GENETIC DIVERSITY ANALYSIS OF GREEN CHILI (*Capsicum frutescens* L.)

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GENETIC DIVERSITY ANALYSIS OF GREEN CHILI (*Capsicum frutescens* L.)

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CERTIFICATE

This is to certify that thesis entitled," ***GENETIC DIVERSITY ANALYSIS OF CHILI (Capsicum frutescens)"*** *submitted to the faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of* ***MASTER OF SCIENCE IN GENETICS AND PLANT BREEDING****, embodies the result of a piece of bonafide research work carried out by* ***ISMAT ARA EMA****, Registration No.:* ***14-06121*** *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 been duly been acknowledged by her.*

Dated: June, 2021
Place: Dhaka, Bangladesh

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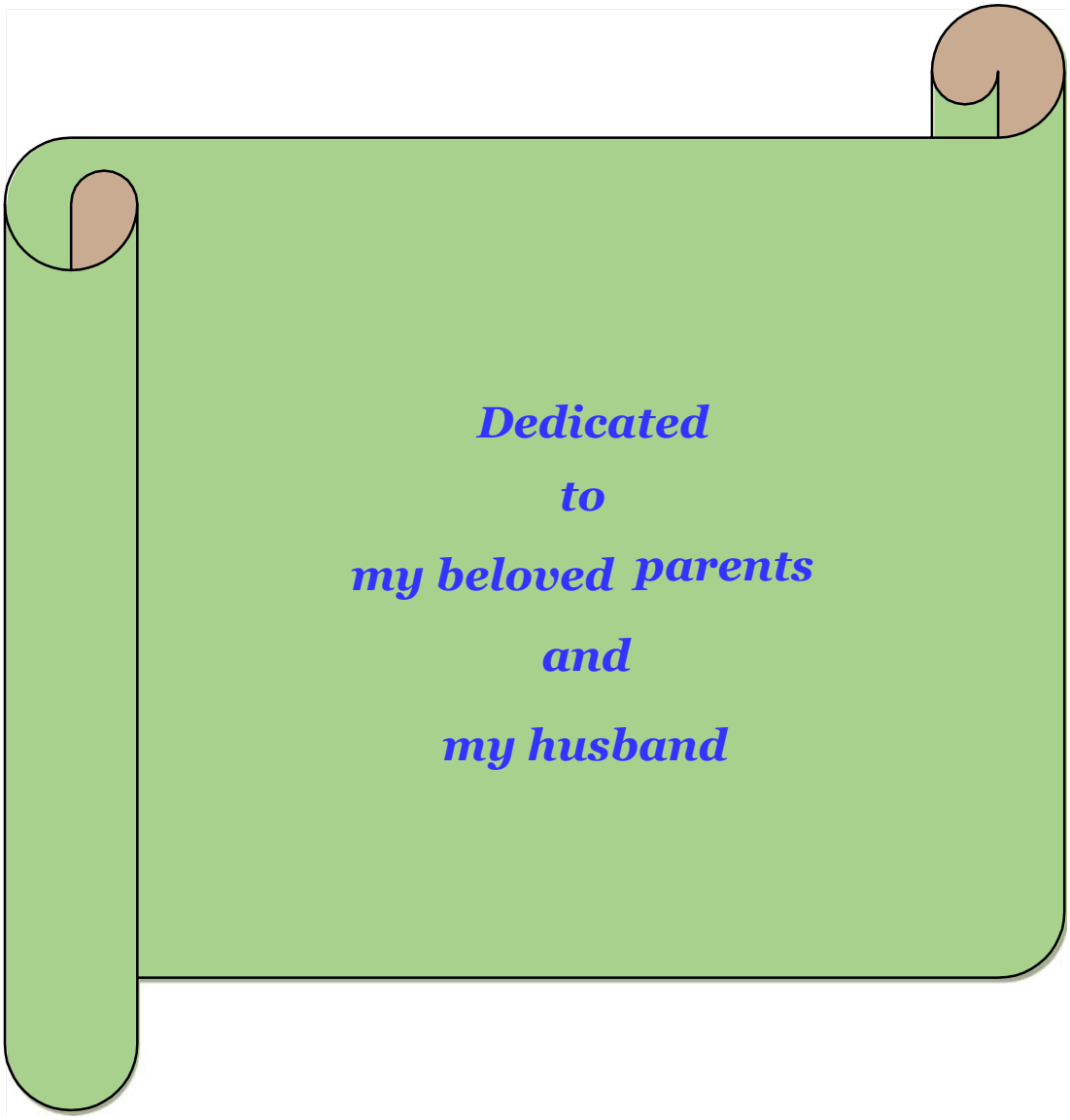
Dedicated
to
my beloved parents
and
my husband

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GENETIC DIVERSITY ANALYSIS OF GREEN CHILI (*Capsicum frutescens* L.)

ABSTRACT

The present research work was conducted to study the characterization and genetic diversity analysis of green chili during the period from October 2019 to March 2020 in rabi season in the experimental field of Sher-e-Bangla Agricultural University, Sher-e-Bangla Nagar, Dhaka 1207. In this experiment 20 chili genotypes were used as experimental material in a randomized complete block design with three replications. Analysis of variance revealed highly significant differences among genotypes for different characters studied. The highest phenotypic co-efficient of variation (70.09) and genotypic co-efficient of variation (69.64) was found in yield per plant (g). High heritability coupled with high genetic advance and genetic advance in percentage of mean was found in yield per plant (g) which indicated predominance of additive gene expression on this character and direct phenotypic selection of this character. The genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients, indicating strong inherent association between the characters under studied. Investigation on character association indicating that yield per plant had the highest significant positive correlation with individual fruit weight in both genotypic and phenotypic level. Path analysis revealed that plant height (cm), number of primary branches and individual fruit weight (g) showed positive direct effect on yield per plant (g) indicating that direct selection based on these traits. Principal component analysis identified three principal components, which contributed 68.06% of cumulative variance. The 20 genotypes were grouped into five different clusters. The highest intra-cluster distance was computed for cluster V. The maximum inter cluster divergence was observed between cluster III and V and the lowest was between cluster I and II. Therefore, considering the magnitude of genetic distance, contribution of character towards divergence, magnitude of cluster mean and agronomic performance the genotypes G18 from cluster V for number of primary branches, G14 from cluster IV for individual fruit weight (g) and days to first harvest and G5, G11 and G13 from cluster III for yield per plant might be considered better parents for future hybridization programme.

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LIST OF ABBREVIATIONS

FULL NAME	ABBREVIATIONS
Analysis of Variance	ANOVA
Agro-Ecological Zone	AEZ
Archives	*Arch.*
Bangladesh Bureau of Statistics	BBS
Biology	*Bio*.
Biological science	*Biosci.*
Bangladesh Agricultural Research Institute	BARI
Centimeter	Cm
Coefficient of Variations	CV
Canonical Variate Analysis	CVA
Days after transplanting	DAT
Degrees of freedom	Df
Fruit Yield	FY
Fruit length	FL
Gram	G
Genotypic Variance	σ^2_g
Genetic Advance	GA
Genotypic Coefficient of Variation	GCV
Hectare	H
Heritability in Broad Sense	h^2b
International	*Intl.*
Journal	*J.*
Kilogram	Kg
Least significant differences	LSD
Phenotypic Coefficient of Variation	PCV
Meter	M
Murate of Potash	MP
Number	no.
Plant Height	P^H
Percent	%
Principal Component Analysis	PCA
Principal Coordinate Analysis	PCO
Phenotypic Variance	σ^2_p
Randomized Complete Block Design	RCBD
Relative Humidity	RH
Research	Res.
Square meter	m^2

Sher-e-Bangla Agricultural University	SAU
And Others	*et al*.

CHAPTER I
INTRODUCTION

Chili (*Capsicum frutescens*) is originated in South and Central America belongs to the family Solanaceae is a spice crop and also used as vegetable and widely cultivated throughout the world (Dias *et al*., 2013; Wahyuni *et al*., 2013). It is one of the most important ingredients used in the everyday diet of the people of south and south-east Asia. Chili has high demand among the consumers due to its diversified uses. The constituents of chili are important for its nutritional value, aroma, texture, color and it is also a good source of oleoresin which has diversified uses in process of food, beverage industries and in pharmaceuticals (Osuna-Garcia *et al*., 1998; Marin *et al*., 2004). Over 100 species have been named under the genus capsicum, but most of the people recognize only two species. *Capsicum annum* L. and *Capsicum frutescens* L. (Purseglove 1968).

Throughout the world, chili is generally consumed either in fresh, dried or in powder (El-Ghoraba *et al*., 2013). In Bangladesh it is an important spice crop. Generally, chili is grown throughout the country but it is largely concentrated in Bogra, Rangpur, Comilla, Noakhali, Faridpur, Chittagong and Mymensingh district. The actual area tinder chili cultivation in Bangladesh is not available due to its seasonal nature of cultivation. In 2020-21, Total area covered by chili was 66,235 hectares with 52,215 million tons per hectare yield. Almost all the varieties of low and medium pungency cultivated on a field scale in Bangladesh are belonged to *Capsicum frutescens*. Most of the varieties cultivated in Rabi season.

Chilies are widely used throughout the tropics and are major ingredients of curry powder in the culinary preparations. They extensively used in Central America as constituents of dishes such as *tamales* and ‘chile con curne’. In its powdered form, it constitutes red or caynee pepper. Extracts of chilies are used in the production of ginger beer and other beverages. Cayenne pepper is incorporated in poultry feeds. *Capsicum frutescens* used in medicine as carminatives internally, besides being in external counter irritant. The green chilies are rich in routine which is of immense pharmaceutical need (Persiglove, 1977). It is quite rich in nutritive value and supposed to contain certain

medicinal properties (Chawdhury, 1976). Commercial cayenne pepper is the preparation of dried, finally grounded, mature of various highly pungent or 'hot' forms of *Capsicum frutescens.* These pungent are used in the manufacture of sauces and curry powders and in the preparation of pickles. The chief constituent of chili (*Capsicum frutescens*) pericarp is a crystalline colorless pungent principle known as capsaicin ($C_{18}H_{27}NO_3$) a condensation product of 3-hydroxy-4-methoxy benzylalamine and decylenic acid which produces a highly irritating vapor on heating (Anon.,1952). Green chilies are rich in vitamin A and C and the seed contain traces of starch (Saimbhi *et al*., 1977; Sayed and Bagavandas, 1980).

Morphological characterization based on qualitative traits of crops is a very crucial and essential first step in any crop improvement and breeding programme. Parental purity judgement and varietal identification are an important factor for the released genotypes Cultivars can be identified and differentiated based on differences in morphology of seed, seedling and grow up plant. Morphological characterization of chili germplasm accessions has been studied for most plant and fruit traits. Evaluation and Characterization of chili germplasm becomes a necessary step for utilizing the available diversity for improvement of the crop.

Genetic diversity is one of the most important criteria for parent selection. Genetic diversity is a pre-requisite for an efficient plant breeding program. Crop improvement largely depends on existence of genetic variability. The plant breeders are always interested to know the genetic diversity among the varieties available due to reasons that crosses between genetically diverse parents are likely to produce high heterotic effect (Ramanujam *et al*., 1974). Analysis of genetic diversity is useful in selecting diverse parental combinations, reliable classification of accessions, and for exact identification of variety. Germplasm characterization is important for conservation and utilization of plant genetic resources (Thul *et al*., 2012).

Moreover, the success of any crop improvement program depends not only on the amount of genetic variation present in a crop but also on magnitude of variation which is heritable from the parent to the progeny (Bello *et al*., 2014). A wide range of variability is available in chili genotypes which provide great scope for improving fruit yield through systematic breeding. Estimation of genetic variability present in the

germplasm of a crop is a pre-requisite for designing effective breeding program (Parkash, 2012). Variability and genetic diversity are the fundamental law of plant breeding which is major tool being used in parent selection to efficient breeding program (Bhatt, 1973).

Moreover, evaluation of genetic diversity is important to know the source of genes for a particular trait within the available germplasm (Tomooka, 1991). Genetic divergence is a basic requirement for effective selection within the existing population or population arising out of hybridization. More diverse the parents within a reasonable range, better are the chances of improving economic characters under consideration in the offspring. Thus, the knowledge of genetic diversity present in a given crop species for the character under improvement is of paramount importance for the success of any plant breeding.

The aim of this study is to characterize various chili genotypes to know their morphological characteristics and differentiate them from each other and to access the variations present in genotypes under consideration and identify promising genotypes and traits which can be used in future breeding program. In order to increase the frequency of desired genotypes in breeding progenies superior parents with high breeding values are needed.

