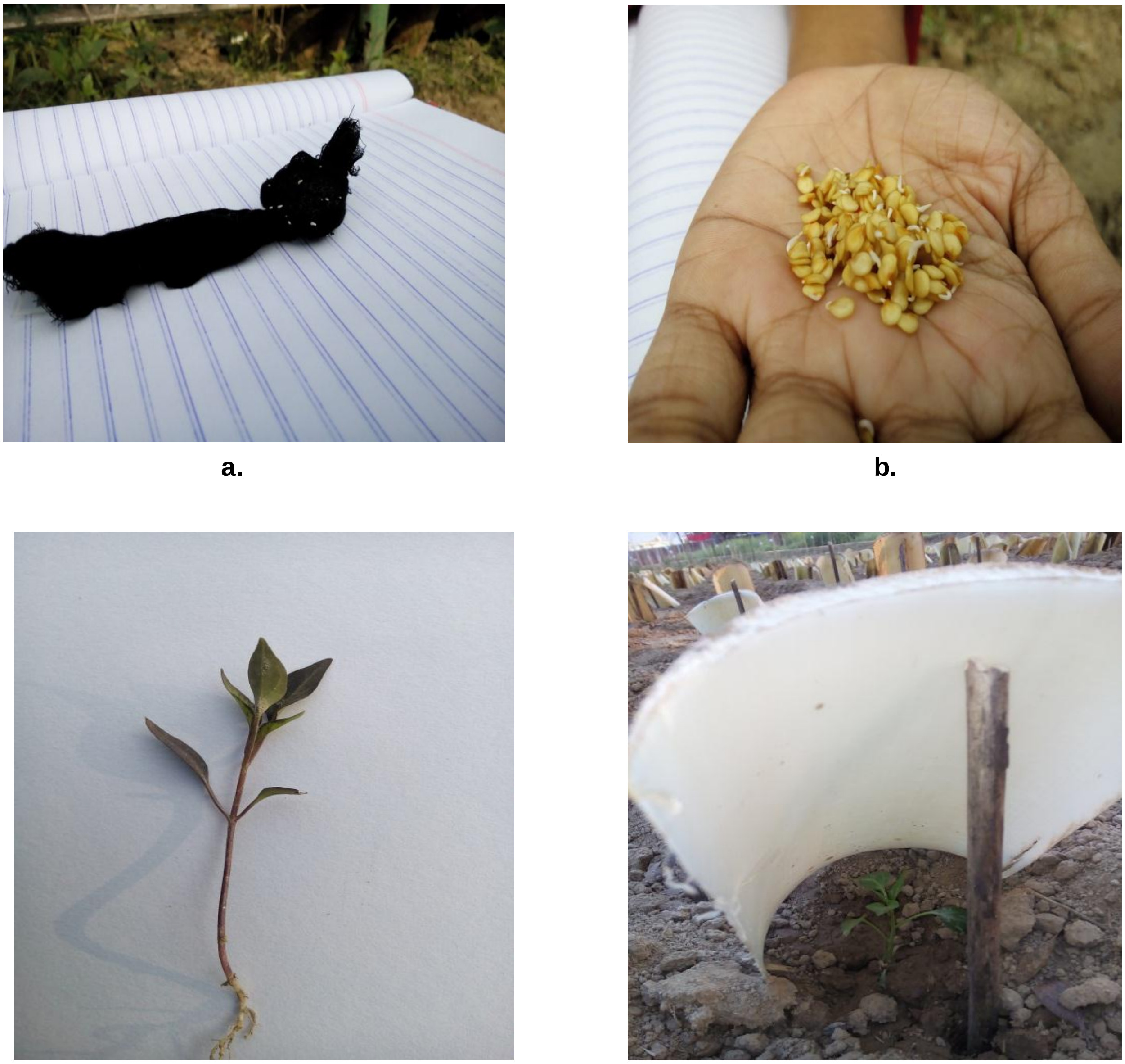
The fertilizers N, P, K, S, Zn and B in the form of urea, TSP, MP, gypsum, zinc oxide and boric acid, respectively were applied. Entire dose of cow dung, TSP, gypsum, zinc oxide and boric acid were applied as basal dose while urea and MP were applied in installments. The dose and method of application of fertilizer are shown in Table 2.

3.10. Transplanting of seedlings

Forty-five days old seedlings with 4-5 leaves were transplanted to the main field on 21 January, 2015. The seedlings were transplanted at afternoon. As a precaution of root-damage of seedlings, the seed beds were watered one hour before uprooting the seedlings and seedlings were uprooted carefully from the seed bed. Seedlings were transplanted by maintaining a spacing of 50 cm of each between the rows and the plants within a row. Immediately after transplanting the field was irrigated lightly.

Table 2. Doses of fertilizers in Chilli field

Manure and Fertilizers	Dose /ha	Amount applied in total plot	Basal dose	Top dressing installment		
				1st at 30 DAT	2nd at 50 DAT	3rd at 70 DAT
Cow dung	5 ton	75 kg	75 kg	---	---	---
Urea	210 kg	3.1 kg	1.0 kg	700 g	700 g	700 g
TSP	300 kg	4.5 kg	4.5 kg	---	---	---
MP	200 kg	3.0 kg	2.1 kg	300 g	300 g	300 g
Gypsum	110 kg	1.6 kg	1.6 kg	---	---	---
ZnO	5 kg	75 g	75 g	---	---	---
Boric acid	1.5 kg	20 g	20 g	---	---	---



a.

b.

c.

d.

Plate 1. Showing seed after treatment (a), seeds before sowing (b), seedling before transplanting (c) and seeding protection measure after transplanting (d)

3.11. Intercultural operations

After transplanting seedlings, various intercultural operations such as plant protection measures, gap filling, weeding, earthing up, irrigation, pest and disease control etc. were accomplished for better growth and development of the capsicum seedlings.

3.11.1. Plant protection measures

Pieces of banana stalk were used to cover the seedlings from extreme sunshine at day. However at afternoon seedlings were exposed to receive dewdrops. It was done approximately for a week while seedling were establishing in field condition.

3.11.2. Gap filling

The transplanted seedlings in the experimental plot were observed carefully and damaged seedlings were replaced by new healthy seedlings from the same stock. The newly transplanted seedlings were taken under special observation for their proper establishment.

3.11.3. Top dressing

Urea and MP were applied at the amount of 700gm and 300gm respectively on 30, 50 and 70 DAT.

3.11.4. Irrigation

Light irrigation was given by a watering cane at every morning and afternoon following transplanting and it was continued for a week for rapid and well establishment of the transplanted seedlings. After establishing, semi-flood irrigation was done when necessary depending on the moisture status of the soil.

3.11.5. Earthing up and stalking

Earthing up was done at 20 and 40 days after transplanting on both sides of rows by taking the soil from the space between the rows by a small spade. Stalking was done to protect the plant from wind and to support it when fruiting.

a.

b.

Plate 2. Showing field view after transplanting (a) and a part of field (b)

3.11.6. Weeding and hoeing

The experimental plot was kept free from weed. Weeding was done when as per requirement. Hoeing was done to ensure easy aeration and to conserve soil moisture.

3.11.7. Pest and disease control

Fungal diseases were a major problem during the crop cultivation. After a mild rain, the plot was infested with anthracnose. Tilt 250 EC was sprayed twice at the rate of 0.5ml per liter water. To protect the plant from viral disease such as leaf curl, Malathion 50EC was sprayed at the rate of 1ml per liter water.

3.12. Harvesting

First harvesting was done at 85 DAT and continued for the following 75 days with an interval of 15 days. Matured chillies were picked by hand during harvesting and were kept separated and leveled from each plant.

3.13. Data collection

Five plants from the middle of the rows of each genotype were randomly selected and tagged in each replication for recording data. With a view to assessing multivariate analysis, the data were collected in respect of the following parameters.

3.13.1. Days to first flowering

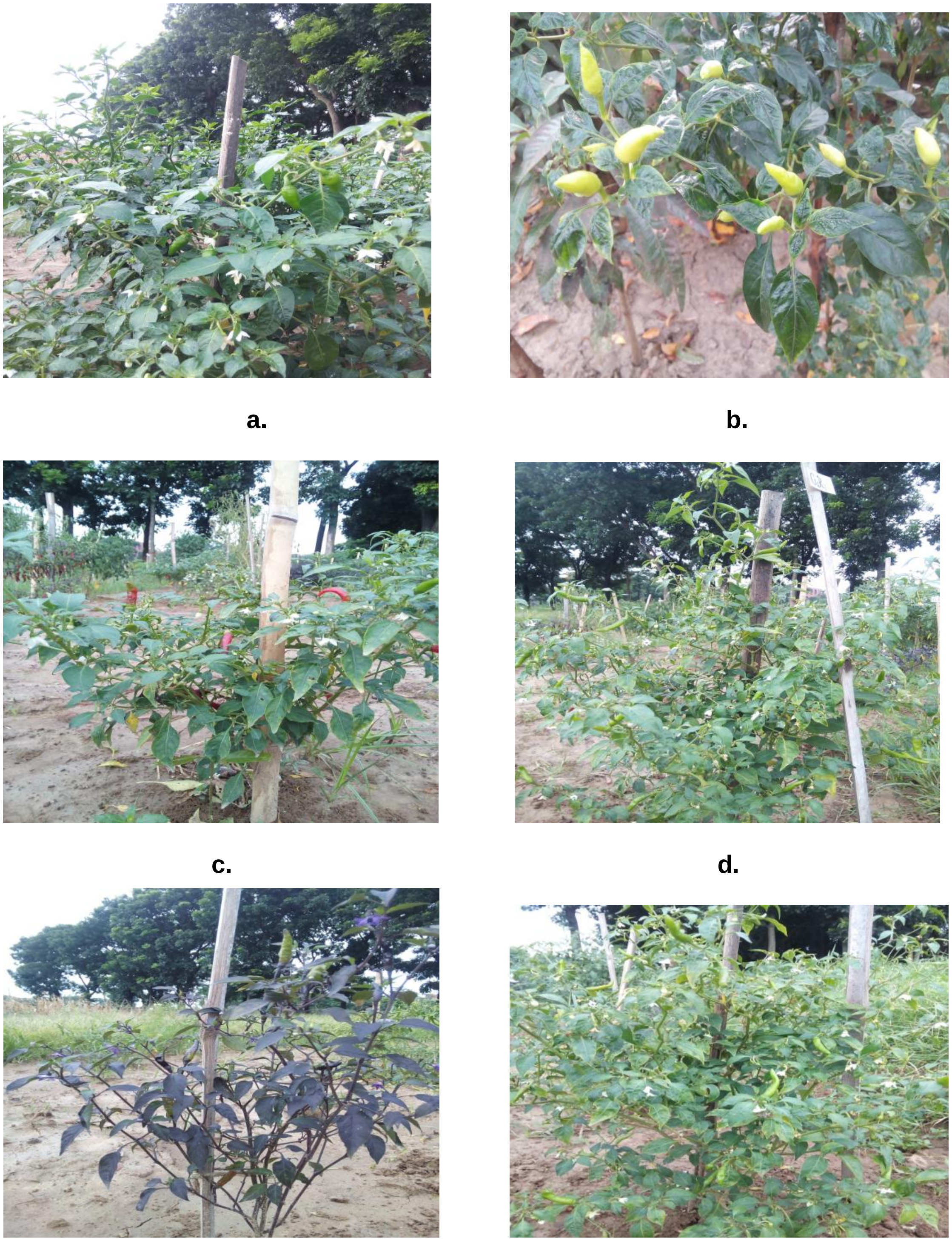
Days from transplanting to first flowering of each plant in a block was counted.

