GENETIC DIVERGENCE ANALYSIS IN LENTIL (*Lens culinaries* Medik.)

BY

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CERTIFICATE

This is to certify that thesis entitled, GENETIC DIVERGENCE ANALYSIS IN LENTIL (Lens culinaries Medik.) submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of MASTER OF SCIENCE in GENETICS AND PLANT BREEDING, embodies the result of a piece of bona fide research work carried out by Fakir Sohag Hossen, Registration No. 05-01707 under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.

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

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Dated:: June, 2011
Place: Dhaka, Bangladesh

(Prof. Dr. Md. Sarowar Hossain)
Supervisor

DEDICATED TO

MY

BELOVED PARENTS

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ABSTRACT

A field experiment was conducted with 35 lentil genotypes at Sher-e-Bangla Agricultural University experimental farm, Sher-e-Bangla Nagar, Dhaka, to study their diversity based on different morphological characteristics during November 2011 to March 2012. The objectives of the study were to identify divergent parents for hybridization program, to identify the characters contributing to genetic diversity, to assess the magnitude of genetic divergence in genotypes, association among the characters and their contribution to yield. The analysis of variance indicated significantly higher amount of variability among the genotypes for all the characters. Different multivariate analysis techniques were used to classify 35 lentil genotypes. Diversity was estimated by cluster distance. All the genotypes were grouped into five clusters. Principal Component Analysis, Cluster Analysis and Canonical Variate Analysis exhibited similar results. Significant variations were observed among the lentil genotypes for all the parameters under study. Cluster III had the maximum (13) and cluster II had the minimum (1) number of genotypes. The highest intra-cluster distance was observed in cluster V followed by I. The highest inter-cluster distance was observed between cluster II and IV and the lowest inter-cluster distance was found between the clusters III and IV. Considering genetic parameters high genotypic co-efficient of variation (GCV) was observed for number of primary and secondary branches, number of pods per plant, seeds per plant and yield per plant whereas days to 50 % flowering, and days to 100% flowering showed low GCV. In all cases, phenotypic variances were higher than the genotypic variance. High heritability with low genetic advance in percent of mean was observed for days to 100% flowering, number of pods per plant, seeds per plant, and yield per plant which indicated that non-additive gene effects were involved for the expression of this character and selection for such trait might not be rewarding. High heritability with high genetic advance in percent of mean was observed for number of pods per plant and seeds per plant indicating that this trait was under additive gene control and selection for genetic improvement for this trait would be effective. Considering all the characters G1 (BARI MASOOR-1); G27 (BD-3827); G9 (BD-3805); G3 (BARI MASOOR-3); G14 (BD-3811) can be selected for future breeding program.

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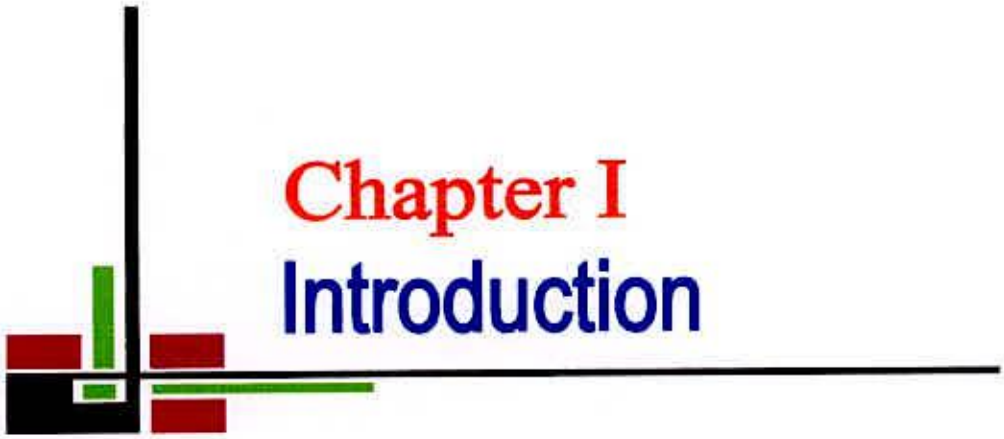
LIST OF ABBREVIATED TERMS

ABBREVIATION	FULL WORD
AEZ	Agro-Ecological Zone
et al.	And others
ACC	Accessions
BARI	Bangladesh Agricultural Research Institute
BBS	Bangladesh Bureau of Statistics
cm	Centimeter
CV	Co-efficient of Variation
G	Genotype
GA	Genetic Advance
GCV	Genotypic Co-efficient of Variation
δ^2_g	Genotypic Variance
g	Gram
h^2b	Heritability in broad sense
j.	Journal
Kg	Kilogram
m	Meter
MSS	Mean Sum of Square
mm	Millimeter
MP	Muriate of Potash
No.	Number
%	Percent
PCV	Phenotypic Co-efficient of Variation
δ^2_p	Phenotypic variance
RCBD	Randomized Complete Block Design
R	Replication
SAU	Sher-e-Bangla Agricultural University
SE	Standard Error
m^2	Square meter
TSP	Triple Super Phosphate



Chapter I
Introduction

CHAPTER 1

INTRODUCTION

Lentil (*Lens culinaris* Medik.) is one of the major legume crops in Bangladesh, which ranks third among the lentil growing countries of Asia Pacific region. It is the second most important pulse crop in area and production, but stands first in the consumer's preference in this country. In 2005-2006 it was grown on about 134,642 ha of land producing 115,370 tonnes of grain, with an average yield of 857 kg ha^{-1} and contributes about 33% to the total pulses production (BBS, 2006). In the humid tropical countries including Bangladesh, leguminous food crops are of special significance because of the low protein content of the major food crops such as cereals (Miah, 1976).

In Bangladesh its cultivation is mostly concentrated in the Gangetic flood plain of western part of the country. Lentil is cultivated during winter (rabi or post rainy season; November-March). Domestic pulse production satisfies less than half of the country's need. The rest, near about 140,000I tonnes, need to be imported at a cost of about US$ 32.2 million per annum. The resulting high prices have led to widespread protein malnutrition especially among vulnerable groups, such as rural children and the aged.

L. culinaris, the only cultivated species (Sindhue and Slinkard,1985), is further divided into two major groups: microsperma with small seeds and macrosperma with

bold seeds.In Bangladesh all the indigenous landraces and varieties are microsperma with orange cotyledons, whereas the exotic macrosperma varieties posses both yellow and orange cotyledons.