The present experiment was conducted to study available characterization, genetic nature and genetic diversity of 20 chili genotypes collected from home and abroad for more promising and necessary to develop new varieties of chili in the country. The specific objectives of the present study were as follows:

1. To estimate the variability for different quantitative characters involved among 20 chili genotypes,
2. To estimate the genetic diversity among 30 chili materials,
3. To characterize and interrelationship among the genotypes on the basis of yield and yield contributing traits and
4. To screen suitable diversified parents for the utilization in future hybridization programme.

CHAPTER II
REVIEW OF LITERATURE

Characterization and genetic diversity are the fundamental law of plant Breeding which is major tool being used in parent selection for efficient hubridization programme. (Bhatt, 1973). It is a prerequisite for effective parent selection. The quantification of genetic diversity through biometrical procedures such as Mahalanobis's D-statistics and Canonical Variate Analysis (CAV) has possible to choose genetically diversed parents. Recent work indicates that the Mahalanobis's generalized distance (D^2-statistics) may be an efficient tool in the quantitative estimation of genetic diversity. Genetic diversity is an essential tool to the diverge goals such as producing cultivars with increased yield, wider adaptation, desirable quality, disease and insect resistance. More diverse the parents exhibit high heterotic F_1 and board spectrum variability in segregating generation (Arunachalam. 1991).

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

Kaouther *et al.* (2015) conducted an agronomic evaluation with five local accessions of chilli pepper namely, Tebourba, Somaa, Korba, Awled Haffouz and Souk Jedid, at Higher Institute of Agronomy, Chott Mariem, Sousse (Tunisia) and stated that Tebourba was the earliest to flowering with 44 days while Somaa took the longest days (58 days).

Chowdhury *et al*. (2015) conducted an experiment with four varieties of Chili V1(Magura), V2(Kajoli), V3(Vaduria) and V4(Bogra Morich) and showed wide differences in their genotypic constituents reflected by morphological status. The maximum number of fruits (265.5/plant) was found from V2, while minimum from V4.

Hasan *et al*. (2014**)** carried out an experiment to study the morpho-physiological and yield performance of four chili lines (coded from L1 to L4) at Sher-e-Bangla Agricultural University, Bangladesh and reported that early flower bud initiation from L1 (30 days) whereas late from L4 (42 days).

Hasan *et al.* (2014) carried out an experiment to study the morpho-physiological and yield performance of four chili lines (coded from L1 to L4) at Sher-e-Bangla

Agricultural University, Bangladesh and recorded the maximum number of fruit from L2 (33.0/plant) which was statistically similar with L3 (28.3/plant) and L4 (26.0/plant), while the minimum from L1 (14.3/pant) which was statistically similar with L4 (26.0/plant).

Tairu *et al*. (2013) observed that although the accessions did not differ significantly in their yield potential but the accessions PP9955-15 had the highest average fruit weight (13.39 g).

Manna and Paul (2012) reported that significant association for average fruit length, number of fruits, fruit length suggests that increase in any one of these traits may result in increase in fruit yield per plant and low for ascorbic acid content.

Acharya *et al*. (2007) reported sufficient genetic variability for many of the horticultural traits studied in chili genotypes and considerable scope for its improvement.

Bhardwaj *et al*. (2007) observed fruit yield per plant (99.60 and 88.98), capsaicin content (99.10 and 81.43), number of fruits per plant (98.00 and 85.43). High heritability and high genetic advance have also been obtained.

Ibrahim *et al*. (2001) reported that high heritability along with moderate to low genetic advance was observed for average fruit weight, days to first harvest, days to flower anthesis, number of branches, fruit length and fruit diameter.

Patil (1998) reported that the screening of genotype variety is most important for getting higher yield as well as higher income and international market. With respect to management, nutrient management is most important factor for higher productivity.

Mishra et al. (1998) observed that the estimates of PCV and GCV were high for fruit yield per plant, number of fruits per plant, capsaicin content and average fruit weight, moderate for days to first harvest**.** Das and Choudhary (1999*)* reported that selection could be made for almost all the traits on the basis of phenotypic expression. High heritability estimates were observed for fruit yield per plant and average fruit weight.

Al-Jibouri *et al*. (1958) reported that the phenotypic and genotypic coefficient of variability were calculated according to the method suggested by Burton and De Vane. Heritability (broad sense), genetic advance and correlation were calculated according to the methods suggested.

Jaisankar *et al.* (2015) carried out a varietal evaluation at research farm of CIARI, South Andaman with twelve varieties of Chili and recorded that the maximum yield was found in V3 (69.74 g/plant) followed by V2 (55.26 g/plant), whereas the minimum was recorded in V5 (37.68 g/plant). On the other hand, Kaouther *et al.* (2015) conducted an agronomic evaluation with five local accessions of chili 11 pepper (Capsicum spp.) namely, Tebourba, Soma, Korba, Awled, Haffouz and Souk Jedid, and stated that yield in g per plant showed that Korba was the most performing accession (870.61 g) while Souk Jedid produce the lowest yield per plant (406.8 g).

Prabhakaran and Nataranjan (2004) conducted an experiment to study genetic variability. Heritability and genetic advance for 8 characters in chili (*Capsicum frutescens*) in Coimbatore, Tamil Nadu, India with 97 genotypes of chili. They recorded high genotypic co-efficient of variation for plant spread, number of fruits per plant, yield per plant, fruit length, mean fruit weight, placenta length and capsaicin. They observed that the heritability estimates were high for most of the characters. They found that the genetic advance as percentage of mean was high for yield per plan, mean fruit weight, placenta length and capsaicin. High heritability estimates coupled with high genetic advance as percentage of mean were recorded by them for yield per plant, mean fruit weight, placenta length and capsicin.

Sharma *et al*. (1975) reported high heritability and high genetic advance for average fruit weight, fruit yield per plant and fruit diameter indicating the role of additive gene action for the inheritance of these traits.

Singh *et al*. (1973) studied genetic divergence through D^2-statistics with 40 potato genotypes growing in 12 environments based on 13 characters. They search the clustering pattern and their inter and inter clusters distance. On the basis of stability, high yield and divergence among the genotypes, nine crosses were recommended as suitable for using in breeding program.

Badigannavar *et al.* (2002) studied on genetic base and diversity in groundnut and reported that cluster analysis of groundnut indicated no relationship between clustering pattern and subspecies among genotypes during rainy or summer seasons. Despite this narrow base, greater diversity could be possible following judicious use of mutation and recombination breeding to bring about genetic improvement.

Genetic divergences were studied by Malik *et al.* (1985) in mungbean. They observed days to flowering, seed yield and plant height-contributed maximum towards divergence. However, genetic diversity in blackgram was studied by Das and Gupta (1984). They observed 100-grain weight and branches per plant were the main components of diversity. Sagar et al. studied the same experiment in 1976 through Mahalanobis`s D^2 in blackgram and found days to flowering, plant height, 100 seed weight and pod length contributed maximum towards diversity.

Adhikari and Pandey (1983) by using D^2 analysis in chickpea reported that in native types seed per pod, pod per plant and in kabuli types primary branches per plant and 100 seed weight contributed maximum towards diversity.

Angadi *et al.* (1979) through multivariate analysis in cowpea reported that the characters 100 seed weight and pod length contributed maximum to the genetic diversity.

Agrawal and Lal (1985) evaluated 500 lentil accessions and reported substantial variations for time to flowering, time to maturity, plant height, 100- seed weight and seed yield.

Katiar and Singh (1979) observed in chickpea that 250-grain weight and primary branches per plant contributed major portion of the total genetic diversity. Fourty five lines of chili were subjected to Mahalanobis analysis by Singh and Singh (1976) and the lines differed significantly for eight characters. The clustering pattern of lines followed geographical distribution. From analysis of 27 varieties of chili,

Raikar *et al.* (2005) studied variability and path-coefficient analysis in chili with 40 strains of chili grown in Pune. Maharastra India. during kharif season They observed (lay-s to flowering, maturity, number of priliminary and secondary branches, plant height & spread, fruit length and girth, seeds per plant, number of fruits per plant, fresh fruit weight per plant, and dry fruit weight per plant. they revealed correlation (genotypic and phenotypic) among these characters and path analysis (direct and indirect effects) for fresh fruit weight and number of fruits per plant as the most important and reliable yield indicators in chili. They demonstrated the interrelationships that tall and spreading plants with higher number of secondary branches and early maturity would be high-yielding types.

Wasule *et al.* (2004) carried out variability in 17 newly developed genotypes of chili (*Capsicum annuum* L) in. Akola. Maharastra. India and revealed that there were a wide range of variability among the genotypes for all the characters. They recorded variability for days to 50% flowering, plant height, number of primary branches per plant, number of fruits per plant, fruit length, fruit girth. 1000-seed weight, seed percentage and yield of red chilies per plant They noted high genotypic co-efficient of variation, number of fruits per plant, wet red chili viscid. fruit girth, number of primary branches per plant, they estimated heritability ranged from 27.60 to 92.70% and 9 characters showed high heritability (>700/0). They described the expected genetic advance ranged from 3.73 to 74.90. They observed high heritability (92.70%) 'was accompanied by high genetic advance (70%) in respect of number of fruits per plant, indicating prevalence of additive gene action which offers good scope for further improvement.

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 chili (*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 on yield in path coefficient analysis. They suggested selecting high yielding chili genotypes on the basis of higher fruit weight, fruits/plant and yield/plant for breeding purpose.

Six parents and their thirty hybrids of chili 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 chili hybrid should have higher no. of 15 fruits/plant, coupled with large fruit length, high fruit girth and high average fruit weight to increase fruit yield/plant.

Jabeen *et al*. (2009) evaluated the performance of twenty-five chili 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.

A field experiment was conducted by Aklilu *et al*. (2016) to evaluated plant morphology and yield contributing characters of 49 capsicums (*Capsicum annuum* 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.

An investigation was carried out by Yatung *et al*. (2015) with 30 accessions of chili 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.

Forty-nine genotypes of chili were examined by Sarkar *et al*. (2009) to study the genetic variability as well as association for 12 growth and fruit characters. There was significant variation among the genotypes. Fruit yield (g)/plant, number of fruits/plant, fruit length (cm), placenta length (cm), fruit weight (g), number of seeds/fruit and plant height (cm) showed high values of GCV and PCV. High heritability in broad sense coupled with high GA in % grand mean was recorded for fruit yield/plant, number of fruits/plant, fruit length, days to 50% flowering and plant height indicating such characters were controlled by additive gene action the phenotypic path-coefficient analysis revealed that number of fruits/plant, fruit weight and 1000 seed weight had positive and high direct effect on fruit yield indicating their reliability as selection criteria to improve yield of chili

CHAPTER III
MATERIALS AND METHOD

This chapter includes the location, materials and methodology of the experiment conducted on chili with different genotypes during the period from October 2019 to March 2020. Due to pandemic situation all data could not be take the last data shot.

3.1 Location of the experimental site

The research work was conducted at the experimental site of Sher-e-Bangla Agricultural University, Dhaka- 1207.

3.2 Climate of the experimental site

The area which was used for experiment under the sub-tropical monsoon climate zone, which is characterized by heavy rainfall, high humidity, high temperature and relatively long day during the Kharif season while hardly rainfall, low humidity, low temperature and short day during the Rabi season. Rabi season is favorable for capsicum cultivation. During the studying period, the crop received total rainfall of 26.50 mm. At that time, the average maximum and minimum temperatures were 28.42-degree C and 16.36-degree C. respectively (appendix III). Details of the meteorological data in respect of temperature, rainfall, relative humidity, total sunshine and soil temperature during the period of experiment were collected from the Abhawa bhaban of Bangladesh. During the period the humidity was low, the temperature was mild with plenty of sunshine. The atmospheric temperature increased from February as the season proceeded towards summer.

3.3 Characteristics of soil

The selected plot was a medium high land. The pH of soil 4.47 to 5.63 while the amount organic carbon content, total N, available P and available K were 0.82%, 0.12%, 21 ppm and .27 mc per 100 gm of soil respectively.