3.13.2. Plant height

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

3.13.3. Number of primary branches per plant

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



a. b.

c. d.

e. f.

Plate 3. Showing some plants of G2 (a), G6 (b), G7 (c), G9 (d), G12 (e), and G13 (f)

3.13.4. Number of fruits per plant

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

3.13.5. Fruit length

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

3.13.6. Fruit circumference

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

3.13.7. Fruit weight

The weight of five randomly selected individual fruit was recorded in gram (gm) by a electrical balance from all fruits of selected plants and the mean was calculated.

3.13.8. Yield per plant

The yield in terms of total harvested fruit weight was recorded in grams on five randomly selected plants during each harvest. Summation of the several harvests was recorded and mean was worked out.

3.14. Statistical analysis

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

Genetic divergence is one of the most important parameters evaluated by plant breeders in starting a breeding program. This is a necessary, but not sufficient, condition for the occurrence of heterosis and the generation of a population with broad genetic variability. Subsequently, heterosis is directly proportional to genetic divergence and to dominance squared (Falconer, 1964; Ferreira, 1993) and also associated with adaptation. A second approach is to use multivariate methods to estimate genetic divergence and then predict hybrid performance. In this case, it is not necessary to make crosses. Furthermore, a large number of materials may be successfully evaluated (Hallauer and Miranda, 1981).A canonical variate technique is often used to reduce the number of these traits, through a linear combination of them, without a significant loss of the total variation. Additionally, this technique takes into account the structure of residual co-variances. The concept of D^2 statistics was originally developed by P.C. Mahalanobis in 1936. Rao (1952) suggested the application of this technique for the assessment of genetic diversity in plant breeding. Now this technique is extensively used plant breeding and genetics for the study of genetic divergence in the various breeding materials.

In plant breeding, Genetic diversity plays an important role because hybrids between lines of diverse origin, generally, display a greater heterosis than those between closely related parents. This has been observed in maize, alfalfa, cotton and several other crops. Genetic diversity arises due to geographical separation or due to genetic barriers to cross ability. Statistical analysis such as Mahalanobis D^2 and Canonical Variate Analysis (CVA), which quantity the differences among several quantitative traits are efficient method of evaluating genetic diversity. Mean data of each quantitative character were subjected to both univariate and multivariate analysis. For univariate analysis of variance, analysis was done individually and least of significance was done by F- Test (Pense and Shukhatme, 1978). Mean, range, co-efficient of variation (CV) and correlation was estimated using MSTAT computer program. Multivariate analysis viz., principal component analysis, principal coordinate analysis, cluster analysis and canonical variate analysis were done by using GENSTAT program. The hierarchical nature of the grouping into various number of classes could impose undue constrains and the statistical properties of the resulting groups were not at all clear (Peyne *et al*. 1989). Therefore, they have suggested non-hierarchical classification, as an alternative approach to optimize some suitability choosing criteria directly from the data matrix. Peyne *et al.* (1989) also reported that the squared distance between means were Mahalanobis's D^2 statistics when all the dimensions were used, could be computed principal coordinate analysis. They also commended the canonical variate analysis for discriminatory purpose.

a. b.

Plate 4. Showing plants of G10 genotype (a & b)

3.14.1. Estimation of genetic parameters

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

3.14.1.1. Analysis of variance (ANOVA)

Data were analyzed by the methods outlined by Panse and Sukhatme (1985) using the mean values of random plants in each replication from all genotypes to find out the significance of genotypes effect. The data for different characters were statistically analysed on the basis of the model suggested by Cochran and Cox (1950) for RBD.

$$Yij = \mu + bi + tj + eij$$

3.14.1.2. Genotypic and phenotypic variances

Genotypic and phenotypic variances were estimated by Johnson *et al.* (1955) Genotypic variance was obtained by subtracting genotype mean sum squire to error mean sum of squire and dividing by the number of replication as given bellow:

$$\text{Genotypic Variance } (\delta^2 g) = \frac{\text{GMS} - \text{EMS}}{\text{r}}$$

$$\text{Environmental Variance} (\delta^2 e) = \frac{\text{EMS}}{\text{r}}$$

$$\text{Phenotypic Variance } (\delta^2 p) = \delta^2 g + \delta^2 e$$

Where,

GMS = Genotypic mean sum of squire
EMS = Error mean sum of squire
r = Number of replication

3.14.1.3. Estimation of Genotypic and Phenotypic Coefficient of Variation

Genotypic and phenotypic coefficients of variation were calculated according to the following formulae by Burton (1952).

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

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

Where,

GCV= Genotypic co-efficient of variation
PCV=Phenotypic co-efficient of variation
$\bar{X}$ = Population mean.

3.14.1.4. Estimation of Heritability

Broad sense heritability was estimated by the following formula suggested by Johnson et al. (1955)

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

Where,

h^2 (b) = Heritability in broad sense
$\delta^2 g$ = Genotypic variance
$\delta^2 p$ =Phenotypic variance

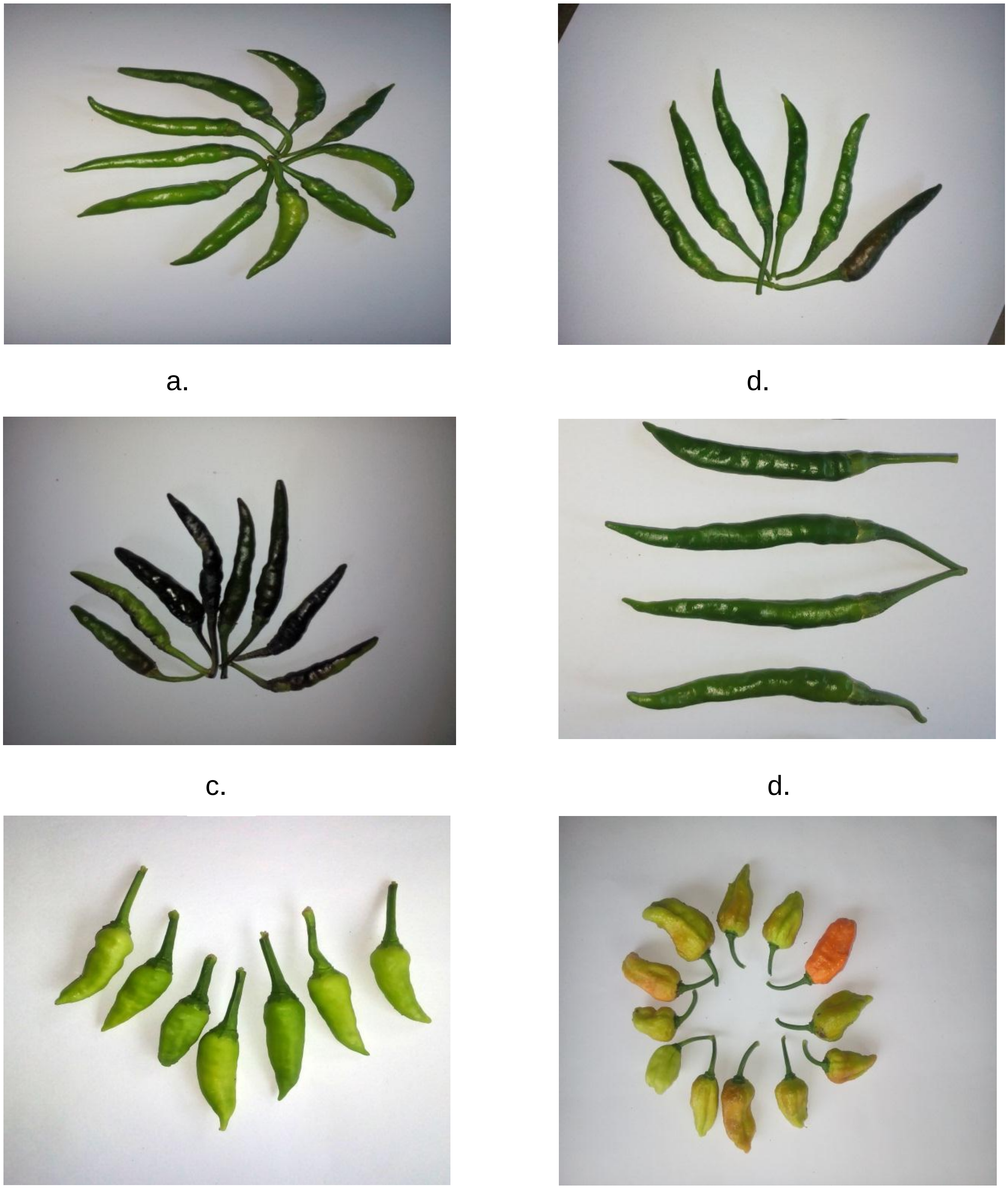
3.14.1.5. Estimation of genetic advance

The following formula was used to estimate the expected genetic advance for different characters under selection as suggested by Allard (1960).

Genetic Advance (GA) =$h^2(b) \times K \times \delta_p$

Where,

h^2 (b) = Heritability in broad sense
δ_p=Phenotypic standard deviation
K= Selection differential which is equal to 2.06 at 5% selection intensity.



a. d.

c. d.

e. **f.**

Plate 5. Some fruits G1 (a), G6 (b), G7 (c), G9 (d), G12 (e), and G13 (f)

3.14.1.6. 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).

$$\text{GA (\%)} = \frac{\mathrm{GA}}{\overline{\mathrm{X}}} \times 100$$

Where,

GA (%) = Genetic Advance in percentage of mean
GA = Genetic Advance
$\overline{\mathrm{X}}$ = Population mean.

3.14.2. Correlation studies

Phenotypic and genotypic correlations were estimated from the replicated data with the help of following formula suggested by Falconer (1964).

3.14.2.1. Phenotypic coefficient of correlation (r_p)

$$r_{(x.y)p} = \frac{\mathrm{COV}_{(xy)p}}{\sqrt{\mathrm{V(x)p}\,.\mathrm{V(y)p}}}$$

Where,

$r_{(x.y)p}$ = Phenotypic correlation between xth and yth character
COV(x.y)p = Phenotypic covariance between xth and yth character
V(x)p = Phenotypic variance of xth character
V(y)p = Phenotypic variance of yth character.