Lentil plays an important role in the agro-economy and national health of Bangladesh. Nutritionally, lentil is very rich in protein content and complementary to any cereal crops including rice. It supplies about four times as much protein and eight times as much riboflavin as does rice; the caloric value of it is equal to rice (Anonymous, 1976). Moreover, it is known as poor man's meat. It is a versatile source of nutrients for man, animal and soil (Miah, 1976). After analyzing 1985 germplasm lines Erskine and Witcombe (1984), reported a mean seed protein content of 25.78%. Lentil also contains 59% carbohydrate, 0.5% fats, 2.1% minerals (Gowda and Kaul, 1982). Sufficient amount of vitamins viz. vitamin A 16 IU; thiamine 0.23 mg and vitamin C 2.5 mg (Anonymous, 1976) are available from a gram of lentil. Because of its high lysine contents, the most limiting amino acid in several cereals, lentil can form a balanced diet when supplemented with cereals (Abu-Shakra and Tannous, 1981).

In spite of so many advantages, lentil in Bangladesh is generally grown under minimum fertility and management practices. The development of high potential genotypes with good, stable yield and higher protein content is important to improve yield status of the crop. The average yield of lentil in Bangladesh is gradually declining. Several factors are responsible for low yield of lentil, such as, less attention on cultural practices, little use of fertilizers, lack of pest control measures, postharvest losses, over

as a function of heterosis, is one of the criteria of parent selection. Therefore, the availability of transgressive segregants in any breeding program depends upon the divergence of test parents. Precise information on the nature and degree of genetic divergence of the parents is the prerequisite of an effective breeding program.

The quantification of genetic diversity through biometrical procedures (Anderson, 1957); Rao, 1952) has made it possible to choose genetically diverged parents for a successful breeding program. The importance of genetic diversity in the improvement of a crop has been stressed in both self and cross-pollinated crops (Griffing and Lindstrom, 1954; Murty and Anad, 1966; Gaur *et al.*, 1978). Moreover, evaluation of genetic diversity is important to know the sources of genes for a particular trait within the available germplasm (Tomooka, 1991).

In Bangladesh, information on genetic diversity in lentil germplasm is scanty. Therefore, the present investigation is undertaken with the following objectives:

(a) To estimate the nature and magnitude of genetic divergence among the lentil genotypes.

(b) To identify the most divergent parents or genotypes for further breeding program.

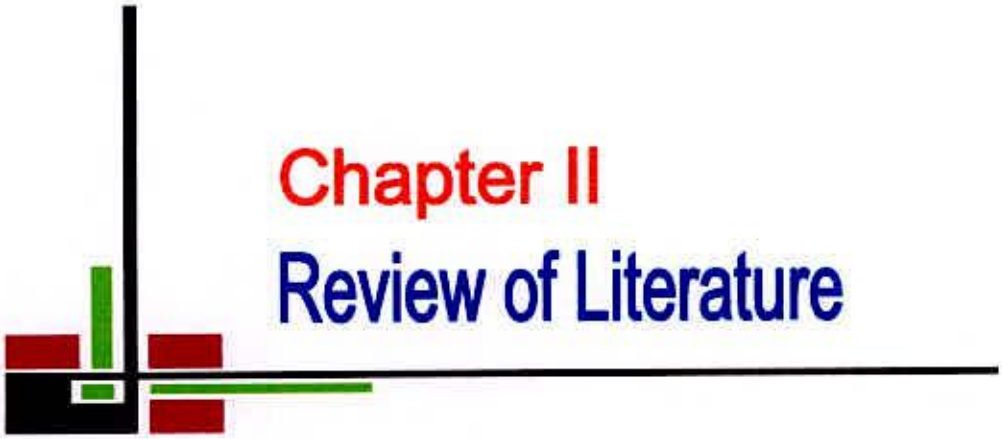
(c) To find out the different gene pool or clustering pattern among the material.

(d) To find out the relationship of genetic diversity with their geographic or ecological background.

and above, the use of traditional varieties or landraces with low genetic potential and instability of yield. The existing varieties in Bangladesh are mostly poor yielding. The development of high yielding and high protein containing lines with other desirable characters is badly needed to improve the yield status of this crop. The research work in this direction is only limited and fragmentary in Bangladesh. More work is needed for making a tangible improvement of this crop. Reportedly, an extensive genetic erosion of lentil occurred in Bangladesh as elsewhere in the World and the need for influx of exotic germplasm into the country has heed stressed (Mia *et al.*, 1986).

In crop improvement program, genetic diversity has been considered as an important factor, essential to meet the diverse goals in plant such as producing cultivars with increased yield, (Joshi and Dhawan, 1966) wider adaptation, desirable quality and pest resistance (Nevo *et al.*, 1982). Diversified genotypes are also a pre-requisite for hybridization program to develop desirable genotypes.

Information on genetic divergence among the plant materials is vital to a plant breeder for an efficient choice of parents for hybridization. It is an established fact that genetically diverse parents are likely to contribute desirable segregates and/or to produce high heterotic crosses. More diverse the parents, greater are the chances of obtaining high heterotic F_1s and broad spectrum of variability in segregating generations (Arunachalam, 1981). The parents identified on the basis of divergence analysis would be more promising in selecting genotypes with desirable character combinations from the segregating generations obtained through hybridization. Furthermore, genetic divergence



Chapter II
Review of Literature

CHAPTER 2

REVIEW OF LITERATURE

2.1 Origin and distribution

The lentil was grown from early times throughout the eastern Mediterranean region as well as in the Nile Valley. Today, it is cultivated throughout the world (Aykroyt and Doughty, 1964). The mountainous region between Hindukush and Himalayas was suggested earlier as the centre of origin but evidence acquired later supported the Near Eastern origin (Zohary, 1972). On the basis of examination and evaluation of archaeological remains and on the identification of the world progenitors and delimitation of their geographic distribution Zohary and Hopt (1973), concluded that pea and lentil should be regarded as founder crops of old world Neolithic agriculture; they were domesticated in the Near East, simultaneously with wheat and barley. Lentil used by the ancient-dwellers and is thought to be one of the earliest domesticated crops (Zohary and Hopt, 1973; Cubero, (1984). Archaeologically, lentil was established as one of the primary domesticated that founded the Neolithic agricultural revolution of wild species *L. orientalis* that is centered inthe Near East. The geographic distribution of wild species .and *L. orientalis* is centered in the Neolithic nuclear area of the Near East arc, i.e. northern Israel, Syria, South Turkey, North Iraq and Western Iran. Ladiginsky (1979) reported that lentil originated in Southern Turkey. Cubero (1984), reported that the region

between Western Turkey and Kurdistan could be its place of origin. According to Azad *et al.* (1991) lentil is thought to have originated in Asia Minor. It spreads quickly to Greece, central and Southern Europe, Egypt, Mediterranean, Afghanistan, Indian subcontinent and China. Lentil is now also cultivated in Argentina, Canada, Colombia, Mexico, Peru and the USA. It is a temperate crop, but is also cultivated in the subtropics during winter months and at high altitudes in the tropics during colder months.