3.4 Genetic materials used for the experiment

The present study was performed with 20 genotypes of chili of BARI. All the 20 genotypes were collected from Bangladesh Agricultural Research Institute (BARl), Gazipur. (Table 1)

Table 1. The code, name and source of collection of the 20 genotypes of chili

Genotypes (code)	Name of the genotypes	Source of genotypes
G1	BD- 11109	Gene Bank, BARI, Gazipur
G2	BD- 11110	Gene Bank, BARI, Gazipur
G3	BD- 11111	Gene Bank, BARI, Gazipur
G4	BD- 11112	Gene Bank, BARI, Gazipur
G5	BD- 11113	Gene Bank, BARI, Gazipur
G6	BD- 11114	Gene Bank, BARI, Gazipur
G7	BD- 11115	Gene Bank, BARI, Gazipur
G8	BD- 11116	Gene Bank, BARI, Gazipur
G9	BD- 11117	Gene Bank, BARI, Gazipur
G10	BD- 11118	Gene Bank, BARI, Gazipur
G11	BD- 11119	Gene Bank, BARI, Gazipur
G12	BD- 11120	Gene Bank, BARI, Gazipur
G13	BD- 11121	Gene Bank, BARI, Gazipur
G14	BD- 11122	Gene Bank, BARI, Gazipur
G15	BD- 11123	Gene Bank, BARI, Gazipur
G16	BD- 11124	Gene Bank, BARI, Gazipur
G17	BD- 11125	Gene Bank, BARI, Gazipur
G18	BD- 11126	Gene Bank, BARI, Gazipur
G19	BD- 11127	Gene Bank, BARI, Gazipur
G20	BD- 11128	Gene Bank, BARI, Gazipur

3.5 Design and layout of the experiment

The experiment was laid out in Randomized Complete Block Design (RCBD) with 3 replications. The field was divided into 3 blocks then the blocks will be further sub-divided into 20 lines where genotypes were randomly assigned. The plot size was 3m with single time. Row to Row distance was 50 cm and plant to plant distance was 50 cm. The genotypes were distributed to cacti line with each block randomly.

3.6 Preparation of the experimental field

Larger clods were broken into small particles and finally attained into a desirable tilth to ensure proper growing conditions. The plot was partitioned into the unit plots according to the experimental design as mentioned earlier. Recommended doses of well decomposed cowdung, manure and chemical fertilizers were applied and mixed well with the soil each plot. Proper irrigation and drainage channels were also prepared around the plots. Each unit plot was prepared keeping 5cm height from the drains. The bed soil was made friable and the surface of the bed was leveled.

3.7 Manure and fertilizers

Manure and fertilizers were applied at the doses indicated below following the methods shown in Table 2. Four days before planting of capsicum seedlings the entire amount of well decomposed cow dung and TSP and other fertilizers were applied to the plots and well mixed with the bed soil. During final bed preparation one fourth of both Urea and MP were applied. The rest of the Urea and MP were top dressed in 3 equal installments, after 30, 45 and 60 days of planting (Table 2).

Table 2. Doses and methods of application of manure and fertilizers for the production of chili

Manure & Fertilizers	Doses Kg/ ha	Dose/plot	Basal dose	Application per plot		
				1st top dressing at 30 DAP	2nd top dressing at 45 DAP	3rd dressing g at 60 DAP
Cowdung	15000	15 kg	15 kg	-	-	-
Urea	275	265 g	85 g	60 g	60 g	60 g
TSP	200	225 g	225 g	-	-	-
MP	200	200 g	75 g	50 g	50 g	50 g
Zypsum	20	20 g	20 g	-	-	-
ZnO	10	10 g	10 g	-	-	-
Boric acid	10	10 g	10 g	-	-	-
Furadon	10	10 g	10 g	-	-	-

3.8 Planting of Chili seedlings

Thirty-five days old seedlings were transplanted in the experimental plots on 03 December, 2019. Planting was done at the afternoon. One seedling was planted in each hole. After planting, the bases of the seedlings were covered with soil and then pressed by hand.

3.9 Intercultural operations

The growing seedlings were always kept under care observation. After planting the seedlings, the following intercultural operations were accomplished for their better growth and development.

3.9.1 Irrigation

The growing seedlings were always kept under care observation. After planting the seedlings, the following intercultural operations were accomplished for their better growth and development.

3.9.2 Gap filling

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

3.9.3 Weeding and mulching

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

3.9.4 Top dressing

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

3.9.5 Plant protection measures

The established plants were affected by aphids. Diazonin 60EC (15cc/10 liter) was applied against aphids and other insects. Chili plants infacted with anthracnose and die back and were controlled by spraying cupravit (3gm/l) at 15 days interval. Few plants

found to be infected by bacterial wilt were uprooted. For crinkle disease Ektara (5gm/10 liter) was used at 15 days interval.

3.10 Harvesting

Harvesting of fruits was started at 70 DAP and continued up to 25 DAP with an interval of 25 days Harvesting was done usually by hand. First harvesting was done on 18th March.

3.11 Data Collection

In order to study the genetic diversity among the genotypes, the data were collected in respects of 7 parameters such as days to first flowering, days to first harvesting, plant height, number of primary branches, fruit length, individual fruit weight, yield per plant. During the plant growth, 10 plants were selected randomly from each unit plot for data collection. The sampling was done iii such a way so that the border effects were completely avoided. For this purpose, the outer two lines and the extreme end of the middle rows were excluded.

3.11.1 Days to first flowering

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

3.11.2 Days to first harvesting

Harvesting of fruits was started at 70 DAP and continued up to 25 DAP with an interval of 25 days Harvesting was done usually by hand. First harvesting was done on 18th March,

3.11.3 Plant height (cm)

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

3.11.4 Number of primary branches

Number of primary branches were recorded from the selected plants at final harvest. It was considered only main lateral shoots with main shoot.

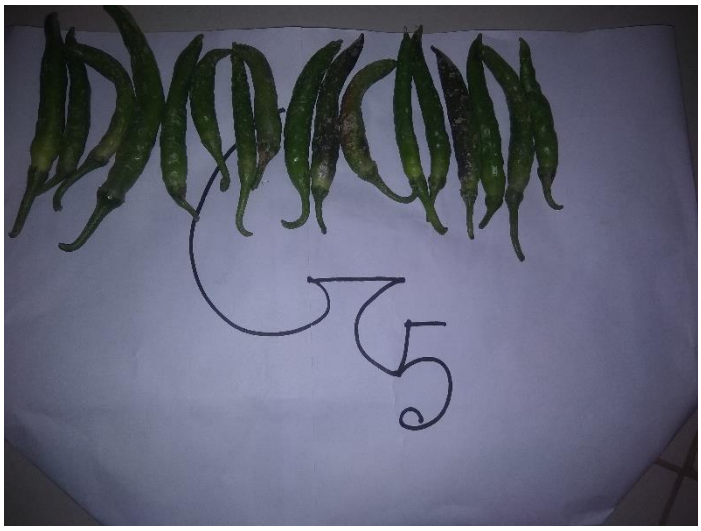
Sticking

Tagging

Weeding

Data collection

Plate 1: Intercultural operations and data collection



Genotype G5

Genotype G14

Plate 2: Different shapes and sizes of chili genotypes

3.11.5 Fruit length (cm)

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

3.11.6 Individual fruit weight (g)

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

3.11.7 Yield per plant (g)

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

3.12 Statistical analysis

The data obtained for different characters were statistically analyzed by using Statistics 10 computer package program. The mean values of all the recorded characters were evaluated and analysis of variance was performed by the 'F' (variance ratio) test. The significance of the difference among the treatment combinations of means was estimated by Duncan's Multiple Range Test (DMRT) at 5% level of probability (Gomez and Gomez, 1984).

3.12.1 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.

3.12.2 Analysis of variance (ANOVA)

Data were analyzed by the methods outlined by Panse and Sukhatme (1978) 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 analyzed on the basis of the model suggested by Cochran and Cox (1950).

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

3.12.3 Estimation of genotypic and phenotypic variances:

Formula given by Chaudhary and Prasad (1968) was used to calculate phenotypic and genotypic variance.

Genotypic variance (σ^2_g) = (TMSS – EMSS) / R

Error variance = σ^2_e

Phenotypic variance = $\sigma^2_p = \sigma^2_g + \sigma^2_e$

Where, TMSS is treatment mean sum of square

EMSS is error mean sum of square

R is number of replication

3.12.4 Estimation of genotypic and phenotypic coefficient of variation (GCV and PCV)

They are expressed as percentage according to Burton and G.W (1952).

Genotypic coefficient of variation (GCV) = $(\sigma_g/\overline{X}) \times 100$

Phenotypic coefficient of variation (PCV) = $(\sigma_p/\overline{X}) \times 100$

Where, σ_g = Genotypic standard deviation

σ_p = Phenotypic standard deviation

$\overline{X}$= General mean of the trait

As indicated by Sivasubramanjan and Menon (1973), GCV and PCV are categorized as follows: 0 – 10 %: Low; 10 – 20 %: Moderate; >20 %: High

3.12.5 Estimation of broad sense heritability (h^2_b)

Hanson *et al.* (1956) estimated broad sense heritability as the ratio of genotypic variance (Vg) to the phenotypic variance (Vp) and expressed in percentage.

Broad sense heritability (h^2_b) = $(V_g / V_p) \times 100$

Robinson *et al.* (1949) categorized broad sense heritability as follows:

0 – 30%: Low; 30% – 60%: Moderate; > 60%: High

3.12.6 Estimation of genetic advance (GA)

It was calculated by using the following formula given by Robinson *et al*. (1949).

$GA = i. \sigma_p. h^2_b$

Where, i = Efficacy of selection (2.06 at 5% selection intensity)

σ_p = Phenotypic standard deviation

h^2_b = Broad Sense Heritability

3.12.7 Estimation of genetic advance as percent of means (GAM)

GA as per cent of mean (GAM) = $(GA/\overline{X}) \times 100$

GA = Genetic advance;

$\overline{X}$ = General mean of the trait

Johnson *et al*. (1955) categorized GAM as follows:

0 - 10 %: Low; 10 -20 %: Moderate; > 20 %: High

3.12.8 Estimation of genotypic and phenotypic correlation co-efficient

For calculating the genotypic and phenotypic correlation coefficient in all possible combination the formula suggested by Johnson *et al*. (1955) and Hanson *et al.* (1956) were adopted. The genotypic covariance components between two traits and of the phenotypic covariance component were derived in the same way as for the corresponding variance components. The covariance components were used to compute genotypic and phenotypic correlation between the pairs of the characters as follows:

Genotypic correlation $=\sigma^2_{gxy}/\sqrt{\sigma^2_{gx}+\sigma^2_{gy}}$

Where, σ^2_{gxy}= Genotypic covariance between the traits x and y.

σ^2_{gx}= Genotypic variance of the trait x

σ^2_{gy}= Genotypic variance of the trait y

Thus, Phenotypic correlation (r_{phxy}) $=\sigma^2_{phxy}/\sqrt{\sigma^2_{phx}+\sigma^2_{phy}}$

Where, σ^2_{phxy}= Phenotypic covariance between the traits x and y.

σ^2_{phx}= Phenotypic variance of the trait x

σ^2_{phy}= Phenotypic variance of the trait y

3.12.9 Path co-efficient analysis

Path co-efficient analysis was done according to the procedure employed by Dewey and Lu (1959) and Dabholkar (1992), using simple correlation values. In path analysis, correlation co-efficient was partitioned into direct and indirect effects of independent variables on the dependent variable.

In order to estimate direct and indirect effect of the correlated characters, say x_1, x_2, and x_3 yield y, a set of simultaneous equations (three equations in this example) is required to be formulated as shown below:

$r_{yx1} = P_{yx1} + P_{yx2rx1x2} + P_{yx3rx1x3}$

$r_{yx2} = P_{yx1rx1x3} + P_{yx2} + P_{yx3rx2x3}$

$r_{yx3} = P_{yx1rx1x3} + P_{yx2rx2x3} + P_{yx3}$

P_{yx1}= the direct effect of x_1 on y

$P_{yx2rx1x2}$=the indirect effect of x_1 via x_2 on y

$P_{yx3rx1x3}$= the indirect effect of x_1 via x_3 on y

After calculating the direct effect and indirect effect of the characters, residual effect (R) was calculated by using the formula given below:

$P^2R_Y = 1-\Sigma P_{iy}.r_{iy}$

Where, $P^2R_Y = (R^2)$ and hence residual effect, $R = (P^2R_Y)\ 1/2$

P_{iy}= direct effect of the character on yield

r_{iy}= correlation of the character with yield

3.12.10 Multivariate analysis

Mean data for each character was subjected to multivariate analysis methods viz, principal component analysis (PCA), principal coordinate analysis (PCO), canonical variate analysis (CVA) and cluster analysis (CLSA) using GENSTAT program.

3.12.10.1 Principal component analysis (PCA)

Principal component analysis is one of the multivariate techniques to know the interrelationships among several characters and can be done from the sum of squares and product matrix for the characters. Principal components were computed from the

correlation matrix and genotypic scores obtained for the first component and succeeding components with latent roots greater than unity (Jager *et al.*, 1983).

3.12.10.2 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 n points using similarity matrix (Digby *et al.,* 1989). Inter-distances between genotypes were studied by PCO.

3.12.10.3 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.

3.12.10.4 Cluster analysis (CLSA)

Genotypes were divided into groups on the basis of a data set into some number of mutually exclusive groups. The clustering was done using non-hierarchical classification. In GENSTAT, the algorithm is used to search for optical values of the chosen criterion. The optimal values of the criteria followed by some initial classification of the genotypes into required number of groups, the algorithm repeatedly transfers genotypes from one group to another so long as such transfer improved the value of the criterion. When no further transfer can be found to improve the criterion, the algorithm switches to second stage that examine the effect of two genotypes of different classes and so on.