3.14.2.2. Genotypic coefficient of correlation (r_p)

$$r_{(x.y)g} = \frac{\mathrm{COV}_{(x.y)g}}{\sqrt{\mathrm{V(x)g}\,.\mathrm{V(y)g}}}$$

Where,

$r_{(x.y)g}$ = Genotypic correlation between xth and yth character
COV(xy)g = Genotypic covariance between xth and yth character
V(x)g = Genotypic variance of xth character

V(y)g = Genotypic variance of y^{th} character

3.14.2.3. Test of significance

Significance of correlation coefficients was tested by comparing phenotypic correlation coefficients with the tabulated values (Fisher and Yates, 1963) at (n-2) degrees of freedom at 5 % and 1 % level by using following formulae.

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

Where,

t = test of significance
r = correlation coefficient and
n = number of paired observations

3.14.3 Path co-efficient analysis

Path co-efficient analysis was done according to the procedure suggested by Wright (1921) and elaborated by Dewey and Lu (1959). In path analysis, correlation co-efficient is partitioned into direct and indirect independent variables on the dependent variable.

In order to estimate various direct and indirect effects of path coefficients, the following simultaneous equations were formed and solved.

$$r_{1y} = P_{1y} + r_{12}P_{2y} + r_{13} P_{3y} + \dots\dots\dots + r_{1k} P_{ky}$$

Where,

r_{1y} = Simple correlation coefficient between x1 and y, the dependent character
P_{1y} = Direct effect of x1 on y, the dependent character
$r_{12}P_{2y}$ = Indirect effect of x1 on y through x2.
r_{12} = Correlation coefficient between x1 and x2.
$r_{1k} P_{ky}$ = Indirect effect of x1 only through kth variable.

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

Residual effect, (Pry) = $\sqrt{1 - \mathrm{R}^2}$

Where,

$R^2 = P_{1y}r_{1y} + P_{2y}r_{2y} + \ldots\ldots\ldots\ldots + P_{iy}r_{iy}$

P_{1y} = Direct effect of x1 on y.

r_{1y} = Correlation coefficient of x1 and y

P_{iy} = Direct effect of xi on y

r_{jy} = Correlation coefficient of xi and y

3.14.4. Genetic diversity analysis

3.14.4.1. Principal component analysis (PCA)

It is a way of identifying patterns in data, and expressing the data in such a way as to highlight their similarities and differences. Since patterns in data can be hard to find in data of high dimension, where the luxury of graphical representation is not available, PCA is a powerful tool for analyzing data. The Purpose of principal component analysis it to derive a small number of linear combinations (principal components) of a set of variables that retain as much of the information in the original variables as possible. Principal Component Analysis one of the multivariate techniques, is used to understand relationships among several characters. It can be done from the sum of squares and products matrix for the characters. Principal components were computed from the correlation matrix and genotype scores obtained for the first components and succeeding components with latent roots greater than unity (Jeger *et al.,* 1983). Contributions of different morphological characters towards divergence were discussed from the first two principal components.

3.14.4.2. Principal coordinate analysis (PCO)

Principal coordinate Analysis is equivalent to PCA but is used to calculate inter unit distances. Through the use of all dimensions of P it gives the minimum distance between each pair of points using similarity matrix (Digby *et al.,* 1989).

3.14.4.3. Clustering

The term cluster analysis encompasses a number of different algorithms and methods for grouping objects of similar kind into respective categories.

In multivariate analysis, cluster analysis refers to methods used to divide up objects into similar groups, or, more precisely, groups whose members are all close to one another on various dimensions being measured. The definition of clusters emerges entirely from the cluster analysis-i.e. from the process of identifying "clumps" of objects.

Cluster analysis is an exploratory data analysis tool for solving classification problems. Its object is to sort cases (People, plant, things, events, etc) into clusters, so that the degree of association is strong between members of the same cluster and weak between members of different clusters. Each cluster thus describes, in terms of the data collected, the class to which its members belong; and this description may be abstracted through use from the particular to the general class or type.

To divide the genotypes of a data set into some number of mutually exclusive groups clustering was done using non-hierarchical classification. In GENSTAT, algorithm was used to search for optimal values of chosen criteria which proceed as follows:

Starting from some initial classification of the genotypes in required number of group, the algorithm repeatedly transferred genotypes from one group to another so long as such transfer improved the value of the criterion when no further transfer could be found to improve the criterion, he algorithm switched to a second stage, which examined the effect of swapping two genotypes of different classes and so on.

3.14.4.4. Canonical variate analysis (CVA)

Discriminate function or canonical variate analysis attempt to establish whether a set of variables can be used to distinguish between two or more groups.

Canonical variate analysis complementary to D^2 statistic is sort of multivariate analysis where canonical vectors and roots representing different axes of differentiation and the amount of variation accounted for by each of such axes respectively and derived. Canonical variate analysis computed linear combination of original variability that maximized the ratio between groups and within group variations, thereby giving functions of the original variables that could be used to discriminate between the groups. Thus in this analysis, a series of orthogonal transformation sequentially maximized the ratio of the groups to within group variations. Several techniques that seek to illuminate the ways in which sets of variables are related one another. The term refers to regression analysis, ANOVA, discrimination analysis, and, most often, to canonical correlation analysis.

3.14.4.5. Cluster diagram

In D^2 analysis a line diagram is constructed with the help of D^2 values which is known as cluster diagram. The squires roots of average intra and inter cluster D^2 value are used in the construction of cluster diagram. This diagram provides information on the following aspects:

- It depicts the genetic diversity in an easily understandable manner.
- The number of cluster represents the number of groups in which a population can be classified on the basis of D^2 analysis.
- The distance between two clusters in the measure of the degree of diversification. The greater the distance between two cluster the greater the divergence and vice versa.
- The genotypes filling in the same cluster are more closely related then those belonging to another cluster. In other words, the genotypes grouped together in one cluster are less divergent than those which are placed in different cluster.
- It provides information about relationship between various clusters.

A cluster diagram was drawn using the values ($\sqrt{D^2}$) of intra and inter-cluster distance. The diagram represented the brief idea of the patter diversity among the genotypes and relationships between different genotypes included in the cluster.

3.14.4.6. Selection of genotypes for future hybridization programme

Genotypes were selected from the study for future hybridization programme considering genetic variability and other performances related to yield (kg), number of fruit per plant, color of fruit and presence, number of primary branches, node number of first male flower, no. of flower per days to first flowering, weight per fruit (kg), percent insect infestation of plants, fruit length (cm), fruit diameter (cm), number of seed per fruit, days to germination etc.

CHAPTER IV

RESULTS AND DISCUSSIONS

A systematic study was conducted to study the genetic variability, correlation, path coefficient analysis and genetic diversity of 13 chilli genotypes. The data on different yield and yield contributing characters of chilli (*Capsicum frutescens* L.) were computed and statistically analyzed. The results obtained are presented under the following headings:

3.1. Genetic variability
3.2. Correlation coefficient analysis
3.3. Path coefficient analysis
3.4. Genetic diversity analysis

4.1. Genetic variability

The analysis of variance indicated that the existence of highly significant variation among the genotypes studied. The mean, range, mean sum of square, variance components, genotypic and phenotypic co efficient of variance, heritability, genetic advance, genetic advance in percent of mean are presented in Table 3 and Table 4.

4.1.1. Days to first flowering

Considerable variations were observed among 13 genotypes of chilli for days to first flowering. Table 3 showed that the earliest flowering genotype was G9 (86.00 days) whereas the genotypes G4 and G13 were the late flowering (115.00 days). The mean value for this trait was 97.17 days. Significant mean sum of square for days to first flowering (236.13) and coefficient of variation (5.68%) indicated considerable variation was present among genotypes studied. The phenotypic variance (99.01) was higher than genotypic variance (68.56) indicated higher influence of environment on the expression of the genes controlling this trait. It also supported by higher differences between PCV (10.24%) and GCV (8.52%) for this trait (Table 4). Low PCV and GCV suggested limited variability indicating need to generate more variability for wider spectrum of selection. High heritability (69.25%) for days to first flowering attached with low genetic advance (14.19%) and low genetic advance in percentage of mean (14.61%) suggested that this trait may be under the control of non-additive gene action and

Table 3. Range, mean, mean sum of square, and genotypic, phenotypic and environmental variances for eight characters in thirteen chilli genotypes

Characters	Range (Genotype)	Mean	Mean Sum of Square (MS)	Genotypic Variance (σ^2_g)	Phenotypic Variance (σ^2_p)	Environmental Variance (σ^2_e)
Days to first flowering	86.00(9)-115.00(4&13)	97.17	236.13**	68.56	99.01	30.45
Plant height (cm)	42.89(5)-88.42(6)	62.84	474.10**	141.21	191.89	50.48
No. of primary branches per plant	5.17(13)-12.33(10)	9.025	11.32**	2.74	5.85	3.11
No. of fruits per plant	5.66(5)-27.44(8)	21.06	171.00**	37.81	95.38	57.57
Fruit length (cm)	3.47(2)-17.95(10)	6.82	38.51**	12.80	12.91	0.11
Fruit Circumference (cm)	2.06(5)-4.82(11)	2.69	1.89**	0.62	0.66	0.04
Fruit Weight (g)	0.60(5)-8.35(10)	2.03	12.48**	4.15	4.17	0.02
Yield Per Plant (g)	19.34(5)-606.23(10)	99.17	71339.60**	23740.91	23857.78	116.88

* Significant at 5% level of probability; ** Significant at 1% level of probability

environmental effect. Heritability estimate alone is not enough to produce a high genetic gain. These results are in agreement with the findings of Bharadwaj *et al.* (2007), Farhad *et al.* (2008), Sharma *et al.* (2010), Shirshat *et al.* (2007) and Kumari *et al.* (2010).

4.1.2. Plant height

In this study, the maximum and the minimum plant height was recorded in G6 (88.42 cm) and G5 (42.89 cm), respectively, with a mean of 62.84 cm (Table 3). The mean sum of square for plant height (474.10) was significant indicating considerable variation among genotypes studied. It was also supported by high (11.31%) coefficient of variation (Table 4). Phenotypic and genotypic variances were observed as 191.89 and 141.21, respectively. The phenotypic variance appeared to be high than the genotypic variance which suggested that environmental effect was high on the expression of the genes controlling this trait. The moderate PCV (22.03%) and low GCV (18.91%) gave information that there was much variation among the genotypes in case of plant height. The difference between PCV and GCV was found wide for the trait indicating that the apparent variation was not only due to genotypes but also due to influence of environment. High heritability (73.67%) coupled with moderate genetic advance (21.01%) and moderate genetic advance in percent of mean (33.43 %) was recorded for this character suggesting additive gene effect in this character that indicated opportunity for selecting taller genotypes.