2.2 Cytotaxonomy

Lentil is essentially a self-pollinated crop although natural cross-pollination occurs through insect (Poehlman and Borthakur, 1969). The crop belongs to the family Fabaceae (Leguminosae), sub-family Papilionaceae.Tauband tribe vicineae Bron (Barulina, 1980).

The *Lens* comprises five annual species of which only *L. culinaris* is cultivated (Sindhue and Slinkard, 1985). Lentil is diploid in nature, cytologically containing 7 pairs of chromosomes (2n=l4). Previously lentil was included in the genus *Ervum*. In the year 1987 Medikus suggested the botanicalname, *Lens. culinaris* for lentil. Moench called it *Lens. esculentus in* 1978. Both the nomenclature can be found in the literature but the name given by Medikus is now internationally accepted and approved. Other important species under the genus Lens are: *Lens ervoids*, *Lens montbretti*, *Lens nigricans* and *Lens orientalis.*

2.3 Genetic Divergence

Genetic divergence means the nature and degree of variability existing among the genotypes under studies, which is measured by range, mean, standard deviation, variance, standard error, coefficient of variation, etc.

Genetic divergence analysis used to identify specific parents for realizing heterosis and recombination in breeding program. Several workers have followed the technique of Mahalanobis D^2 statistics on wide range of crop spices to measure the genetic distance among the breeding materials and to identify the character(s) responsible for such type of divergence.

The utility of multivariate analysis for measuring the degree of divergence and for assessing the relative contribution of different characters to the total divergence in self-pollinated crops has been established by several workers (Golakia and Makne, 1992; Natarajan *et al.*, 1988; Das and Gupta, 1984; Sindhu *et al.*, 1989).

Genetic diversity analysis is mainly based on multivariate techniques. During last decade different multivariate techniques are developed through the development of computer program. However, literature related to efficient multivariate techniques for diversity analysis are reviewed in the following paragraphs.

Lentil (*Lens culinaris* M.) is one of the most important pulse crops under the family Leguminosae & sub-family Papilionaceae grown in both tropical and arid regions of the world. Research effort on diversity analysis of lentil seems to be limited in world

literature especially in Bangladesh. Therefore, information related to the diversity of lentil and some other self-pollinated oil and pulse crops available in the literature are reviewed in this section. Beside these, literatures pertaining to the efficient multivariate technique for diversity analysis are also reviewed.

Adhikari and Pandey (1983) by using D^2 analysis in chickpea reported that in native types seeds per pod, pods per plant and in kabuli types primary branches per plant and 100 seed weight contributed maximum towards diversity. In addition to this, 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. On the other hand, Katiar and Singh (1979) observed in chickpea that 250-grain weight and primary branches per plant contributed major portion of the total genetic diversity.

An investigation was carried out for the divergence in eight genotypes of mungbean and their 15 hybrids by Natarajan and Palanisamy (1990). They utilized generalized distance and canonical analysis and found five clusters. The canonical analysis confirmed to a large extent the clustering pattern obtained by multivariate analysis.

Analyzing the data on pod yield/plant and 12 related traits, using the Mahalanobis`s D^2 statistic, Reddy *et al.* (1987) found that 20 germplasms of groundnut, investigated for two years divided into six clusters in both the years. They also observed that genetic diversity was not related to geographical distribution.

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.

Bartual *et al.* (1985) grouped 125 soybean genotypes by PCA, where maximum likelihood factor analysis and cluster analysis were based on morphological and physiological characters. The identified groups were quite stable in their performance through change in environments. Some genotypes were identified as parents for future use.

Chowdhury *et al.* (1998) observed D^2 analysis of yield components of30 groundnut genotypes classified them into 5 clusters. Cluster III had the maximum (10) and cluster V had the minimum (1) number of genotypes. Maximum inter cluster distance was observed between cluster I and V. Metroglyph analysis with a few exception, showed similar types of clustering patterns. In 1996, Varman and Raveendran also

studied genetic diversity in groundnut cross combinations and grouped them into 5 clusters. Cluster V recorded the highest values for 100-pod weight, 100 kernel weight, pod yield and oil content. Cluster IV recorded the highest values for maturing index and recovery percentage.

Dixit (1980) in the investigation in lentil observed that primary branches per plant and yield per plant contributed a large to the total genetic diversity In the same crop Sharma and Luthra reported that pods per plant, seeds per plant and yield per plant contributed maximum towards diversity in 1987.

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 black gram and found days to flowering, plant height, 100 seed weight and pod length contributed maximum towards diversity.

Godshalk and Timothy (1988) in their study reported comparisons of index selection with principal component analysis, principal factor analysis, and maximum likelihood factor analysis. Multivariate analysis was accomplished on both simple and genotypic correlation matrix for three sets of are Characters (5 characters per set) in Switch grass (*Panicum virgatum*). Comparisons were made by computing Spearman's rank correlations between selection index plant scores computed from multivariate

analysis and by determining the number of plants selected in common for the selection methods. Among the multivariate analysis method PCA had the highest correlation with the index selection. They also suggested that PCA is more economic than the other analysis.

Golakia and Makne (1992) investigated diversity in 35 genotypes of Virginia runner groundnut using Mahalanobis's D^2 statistic. These genotypes were grouped into seven clusters, but there was no relationship between genetic and geographical diversity.

Golakiya and Makne (1991) and Nadaf *et al.* (1986) found that grouping of genotypes in indifferent clusters were not related to their geographical origin. It was indicated that the geographical isolation might not be the only factor for genetic diversity. The same authors (1992) found that the genotypes of common geographic origin or same location were grouped into different clusters that suggested lack of relationship between genetic and geographic diversity. In 1991, Katule *et al.* suggested that geographic diversity was not related to genetic diversity. Reddy *et al.* (1987) also found similar result.

Golakiya and Makne (1991) carried out divergence analysis and revealed that the 23 genotypes of groundnut were grouped into six clusters. Same authors (1992) analyzed genetic diversity with 27 varieties of groundnut over two years and divided them into 6 clusters in both the years. Katule *et al.* (1991) studied genetic divergence among eighteen geographically diverse genotypes of semi-spreading groundnut and reported eight different groups of clusters.

In 60 early maturing genotypes of pigeon pea, Murty and Dorairaj (1990) studied genetic diversity through D^2 and canonical analysis from different origin. The genotypes were grouped into three clusters. Genetic diversity was found independent of genotypic origin also.

In cowpea, days to flowering, maturity, pod length, pod girth and 100 grain weight contributed considerably towards diversity reported by Kumar *et al.* (1982). On the contrary, in pigeon pea, Bainiwal and Jatastra (1980) observed through D^2 analysis that plant height, pod length, and days to flowering were the principal component of diversity.