3.12.10.5 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 root 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 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.

CHAPTER IV
RESULTS AND DISCUSSION

The study of generic variability and genetic diversity within chili genotypes would be help to screen better genotypes. So, to generate information in the degree of diversity among 20 lines of chili were raised in the field of Sher-e-Bangla Agricultural University. Dhaka 1207. The data in respect of days to first flowering, days to first harvesting, plant height (cm), number of primary branches, fruit length (cm), individual fruit weight (g) and yield per plant (g) were recorded, analyzed and presented in this chapter. Performance of 20 genotypes of chili was investigated in winter season and the findings of present study have been discussed under different morphological characters. The results of the study showed marked variation in different characters and the variation of different characters is presented in the following tables, figures and plates. The data pertaining to seven characters were computed, statistically analyzed and the results obtained are described below.

4.1 Variability among 20 chili genotypes
4.2 Heritability, genetic advance and genetic advance in percentage of mean
4.3 Correlation coefficients among 7 yield contributing characters
4.4 Path co-efficient analysis
4.5 Genetic diversity for 20 genotypes of chili

4.1 Genetic variability among 20 chili genotypes

The analysis of variance indicated that the existence of highly significant variation among the genotype studied (Table 3). The mean, performance of seven characters are presented in Table 4. variance components, genotypic and phenotypic co efficient of variance, heritability, genetic advance, genetic advance in percent of mean are presented in Table 5.

Table 3. Analysis of variance of seven characters of chili genotypes

Source of variance	d.f	Mean sum of square						
		Days to first flowering	Days to first harvesting	Plant height (cm)	Number of primary branches	Fruit length (cm)	Individual fruit weight (g)	Yield per plant (g)
Replication	2	15.52	187.02	14.00	2.12	0.03	0.01	43.40
Genotype	19	179.52**	174.41**	79.75**	5.42**	2.82**	0.15**	46552.70**
Error	38	16.96	52.53	31.59	1.75	0.70	0.06	201.20
CV (%)		9.07	10.46	12.55	26.80	10.78	15.27	7.95

****, 1% level of significance**

Table 4. Mean performance of seven characters of 20 chili genotypes

Genotypes	Days to first flowering	Days to first harvesting	Plant height (cm)	Number of primary branches	Fruit length (cm)	Individual fruit weight (g)	Yield per plant (g)
G1	39.33c	65.33b-e	47.83a-d	5.67 a-d	5.10f	1.14d	181.00g
G2	43.67c	61.00d-f	44.30c-e	4.33c-f	7.10de	1.50b-d	173.67g
G3	42.33c	69.67a-d	44.37c-e	4.33c-f	9.50a	1.67b	123.00h
G4	38.00c	62.00c-f	49.73a-c	4.33c-f	8.33a-d	1.72b	226.00de
G5	38.67c	72.33a-d	45.87b-e	4.33c-f	9.07ab	1.72b	418.67a
G6	42.67c	68.33a-e	39.47df	2.67f	7.17de	1.75b	92.00ij
G7	40.00c	72.00a-d	45.62b-e	5.00b-e	7.60c-e	1.53b-d	186.67fg
G8	40.67c	78.33a	46.57b-e	6.33a-c	8.17a-d	1.71b	43.67l
G9	42.00c	69.00a-d	41.36c-f	2.67f	6.50e	1.40b-d	242.33d
G10	44.33c	73.00a-c	45.50b-e	6.67ab	8.33a-d	1.55bc	205.00ef
G11	40.00c	78.33a	53.83ab	5.00b-e	8.00b-d	1.69b	389.33b
G12	43.00c	76.00ab	45.10 b-e	4.67b-f	7.33de	1.68b	85.00ij
G13	41.33c	57.00ef	37.47ef	5.67a-d	8.13 a-d	1.71b	418.33a
G14	41.67c	53.33f	47.93 a-d	4.00d-f	7.67c-e	2.20a	326.00c
G15	40.33c	57.00ef	42.47 c-f	6.00a-d	8.73a-c	1.27cd	132.67h
G16	55.33ab	72.33a-d	38.83d-f	3.33ef	8.17 a-d	1.40b-d	69.67jk
G17	58.00ab	74.33ab	44.73b-e	7.33a	7.67c-e	1.47b-d	83.00ij
G18	60.33ab	76.33ab	43.32c-f	7.33a	8.17a-d	1.36b-d	29.00l
G19	61.67a	78.33a	56.50a	4.67b-f	7.00de	1.47b-d	51.00kl
G20	54.33b	71.33a-d	34.80f	4.33c-f	7.00de	1.67b	94.00i
Mean	45.38	69.27	44.78	4.93	7.74	1.58	178.50
Minimum	38.00	53.33	34.80	2.67	5.10	1.14	29.00
Maximum	61.67	78.33	56.50	7.33	9.50	2.20	418.67
SE	3.36	5.92	4.59	1.08	0.68	0.20	11.58
LSD (%)	6.81	11.98	9.29	2.19	1.38	0.40	23.45

Table 5. Estimation of genetic parameters of the seven characters of chili

Genetic parameter	Days to first flowering	Days to first harvesting	Plant height (cm)	Number of primary branches	Fruit length (cm)	Individual fruit weight (g)	Yield per plant (g)
Phenotypic variance	71.14	93.15	47.64	2.97	1.40	0.09	15651.70
Genotypic variance	54.19	40.63	16.06	1.23	0.71	0.03	15450.50
Phenotypic coefficient of variance	18.59	13.93	15.41	34.96	15.31	18.92	70.09
Genotypic coefficient of variance	16.22	9.20	8.95	22.44	10.87	11.17	69.64
Heritability	76.17	43.61	33.70	41.21	50.41	34.85	98.71
Genetic advance	13.23	8.67	4.79	1.46	1.23	0.21	254.41
Genetic advance in percentage of mean	29.16	12.52	10.70	29.67	15.90	13.58	142.52

4.1.1 Days to first flowering

The analysis of variance for days to first flowering showed highly significant variation among the genotypes (Table 3). The highest 61.67 days for first flowering was recorded in G19 followed by 60.33 in G18, 58.00 in G17 (Table 4). On the other hand, the genotype G4 required the minimum number of days for first flowering (38.00) and the mean value was 45.38 (Table 4). Phenotypic variance (71.14) was considerably higher than genotypic variance (54.19), while phenotypic co-efficient of variation (18.59) slightly higher than genotypic co-efficient of variation (16.22) (Table 5). From this discussion it was revealed that environmental effect for this trait was considerable. These results were in agreement with the findings of Bharadwaj *et al.* (2007), Sharma *et al.* (2010) and Kumari *et al.* (2010). In contrast Monamodi *et al.* (2013) and Aditya *et al*. (1995) found in significant difference in days to first flowering.

4.1.2 Days to first harvesting

Days to first harvest showed significant variation among genotype mean sum of square (174.41) (Table 3). The maximum duration was observed 78.33 days in G8, G11 and G19 and the minimum duration was 53.33 in G14 with mean value 69.27 (Table 4). The difference between phenotypic variance (93.15) and genotypic variance (40.63) was higher indicating high influence of environment on this character (Table 5). The genotypic coefficient of variation and phenotypic co-efficient of variation was observed 9.20% and 13.93%, respectively was indicated presence of low variability in this trait.

4.1.3 Plant height (cm)

Significant difference was observed for plant height (cm) among the genotypes under study (Table 3). The significant varietal differences indicated that there was a wide range of variation among the genotypes for plant height (cm) with the mean value 44.78 (Table 4). The highest plant height (cm) was recorded in G19 (56.50 cm) which was statistically similar with G11 (53.83 cm) and the minimum plant height (cm) was observed 34.80 cm in G20 (Table 4). The genotypic variance was (16.06) considerably lower than the phenotypic variance (47.64) for plant height (cm) in chili genotypes suggesting highly influence of environment of this trait (Table 5). Genotypes co-efficient of variation (8.95)

was also lower than phenotypic co-efficient of variation (15.41). The wide range of variation between genotypic and phenotypic variance for plant height (cm) indicated that the genotypes represented differently even when grown under the same environment. Moderate phenotypic coefficient of variation and genotypic coefficient of variation was found by Manju and Sreelathakumary (2004), Kashinath *et al*. (2003) and Krishna *et al.* (2007).

4.1.4 Number of primary branches

The mean squares due to number of primary branches were found statistically significant at 1% level including highly significant variation among the genotypes selected for the study (Table 3). The mean value for this trait was 4.93 (Table 4). The highest number of primary branches 7.33 was observed in G17 and G18 followed by G10 with 6.67 and G8 with 6.33. The least primary branches 2.67 in G9 (Table 4). Similar significant differences were reported for this trait by Raikar *et al.* (2005), Smitha *et al.* (2006). Phenotypic variance (2.97) was slightly higher than genotypic variance (1.23). Phenotypic coefficient of variation (34.96) was considerably higher than genotypes co-efficient of variation (22.44) indicating a considerable influence of environment of expression of this characters (Table 5). But Wasule *et al.* (2004) noted high genotypes co-efficient of variation for number of primary branches.

4.1.5 Fruit length (cm)

Highly significant variation for the fruit length was observed among the genotypes (Table 3). The genotypes G3 gave the highest mean value of fruit length 9.50 cm followed by 9.07 in G5 which was significantly superior to all other varieties. The lowest mean value was observed in 5.10 cm in G1 and mean value was 7.74 (Table 4). Phenotypic variance (1.40) was slightly higher than genotypic variance (0.71) (Table 5). Phenotypic coefficient of variation (15.31) was also slightly higher than genotypes co-efficient of variation (15.31) indicating a moderate influence of environment of expression of this characters. Similar results were reported by Kashinath (2003), Farhad *et al*. (2008), Prabhakaran and nataranjan (2004) recorded high genotypic co-efficient of variation for fruit length (cm).

4.1.6 Individual fruit weight (g)

The analysis of variance for this character showed highly significant differences among the genotypes (Table 3). The genotype G14 gave the highest mean value of individual fruit weight 2.20 g which was statistically similar with G6 (1.75 g) and significantly superior to all other lines (Table 4). The lowest individual fruit weight 1.14 g was observed in G1 that was statistically similar with some of lines and different from all other lines (Table 4). Phenotypic variance (0.09) and genotypic variance (0.03) were for this trait with little differences in genotypic coefficient of variation (11.17) and phenotypic co-efficient of variation (18.92) indicating negligible environmental effect (Table 5). Sudre *et al.* (2005) and Smitha *et al.* (2006) recorded high genotypic and phenotypic coefficient of variation for individual fruit weight (g).

4.1.7 Yield per plant (g)

Highly significant difference was observed among the genotypes for yield per plant (Table 3). According to mean values the maximum yield per plant (g) 418.67 g was produced by the genotypes G5 and G13 which statistically similar and followed by G11 (389.33 g). Whereas minimum yield per plant was 29.00 g was produced by the genotype G18 (Table 4). The phenotypic variance (15651.70) was considerably higher than genotypic variance (15450.50) indicating environmental influence on this trait (Table 5) and genotypic co-efficient variation (69.64) to that of phenotypic coefficient variation (70.09) was considerable which indicated environmental influence on yield per plant (Table 5). These results were in agreement with those reported by many earlier workers viz., Bharadwaj *et al.* (2007), Sreelathakumary and Rajamony (2004).

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

The estimate of heritability, genetic advance and genetic advance in percentage of mean are presented in Table 5.

4.2.1 Days to first flowering

Days to first flowering exhibited high heritability (76.17%) in hoard sense (h^2b) coupled with moderate genetic advance 13.23 and high genetic advance in percentage of mean

29.16% (Table 5) indicated the possibility of "additive and non-additive" genes effect for the expression of this character. Therefore, selection would he effective for producing varieties.

4.2.2 Days to first harvesting

Heritability showed moderate (43.61%) with low genetic advance (8.67) and moderate genetic advance in percentage of mean (12.52%) revealed that which indicated character was controlled by non-additive genes the selection based on this character would not be effective.

4.2.3 Plant height (cm)

Plant height (cm) showed moderate heritability (33.70%) of this trait; genetic advance (4.79) and GA% mean was moderate (10.70%) (Table 5). It revealed non-additive gene action present in this trait and selection may be effective for this trait. 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), they found high heritability with moderate genetic advance for this trait.

4.2.4 Number of primary branches

The magnitude of heritability 41.21% in board sense (h^2b) for number of primary branches was moderate with considerably low genetic advance 1.46 and high genetic advance in percentage of mean 29.67% (Table 5) which indicated non additive gene action i.e there is no or limited scope of isolating superior genotypes.