Moderate phenotypic coefficient of variation and genotypic coefficient of variation was also found by Manju and Sreelathakumary (2002), Kashinath *et al*. (2003) and Krishna *et al.* (2007). High heritability coupled with moderate expected genetic advance for this trait was reported by Sharma *et al.* (2010), Bharadwaj *et al.* (2007), Farhad *et al.* (2008) and Berhanu *et al.* (2011).

4.1.3. Number of primary branches per plant

Among the 13 genotypes the maximum number of primary branches per plant was recorded in G10 (12.33) whereas the minimum was found in G5 (5.17) with a mean of 9.025 (Table 3). The highly significant mean sum of squares (11.32) and higher coefficient of variation (19.52%) indicated that there were significant differences among the genotypes for the trait under study. Phenotypic variance (5.85) was higher than genotypic variance (2.74) emphasized the significant role of environment in the inheritance of the character. The estimates of PCV and GCV were moderate and low with 26.79% and 18.33% respectively (Table 4), suggested that these character account for the considerable variation in chilli. The trait with moderate estimate of heritability (46.81%) suggesting these characters are governed by additive genetic effect to a great extent. However heritability estimate alone is not enough to express a character. Low genetic advance (2.33) and moderate genetic advance as percent of mean (23.83%) explained the combined effect of non-additive genes and environment to express this character.

These results are in agreement with those reported by many earlier workers viz., Manju and Sreelathakumary (2002), Berhanu *et al.* (2011) and Bendale *et al.*(2006). However Farhad *et al*. (2008) and Kumari *et al*. (2010) reported high GCV and high PCV with high heritability coupled with high genetic advance.

4.1.4. Number of fruits per plant

Number of fruits per plant showed significant variation with significant value of mean sum of squares (171.00) and the highest coefficient of variation (36.04%) among the genotypes for this character under study (Table 3). The maximum number of fruits were harvested from G8 (27.44) and the minimum from G5 (5.66) with an average of 21.06. The phenotypic variation (95.38) was considerably higher than that of the genotypic (37.81) variation suggesting the presence of environmental influence to some extent in the expression of this character. It was also supported by the significant difference between the PCV (46.37%) and GCV (19.29%) of number of fruits per plant (Table 4). The moderate heritability (39.64%) coupled with low genetic advance (7.98) and medium genetic advance as percent of mean (37.87%) for this trait indicated that this character was predominantly controlled by environment with complex gene interaction.

Shirshat *et al.* (2007) reported that phenotypic coefficient of variation was higher than genotypic coefficient of variation for this trait. However Farhad et al. (2008), Kumari et al. (2010) and Krishna *et al.*

Table 4. Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), broad sense heritability (h^2_b), genetic advance (GA), genetic advance in percent of mean (GAPM) and coefficient of variance (CV) for eight characters in *Capsicum frutescens* L. genotypes

Characters	GCV	PCV	h^2_b	GA (5%)	GAPM (5%)	CV (%)
Days to first flowering	8.52	10.24	69.25	14.19	14.61	5.68
Plant height (cm)	18.91	22.03	73.67	21.01	33.43	11.31
No. of primary branches per plant	18.33	26.79	46.81	2.33	23.83	19.52
No. of fruits per plant	19.29	46.37	39.64	7.98	37.87	36.04
Fruit length (cm)	52.46	52.68	99.15	7.34	107.60	4.87
Fruit Circumference (cm)	26.53	27.38	93.91	1.57	52.96	6.69
Fruit Weight (g)	100.39	100.63	99.52	4.19	206.31	6.05
Yield Per Plant (g)	155.37	155.75	99.51	316.63	319.27	10.90

4.1.5. Fruit length

There were significant differences among 13 genotypes of chilli for the character fruit length. It was explained by significant value of mean sum of squares (38.51) and high coefficient of variation (4.87%) among genotypes (Table 3). G10 contained the largest fruit (17.95 cm) whereas G2 contained the smallest fruit of 3.47 cm length. The average fruit length was 6.82 cm. The phenotypic variation (12.91) was very close to the genotypic (12.80) variation suggesting the minimum influence of environment on the character. The PCV (52.68%) in general, was higher than the GCV (52.46%) for the trait, but the differences were very narrow indicating the trait was least affected by the environment and selection for these traits based on phenotypic would be rewarding. However higher value of PCV and GCV indicated the higher magnitude of variability for these traits and consequently more scope for their improvement through selection. The heritability estimate (99.15%) was near about 100% suggesting additive gene interaction thus this trait should be found in next generation. The low genetic advance (7.34) and high genetic advance in percent of mean (107.60%) suggesting more reliable indicator of additive gene action and therefor their improvement can be achieved through mass selection.

Similar results were reported by Kashinath (2003), Farhad *et al*. (2008), Tembhurne *et al*. (2008), Gupta *et al*. (2009), Singh *et al*. (2009), Kumari *et al*. (2010), Berhanu *et al.* (2011), Sreelathakumary and Rajamonyn(2004) and Gogoi and Gautam (2002).

4.1.6. Fruit circumference

Fruit circumference showed considerable variation among 13 genotypes with significant mean sum of squares (1.89) and higher value of coefficient of variation (6.69%). The maximum and minimum value of fruit circumference was found in G11 (4.82 cm) and G5 (2.06 cm) respectively (Table 3). The mean performance for this trait was 2.69 cm. The phenotypic variation (0.66) was a bit more than the genotypic (0.62) variation suggesting the minimum influence of environment on the character. It was also supported by narrow difference between PCV (27.38%) and GCV (26.53%)(Table 4). However medium value of PCV and GCV indicated the considerable amount of variability for these traits thus avail scope of improvement through selection. The trait with high heritability (93.91%), low genetic advance (1.57) and high genetic advance in percent of mean (52.96%) indicated influence of additive gene effect and therefor suggested that any selection in chilli will be effective in fruit yield. These findings are in agreement with reported by Bharadwaj *et al.* (2007), Krishna *et al.* (2007), Gogoi and Gautam (2002), Tembhurne *et al.* (2008), Singh *et al.* (2009) and Gupta *et al.* (2009).

4.1.7. Fruit weight

Significant mean sum of square for fruit weight (12.48) and high coefficient of variation (6.05%) indicated considerable difference among the genotypes studied (Table 3 & Table 4). The maximum fruit weight was found in G10 (8.35 g) and the minimum weight was found in G5 (0.60 g) with an average of 2.03 g. The trait showed very close phenotypic (4.17) variance with the genotypic (4.15) variation suggesting the minimum influence of environment on the character. The PCV (100.63%) in general, was higher than the GCV (100.39%) for the trait, but the difference was very narrow indicating the trait was least affected by the environment and selection for these traits based on phenotypic would be rewarding. However higher value of PCV and GCV indicated the higher magnitude of variability for these traits and consequently more scope for their improvement through selection. The heritability estimate (99.52%) was near about 100% suggesting additive gene interaction thus this trait should be found in next generation. The low genetic advance (4.19) and high genetic advance in percent of mean (206.31%) indicating the preponderance of additive gene action making selection effective.

These results are in conformity with those reported by Sreelathakumary and Rajamony (2004), Sood *et al.* (2006), Shirshat *et al.* (2007), Farhad *et al.* (2008), Manju and Sreelathakumary (2002), Gupta *et al.* (2009) and Singh *et al.* (2009).

4.1.8. Yield per plant

The significant mean sum of square for yield per plant (71339.60) and coefficient of variation (10.90) indicated considerable difference among the genotypes under study (Table 3 & Table 4). The maximum and the minimum yield per plant were recorded as 606.23 g in G10 and 19.34 g in G5 respectively with mean value of 99.17gm. The difference between phenotypic (23857.78) and genotypic (23740.91) variances was low for this trait indicating considerably low environmental influence on this character which was supported by narrow difference between phenotypic (155.75%) and genotypic (155.37%) co-efficient of variation. The heritability (99.51%) for this trait was very close to 100% that indicated additive gene effect on this character. High heritability attached with high genetic advance (316.63) and high genetic advance in percentage of mean

(319.27) indicated the importance of additive genetic effects for the control of this character. Genetic improvement of this character would therefore be highly effective. These results are in agreement with those reported by many earlier workers viz., Bharadwaj *et al.* (2007), Farhad *et al.* (2008), Gupta *et al.* (2009), Singh *et al.* (2009), Kumari *et al.* (2010), Sreelathakumary and Rajamony (2004), Manju and Sreelathakumary (2002), Sood *et al.* (2006) and Shirshat *et al.* (2007).

4.2. Correlation coefficient analysis

Yield is a complex product being influenced by several interdependent quantitative characters. Selection for yield may not be effective unless the directly or indirectly influences of other yield components are taken into consideration. When selection pressure is exercised for improvement of any character highly associated with yield, it simultaneously affects a number of other correlated traits. Hence knowledge regarding association of character with yield and among themselves provides guidelines to the plant breeder for making improvement through selection provide a clear understanding about the contribution in respect of establishing the association by genetic and non-genetic factors. In the present investigation, phenotypic and genotypic correlation coefficients were estimated and are presented in table 5.

4.2.1. Days to first flowering

Days to first flowering showed negative and significant association with number of primary branches per plant at both phenotypic (-0.6204*) and genotypic (-0.8264**) level (Table 5), where increase in one variable cause decrease in another variable and vice-verse and indicating simultaneous selection for these traits is possible. At both genotypic and phenotypic levels, this trait showed non-significant negative association with plant height (-0.4453 and -0.4469), fruit length (-0.4691 and -0.4067), fruit weight (-0.3585 and -0.3182), fruit circumference (-0.0034 and -0.0468) and yield per plant (-0.3544 and -0.3174). Number of fruit per plant showed positive non-significant (0.1212) but negative non-significant (-0.0148) genotypic correlation with this trait. These findings are in agreement with Reddy *et al.* (2008). Farhad *et al.* (2008) reported non-significant and negative association with number of primary branches per plant. However Acharya and Rajput (2003) found significant positive correlation between days to 50% flowering and number of primary branches per plant.

4.2.2. Plant height

Plant height showed significant and positive correlation with number of primary branches per plant at both phenotypic (0.6165*) and genotypic (0.7471**) levels (Table 5), that indicates increase in one trait cause increase in another trait and vice-verse and thus simultaneous selection for these traits is possible. Positive non-significant association was found at phenotypic and genotypic level with number of fruits per plant (0.3496 and 0.4068) and fruit length (0.1046 and 0.1338). This trait was negatively and non-significantly correlated with plant height (-0.4469 and -0.4453), fruit circumference (-0.0184 and -0.0420), fruit weight (-0.0318 and -0.0346) and fruit yield per plant (-0.0439 and -0.0560) at phenotypic and genotypic levels respectively. These findings are in agreement with those of Acharya and Rajput (2003) and Reddy *et al.* (2008). Farhad *et al.* (2008) found positive and non-significant correlation of this trait with number of primary branches per plant in chilli.