Islam *et al.* (1995) studied genetic divergence among 90 genotypes of groundnut using D^2 and principal components analysis and grouped the varieties into 5 clusters. The inter-cluster distances were larger than the intra cluster distance suggesting wider genetic diversity among the genotypes of different groups. The intra-cluster value was maximum in cluster IV and minimum in cluster III. Cluster III showed the lowest mean values for days to first flowering, days to fifty percent flowering, days to maturity, primary branches per plant and highest shelling percentage, while cluster IV revealed the highest mean values for days to first flowering, days to 50 percent flowering, days to maturity and branches per plant. Germplasms much in use of the above mentioned four characters both in cluster III and IV would offer a good scope of improvement of the crop through rational selection.

Joel and Mylsamy (1998) studied Mahalanobis D^2 statistics to assess the genetic diversity of 26-groundnut genotype of diverse origin and to find out best parents for pod

yield and rust resistance breeding. The genotypes were grouped into 3 clusters. Cluster I had the maximum of 22 genotypes, while cluster II and III had 3 and 1 respectively. It is suggested that the genotypes from cluster I and III may be utilized in crossing to create a wide spectrum of variability and to select from segregants with high pod yield with rust resistance.

Juned *et al.* (1988) investigated genetic diversity in 22 accessions of wild potato from Paraguay and Argentina. They observed a close relationship between the geographical groups using Principal Component Analysis (PCA), is Cluster analysis and genetic diversity.

Katiar and Singh (1990) investigated the genetic diversity of 40 indigenous and exotic strains of fababean (*Vicia faba* L) using Mahalanobis's D^2 statistic. The strains were grouped into 12 different clusters. They found no direct association between geographic distribution and genetic divergence.

Malik *et al.* (1984) in an evaluation-cum-observation trial with 55 lentil accessions collected from Sind and Panjab province of Pakistan, found that the time to flowering varied from 117-150 days with mean value of 124.3 days; time to maturity varied from 130-165 days with a mean of 151.3 days; plant height ranged from 29.0-45.5 cm and the mean was 35.6 days. Pod / plant and yield/ plant ranged between 22-154.8 and 0.48-3.95g with the coefficients of variation 47.3% and 45.2%, respectively. Variability for these traits in lentil germplasm was also reported by Tiwari and Singh (1980).

Mishra and Rao (1990) reported that metroglyph analysis did not show similar type of clustering pattern as observed in D^2 analysis carried out in a comparative study of D^2 and metroglyph analysis with 117 genotypes of chickpea. Similarly, Kotaiah *et al.* (1986) compared the Mahalanobis D^2 and metroglyph analysis in 26 genotypes of groundnut and observed deviation between D^2 and metroglyph method regarding the number of clusters formed and number of genotypes in the clusters. It was suggested that the metroglyph 5 analysis would be suitable for preliminary grouping before taking up D^2 analysis.

Muchlbauer (1974) conducted an experiment to find out the variability and association of characters in 45 lentil cultivars and found the greater variability in three characters viz. yield (kg/ha), seeds/plant and pods/plant with the standard high variation (31.37%) was found for yield/plant and number of pods/plant (23.88%). Todorov (1980) found in his study that plant height, number of pods/plant, seeds/ plant, seed weight/ plant and pod length has got greater variation among the 35 lines and 18 initial populations.

Multivariate analysis using Mahalanobis D^2 statistic was used to group 83 genotypes from 18 countries on the basis of yield/plot and six other agronomic characters of bunch groundnut by Nadaf *et al.* (1986). They found nine clusters, which were not related to the grouping formed by geographical origin. They also observed that variation in pod yield accounted for 88% of the total variation between clusters but number of developed pods. Days to 50% flowering and 100 seed weight were important in accounting for divergence with clusters.

Natarajan *et al.* (1988) studied genetic association and diversity using D^2 analysis among 45 genotypes of diverse origin of green gram. 45 genotypes were grouped in to four clusters. They reported that, in selected materials seed weight contributed maximum followed by days to flower towards the genetic divergence.

Payne *et al.* (1989) reported that the hierarchical nature of the grouping into various number of classes can impose undue constrains and the statistical properties of the resulting groups are not at all clear. Therefore, they have suggested non-hierarchical classification, as an alternative approach to optimize some suitabilities choosing criteria directly from the data matrix. They also reported that the squared distance between means are Mahalanobis's D^2 statistics when all the dimensions are used can be computed using Principal Coordinate Analysis (PCO). They also recommended the Canonical Variate Analysis (CVA) for discriminatory purposes.

Pod length and 100 seed weight contributed maximum towards divergence in mungbean reported by Gupta and Singh (1970). Whereas Ramanujam *et al.* (1974) investigated diversity in mungbean using D^2 and found flowering time, maturity, seed density and 100 seed weight contributed considerably.

Reddy and Reddy (1993) reported on forty-eight genotypes of groundnut, which were grouped into 11 clusters. Cluster I was the largest with 23 genotypes followed by cluster V1 and 111 with 9 and 7 genotypes respectively. Genetic diversity indicated that 100 pod weight (36%) number of branches /plant (31%) and harvest index (15%)

accounted for more than 80% of the total divergence. These 3 characters may be considered in future breeding program.

Reddy *et al.* (1986) analyzed the data on pod yield and 12 related traits using Mahalanobis D^2 statistic in 20-groundnut genotypes for two years. He reported that genetic diversity was not related to geographical distribution of the varieties. The greater inter cluster distance, occurred between clusters I (with 10-11 varieties) and I1 (with 4-6 varieties) and between clusters I and IV (1 variety), depending on year.

Sangha and Sandhu (1973) studied twenty spreading groundnut varieties from diverse sources in respect of secondary branches, number of pods, pod yield and 100 kernel weights. Highly significant differences were observed among the varieties, when tested by multivariate dispersion analysis. The varieties were grouped into six and spatial pattern of groups was not corresponding to geographical diversity.

Shahi *et al.* (1986), from a study involving 57 accessions of lentil germplasm from different parts of Madhya Prodesh, India, reported that wide range of variability for seed size with the range 1.4-3.4 g/100-seed (mean 2.4) seed permeability 5.0-55.8 (mean 26.4%) as well as for germination, 44.2-89. 46 (mean 72.9%).

Shamnugam and Rangasamy (1982) observed that the characters yield per plant and pod cluster per plant contributed considerably towards diversity in black gram. Again the same authors in 1982 assigned 45 genotypes of blackgram to ten clusters by analyzing data on yield and nine yield components using Mahalanobis`s D^2 statistic and

stated that geographical diversity was not the only factor for determining genetic diversity. The clustering pattern more or less confirmed the canonical (vector) analysis. They found that yield per plant contributed most to genetic divergence. Furthermore, Sindhu *et al.* (1989), investigated diversity in 20 strains of blackgram from different agro-ecological zones of India using Mahalanobis's D^2 statistic. They observed no parallelism between geographical and genetic diversity.