4.2.5 Fruit length (cm)

Fruit length showed moderate heritability (50.41%) of this trait; genetic advance (1.23) and GA% mean was also low (15.90%) (Table 5). It revealed non-additive gene action involved in the maintenance of this trait and almost moderate heritability was showed due to influence of favorable environment rather than genotypes, so selection may not be rewarded. Similar results were reported by Kashinath (2003), Tembhurne *et al*. (2008) and Singh *et al*. (2009); they found high heritability with low genetic advance.

4.2.6 Individual fruit weight (g)

Individual fruit weight showed moderate heritability (34.85%) coupled with low genetic advance (0.21) and moderate genetic advance in percentage of mean (13.58%) (Table 5). The results of individual fruits weight through selection would be ineffective.

4.2.7 Yield per plant (g)

Yield per plant showed high heritability (98.71%) of this trait; genetic advance (254.41) was high and GA% mean (142.52%) was high (Table 5), which indicating very low or no influence of environment and apparent variability due to additive gene and selection may be effective in early generations for this trait. Similar findings were in agreement with Reddy *et al.* (2008), Acharya and Rajput (2003) they found high heritability with additive gene effect for this trait.

4.3 Correlation coefficients among seven yield contributing characters

Identification of simple genotypic and phenotypic correlation co-efficient was made among yield and yield contributing characters of the 20 chili genotypes in all possible one way paired combinations. Genotypic correlation co-efficient were higher than phenotypic correlation coefficient in all most of cases were suggested that character association had not been largely influenced by environment in this case.

4.3.1 Days to first flowering

Correlation among the yield and yield contributing traits showed that days to first flowering had highly significant and positive correlation with days to first harvesting (r_g= 0.478, r_p= 0.387) at both genotypic and phenotypic levels and number of primary branches (r_g= 0.349) at genotypic levels (Table 6). Days to first flowering also exhibited highly significant but negative correlation with individual fruit weight (g) (rg= -0.408) and yield per plant (g) (r_g= -0.618, r_p= -0.541). It also showed positive but non-significant correlation with number of primary branches (r_p= 0.128) and negative but non-significant correlation with plant height (cm) (r_g= 0.090, r_p= -0.038) and individual fruit weight (g) (r_p= -0.157).

Table 6. Coefficients of phenotypic and genotypic correlation among different yield

Character		Days to first flowering	Days to first harvesting	Plant height (cm)	Number of primary branches	Fruit length (cm)	Individual fruit weight (g)
Days to first harvesting	r_g	0.478**					
	r_p	0.387**					
Plant height (cm)	r_g	-0.090	0.401**				
	r_p	-0.038	0.155				
Number of primary branches	r_g	0.349**	0.260*	0.169			
	r_p	0.128	0.146	0.156			
Fruit length (cm)	r_g	-0.129	-0.023	-0.081	0.222		
	r_p	-0.053	0.052	0.002	0.131		
Individual fruit weight (g)	r_g	-0.408**	-0.233	-0.092	-0.562**	0.557**	
	r_p	-0.157	-0.184	0.174	-0.097	0.133	
Yield per plant (g)	r_g	-0.618**	-0.467**	0.159	-0.199	0.176	0.502**
	r_p	-0.541**	-0.340**	0.085	-0.132	0.133	0.306*

4.3.2 Days to first harvesting

Days to first harvesting showed significant and positive correlation with plant height (cm) (r_g= 0.401) and number of primary branches (r_g= 0.260) at genotypic level. It exhibited positive but non-significant correlation with plant height (cm) (r_p= 0.155), number of primary branches (r_p= 0.146), fruit length (cm) (r_p= 0.052). It also revealed that negative and significant correlation with yield per plant (g) (r_g= -0.467 and r_p= -0.340) at both genotypic and phenotypic level and negative but non-significant correlation with fruit length (cm) (r_g= -0.023) at genotypic level and individual fruit weight (g) (r_g= -0.233 and r_p= -0.184) at both genotypic and phenotypic level.

4.3.3 Plant height (cm)

Interrelationships among the yield contributing traits showed that plant height (g) had non-significant and positive correlated with number of primary branches (r_g= 0.169 and r_p= 0.156) and yield per plant (g) (r_g= 0.159 and r_p= 0.085) at both genotypic and phenotypic levels and fruit length (cm) (r_p= 0.002) and individual fruit weight (g) (r_p= 0.174) at phenotypic level. Plant height (cm) was exhibited non-significant and negative correlation with fruit length (cm) (r_g= -0.081) and individual fruit weight (g) (r_g= -0.092) at genotypic level. This result indicated that taller plants enhancement of taller plant no changing in vegetative growth like more primary branches per plant and yield per plant.

4.3.4 Number of primary branches

Correlation co-efficient revealed that number of primary branches were and negatively significant relationship with individual fruit weight (g) (r_g= -0.562) at genotypic level. It was positively but non-significant correlated with fruit length (r_g= 0.222 and r_p= 0.131) at both genotypic and phenotypic level and negatively non-significant correlation with individual fruit weight (g) (r_p= -0.097) at phenotypic level and yield per plant (g) (r_g= -0.199 and r_p= -0.132) at both genotypic and phenotypic level (Table 6). The result indicated more number of primary branches enhanced less vegetative growth and produced less yield per plant (g).

4.3.5 Fruit length (cm)

Significant and positive correlation was observed of fruit length with individual fruit weight (g) (r_g= 0.557) at genotypic level. While it showed non-significant positive association with individual fruit weight (g) (r_p= 0.133) at phenotypic level and with yield per plant (r_g= 0.176 and r_p= 0.133) at both levels. So fruit length promoted fruit weight resulting increased fruit yield. When fruit length was increased the individual fruit yield (g) was increased.

4.3.6 Individual fruit weight (g)

Interrelationships among the yield contributing traits showed that individual fruit weight (g) had highly significant and positive correlation with yield per plant (r_g= 0.502 and r_p= 0.306) at both genotypic and phenotypic level. The correlation showed when individual fruit weight (g) was increased the fruit yield increased.

4.4 Path co-efficient 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 on seed yield per plant. In order to find out a clear picture of the inter-relationship between seed yield per plant and other yield attributes, direct and indirect effects were worked out using path analysis at phenotypic level which also measured the relative importance of each component. Though correlation analysis denotes the association pattern of components traits with yield, they basically represent the overall effect of a particular trait on yield rather than providing cause and effect relationship. The technique of path coefficient analysis developed by Wright (1921) and demonstrated by Dewey and Lu (1959) facilitates the portioning of correlation coefficients into direct and indirect contribution of various characters on yield. It is standardized partial regression coefficient analysis. As such, it measures the direct effect of one variable upon other. Such information would be of great value in enabling the breeder to exclusively identify the important component traits of yield and use the genetic resources for improvement in a planned way. In path coefficient analysis the direct effect of a trait on seed yield per plant and its indirect effect through other characters were calculated and the results are presented in Table 7.

4.4.1 Days to first flowering

Path co-efficient analysis revealed that days to first flowering had a negative direct effect (**-0.332**) on yield per plant (g). Days to first flowering had positive indirect effect on number of primary branches (0.214) and fruit length (0.067) while negative indirect effect on days to first harvesting (-0.165), plant height (cm) (-0.019) and individual fruit weight (g) (-0.382). It showed significant negative genotypic correlation (**-0.618**) with yield per plant (g). (Table 7)

4.4.2 Days to first harvesting

According to path co-efficient analysis days to first harvesting had a negative direct effect (**-0.344**) on yield per plant (g). Days to first harvesting had positive indirect effect on plant height (cm) (0.083), number of primary branches (0.159) and fruit length (cm) (0.012) while negative indirect effect on days to first flowering (-0.159) and individual fruit weight (g) (-0.218). It showed significant negative genotypic correlation (**-0.467**) with yield per plant (g). (Table 7)

4.4.3 Plant height (cm)

Through, path co-efficient analysis plant height (cm) had a positive direct effect (**0.208**) on yield per plant (g). Plant height (cm) had positive indirect effect on days to first flowering (0.030), number of primary branches (0.103) and fruit length (cm) (0.042) while negative indirect effect on days to first harvesting (-0.138) and individual fruit weight (g) (-0.086). It showed significant positive genotypic correlation (**0.159**) with yield per plant (g). (Table 7)

Table 7. Partitioning of genotypic into direct and indirect effects of morphological characters of 20 chili genotypes by path coefficient analysis

Trait	Direct effect	Days to first flowering	Days to first harvesting	Plant height (cm)	Number of primary branches	Fruit length (cm)	Indivi fruit weigh
Days to first flowering	**-0.332**		-0.165	-0.019	0.214	0.067	-0.3
Days to first harvesting	**-0.344**	-0.159		0.083	0.159	0.012	-0.2
Plant height (cm)	**0.208**	0.030	-0.138		0.103	0.042	-0.0
Number of primary branches	**0.613**	-0.116	-0.089	0.035		-0.115	-0.5
Fruit length (cm)	**-0.517**	0.043	0.008	-0.017	0.136		0.5
Individual fruit weight (g)	**0.937**	0.136	0.080	-0.019	-0.345	-0.288	

4.4.4 Number of primary branches

Number of primary branches had a positive direct effect (**0.613**) on yield per plant (g). Number of primary branches had positive indirect effect on plant height (cm) (0.035) while negative indirect effect on days to first flowering (-0.089), days to first harvesting (-0.115), fruit length (cm) (-0.115) and individual fruit weight (g) (-0.527). It showed non-significant negative genotypic correlation (**-0.199**) with yield per plant (g). (Table 7)

4.4.5 Fruit length (cm)

Path co-efficient analysis revealed that fruit length (cm) had a negative direct effect (**-0.517**) on yield per plant (g). Fruit length (cm) had positive indirect effect on days to first flowering (0.043) and days to first harvesting (0.008) and number of primary branches (0.136) and individual fruit weight (g) (0.522) while negative indirect effect on plant height (cm) (-0.017). It showed non-significant positive genotypic correlation (0.176) with yield per plant (g). (Table 7)

4.4.6 Individual fruit weight (g)

According to path co-efficient analysis individual fruit weight (g) had a positive direct effect (**0.937**) on yield per plant (g). Individual fruit weight (g) had positive indirect effect on days to first flowering (0.136) and days to first harvesting (0.080) while negative indirect effect on plant height (cm) (-0.019), number of primary branches (-0.345) and individual fruit length (-0.288). It showed significant positive genotypic correlation (**-0.502**) with yield per plant (g). (Table 7)

4.5 Genetic diversity analysis of chili genotypes

Genetic divergence in chili was analyzed by using GENSTAT software programme. Genetic diversity analysis involved several steps i.e., estimation of principal component analysis, 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 finders (Bashar. 2002; Uddin, 2001; Juned *et al.,* 1988 and Ario, 1987). In the analysis of genetic diversity in chili multivariate techniques were used.

4.5.1 Principal component analysis (PCA)

Genetic divergence analysis quantifies the genetic distance among the selected genotypes and reflects the relative contribution of specific traits towards the total divergence and is an important tool for breeding program. The diversity analysis is useful to determine the magnitude of divergence among population (Murthy and Quadri 1966). The Principal component analysis was studied with twenty genotypes of chili. Eigen values and latent vectors of corresponding seven principal component axes and percentage of total variation accounting for them obtained from the principal component analysis are presented in (Table 8). It was represented that the cumulative Eigen values of first three principal components accounted for 68.06% of the total variation; the first principal component accounted for 33.68% of the total variation; the second and third components accounted for 18.87%, and 15.51% of the total variation, respectively. The rest of the components accounted for only 31.94% of the total variation.

Table 8. Eigen value, % variance and cumulative (%) total variance of the principal components

Principle component axes	Eigen value	% Variance	Cumulative (%) total variance
I	2.36	33.68	33.68
II	1.32	18.87	52.55
III	1.09	15.51	68.06
IV	0.94	13.46	81.52
V	0.53	7.61	89.13
VI	0.41	5.84	94.97
VII	0.35	5.03	100

4.5.2 Construction of scatter diagram

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. 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 2 as X-axis and component score 1 as Y-axis was constructed, which has been presented in Figure 1. The position of the genotypes in the scatter diagram was apparently distributed into six groups, which indicated that there existed considerable diversity among the genotypes.

4.5.3 Cluster analysis

The experiment was conducted to investigate the genetic diversity of twenty genotypes of chili. The genotypes were divided into five different cluster according to D^2 analysis (Table 9). The cluster V had (G6, G8, G12, G16, G17, G18, G19 and G20) maximum number of genotypes (8) followed by cluster I which had 5 genotypes. Cluster II and III had 3 genotypes respectively. Remarkably cluster I had (G1, G2, G3, G7 and G15) whereas cluster II had (G4, G9 and G10). Furthermore, cluster III had (G5, G11 and G13), cluster IV showed one genotype (G14). Clustering was done at random that indicated a broad genetic base of the genotypes.