4.2.3. Number of primary branches per plant

At both phenotypic and genotypic levels this trait showed (Table 5) significant and positive association with plant height (0.6165* and 0.7471**), fruit length (0.5766* and 0.7799**), fruit weight (0.5217* and 0.6798**), and fruit yield per plant (0.4879* and 0.6361*), where increase in one variable cause increase in another variable and vice-verse and indicating simultaneous selection for these traits is possible. Number of primary branches per plant showed negative and significant correlation with days to first flowering (-0.6204* and -0.8264**) at both phenotypic and genotypic levels, which indicated the simultaneous selection of these traits is not possible. Number of fruits per plant (0.3328 and 0.3118) and fruit circumference (0.1786 and 0.2135) showed positive but non-significant correlation with this trait at phenotypic and genotypic levels. Similar findings are noticed by Acharya and Rajput (2003), Farhad *et al.* (2008) and Reddy *et al.* (2008).

Table 5. Correlation coefficient between yield and yield contributing traits in thirteen chilli genotypes

Characters		DFF	PH	NPB	NFP	FL	FC	FW	FY
DFF	r_g		-0.4453	-0.8264**	0.1212	-0.4691	-0.0034	-0.3585	-0.3544
	r_p		-0.4469	-0.6204*	-0.0148	-0.4067	-0.0468	-0.3182	-0.3174
PH	r_g			0.7471**	0.4068	0.1338	-0.0420	-0.0346	-0.0560
	r_p			0.6165*	0.3496	0.1046	-0.0184	-0.0318	-0.0439
NPB	r_g				0.3118	0.7799**	0.2135	0.6798**	0.6361*
	r_p				0.3328	0.5766*	0.1786	0.5217*	0.4879*
NFP	r_g					0.2886	-0.2038	0.1504	0.1908
	r_p					0.2031	-0.1094	0.1151	0.1482
FL	r_g						0.1282	0.9386**	0.9577**
	r_p						0.1279	0.9352**	0.9539**
FC	r_g							0.4008	0.2483
	r_p							0.3938	0.2449
FW	r_g								0.9699**
	r_p								0.9683**

r_g and r_p represents genotypic and phenotypic correlation coefficient, respectively; * and ** indicates significant at 5% and 1% level of significance, respectively; DFF = Days to first flowering, PH = Plant height (cm), NPB = Number of primary branches per plant, NFP = Number of fruit per plant, FL = Fruit length (cm), FC = Fruit circumference (cm), FW = individual Fruit weight (g) and FY = Fruit yield per plant (g)

4.2.4. Number of fruits per plant

Number of fruits per plant showed no significant correlation with any other traits studied (Table 5). But this trait showed positive non-significant association with plant height (0.3496 and 0.4068), number of primary branches per plant (0.3328 and 0.3118), individual fruit length (0.2031 and 0.2886), individual fruit weight (0.1151 and 0.1504) and fruit yield per plant (0.1482 and 0.1908) whereas fruit circumference showed negative non-significant correlation (-0.1094 and -0.2038) at both phenotypic and genotypic levels. Days to first flowering showed non-significant negative (-0.0148) correlation at phenotypic level while non-significant positive (0.1212) correlation at genotypic level. Acharya and Rajput (2003) reported positive and non-significant correlation of this trait with fruit yield per plant while Farhad *et al.* (2008) and Reddy *et al.* (2008) reported positive and significant association between number of fruits per plant and fruit yield per plant.

4.2.5. Fruit length

Positive and highly significant correlation was found with individual fruit weight (0.9352** and 0.9386**) and yield per plant (0.9539** and 0.9577**) for this trait at phenotypic and genotypic levels respectively (Table 5). This trait showed positive and significant association with number of primary branches per plant (0.5766* and 0.7799**). This indicated increase in one variable cause increase in another variable and vice-verse. Number of fruits per plant (0.2031 and 0.2886), Plant height (0.1046 and 0.1338) and fruit circumference (0.1279 and 0.1282) showed positive but non-significant correlation with this trait at phenotypic and genotypic levels. But days to first flowering showed negative but non-significant (-0.4067 and -0.4691) correlation with this trait. These results are supported by the reports of Tembhurne *et al*. (2008), Reddy *et al.* (2008), Farhad *et al.* (2008) and Berhanu *et al.* (2011).

4.2.6. Fruit circumference

No other traits showed significant correlation with fruit circumference (Table 5). But this trait showed positive non-significant association with individual fruit weight (0.3938 and 0.4008), number of primary branches per plant (0.1786 and 0.2135), individual fruit length (0.1279 and 0.1282) and fruit yield per plant (0.2449 and 0.2483) while negative non-significant correlation were found with days to first flowering (-0.0468 and -0.0034), fruit length (-0.1094 and -0.2038) and number of primary branches per plant (-0.0184 and -0.0420) at both phenotypic and genotypic levels which clearly indicated the independent nature of this character. Acharya and Rajput (2003) reported positive and non-significant correlation of this trait with most of the traits except plant height with positive and significant correlation. Farhad *et al.* (2008) reported positive and significant correlation of this trait with fruit weight.

4.2.7. Fruit weight

Fruit weight showed significant and positive association with yield per plant (0.9683** and 0.9699**), fruit length (0.9352** and 0.9386**) and number of primary branches per plant (0.5217* and 0.6798**) at both phenotypic and genotypic levels (Table 5), thus indicating selection for these traits based on fruit weight is beneficial. This trait showed non-significant and positive association with number of fruits per plant (0.1151 and 0.1504) and fruit circumference (0.3938 and 0.4008) at both levels. Days to first flowering (-0.3182 and -0.3585) and plant height (-0.0318 and -0.0346) showed negative and non-significant association with this trait. These findings are in agreement with those of Acharya and Rajput (2003), Reddy *et al.* (2008), Farhad *et al.* (2008) and Berhanu *et al.* (2011).

4.2.8. Yield per plant

The yield per plant had significant and positive association with fruit length (0.9539** and 0.9577**), individual fruit weight (0.9683** and 0.9699**) and number of primary branches per plant (0.4879* and 0.6361*) at phenotypic and genotypic levels (Table 5). These findings suggested that selection for these traits based on yield per plant is beneficial. This trait showed positive non-significant correlation with number of fruits per plant (0.1482 and 0.1908) and fruit circumference (0.2449 and 0.2483) while negative non-significant correlation was found with days to first flowering (-0.3174 and -0.3544) and plant height (-0.0439 and -0.0560) at at phenotypic and genotypic levels respectively. These results were supported by the reports of Das and Choudhary (1999), Tembhurne *et al*. (2008), Reddy *et al.* (2008), Farhad *et al.* (2008) and Berhanu *et al.* (2011).

4.3. Path analysis

Association of character determined by correlation co-efficient may not provide an exact picture of the relative importance of direct and indirect influence of each of yield components. In order to find out a clear picture of the inter relationship between yield per plant and other yield attributes, path analysis was done. Direct and indirect effects were worked out using path analysis at genotypic level which also measured the relative importance of each component. Estimation of direct indirect effect of path co-efficient analysis for chilli was done and represented in Table 6.

4.3.1. Days to first flowering

The direct contribution of this character on yield per plant was negligible and positive (0.0470). At genotypic level (Table 6), this trait exhibited negligible and positive indirect effect on yield per plant via fruit circumference (0.0001) and plant height (0.0604) whereas negligible and negative indirect effect via number of fruits per plant (-0.0004) and number of primary branches per plant (-0.0515) and low and negative indirect effect via fruit weight (-0.1630) and fruit length (-0.2469). Days to first flowering showed negative and non-significant correlation with yield per plant (-0.3544) at genotypic level. Negligible positive direct effects and negative non-significant correlation indicating the indirect effects seem to be the cause of the correlation. In such situations, the indirect causal factors are to be considered simultaneously for selection. These findings are in agreement with those reported by Farhad *et al.* (2008) and Reddy *et al.* (2008).

4.3.2. Plant height

This character showed a low and negative direct effect (-0.1357) on yield (Table 6) at genotypic level. Plant height showed low and positive indirect effect on yield per plant via fruit length (0.0704), number of primary branches per plant (0.0466) and fruit circumference (0.0009) at genotypic level. This trait showed negligible and negative indirect effect via number of fruits per plant (-0.0015), individual fruit weight (-0.0157) and days to first flowering (-0.0209) at genotypic level which finally produced a negative non-significant genotypic correlation with yield (-0.0560). Negligible direct effects with negative non-significant correlation indicating dropping the selection based on this character.

Table 6. Path coefficient showing direct (diagonal) and indirect effects of some yield contributing traits on fruit yield in thirteen chilli genotypes

Characters	**DFF**	**PH**	**NPB**	**NFP**	**FL**	**FC**	**FW**	**FY (r_g)**
DFF	**0.0470**	0.0604	-0.0515	-0.0004	-0.2469	0.0001	-0.1630	-0.3544
PH	-0.0209	**-0.1357**	0.0466	-0.0015	0.0704	0.0009	-0.0157	-0.0560
NPB	-0.0388	-0.1014	**0.0624**	-0.0011	0.4104	-0.0045	0.3091	0.6361*
NFP	0.0057	-0.0552	0.0194	**-0.0036**	0.1519	0.0043	0.0684	0.1908
FL	-0.0220	-0.0182	0.0486	-0.0011	**0.5263**	-0.0027	0.4267	0.9577**
FC	-0.0002	0.0057	0.0133	0.0007	0.0674	**-0.0210**	0.1822	0.2483
FW	-0.0168	0.0047	0.0424	-0.0005	0.4939	-0.0084	**0.4547**	0.9699**

Residual effect, R = 0.174

* and ** indicates significant at 5% and 1% level of significance, respectively; DFF = Days to first flowering, PH = Plant height (cm), NPB = Number of primary branches per plant, NFP = Number of fruit per plant, FL = Fruit length (cm), FC = Fruit circumference (cm), FW = individual Fruit weight (g) and FY = Fruit yield per plant (g).

These findings are in agreement with those reported by Ajjappalavara *et al*. (2005) and Farhad *et al.* (2008). They found negative and direct effect of this trait on yield.

4.3.3. Number of primary branches per plant

This trait showed negligible and positive direct effect (0.0624) on yield per plant at genotypic level (Table 6). This trait showed moderate and positive indirect effect on yield per plant via fruit length (0.4104) and fruit weight (0.3091); negligible and negative indirect effect via number of fruits per plant (-0.0011), days first flowering (-0.0388), fruit circumference (-0.0045) and plant height (-0.1014). This trait showed significant and positive association (0.6361*) with yield per plant at genotypic level. Positive direct effects and positive correlations indicated that direct selection for yield per plant through this trait will be effective. These results are in conformity with the earlier observations of Bharadwaj *et al*. (2007), Farhad *et al*. (2008), Reddy *et al.* (2008).