Singh and Singh (1969), in a study comprising 20 indigenous and 20exotic lines of lentil; found that pod number, branch numbers and days to flowering had high variability. They also observed that the characters, which had high phonotypic variability, also exhibited high genotypic variability and wide ranges. Number of branches and number of pods had very wide ranges and also had very high phenotypic variability. Practically exotic lines had very small number of branches and pods per plant whereas the indigenous lines had very high no. of branches and pods, and these wide differences accounted for larger phenotypic variability.

Singh and Singh (1989) studied the genetic diversity and stability in chickpea entries. They suggested crossing among the 14 selected genotypes on the basis of intra/inter cluster distances to recombine the genes for stability and high yield.

Swarup and Lal (1987) evaluated 28 high yielding and bold seeded (22.5g/ 100 seed) for time to 50 flowering, time to maturity, plant height, and 100-seed weight at Sehore, India. They observed the time to 50% flowering ranged from 55-69 days, time to maturity ranged from 113 to 134 days after sowing in SL-904 and SL-397, respectively.

Plant height varied from 28.7 cm (SL 945) to 33.9 cm (SL 598) and 100-seed weight from 2.90 g (SL 666) to 4.30g (SL 143).

Teng and Hor (1994) reported the analysis of 15 agronomic characters in 35 groundnut varieties that were divided into 6 clusters of different genetic divergences. Little variation was found within clusters but large differences were observed between clusters. It was suggested that single plant productive capacity, quality and quantity of branches, and shelling percentage were the primary characters influencing yield.

The clustering and ordination methods used often cannot deal explicitly with the computational consequences of large data sets with incomplete information. However, it is shown that the ordination technique of principal component analysis and the mixture maximum likelihood method of clustering can be employed to achieve such analysis (Harch *et al.*, 1999). Genotypes within the cluster are having a smaller D^2 value among themselves than those from group belonging to two different clusters. On the other hand the inter cluster distance is the criterion used for selecting genotypes as parent for hybridization. The genotypes those in clusters with maximum inter cluster distance are genetically more divergent. Variation within the cluster is measured by inter cluster distance. The inter and intra cluster values (D) of groundnut were reported to be ranged from 9.50 to 22.20 and 5.18 to 8.45 (Katule *et al.*, 1991), 3.84 to 7.35 and 4.24 to 4.81 (Golakiya and Makne, 1991) to 7.09 and 3.61 to 4.51 (Golakiya and Makne, 1992).

The coordinates obtained from the PCA are used as input of PCO analysis to calculate distances among the points reported by Digby *et al.* (1989). PCA is used for

graphical representation of the points while PCO is used to calculate the minimum distance in a straight line between each pair of points.

The genetic divergence among 7 parents and their 12 hybrids of cowpea were studied by Thiagarajan *et al.* (1988) using Mohalanobis's D^2 statistics. They observed that the characters namely 50% flowering, 100-grain weight and plant height contribute maximum toward genetic divergence. Similar reports were made by Ramanujam *et al.* (1974) in the study of 10 parents and their $25F_1$s in mungbean.

The genetic diversity of 40 newly developed soybean lines and ten parents were studied by Singh and Ram (1985). The cultivars were grouped into nine clusters by D^2 analysis. They observed lines originating from one or related crosses tended to be included in the same cluster and potential crosses based on inter cluster distance.

The range of variability was studied in some ICARDA collections grown at Tel Hadya, Syria during 1978-79 seasons (Solh and Erskine, 1984). They observed that the range of 100-seed weight (g), Crude protein %, time to maturity, plant height (cm), lowest pod height (cm) and pod number per peduncle were reported as being 1.1-3.6, 20.6-35.6, 154-197, 10-45, 6-30 and 1.0-1.7 respectively, with the corresponding mean value of 3.2, 28.1, 170.3,25.5,14.1,1.1.

Thinking about magnitude of genetic variability for yield and its component characters has been of considerable interest to the plant breeders for planning and execution of genetic improvement program. A large number of such investigations have

been carried out in different crops including Lentil (Malhotra *et al.*, 1974), Groundnut (Reddy *et al.*, 1987), Soybean (Singh and Ram, 1985, Mishra *et al.*, 1987, Broich and Palmer, 1980), Black gram (Singh *et al.*, 1973; Das, 1978; Singh and Mishra, 1983), Mungbean (Gupta and Singh, 1969; Yohe and Poehlman, 1972; Malik *et al.*, 1983, Chickpea, (Chandra,1968; Dumber and Deshmukh, 1983), pigeon pea (Heermath and Talwar, 1971; Dumbre and Deshmukh, 1983) and Pea (Singh *et al.*, 1973; Singh, 1985). All these studies were on the basis of simple analysis of variance, which enabled to compute genetic variance for different characters. But total genetic diversity among different natural populations of these crops could not be obtained, which is important from evolutionary and breeding point of view. Under these circumstances, multivariate analysis is of great importance.

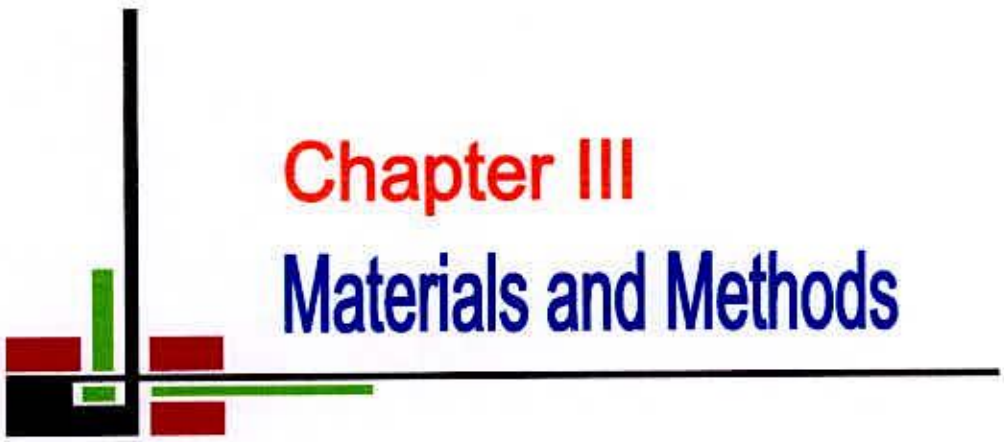
Through Mahalanobis`s D^2 analysis in pea (*Pisum salivum* L.), Narshighani *et al.* (1978) found that seed size, plant height and days to maturity contributed a major portion to the total diversity whereas Ranalli (1982) found a major role of days to flowering. Moreover, Singh *et al.* (1976) reported that pod length, days to flowering and seed yield contribute maximum towards divergence in mungbean through D^2 analysis.