Table 9. Number, percent and name of genotypes in different cluster

Cluster number	Number of genotypes	Percent (%)	Name of genotypes
I	5	25	G1, G2, G3, G7, G15
II	3	15	G4, G9, G10
III	3	15	G5, G11, G13
IV	1	5	G14
V	8	40	G6, G8, G12, G16, G17, G18, G19, G20

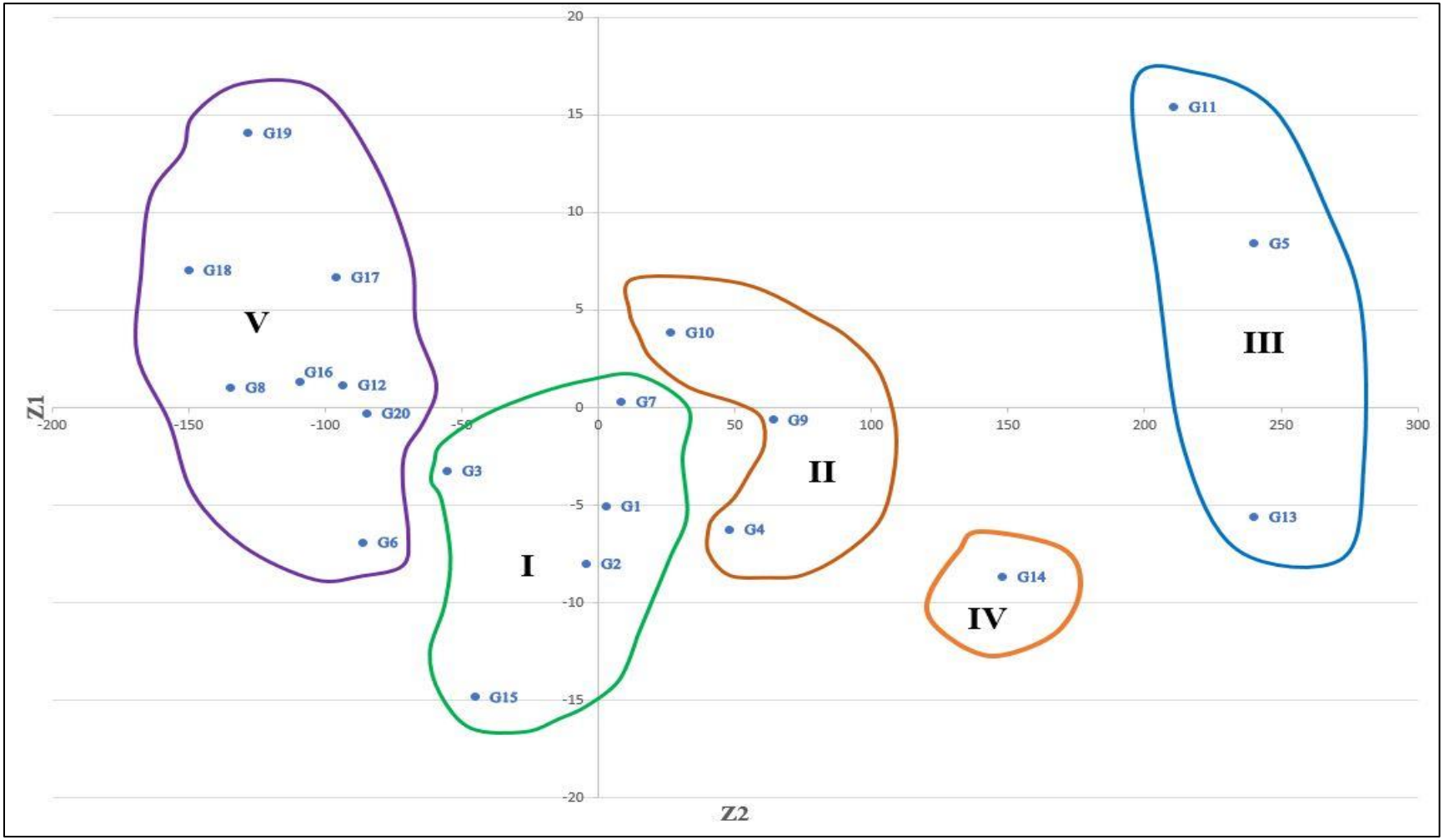


Figure 1. Scatter diagram of 20 chili genotypes based on their principal component scores

4.5.4 Principal coordinate analysis

Principal coordinate analysis (PCO) was estimated on auxiliary principal component analysis. This analysis helps in estimating distances. Principal coordination analysis (PCO) indicated that the highest inter genotypes distance (2.72) was observed between the chili genotypes G5 and G18 followed by the genotypes G13 and G18 (Table 10). In figure number 1 the tenth highest pair distance was (2.16) observed between G5 and G19. The lowest distance (0.24) was observed between the genotypes G2 and G7 followed by the genotypes G5 and G11. The tenth lowest distance (0.42) was observed between the genotypes G16 and G20. The difference between the highest and the lowest inter-genotypes distance indicated the prevalence of variability among the 20 genotypes of chili.

4.5.5 Non-hierarchical clustering

Twenty chili genotypes were grouped into five different clusters non-hierarchical clustering. These results confirmed the clustering pattern of the genotypes obtained through PCA. Cluster means were computed for all the seven characters studied and presented in Table 11. However, if we consider the characters of the experiment then the following scenario would capture our attention:

4.5.5.1 Days to First Flowering

It was observed that minimum days required in the cluster III (40 days). It revealed that most of the early flowering materials are laying in this group. On the other hand, late flowering materials were present in the cluster group V (52 days).

4.5.5.2 Days to first harvesting

The lowest days to first harvesting materials were present in the cluster IV (53.33 days) and the highest days to first harvesting materials were presented in the cluster group III (74.41 days).

Table 10. The nearest and farthest clusters from each cluster between D^2 values in 20 chili genotypes

Highest Distance			Lowest Distance		
Genotypes		Distance	Genotypes		Distance
G5	G18	2.72	G2	G7	0.24
G13	G18	2.70	G5	G11	0.25
G11	G18	2.63	G7	G10	0.29
G14	G18	2.52	G4	G7	0.31
G9	G18	2.29	G2	G4	0.36
G8	G13	2.27	G12	G20	0.37
G5	G8	2.27	G3	G15	0.39
G13	G19	2.20	G5	G13	0.40
G8	G11	2.18	G1	G7	0.41
G5	G19	2.16	G16	G20	0.42

Table 11. Cluster mean for twelve yield and yield characters of 20 chili genotypes

Characters	I	II	III	IV	V
Days to first flowering	41.13	41.44	40	41.67	52
Days to first harvesting	65	68	69.22	53.33	74.41
Plant height (cm)	44.92	45.53	45.72	47.93	43.67
Number of primary branches	5.07	4.56	5	4	5.08
Fruit length (cm)	7.61	7.72	8.4	7.67	7.59
Individual fruit weight (g)	1.42	1.56	1.71	2.2	1.56
Yield per plant (g)	159.4	224.44	408.78	326	68.42

4.5.5.3 Plant height (cm)

The highest plant height (cm) was observed in the cluster IV (47.93) and the lowest plant height (cm) was observed in cluster V (43.67).

4.5.5.4 Number of primary branches

It was observed that the highest number of primary branches in the cluster V (5.08) and the lowest number of primary branches was observed in cluster IV (4).

4.5.5.5 Fruit length (cm)

The highest fruit length (cm) was observed in the cluster III (8.4) and the lowest fruit length (cm) was observed in cluster V (7.59).

4.5.5.6 Individual fruit weight (g)

In the experiment the highest individual fruit weight (g) was observed in the cluster IV (2.2) and the lowest individual fruit weight (g) was observed in cluster I (1.42).

4.5.5.7 Yield per plant (g)

It was observed that the highest yield per plant (g) in the cluster III (408.78) and the lowest yield per plant (g) was observed in cluster V (68.42).

4.6 Conical variate analysis

Conical variate analysis (CVA) was done to identify the inter-cluster distance. Table (12) were presented intra and inter-cluster distance (D^2) values. In this experiment the inter-cluster distances were higher from intra-cluster distances. It showed that the wide range of genetic variability among genotypes of chili. Based on the result it indicated that the highest inter cluster distance was observed between cluster III and cluster IV (25.026), followed by cluster I and cluster III (17.846), cluster IV and cluster V (17.385), cluster II and cluster III (13.515) and cluster I and cluster IV (11.722). The lowest inter-cluster distance was observed between cluster I and cluster II (4.376) followed by cluster I and cluster V (7.661) and cluster II and cluster IV (7.849), whereas there is no any similar type of distance was found. However, the maximum inter-cluster distance was recorded between clusters III and

IV followed by between I and III. Genotypes from these clusters can be used in hybridization programme. The intra-cluster divergence varied from 0 to 0.750, maximum for cluster V, which was comprised of eight genotypes of diverse origin, while the minimum distance was observed in cluster IV that comprised one genotype. Results obtained from different multivariate techniques were superimposed from which it may be concluded that all the techniques gave more or less similar results and one technique supplemented and confirmed the results of another one.

Table 12. Intra (Bold) and inter cluster distances (D^2) for 20 chili genotypes

Characters	I	II	III	IV	V
I	**0.379**				
II	4.376	**0.586**			
III	17.846	13.515	**0.381**		
IV	11.722	7.849	9.568	**0.000**	
V	7.661	11.619	25.026	17.385	**0.750**

4.7 Contribution of characters towards divergence of the cultivars

For deciding on the cluster for the purpose of further selection and choice of parents for hybridization the character contributing maximum to the divergence were given greater emphasis. The PCA revealed that in vector I (Z1) the important characters responsible for genetic divergence in the major axis of differentiation were days to first flowering, days to first harvesting and individual fruit weight (g) (Table 13). ln vector II (Z2) that was the second axis of differentiation days to first flowering, plant height (cm), number of primary branches, individual fruit weight (g) and yield per plant (g) were important. The role of days to first flowering and individual fruit weight (g) in both the vectors were positive across two axes indicating the important components of genetic divergence in those materials.

4.8 Selection of genotypes as parent for hybridization programme

Genetically dissimilar parent selection is the fundamental works for hybridization programme. So, the genotypes were chosen according to specific trait, maximum heterosis could be shown in offspring from the crosses between genetically diverse parents. Based on cluster mean and agronomic performance the genotype G4 for earlier days to flowering, G14 for days to first harvesting and individual fruit weight (g), G19 for plant height (cm), G3 for fruit length (cm), G17 and G18 for number of branches and G5, G13 and G11 for yield per plant (g). Therefore, considering group distance and other agronomic performance the inter genotypic crosses between G5, G11, G13, G14 and G18 and other improved variety and might be suggested for future hybridization program.

Table 13. Relative contributions of the seven characters of 20 genotypes to the total divergence

Characters	Vector 1	Vector 2
Days to first flowering	0.014	0.146
Days to first harvesting	0.007	-0.028
Plant height (cm)	-0.115	0.008
Number of primary branches	-0.163	0.153
Fruit length (cm)	-1.256	-0.553
Individual fruit weight (g)	3.216	8.248
Yield per plant (g)	-0.071	0.001

CHAPTER V

SUMMARY AND CONCLUSION

The experiment was conducted at the Sher-e-Bangla Agricultural University farm, Bangladesh during October, 2019 to March, 2020 in Rabi season for study on characterization and genetic diversity analysis of green chili. The field experiment was laid out in the main field in Randomized Complete Block Design (RCBD) with three replications. In this experiment twenty chili genotypes were used as experimental materials. It was observed that significant variation exists among all the genotypes used for most of the characters studied. The experiment was conducted to study the genetic divergence considering seven important yield and yield contributing characters, viz., days to first flowering, days to first harvesting, plant height (cm), number of primary branches, fruit length (cm), individual fruit weight (g) and yield per plant (g). The phenotypic variance was higher than the corresponding genotypic variance for all the characters indicating greater influence of environment for the expression of these characters. Characters like, number of primary branches per plant and yield per plant (g) exhibited high genotypic and phenotypic co-efficient of variation. The phenotypic co-efficient of variation was higher than the genotypic coefficient of variation for all the characters. Maximum difference between phenotypic and genotypic coefficient of variation were 34.96 and 22.44, respectively which indicated that the number of primary branches was mostly depended on the environmental condition. Highest phenotypic co-efficient of variation (70.09) and genotypic co-efficient of variation (69.64) was found in yield per plant. High heritability coupled with high genetic advance and genetic advance in percentage of mean was found in yield per plant which indicated that additive gene expression on this character. Days to first flowering showed high heritability with moderate genetic advance and high genetic advance in percentage of mean that might be presence of additive and non-additive gene expression. Moderate heritability and low genetic advance were found in days to first harvesting, plant height (cm), number of primary branches, fruit length (cm) and individual fruit weight (cm). According to the mean performance, the highest 61.67 days required for first flowering was recorded in G19 and minimum number of days for first flowering (38.00) was in G4. The maximum duration of fruit harvesting

was observed 78.33 days in G8, G11 and G19 and the minimum duration was 53.33 in G14. The highest plant height (cm) was recorded in G19 (56.50 cm) and the minimum plant height (cm) was observed 34.80 cm in G20. The highest number of primary branches 7.33 was observed in G17 and G18 and the least primary branches 2.67 in G9. The genotypes G3 gave the highest mean value of fruit length 9.50 cm and the lowest mean value was observed in 5.10 cm in G1. The genotype (G14) gave the highest mean value of individual fruit weight (g) 2.20 g and the lowest individual fruit weight (g) 1.14 g was observed in G1. According to mean values the maximum yield per plant (g) 418.67 g was produced by the genotypes G5 and G13 whereas minimum yield per plant (g) was 29.00 g. Investigation on character association indicating that yield per plant had highest significant positive correlation with individual fruit weight in both genotypic and phenotypic level indicating the importance of these trait 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 chili. Path analysis revealed that plant height (cm), number of primary branches and individual fruit weight (g) showed positive direct effect on yield per plant (g) indicating that direct selection based on these traits may be helpful in evolving high yielding varieties of chili.