4.3.4. Number of fruits per plant

At genotypic level, the direct contribution of number of fruits per plant on yield per plant was negligible and negative (-0.0036) (Table 6). This trait showed negligible and negative indirect effect on yield per plant through plant height (-0.0552); negligible and positive indirect effect through fruit circumference (0.0043), days to first flowering (0.0057), number of primary branches per plant (0.0194), fruit weight (0.0684) and fruit length (0.1519), which finally produced a positive insignificant genotypic correlation with yield (0.1908). Negative negligible direct effects and positive correlation indicating the indirect effects seem to be the cause of positive correlation. In such situations, the indirect causal factors are to be considered simultaneously for selection. These findings are in agreement with Berhanu *et al*. (2011)

4.3.5. Fruit length

Fruit length showed moderate and positive direct effect (0.5263) on yield per plant at genotypic level (Table 6). It exhibited negligible and positive indirect effect on yield per plant through number of primary branches per plant (0.0486); moderate and positive indirect effect via fruit weight (0.4267); negligible and negative indirect effect via number of fruits per plant (-0.0011), fruit circumference (-0.0027), plant height (-0.0182) and days to first flowering (-0.0220). This trait showed positive and highly significant association with yield per plant (0.9577**) at genotypic level. The positive direct effects and significant positive correlations indicated that direct selection for yield per plant through this trait will be effective. These findings corroborate with the reports of Ajjappalavara *et al.* (2005), Krishna *et al.* (2007), Reddy *et al.* (2008) and Berhanu *et al.* (2011).

4.3.6. Fruit circumference

The direct contribution of fruit circumference on yield per plant was negligible and negative (-0.0210) at genotypic level (Table 6). This trait showed negligible and positive indirect effect on yield per plant via number of fruits per plant (0.0007), plant height (0.0057), number of primary branches per plant (0.0133) and fruit length (0.0674); low and positive indirect effect via fruit weight (0.1822) and negligible and negative indirect effect via days to first flowering (-0.0002). This trait showed non-significant and positive association with yield per plant (0.2483) at genotypic level. Negative negligible direct effects and positive correlation indicating the indirect effects seem to be the cause of positive correlation. In such situations, the indirect causal factors are to be considered simultaneously for selection. These findings are in agreement with those of Jabeen *et al.* (2009), Berhanu *et al.* (2011), Farhad *et al.* (2008) and Reddy *et al.* (2008).

4.3.7. Fruit weight

At genotypic levels, the direct contribution of this character on yield per plant was moderate and positive (0.4547) (Table 6). At genotypic level, this trait showed negligible and positive indirect effect on yield per plant via plant height (0.0047) and number of primary branches per plant (0.0424); moderate and positive indirect effect through fruit length (0.4939) and negligible and negative indirect effect via number of fruits per plant (-0.0005), fruit circumference (-0.0084) and days to first flowering (-0.0168). Finally this trait showed significant and positive association with yield per plant (0.9699**) at genotypic level. The moderate positive direct effect of this trait and its pronounced association with yield per plant reveals its true relationship with yield and direct selection for this trait will be rewarding. These findings corroborate with the reports of Farhad *et al*. (2008), Reddy *et al.* (2008), Jabeen *et al*. (2009) and Berhanu *et al*. (2011).

4.4. Genetic diversity analysis

Genetic divergence was analyzed by using GENSTAT software programme. Genetic diversity analysis involved several steps i.e., estimation of distance between the genotypes, clusters and analysis of inter-cluster distance. Therefore, more than one multivariate technique was required to represent the results more clearly and it was obvious from the results of many researchers (Bashar, 2002 and Uddin, 2001). In the analysis of genetic diversity multivariate techniques were used.

4.4.1. Principal component analysis

Principal components were computed from the correlation matrix from genotype scores obtained from first components and succeeding components with latent roots greater than the unity. The principal component analysis yielded eigen values of each principal component axes. The first two components (days to first flowering and plant height) with Eigen values greater than 1 contributed 91.26% of the variability among thirteen genotypes evaluated for eight quantitative traits (Table 7).

Genotypes were grouped into three clusters. Cluster I consists of one genotypes, which is smallest cluster. Cluster II composed of eight genotypes that was largest cluster. Finally, cluster III composed of four genotypes (Table 8). Genotypes in each cluster produced the highest mean for fruit yield per plant and the lowest mean value was for fruit circumference (Table 9). It was observed that all the cluster mean values for plant height, number of fruits per plant, fruit length and fruit circumference were more or less similar. Thul *et al.* (2009), Farhad *et al.* (2010) and Sudre *et al.* (2010) studied the utilization of principal component analysis in genetic divergence studies in chilli.

4.4.2. Construction of scatter diagram

In multivariate analysis, Cluster analysis is the technique used to divide up objects into similar groups, or more precisely, groups whose members are all close to one another on various dimensions being measured. Depending on the values of principal component scores 2 and 1 obtained from the principal component analysis, a two dimensional scatter diagram (Z1 - Z2) using component score 1 as X-axis and component score 2 as Y-axis was constructed, which has been presented in Figure 1.

Table 7. Eigen values, percentage of variation and cumulative percentage in respect of eight axes in thirteen genotypes of chilli

Principal Component axes	Eigen values	Percent of variation	Cumulative percentage
I	13.25	78.84	78.84
II	2.09	12.42	91.26
III	0.73	4.37	95.63
IV	0.51	3.03	98.66
V	0.13	0.79	99.45
VI	0.06	0.35	99.80
VII	0.02	0.14	99.94
VIII	0.01	0.06	100

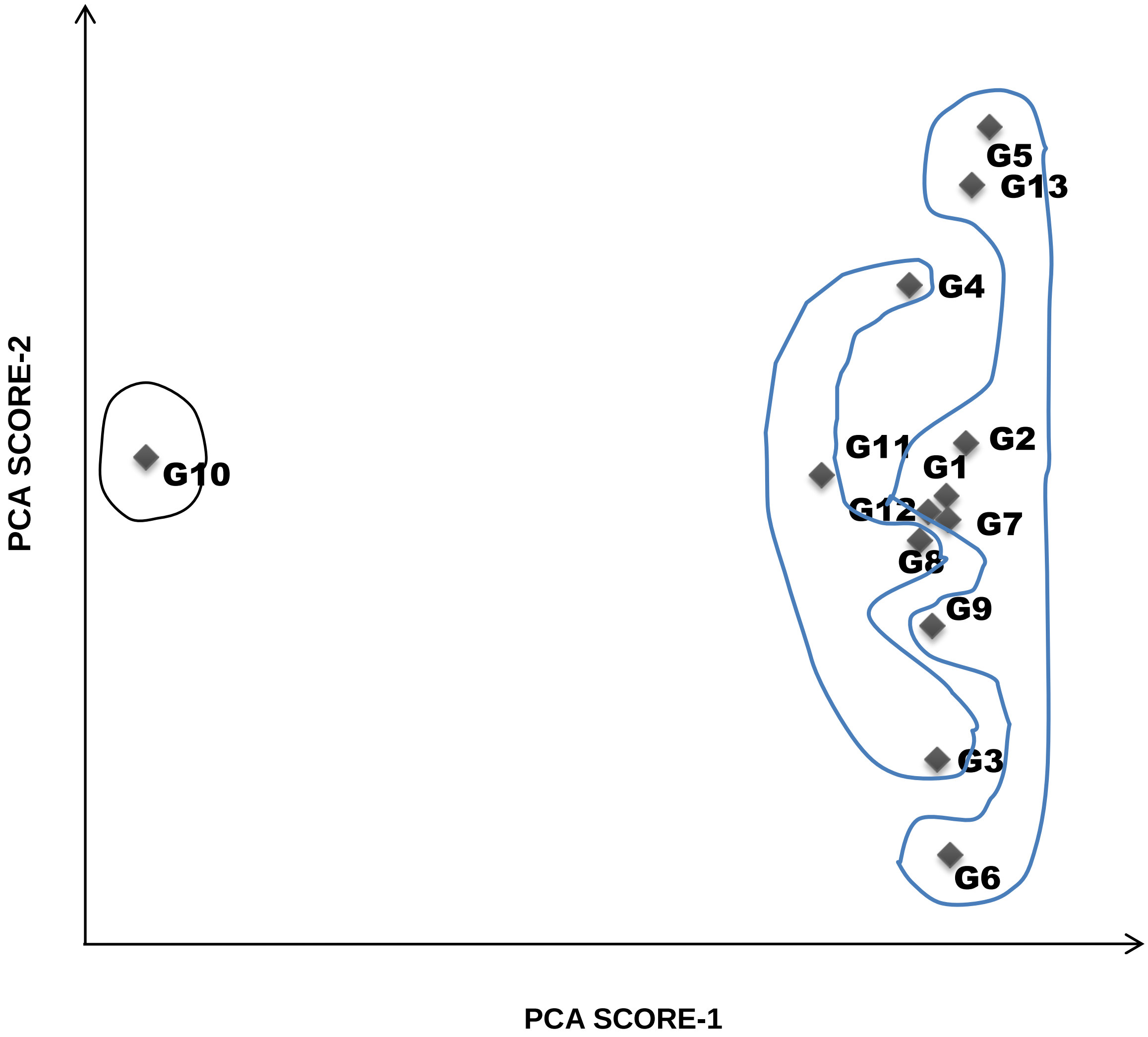


Figure 1. Scatter diagram of thirteen chilli genotypes based on their principal component scores

The position of the genotypes in the scatter diagram was apparently distributed into three groups, which indicated that there existed considerable diversity among the genotypes.

4.4.3. Non-hierarchical clustering

Thirteen genotypes were grouped into three clusters through non-hierarchical clustering. Cluster analysis grouped genotypes together with greater genetic similarity; the clusters did not necessarily include all genotypes from same origin. Srinivas *et al* (2015) categorized 78 genotypes using multivariate analysis into nine well-characterized groups. Saleh *et al.* (2016) also clustered sixty accessions into five distinct groups. Compositions of different clusters with their corresponding genotypes in each cluster are presented in Table 7.

4.4.3.1. Cluster I

Cluster I had only one genotype namely G10 (Table 8). From the clustering mean values (Table 9), it was observed that cluster-I showed the lowest days to first flowering (59.49 DAS) and shortest plant (7.73 cm). This cluster showed moderate value for the traits number of primary branches per plant (18.01), fruit length (2.91 cm) and individual fruit weight (48.59 g). It also produced lowest number of fruits per plant (5.12), minimum fruit circumference (1.12 cm) with maximum fruit yield per plant (99.73 g).