Two hundred and seventy lentil lines were evaluated by Sinha and Chowdhary (1984) at Bihar, India for different morphological and quantitative characteristics. Lines varied little from each other in growth habit, flower color and seed color. Enough variability was found providing scope for selection in quantitative characters such as

plant height (cm), time to flowering (days), 100-seed weight (g) and seed yield (g) per meter row within the range of 20-25, 51-80, 1.02-2.66 and 7.2-71.5 respectively.

Using PCA Mian *et al.* (1991) studied the genetic divergence in 128 germplasms of pea. They reported that the whole population divided into 16 broad based groups and random distribution of genotypes in the clusters suggested no parallel relationship between genetic and geographical diversity in pea.

Working with two hundred early maturing exotic lentil lines Mia *et al.* (1986) found very low coefficient of variation for time to maturity (3.94%) with a mean value 122.30 days, time to flowering (9.65%) with a mean value 74.70 days, and plant height (109.00 %) with a mean value 55.50 cm, but high for seed yield per plant (43.90 %) and 1000 seed weight (29.02%) with mean value of 0.96g and 22.80 g respectively.



Chapter III

Materials and Methods

CHAPTER 3

MATERIALS AND METHODS

Agricultural research uses a large number of procedures and techniques for successful conduction of field experiment. The techniques to be adopted depend on the nature of the research trial and its objectives. Success of field experiment largely depends on the appropriateness of establishment. This means how precisely different aspects of field plot techniques are considered and adopted to maximize non-treatment variations or errors.

3.1 Site of experiment

The experiment was conducted at the field laboratory of the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka during the period from November 2011 to March 2012. The experimental site was at 90°22" E longitude and 23°41" N latitude at an altitude of 8.6 meters above the sea level.

3.2 Materials

A total of thirty five genotypes (35) of lentil, originated from BARI (Bangladesh Agricultural Research Institute) were used in this experiment.

3.3 Soil and climate

The land belongs to Agro-ecological region of 'Madhupur Tract' (AEZ-28) of Nodda soil series. The soil was sandy loam in texture having pH 5.47-5.63. The mean

temperature of the growing period was 24.36° C with average maximum and minimum being 30.0^0 C and 18.67^0 C respectively.

3.4 Experimental design and layout

The study was laid out in Randomized Complete Block Design (RCBD) with three (3) replications (Figure 1). The plant to plant distance was 10 cm and line to line distance was 30 cm. The total land size was 19m X 12.2m. There were three long plots measuring 4 meters width and 18 meters length. The plot to plot distance was 2.5 m. The genotypes were randomly distributed to each row within each line.

3.5 Land preparation

The experimental plot was prepared by ploughing with tractor followed by harrowing and laddering by cows. Weeds and stubbles were removed. Manures and fertilizers were applied as per the recommended dose before the final land preparation. Irrigation channels were made around each plot. The final land preparation was done on 14 November.

3.6 Manure and fertilizer

Due to its ability of nitrogen fixation from the atmosphere lentil require less nitrogen application. But for initial establishment of plant up to the stage of nodule formation a starter dose of 20-40-20 NPK respectively was applied.

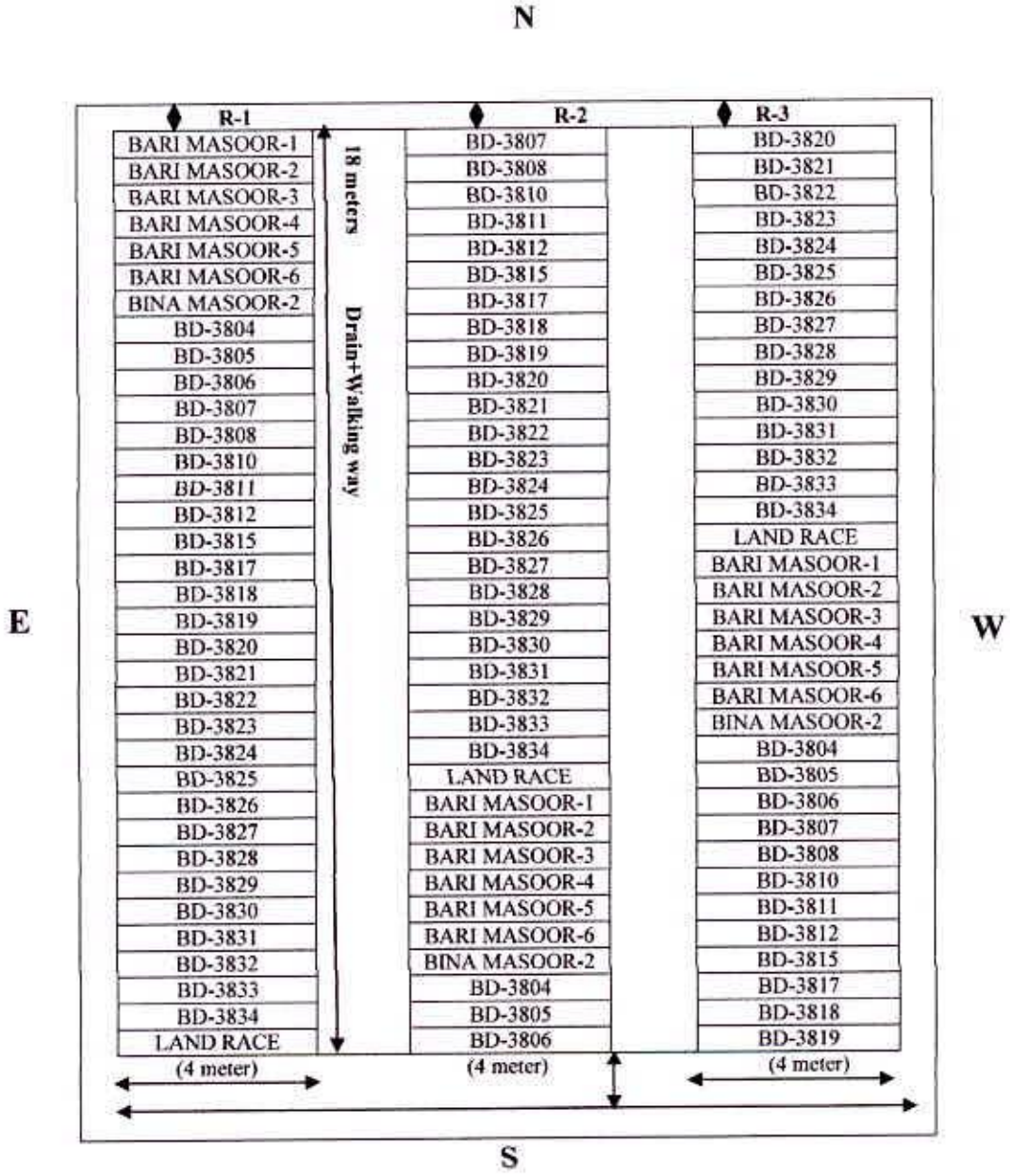


Figure 1. Layout of the experimental field.