Genetic diversity among chili genotypes was performed through Principal Component Analysis (PCA), Cluster Analysis, Canonical Variate Analysis (CVA) using GENSTAT According to PCA, PCO and Cluster analysis, the genotypes were grouped into five different clusters. The first three principal component characters with eigen values were greater than unity contributed a total of 68.08% variation towards divergence. As per as principal component analysis (PCA). The cluster V comprised the maximum number 8 of genotypes, followed by cluster I comprised of 5 genotypes. The cluster II, III and IV comprised 3, 3 and 1 genotypes, respectively. In respect of cluster mean of different cluster showed that cluster V can be selected for days to first flowering, days to first harvesting and number of primary branches and Cluster III can be selected for fruit length (cm), individual fruit weight (g) and yield per plant (g). The highest inter-cluster distance was observed between III and V suggested that the genotypes selected from the more diversified cluster-III and cluster V could be used as parents for future breeding programs and the lowest inter-cluster distance was observed between I and II also observed in this study for

Contribution of individual characters towards divergence. The highest and lowest intra-cluster distances were observed in cluster IV and V, respectively. When these genotypes from this cluster will be crossed, it will be claimed that selecting genotypes from these more diverse groups result in better segregation. The higher genetic distance between genotypes as a result of these features in clusters would also be an advantage for developing a high-yielding chili variety. Considering diversity pattern, genetic status and other agronomic performances, considering the magnitude of genetic distance, contribution of character towards divergence, magnitude of cluster means and agronomic performance the genotypes G18 from cluster V for number of primary branches, G14 from cluster IV for individual fruit weight (g) and days to first harvest and G5, G11 and G13 from cluster III for yield per plant. Diverse genotypes in crossing programme may produce desirable segregants. So, divergent genotypes (G5, G11, G113, G14 and G18) were recommended to use as parent in future hybridization programme.

REFERENCES

Acharya, P. and Rajput, C.B.S. (2003). Variability and correlation studies for different traits in Capsicum with respect to leaf curl complex. *Indian J. Hort.* **60**(4): 381-387.

Acharya, P. and Sengupta, S (1992). Genetic variability in pepper (*Capsicum annuum*). *Envir. and Eco*. **25**(4): 808-812.

Adhikary, G. and Pandey, M. P. (1983). Genetic divergence in chickpea. Indian J. Genet. **43** (2): 188-192.

Aditya, P.M. and Phir, K. (1995). Studied on genetic variability in chilli. *Progr. Hort*. **32**(2): 172-182.

Ahmed, M.S. and Uaque. M.A. (1980). Morphological characters and yields of five characters of chilli Bangladesh *Hort.* **8**(l): 3-16

Al-Jibouri, H. A., Millar, P. A., Robinson, H.P. (1958). Genotypic and environmental variances and covariance in upland cotton crosses in inter-specific origin. Agronomy journal, **50**:633-637.

Anderson, E. (1957). A semi graphical method for the analysis of complex problems. *Proc. Mat. Acad. Sci. Wash. M.* 43: 917-927.

Angadi, S. P., Subramani, A. and Kulkarani, R. S. (1979). Multivariate analysis on cowpea. Genet. Agr. **33** (2-3): 121-132.

Anonymous. (1987). Annual reports on spices research. BARI. Gazipur. pp. 1-3.

Ario, O.J. (1987). Multivariate analysis and choice of parents for hybridization in okra. *Theor. Appl. Genet*. **74**: 361-363.

Arunachalam. V. (1981). Genetic distances in plant Breeding. Indian *J*. Genet. 41: 226236.

Badigannavar, A. K., Kale, D. M. and Murty, G. S. S. (2002). Genetic variability and diversity in groundnut genotypes. Plant Breeding. **121** (4): 348-353.

Bashar, M. K. (2002). Genetics and morpho-physiological basis of heterosis in rice. Ph.D. Thesis, BSMRU, Gazipur.

BBS. (2016). Year Book of Agricultural Statistics of Bangladesh. Government of the People's Republic of Bangladesh, Dhaka, Bangladesh. P.144.

Berhanu, Y., Derbew, B., Wosene, G. and Fekadu, M. (2011). Variability, heritability and genetic advance in Hot Pepper (*Capsicum annuum L.)* genotypes in west shoa, Ethiopia. *American – Eurasian J. Agric. Environ. Sci.* **10**(4): 587- 592.

Bharadwaj, D.N., Singh, H. and Yadav, R.K. (2007). Genetic variability and association of component characters for yield in chili (*Capsicum annum* L.). *Progressive. Agric.* **7** (1/2): 72-74.

Bhatt. G.M. (1973). Comparison of various methods of selecting parents for hybridizasion in common breed wheat (*Triticum aestivum*). Aus. *J. Agric. Res*. **24**: 457-464.

Burton, G. W. (1952). Quantitative inheritance in grass pea. *Proceed.6th grassl. Cong.* ***1***:277-283.

Chaudhary, L.B., and Prasad, B. (1968). Genetic variation and heritablity of quantitative characters in Indian mustard (*Brassica Juncea*). *Indian J. Agril. Sci.* **38**: 820-825.

Choudhury, B. (1976). Vegetables (4th edn.). National Book. Trust, New Delhi, India. pp. 50-58.

Chowdhury, M.S.N., Hoque, F., Mehraj, H. and Jamal Uddin, A.F.M. (2015). Vegetative Growth and Yield Performance of Four Chilli (Capsicum frutescens) Cultivars. American-Eurasian *J. Agric. Env. Sci.* **15**(4): 514- 517.

Cochran, W.G. and Cox, G. (1957). Experimental design. W.S John, (2nded.). New York. p.615

Dias GB, Gomes VM, Moraes TM, Zottich UP, Rabelo GR, Carvalho AO, Moulin M, Gonçalves LS, Rodrigues R, Da Cunha M (2013). Characterization of Capsicum species using anatomical and molecular data.

Dabholkar, A.R. (1992). Elements of biometrical genetics. Concept Publishing, New Dhelhi, *India. pp*. 126-128

Das, P. K. and Gupta, T. D. (1984). Multivariate analysis in black gram. *Indian J. Genet.* **44** (2): 243-247

Deway, D.R. and Lu, K.N. (1959). A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agron. J.*, **51:** 515-518.

Digby, P., Galway, N. and Lane, P. (1989). GENSTAT 5: A Second Course. Oxford Science. Oxford Science Publications, Oxford. pp. 103-108.

Dutonde, S.N., Bhalekar, M.N., Patil, B.T., Kshirsagar, D.B. and. Dhumal, S.S. (2008). Genetic diversity in chili (Capsicum annuum L.). *Agric. Sci. Digest* **28** (1): 45-47

Farhad, M., Hasanuzzaman, M., Biswas, B.K., Azad, A.K. and Arifuzzaman, M. (2008). Reliability of yield contributing characters for improving yield potential in chili (*Capsicum annum*). *Intl. J. Sustain. Crop Prod.* **3**(3): 30-38.

Farhad, M.I., Hasanuzzaman, M., Biswas, B.K., Arifuzzaman, M. and Islam, M.M. (2010). Genetic divergence in chilli (Capsicum annuum L.). *Bangladesh Res. Publ. J.* **3** (3): 1045-1051.

El-Ghoraba AH, Javedb Q, Anjumb FM, Hamedc SF, Shaabana HA (2013). Pakistani Bell Pepper (*Capsicum annum* L.): Chemical Compositions and its Antioxidant Activity. International Journal of Food Properties, 16(1):18-32

Gomez. K.A. and Gomez, A.A. (1984). Statistical procedure for agricultural research (2nd ed). Wiley. *New York. pp.* 28-192.

Hanson, C.H., Robinson, H.F. and Comstock, R.E. (1956). Biometrical studies on yield in segregating population of Korean *lespedesa. Agron. J*. **48**: 268-272

Hasan, M.J., Kulsum, M.U., Ullah, M.Z., Hossain, M.M. and Mahmud, M.E. (2014). Genetic diversity of some chilli (*Capsicum annuum* L.) Genotypes. *Int. J. Agril. Res. Innov. Tech*. **4**(1): 32-35.

Ibrahim, M., Ganigar, V.M. and Yenjer Appa, S.T., (2001) Genetic variability, heritability, genetic advance and correlation studies in chilli. *Karnataka J. Agric Sci.* **14**: 784-787.

Jabeen, N., Sofi, P.A. and Wani, S.A. (2009). Character association in chili. Revista Científica UDO Agrícola. **9**(3): 487-490.

Jeger, M.I., Genethojones, D. and Griffith, E. (1983). Components of partial resistance of wheat seedlings of septoria nod rum. *Euphytica.* **32**: 575-584.

Johnson, H.W., Robinson, H.F. and Comstock, R.E. (1955). Estimation of genetic and environmental variability in soybeans. *Agron. J*. 47: 314-318.

Juned, S.A., Jackson, M.T. and Catty, J.P. (1988). Diversity in the wild potato species *Chacoense Bitt. Euphytica*. **37**(2): 149-156.

Kaouther, Z., Hamdi, W., Sedraoui, S., Fendri R., Lajimi, O. and Hannachi, C. (2015). A comparative study of morphological characterization of Tunisian accessions of Chilli pepper (*Capsicum frutescens* L.). *IRJET*. **2**(4): 87-94.

Karad, S.R., G.R. Raikar. and Navale P.A., (2002). Genetic divergence in chilli. Maharashtra *J. Agric. Univ*. **27**(2): 143-145.

Kashinath, C.B. (2003). Evaluation and genetic variability studies in chili genotypes (*Capsicum annum* L.). M.Sc. (Agri.) Thesis.

Katiar, R. P. and Singh, S. P. (1979). Genetic divergence in chickpea. *Indian J. Genet.* **39** (2): 345-358.

Khurana, D.S., P. Singh. and Hundal. J.S. (2003). Studies on Genetic diversity for growth, yield and quality traits in chilli (*Capsiciun annum L*). *Indian J Hort.* **60**:277-282.

Krishna, U., Patil, M.P., Madalageri, M.B., Mulge, R. and Jagadeesha, R.C. (2007). Character association and path analysis studies in green chili for yield and yield attributes. *Karnataka J. Agril. Sci*. **20**(1): 99-101.

Kumar, A., Mishra, S. N. and Verma, J. S. (1982). Studies on Genetic Diversity in cowpea. Crop improvement. **9** (2): 160-163.

Marín, A., F. Ferreres, F.A. Tomás-Barberán and M.I. Gil, (2004). Characterization and quantitation of antioxidant constituents of sweet pepper (*Capsicum annuum* L.). J. Agric. Food Chem., 52: 3861–3869

Mahalanobis PC (1936). On the generalized distance in Statistics. *Proc Nat Inst Sci* India 249-55.

Manju. P.R. and Sreelathakumary. (2004). Genetic divergence in hot chili *Capsicum Chinese jacq*.). **23**: 69-72.

Manna A., Paul A. (2012). Studies on genetic variability and characters association of fruit quality parameters in tomato, Hort Flora Research Spectrum, Vol 1, 110-116,2012

Mehra, C.S. and Peter, K.V. (1980). Genetic divergence in chilli. *Indian J. Agric. Sci.* **50**:477-481.