4.4.3.2. Cluster II

Cluster II was composed of eight genotypes namely G1, G2, G5, G6, G7, G9, G12 and G13 (Table 8). This is the largest cluster. From the clustering mean values (Table 9), these genotypes were late flowering (69.07 DAS), produced the highest mean for plant height (9.63 cm) with maximum number of primary branches per plant (23.03). This cluster showed moderate number of fruits per plant (6.51), fruit circumference (1.44 cm), individual fruit weight (54.91 g) with minimum fruit length (2.66 cm) and fruit yield per plant (91.75 g).

4.4.3.3. Cluster III

From the table no 8, it was observed that Cluster III was composed of four genotypes namely G3, G4, G8 and G11. From the clustering mean value (Table 9), it was observed that the genotypes of cluster III produced the moderate mean for days to first flowering

(65.76 DAS), plant height (9.24 cm) but lowest number of primary branches per plant (16.60). This cluster showed maximum number of fruits per plant (9.25), fruit length (3.34 cm), fruit circumference (3.75 cm) and individual fruit weight (219.17 g) but these genotypes produced medium yield per plant (98.83 g) among the clusters.

4.4.4. Principal coordinate analysis

The average intra and inter-cluster D^2 values estimated as per the procedure given by Singh and Chowdhary (1979) are presented in the table 10. The mean intra-cluster D^2 values ranged from 0.00 to 1.23, where the maximum intra-cluster distance was 1.23 in cluster II followed by 1.15 in cluster III and minimum intra-cluster distance was zero in cluster I, which composed of only one genotype. The coordinates obtained from the Principal Component analysis (PCA) were used as input at Principal Coordinate Analysis (PCO) to calculate distances among the points reported by Digby *et al.* (1989).

4.4.5. Canonical variate analysis

To compute the inter-cluster Mahalanobis's D^2 values canonical variate analysis was used. Table 10 and Figure 2, indicates the intra and inter-cluster distance (D^2) values. The inter-cluster distances indicating wider genetic diversity among the genotypes of different groups. Results indicated that the highest inter cluster distance was observed between cluster I and Cluster II (607.55) followed by between cluster I and cluster III (513.60). The lowest inter-cluster distance was observed between the Cluster II and Cluster III (94.16). Inter-cluster distances were larger than the intra-cluster distances indicating wider genetic diversity among the genotypes of different groups thus crosses can be made between genotypes of these clusters to obtain heterotic hybrids and desirable segregants.

Yatung *et al* (2014); studied genetic diversity in 30 chilli and reported the highest (459.81) inter cluster distance between cluster II and IV and the lowest (36.04) between cluster I and IV. Cluster III (D^2= 67.66) have exhibited highest intra cluster distance and the lowest was observed in cluster II (D^2=11.19).

However Matin *et al*. (2016); screened out suitable parents for hybridization programme. They found the maximum inter-cluster distance between cluster II and V (532.214) and the minimum inter-cluster distance was obtained between the cluster I and IV (91.948).

Table 8. Grouping of thirteen chilli genotypes into three clusters

Clusters	No. of Genotypes	Description
I	1	G10
II	8	G1, G2, G5, G6, G7, G9, G12 and G13
III	4	G3, G4, G8 and G11

Table 9. Cluster means for eight traits in thirteen chilli genotypes

	Clusters		
Characters	**I**	**II**	**III**
Days to first flowering	59.49	69.07	65.76
Plant height (cm)	7.73	9.63	9.24
Number of primary branches per plant	18.01	23.03	16.60
Number of fruits per plant	5.12	6.51	9.25
Fruit length (cm)	2.91	2.66	3.34
Fruit circumference (cm)	1.12	1.44	3.75
Individual Fruit weight (g)	48.59	54.91	219.17
Fruit yield per plant (g)	99.73	91.75	98.83

Table 10. Intra (bold) and inter cluster distances of three clusters for chilli genotypes

Cluster	I	II	III
I	**0.00**	607.55	513.60
II		**1.23**	94.16
III			**1.15**

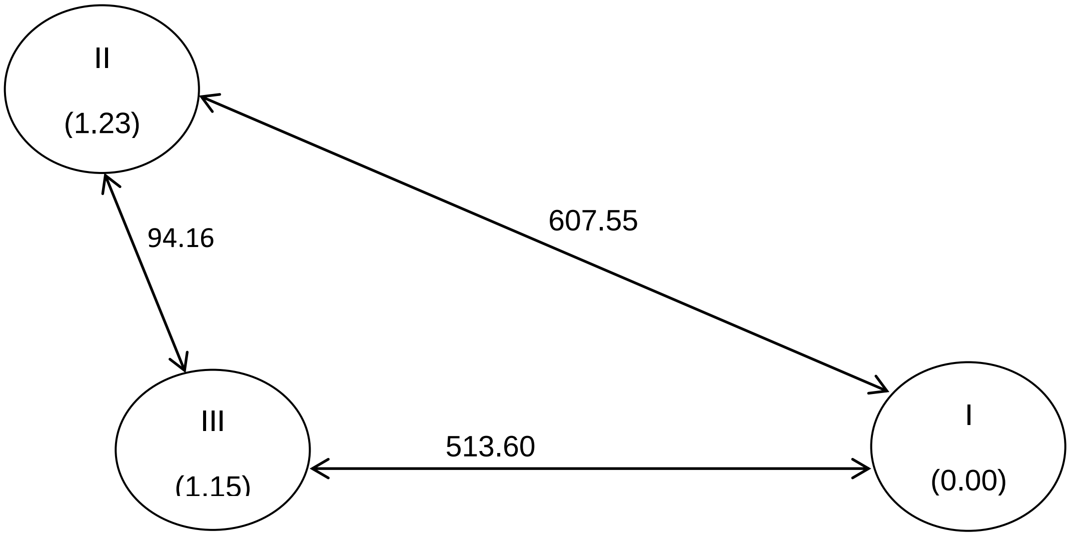


Figure 2. Cluster diagram showing the average intra and inter cluster distances

4.4.6. Relative contribution of individual characters towards divergence

Relative contribution of individual characters towards divergence was measured through latent vectors (vector I and II) for different quantitative traits. Latent vectors (Vector I and II) for different quantitative traits in this experiment are presented in Table 11. Fruit yield per plant was positive for both vectors (0.02536 and 0.42278 respectively) indicating this trait contributes maximum towards divergence. However number of primary branches per plant (-0.00056 and -0.15839) showed maximum negative value for both latent vectors, following plant height (-0.00706 and -0.12820), number of fruits per plant (-0.02010 and -0.05491), fruit circumference (-0.01178 and -0.00427) and fruit length (-0.00126 and -0.00075), indicating less involvement of these towards divergence. Days to first flowering (0.00763 and -0.88128) and individual fruit weight (-0.99935 and 0.00615) showed moderate contribution towards divergence. Srinivas et al (2015) and Hasan *et al.* (2015) found similar result that was maximum contribution of yield per plant towards divergence. However Matin *et al.* (2016) found fruit diameter (16%) contributed maximum to the total divergence.

4.4.7. Comparison of Different Multivariate Techniques

The cluster pattern of D^2 analysis though non-hierarchical clustering has taken care of simultaneous variation in all the characters studied. However, the distribution of genotypes in different cluster of the D^2 analysis has followed more or less similar trend of principal component analysis which was found to be alternative method in giving the information regarding the clustering pattern of genotypes. However the principal component analysis provides the information regarding the contribution of characters towards divergence of chilli.

Table 11. Latent vectors for eight traits of thirteen chilli genotypes

Characters	Vector-I	Vector-II
Days to first flowering	0.00763	-0.88128
Plant height (cm)	-0.00706	-0.12820
Number of primary branches per plant	-0.00056	-0.15839
Number of fruit per plant	-0.02010	-0.05491
Fruit length (cm)	-0.00126	-0.00075
Fruit circumference (cm)	-0.01178	-0.00427
Individual Fruit weight (g)	-0.99935	0.00615
Fruit yield per plant (g).	0.02536	0.42278

4.4.8. Selection of Genotypes for Further Hybridization

Selection of genetically divergent genotypes is an important step for hybridization programme. So, the genotypes were to be selected on the basis of specific objectives. A higher heterosis could be produced from the crosses between genetically distant parents (Falconer, 1964; Moll *et al.* 1962; Raminujam *et al.* 1974; Ghaderi *et al.* 1984; Mian and Bhal, 1989). Considering the magnitude of genetic distance and agronomic performance, the genotypes G10 from cluster I and G6, G7 and G12 from cluster II would be suitable for maximum yield per plant. Selection of genetically diverse parents is the prime task for any plant breeding activities. Therefore, considering the magnitude of genetic distance, contribution of character towards divergence, magnitude of cluster mean and agronomic performance the genotype G10 (GPB0010/14) for maximum number of primary branches per plant, fruit length, fruit weight and fruit yield per plant from cluster I, G6 (GPB0006/14) for maximum fruit weight from cluster II, G7 (GPB0007/14) for maximum fruit length from cluster II and G12 (GPB0012/14) for moderate values of all traits viz. number of primary branches per plant, fruit length and fruit weight from cluster II. Therefore considering group distance and other agronomic performances of the inter-genotypic crosses between G10 (GPB0010/14) and G6 (GPB0006/14); G10 (GPB0010/14) and G7 (GPB0007/14), G10 (GPB0010/14) and G12 (GPB0012/14) may be done for future hybridization program.

CHAPTER V

SUMMARY AND CONCLUSION

The present investigation was carried out during the season of kharif in 2014-15 at the experimental field of Sher-e-Bangla Agricultural University, Dhaka, with 13 genotypes of chilli (*Capsicum frutescens* L.). The mean, genetic variability, heritability, genetic advance as per cent of mean, genetic divergence, character association and the magnitude of direct and indirect effects of yield component traits on dry fruit yield per plant were studied for 8 characters viz. days to first flowering, plant height, number of primary branches per plant, number of fruits per plant, fruit length, fruit circumference, individual fruit weight and yield per plant.

The analysis of variance revealed significant differences and high coefficient of variance among the genotypes for all the characters studied indicating the presence of variability in the studied material. The phenotypic coefficients of variation (PCV) were higher than the genotypic coefficients of variation for all the characters indicating the interaction of environment to express the characters. High magnitude of PCV and GCV were observed for fruit length, fruit weight and fruit yield per plant indicating the existence of wide range of genetic variability in the germplasm for these traits. These traits also showed high broad sense heritability indicating the control of additive genes and hence there is a good scope for the further improvement of these characters through selection. High heritability (h^2_b) coupled with high genetic advance as percent of mean (GAPM) were observed for fruit length (h^2_b- 99.15% & GAPM- 107.60), fruit circumference (h^2_b - 93.91% & GAPM- 52.96), individual fruit weight (h^2_b- 99.52% & GAPM- 206.31) and yield per plant (h^2_b- 99.51% & GAPM-319.27) indicating the predominance of additive gene action and hence direct phenotypic selection is useful for these traits. High heritability coupled with moderate genetic advance as percent of mean was observed for plant height (h^2_b- 73.67% & GAPM- 33.43) indicating the role of additive and non-additive gene action and further improvement of this character would be easier through mass selection, progeny selection to exploit the additive gene effects rather than simple selection.