R-Replication, m=meter, BD-Bangladesh, N-North, S-South, W-West, E-East

In this study fertilizer was applied as per the recommendation of Bangladesh Agricultural Research Institute (BARI). The following doses of fertilizers and manures were applied to the plot for lentil cultivation (Table 1).

Table 1. Doses of manure and fertilizers used in the study

Fertilizers/Manures	Dose (kg)	
	Applied in the plot	Quantity/ha
Urea	1.71	45
TSP	3.23	85
MP	1.33	35
Cow dung	Applied earlier	1.5 ton

Urea, TSP, MP and Gypsum were applied at the time of final land preparation. Cow dung was applied two weeks before sowing during the land preparation.

3.7 Sowing of seeds and intercultural operation

The seeds of 35 lentil genotypes (Table 2) were sown in the field on 23th November 2010. Intercultural practices were done uniformly for all the genotypes. Thinning was done 25 days after sowing and wedding was done twice-the first during thinning and the second after about two months of sowing.

3.8 Harvesting

Different genotypes matured at different times. The harvesting was completed by 18 March 2011. Ten plants from each plot were randomly selected to collect data and these were harvested by uprooting. Border plants were discarded to avoid border effect.

Table 2. List of lentil genotypes with their sources

Genotype No.	Name/Acc No. (BD)	Source
1.	BARI MASOOR-1	PGRC,BARI
2.	BARI MASOOR-2	PGRC,BARI
3.	BARI MASOOR-3	PGRC,BARI
4.	BARI MASOOR-4	PGRC,BARI
5.	BARI MASOOR-5	PGRC,BARI
6.	BARI MASOOR-6	PGRC,BARI
7.	BINA MASOOR-2	BINA.BAU
8.	BD-3804	PGRC,BARI
9.	BD-3805	PGRC,BARI
10.	BD-3806	PGRC,BARI
11.	BD-3807	PGRC,BARI
12.	BD-3808	PGRC,BARI
13.	BD-3810	PGRC,BARI
14.	BD-3811	PGRC,BARI
15.	BD-3812	PGRC,BARI
16.	BD-3815	PGRC,BARI
17.	BD-3817	PGRC,BARI
18.	BD-3818	PGRC,BARI
19.	BD-3819	PGRC,BARI
20.	BD-3820	PGRC,BARI
21.	BD-3821	PGRC,BARI
22.	BD-3822	PGRC,BARI
23.	BD-3823	PGRC,BARI
24.	BD-3824	PGRC,BARI
25.	BD-3825	PGRC,BARI
26.	BD-3826	PGRC,BARI
27	BD-3827	PGRC,BARI
28.	BD-3828	PGRC,BARI
29.	BD-3829	PGRC,BARI
30.	BD-3830	PGRC,BARI
31.	BD-3831	PGRC,BARI
32.	BD-3832	PGRC,BARI
33.	BD-3833	PGRC,BARI
34.	BD-3834	PGRC,BARI
35.	LAND RACE	PGRC,BARI

3.9 Recording of Experimental Data

Data on the following characters were recorded on individual plant basis from l0 randomly selected plants per genotypes in each replicate. Out of 12 characters, days to 50% flowering and days to maturity were recorded in the field condition and the data on the other characters were recorded in the field Laboratory after harvest.

3.9.1 Days to 50% & 100 % flowering:

Data on days to 50% and 100 % flowering was recorded from the date of sowing to date when 50% and 100 % of plants within a line had flowered.

3.9.2 Days to maturity:

Data on days to maturity was recorded from date of sowing to date of pod maturity.

3.9.3 Plant height (cm):

The height of plant from the ground level to tip of the plant was measured in centimeter as plant height.

3.9.4 Pods per plant:

The total number of pods in individual plants was recorded.

3.9.5 Branches per plant (primary and secondary):

The total number of primary branches and secondary branches including the main stem was counted.

3.9.6 Yield per plant (g):

Weight of the total seeds from each of the sample plant was recorded in gram (g).

3.9.7 Seeds per pod:

Total number of seeds in each pod within the individual plants was counted.

3.9.8 Weight of 100 seed (g):

One hundred clean sun dried seeds were randomly taken from each line and weighted in gram (g).

3.9.9 Seeds per plant:

Total number of seeds in each plant was counted.

Plate 1: One replication view of the experimental field

Plate 2: A single lentil plant in the experimental field

Plate 3: A taller plant with pods

Plate 4: A bushy plant with pods

3.10 Statistical analysis

3.10.1 Estimation of genotypic and phenotypic variances

Genotypic and phenotypic variances were estimated according to the formula given by Johnson *et al.* (1955).

$$\text{Genotypic variance } (\sigma^2_g) = \frac{GMS - EMS}{r}$$

Where,

GMS = Genotypic mean sum of square

EMS = Error mean sum of square

r = number of replications

$$\text{Phenotypic variance } (\sigma^2_{ph}) = \sigma^2_g + EMS$$

Where, σ^2_g = Genotypic variance

EMS = Error mean sum of square

3.10.2 Estimation of genotypic and phenotypic co-efficient of variation

Genotypic and phenotypic co-efficient of variation were calculated by the formula suggested by Burton (1952).

$$\text{Genotypic co-efficient of variation (GCV \%)} = \frac{\sqrt{\sigma^2 g}}{\bar{x}} \times 100$$

Where, σ^2_g = Genotypic variance

$\bar{x}$ = Population mean

Similarly,

The phenotypic co-efficient of variation was calculated from the following formula.

$$\text{Phenotypic co-efficient variation (PCV)} = \frac{\sqrt{\sigma^2 ph}}{\bar{x}} \times 100$$

Where,

σ^2_{ph} = Phenotypic variance

$\bar{x}$ = Population mean

3.10.3 Estimation of heritability

Broad sense heritability was estimated (Lush, 1943) by the following formula, suggested by Johnson *et al.* (1955).

$$h^2_b\% = \frac{\sigma^2_g}{\sigma^2_{ph}} \times 100$$

Where,

h^2_b = Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_{ph} = Phenotypic variance

3.10.4 Estimation of genetic advance

The expected genetic advance for different characters under selection was estimated using the formula suggested by Lush (1943) and Johnson *et al.* (1955).