Mishra, P.K., N. P. Singh and N.H. Ram. (2002). Genetice divergence among adbavanceed hybrids and varieties of potato. *J. Indian potato Assoc*. **29**(1-2):175-176

Monamodi, E.L., Lungu, D.M. and Fite, G.L. (2013). Analysis of fruit yield and its components in determinate chili using correlation and path coefficient. *Bots. J. Agric. Appl. Sci*. **9**(1): 29-40.

Murty, B. R. and Arunachalam, I. J. (1966). The nature of genetic divergence in relation to breeding system in crop plants. *Indian J. Genet*. **26**:188-198.

Nandi, A. (1992). Variability studies in chilli. Genetic Publishers, New Delhi, p.318.

Natarajan, C., Thiyagarajan, K. and Rathanaswamy, R. (1988). Association and genetic diversity studies in greengram. *Madras Agric. J.* **75** (7-8): 238- 245.

Osuna-García, J.A., M.M. Wall and C.A. Waddell, (1998). Endogenous levels of tocopherols and ascorbic acid during fruit ripening of new mexican-type chile (*Capsicum annuum* L.) cultivars. J. Agric. Food Chem., 46: 5093–5096

Patil, M.Z.; Raddy. M.V.; Rana, B.S.P and B.J. Reddy. (1989). Genetic divergence in safflower. *Indian. J. Genet*. 49A: 188-198

Pawar, (2000). Intra and Inter cultivar molecular polymorphism in native chilli (*Capsicum annuum L.)*. M.Sc. Thesis University of Agricultural Sciences, Dharwad.

Pense, V.G. and Shukhatme, P.V. (1978). Statistical Method for Agricultural Workers. 3rd edition. Indian Council of Agricltural Research, New Delhi. pp. 258-268.

Prabhakaran, T.S. and Nataranjan S. (2004). Studies on genetic variability, heritability and genetic divergence in chilli (*Capsicum annuum L*.). *South Indian Horticulture*. **5291** (6): 70-72.

Purseglove, J.W. (1968). TropicaL crops, Dichotyledons. John Wiley and Sons, New York. Vol. **2**: 524-530.

Raikar, G.N., S.R. Karad. and P. A. Navale. (2005). Variability and path co-efficient analysis in chilli. *Maharastra. J. Agric Univ*. **30**(1):90-91.

Ramanujam, S., Tiwary, A.S. and Mehra, R.B. (1974). Genetic divergence and hybrid performance in mungbean. *Theor. Appl. Genet*. **44** (5): 211-214.

Rani, K. Natarajan, S. and Thamburaj, S., (1996). Correlation and path analysis in chilli (*Capsicum annuum L*.). *South Indian Horticulture*. **44**: 8-11.

Reddy, M.G., Kumar, H.D.M. and Salimath, P.M. (2008). Correlation and path coefficient analysis in chili (*Capsicum annuum* L.). *Karnataka J. Agril. Sci*. **21**(2): 259-261.

Robinson, H.F., Cornstock, R.E. and Harvey, P.H. (1949). Estimates of heritability and degree of dominance in corn. *Agron. J*. **41**: 353-359.

Sarkar, S., Murmu, D., Chattopadhyay, A. and Hazra, P. (2009). Genetic variability, correlation and path analysis of some morphological characters in chilli. *J. Crop Weed.* **5**(1): 157-161.

Senapati, B.K., Sahu, F.K. and Sarkar, G., (2003). Genetic divergence in chilli. *Crop Res. Hisar.* **26** (2): 314-317

Sharma, D. D.; Gill, R. S., (1968). Nutritive value of Palampur hay. Evaluation as a sole feed and in combination with *Pueraria thumbergiana* (kudzu). J. Research, Punjab Agricultural University, **5** (3, Suppl.): 98-102

Sharma, H.C. (1975). Pungent principle of chillies. Arecaunt and spice bull., U.P. Rice Res. Station. Faizbad, India. 6(4): 78-81. Cited from *Hort Abstr*. **46**(11): 10365. (1977).

Sharma, V.K., Semwal, C.S. and Uniyal, S.P. (2010). Genetic variability and character association analysis in bell pepper (*Capsicum annum* L.). *J. Hort. Forestry*. **2**(3): 58-65.

Sing, S.P. and Singh. H.N. (1979). Genetic divergence in okra. *Indian J. Hors*. **20**:166170.

Singh, H.; Hardevinder, S. Cheema. D.S. (2005). Studies on genetic variability and heritability for quality traits of tomato (*Lycopersicon esculentum*). *J. of Appl. Hors. Indian*. **7**:55-57.

Singh, R.K. and Choudhary, B.D. (1985). Biometrical Methods in Quantitative Genetic Analysis. Kalyani

Singh, Y., Sharma, M. and Sharma, A. (2009). Genetic variation, association of characters, and their direct and indirect contributions for improvement in chili peppers. *Int. J. Veg. Sci*. **15**(4): 340-368.

Sivasubramanjan, S. and Menon, M. (1973). Heterosis and inbreeding depression in rice. *Advances in Agronomy*. **47**: 85-140.

Smitha, R.P. and N. Basavaraja. (2006). Genetic divergence studies in chilli (*capsicum annuum*) Karnataka. *Agric. Sci*. **19**(4):975-977.

Sreelathakumary, I. and Rajamony, L. (2004). Variability, heritability and genetic advance in chili (*Capsicum annuum L.*). *J. Trop. Agric.* **42**: 35-37.

Sudre, C.P.R., Rodrigues, R., Riva, E.M., Karasawa, M. and Amaral. A.T. (2005). Genetic divergence between chili and sweet pepper accessions using multivanate techniques. *Hort.* **23**(1): 22-27.

Sumabai, D.I., D. Chandramony and Nayar. N.K. (1987). Genetic divergence in chilli. Indian *J. Agric. Sci*. **579**(12): 941-942.

Sundaranm, A.; Ramakrishan. A.; Renganathan, C.R. and Ramalingam, S. (1980). Genetic divergence of chilli (*Capsicum frutescens L*), Indian *J. of Agric. Sci.* **50**(5): 391-39.

Tairu, F.M., Olufolaji, A.O., Abdul, R.M.A. and Kouame, C. (2013). Comparative study on the performance of some exotic chilli pepper accessions in ibadan, southwestern Nigeria. Acta Hort. 1007: 29-35

Tembhurne, B.V., Revanappa, R. and Kuchanur, P.H. (2008). Varietal performance, genetic variability and correlation studies in chili (*Capsicum annuum* L.). *Karnataka J. Agril. Sci*. **21**(4): 541-543.

Thul, S. T., Lal, R. K., Shasany, A. K., Darokar, M. P., Gupta, A. K., Gupta, M. M., Verma, R. K. & Khanuja, S.P.S. (2009). Estimation of phenotypic divergence in a collection of Capsicum species for yield related traits.

Tomooka, N. (1991). Genetic diversity and landrace differentiation of mungbean, (*Vigna radiata* L.) Wilczek, and evaluation of its wild relatives (The subgenus Ceratotropics) as breeding materials. Tech. Bull. Trop. Res. Centre, Japan No. 28. Ministry of Agriculture, Forestry and Fisheries. Japan. p.1.

Uddin, M.J. (2001). Morphogenetic diversity and gene antion in sesame (*Sesame indicum* L.). Ph.D. thesis, Department of Genetics and Plant Breeding, BSMRAU, Gazipur.

Varalakshami. B. and Babu, K. H. (1991). Genetic divergence, heritability and genetic advance in chilli (*Capsicum aunnum L*.) Indian *J. Genet. Pl. Br.* **51**(2): 174-178.

Verma, S.K. Singh, R.K. and Arya, R.R. (2004). Genetic variability and correlation studies in chili lines.

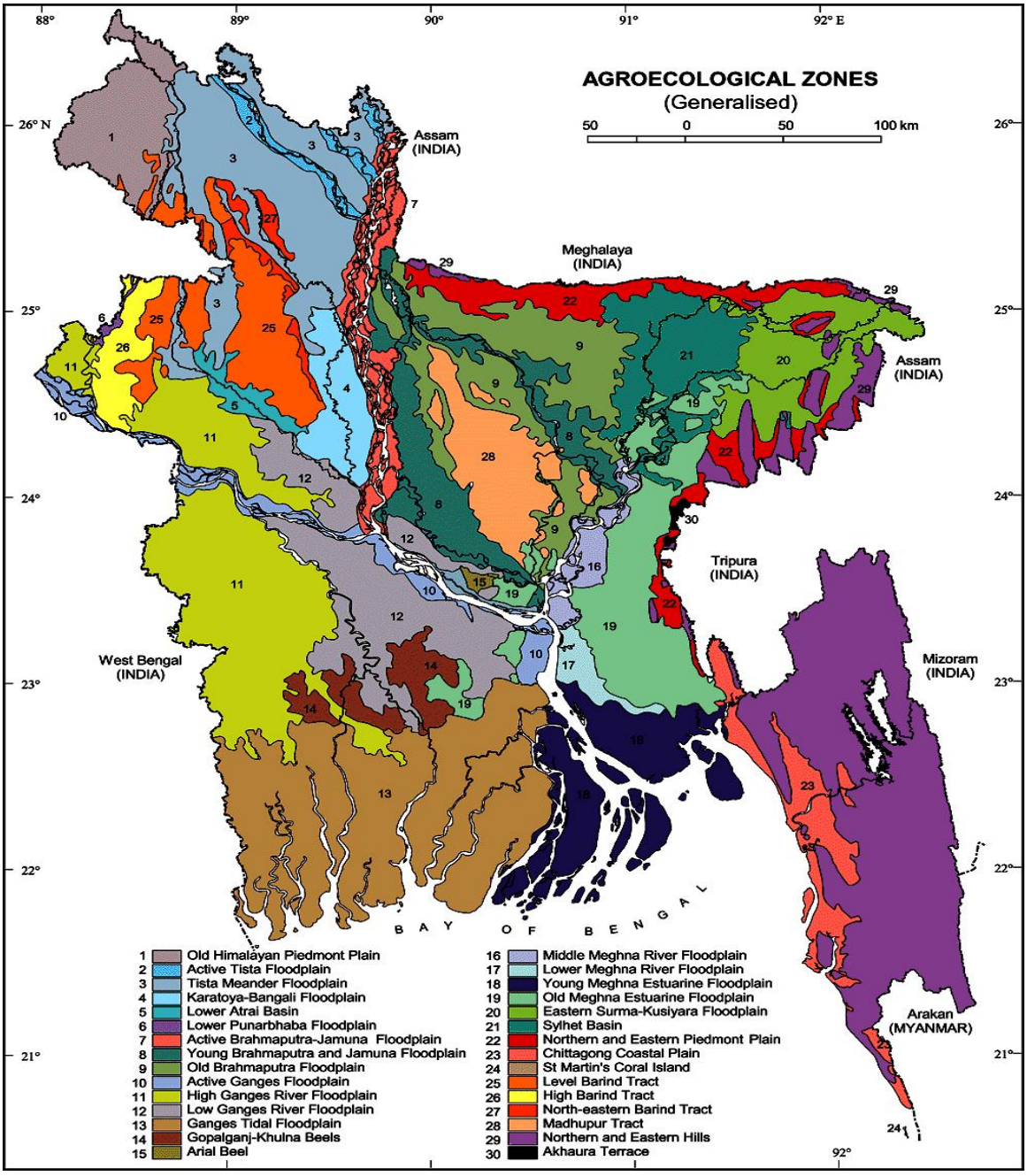
Wasule, J.H., I N. Parmar., N.R. Potdukhe. and Deshmukh. D.T. (2004). Variability studies in chilli. *Ann. Plant Phy; Biol*. **18**(2): 187-191.

Wright, S. (2007). Correlation and causation. *J. Agric. Res*. **20**: 202-209.

Yatung, T., Dubey, R.K., Singh, V., Upadhyay, G. and Pandey, A.K. (2015). Selection parameters for fruit yield and related traits in chilli (*Capsicum annum* L.). *Bangladesh J. Bot.* **43** (3): 283-291.

APPENDICES

Appendix I. Map showing the experimental site under the study



Legend showing the research site

Appendix II: Physical and chemical characteristics of initial soil depth of the experimental site.

A. Physical composition of the soil:

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

B. Chemical composition of the soil:

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

Appendix III: Monthly average temperature, average relative humidity and total rainfall and total sunshine of the experimental site during the period from October, 2019 to March, 2020.

Month	Air temperature (°C)		Relative humidity (%)	Total rainfall (mm)	Sunshine (hr)
	Minimum	Maximum			
October, 2019	19	32	66	13.2	6.5
November, 2019	18	31	63	12.6	5.8
December, 2019	16	28	61	1.9	7.9
January, 2020	13.0	27	57	3.5	3.9
February, 2020	18	28	58	12.3	5.7
March, 2020	20	31	60	15.1	7.5