Investigation on character association indicated that significant and positive correlations were observed at both phenotypic (P) and genotypic (G) levels for number of primary branches per plant (P = 0.4879, G = 0.6361), fruit length (P = 0.9539, G = 0.9577) and fruit weight (P = 0.9683, G = 0.9699) with yield per plant indicating the importance of these traits in selection for increasing yield and were identified as yield attributing characters. Thus selection can be relied upon these characters for the genetic improvement of yield of chilli. The path analysis revealed that fruit length (0.5263), individual fruit weight (0.4547), days to first flowering (0.0470) and number of branches per plant (0.0624) had positive direct effect on yield per plant indicating that direct selection based on these traits may be helpful in evolving high yielding varieties of chilli. Fruit length via fruit length (0.4939) had highest positive indirect effect on yield per plant. The highest negative indirect effect was recorded for days to first flowering via fruit length (-0.2469) on yield per plant.

From the results of multivariate analysis, the presence of considerable genetic divergence among the 13 genotypes was revealed. Days to first flowering and plant height with Eigen values greater than 1 contributed 91.26% of the variability. All the genotypes were grouped into 3 clusters. Cluster I, cluster II and cluster III were composed of one, eight and four genotypes respectively. The highest inter-cluster distance was observed between cluster I and II (607.55), followed by between cluster I and III (513.60) and cluster II and III (94.16). On the other hand, the maximum intra-cluster distance was found in cluster II (1.23), while the minimum distance was found in cluster I (0.00). Based on intra and inter-cluster distance, it is suggested to make crosses between the genotypes of cluster I (GPB0010/14) and the cluster II (GPB0001/14, GPB0002/14, GPB0005/14, GPB0006/14, GPB0007/14, GPB0009/14, GPB0012/14 and GPB0013/14). Therefore, considering the magnitude of genetic distance, contribution of character towards divergence, magnitude of cluster mean and agronomic performance the genotype G10 (GPB0010/14) for maximum number of primary branches per plant, fruit length, fruit weight and fruit yield per plant from cluster I, G6 (GPB0006/14) for maximum fruit weight from cluster II, G7 (GPB0007/14) for maximum fruit length from cluster II and G12 (GPB0012/14) for moderate values of all traits viz. number of primary branches per plant, fruit length and fruit weight from cluster II. Therefore considering group distance and other agronomic performances of the intergenotypic crosses between G10 (GPB0010/14) and G6 (GPB0006/14); G10 (GPB0010/14) and G7 (GPB0007/14), G10 (GPB0010/14) and G12 (GPB0012/14) may be exploited for the development of heterotic hybrids in future breeding programmes.

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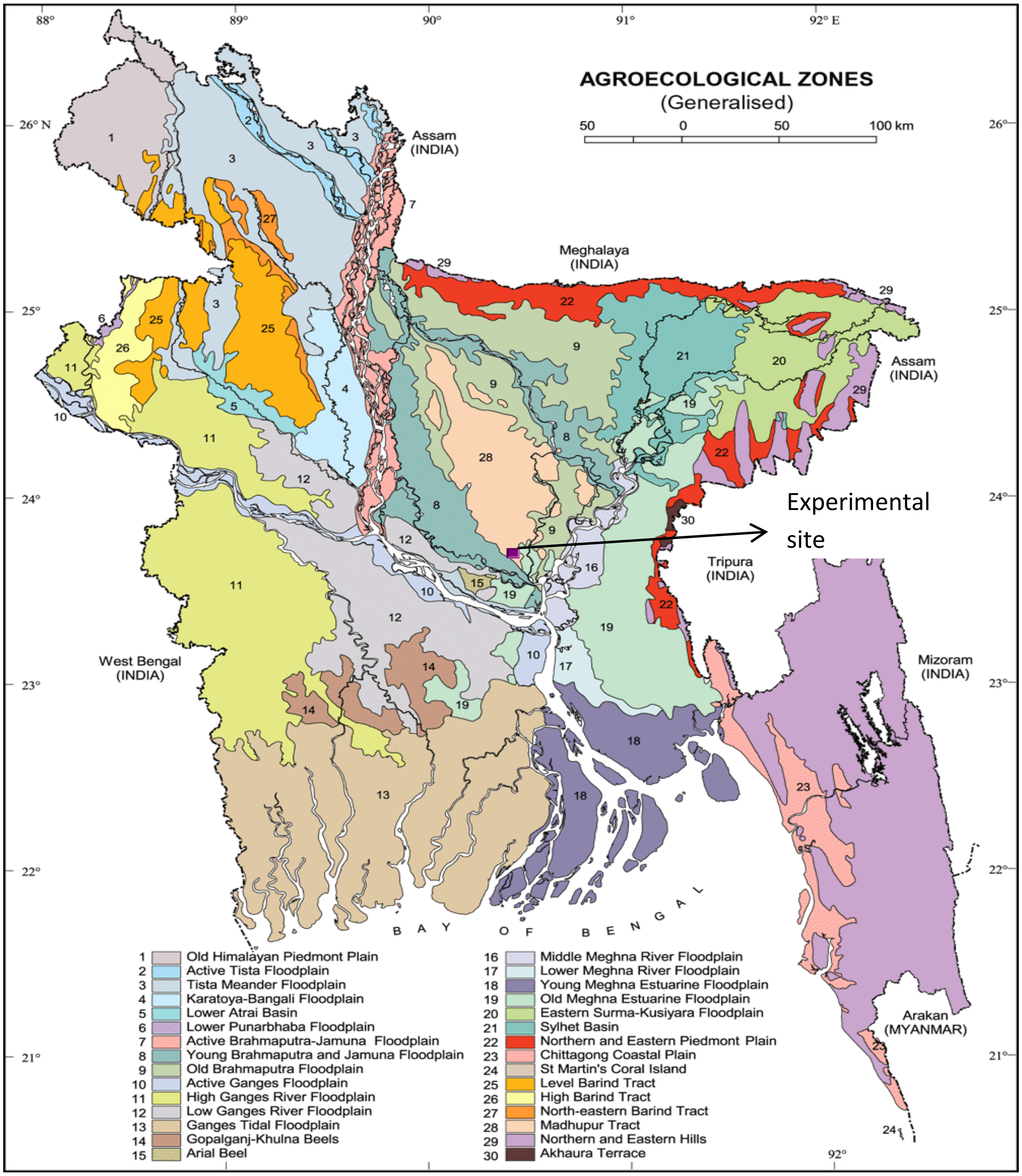
APPENDICES

Appendix I. Map showing the experimental site under study



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

A. Physical composition of the soil

Soil separates	Percentage (%)	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
01.	Organic carbon (%)	0.82	Walkley and Black, 1947
02	Total N (kg/ha)	1790.00	Bremmer and Mulvaney,1965
03	Total S (ppm)	225.00	Bardsley and Lanester,1965
04	Total P (ppm)	840.00	Olsen and Sommers, 1982
05	Available N (kg/ha)	54.00	Bremner, 1965
06	Available P (kg/ha)	69.00	Olsen and Dean ,1965
07	Exchangeable K (kg/ha)	89.00	Pratt, 1965
08	Available S (ppm)	16.00	Hunter,1984
09	PH (1:2.5 soil to water)	5.55	Jackson,1958
10	CEC	11.23	Chapman, 1965

Source: Central library, Sher-e-Bangla Agricultural University, Dhaka-1207.

Appendix III. Monthly average temperature, relative humidity, rainfall and day-length of the experimental site during the period from December, 2014 to June, 2015

Month	Temperature			Relative Humidity (%)	Rainfall (mm) (total)	Day-length (hr)
	Min	Max	Avg			
December, 2014	14.1	26.4	20.4	73	12.8	10.7
January, 2015	12.2	25.4	18.0	71	7.7	11.0
February, 2015	20.4	28.1	24.3	64	28.9	11.2
March, 2015	23.6	32.5	28.1	62	65.8	12.0
April, 2015	23.6	33.7	28.7	71	156.3	12.4
May, 2015	24.5	32.9	28.7	76	339.4	13.1
June, 2015	26.1	32.1	29.1	82	340.4	13.5

Source: Bangladesh Metrological Department (Climate division), Agargaon, Dhaka1212.

Appendix IV. Analysis of variance for different morphological plant characters of thirteen Chilli genotypes

Sources of variations	Degrees of freedom	Days to first flowering	Plant height	Number of primary branches per plant	Number of fruits per plant	Fruit length	Fruit circumference	Fruit weight	Fruit yield per plant
Replication	2	7.72	28.27	1.01	6.57	0.02	0.06	0.03	55.46
Genotype	12	236.13**	474.1**	11.32**	171.0**	38.51**	1.89**	12.48**	71339.6**
Error	24	30.45	50.48	3.12	57.57	0.11	0.11	0.02	116.88

** indicates significant at 0.01 probability level

Appendix V. Mean performance of thirteen Chilli genotypes.

Genotypes	DFF	PH	NPB	NFP	FL	FC	FW	YP
G1	100.00	65.89	9.11	18.63	5.13	2.97	1.17	52.9
G2	99.33	62.89	8.22	14.67	3.47	4.30	1.00	38.21
G3	95.00	81.61	9.97	17.11	7.77	2.71	1.47	69.69
G4	115.00	53	6	34	5.16	2.52	1.36	67.67
G5	92.50	42.89	5.33	5.66	4.09	2.06	0.60	19.34
G6	91.67	88.42	10.38	17.81	6.69	2.55	1.41	58.50
G7	94.33	65.11	7.9	19.78	7.14	2.62	1.32	58.98
G8	95.00	65.78	8.11	27.44	5.95	2.91	1.65	79.60
G9	86.00	67.11	12.11	27.11	6.26	2.54	1.39	40.71
G10	87.50	58.65	12.33	17.96	17.95	3.40	8.35	606.23
G11	94.33	63.11	9.99	14.72	7.23	4.82	3.81	115.04
G12	97.50	67.8	9.46	22.57	6.9	2.19	1.43	48.44
G13	115.00	51.17	5.17	11.16	4.9	2.95	1.4	33.87

DFF = Days to first flowering, PH = Plant height (cm), NPB = Number of primary branches per plant, NFP = Number of fruit per plant, FL = Fruit length (cm), FC = Fruit circumference (cm), FW = individual Fruit weight (g) and FY = Fruit yield per plant (g).