Genetic advance (GA) = K. h^2. σ_{ph}

$$GA = K.\frac{\sigma^2_g}{\sigma^2_{ph}}.\sigma_{ph}$$

Where,

K = Selection intensity, the value which is 2.06 at 5% selection intensity

σ_{ph} = Phenotypic standard deviation

h^2_b = Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_{ph} = Phenotypic variance

3.10.5 Estimation of genetic advance mean's percentage

Genetic advance as percentage of mean was calculated from the following formula as proposed by Comstock and Robinson (1952):

$$\text{Genetic advance (\% of mean)} = \frac{\text{Genetic Advance}}{\text{Population mean } (\bar{x})} \times 100$$

3.11. Multivariate analysis

The genetic diversity among the genotypes was assessed by Mahalanobis's (1936) general distance (D^2) statistic and its auxiliary analyses. The parent selection in hybridization program based on Mahalanobis's D^2 statistic is more reliable as requisite

knowledge of parents in respect of a mass of characteristics is available prior to crossing. Rao (1952) suggested that the quantification of genetic diversity through biometrical procedures had made it possible to choose genetically diverse parents for a hybridization program. Multivariate analysis viz. Principal Component analysis, Principal Coordinate analysis, Cluster analysis and Canonical Vector analysis (CVA), which quantify the differences among several quantitative traits, are efficient method of evaluating genetic diversity. These are as follows:

3.11.1. Principal Component analysis (PCA)

Principal Component analysis, one of the multivariate techniques, is used to examine the inter-relationships among several characters and can be done from the sum of squares and products matrix for the characters. Thus, PCA finds linear combinations of a set variate that maximize the variation contained within them, thereby displaying most of the original variability in a smaller number of dimensions. Therefore, Principles components were computed from the correlation matrix and genotypes scores obtained for first components (which has the property of accounting for maximum variance) and succeeding components with latent roots greater than unity. Contribution of the different morphological characters towards divergence is discussed from the latent vectors of the first two principal components.

3.11.2 Principal Coordinate analysis (PCO)

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

3.11.3. Cluster analysis (CA)

Cluster analysis divides the genotypes of a data set into some number of mutually exclusive groups. Clustering was done using non-hierarchical classification. In GENSTAT, the algorithm is used to search for optimal values of chosen criterion proceeds as follows. Starting from some initial classification of the genotypes into required number of groups, the algorithm repeatedly transferred genotypes from one group to another so long as such transfer improved the value of the criterion. When no further transfer can be found to improve the criterion, the algorithm switches to a second stage which examines the effect of swooping two genotypes of different classes and so on.

3.11.4. Canonical Vector analysis (CVA)

Canonical vector analysis (CVA) finds linear combination of original variabilities that maximize the ratio of between group to within group variation, thereby giving functions of the original variables that can be used to discriminate between the groups. Thus, in this analysis a series of orthogonal transformations sequentially maximizing of the ratio of among groups to the within group variations. The canonical vector are based upon the

roots and vectors of WB, where W is the pooled within groups covariance matrix and B is the among groups covariance matrix.

3.11.5 Calculation of D^2 values

The Mahalanobis's distance (D^2) values were calculated from transformed uncorrelated means of characters according to Rao (1952), and Singh and Chaudhury (1985). The D^2 values were estimated for all possible combinations between genotypes. In simpler form D^2 statistic is defined by the formula

$$D^2 = \sum_{i}^{x} d_i^2 = \sum_{i}^{x} (Y_i^j - Y_j^k) \qquad (j \neq k)$$

Where,

Y = Uncorrelated variable (character) which varies from i = 1 ------to x

x = Number of characters.

Superscript j and k to Y = A pair of any two genotypes.

3.11.6 Computation of average intra-cluster distances

Average intra-cluster distances were calculated by the following formula as suggested by Singh and Chuadhury (1985).

$$\text{Average intra-cluster distance} = \frac{\sum D_i^2}{n}$$

Where,

D_i^2 = the sum of distances between all possible combinations (n) of genotypes included in a cluster.

n = Number of all possible combinations between the populations in cluster.

3.11.7 Computation of average inter-cluster distances

Average inter-cluster distances were calculated by the following formula as suggested by Singh and Chuadhury (1985).

$$\text{Average inter-cluster distance} = \frac{\sum D_{ij}^2}{n_i \times n_j}$$

Where,

$\sum D_{ij}^2$ = The sum of distances between all possible combinations of the populations in cluster i and j.

n_i = Number of populations in cluster i.

n_j = Number of populations in cluster j.

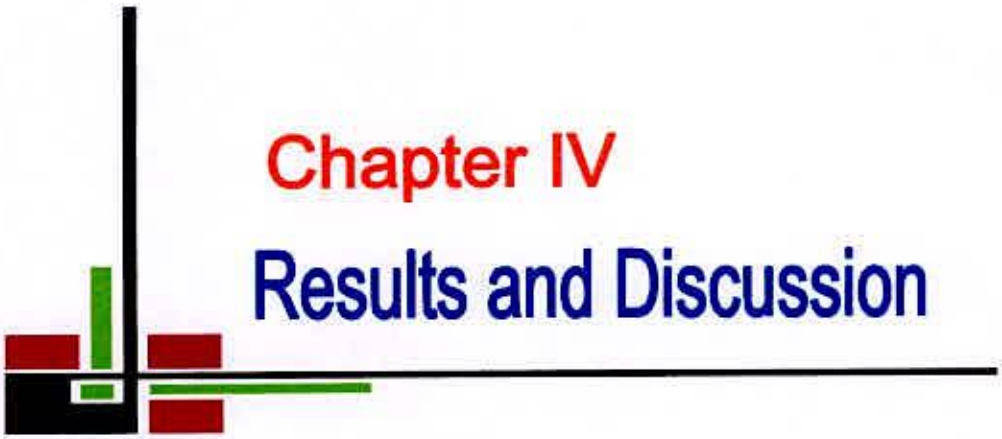
3.11.8 Cluster diagram

Using the values of intra and inter-cluster distances ($D = \sqrt{D^2}$), a cluster diagram was drawn as suggested by Singh and Chuadhury (1985). It gives a brief idea of the pattern of diversity among the genotypes included in a cluster.

3.11.9 Selection of varieties for future hybridization program

Divergence analysis is usually performed to identify the diverse genotypes for hybridization purposes. The genotypes grouped together are less divergent among themselves than those, which fall into different clusters. Clusters separated by largest statistical distance (D^2) express the maximum divergence among the genotypes included into these different clusters. Variety (s) or line(s) were selected for efficient hybridization program according to Singh and Chuadhury (1985). According to them the following points should be considered while selecting genotypes for hybridization program:

- Choice of cluster from which genotypes are selected for use as parent (s)
- Selection of particular genotype(s) from the selected cluster(s)
- Relative contribution of the characters to the total divergence and Other important characters of the genotypes performance.



Chapter IV

Results and Discussion

CHAPTER 4

RESULTS AND DISCUSSION

Diversity is the function of parent selection and also heterosis. The availability of transgressive segregants in a breeding program depends upon the divergence of parents. Thus, the accurate information on the nature and degree of diversity of the parents is the pre-requisite of an effective breeding program. The knowledge of genotypic variation within genotypes in relation to morphology, phenology and yield would help to Screen better genotypes for hybridization program. Therefore, to generate information in the degree of diversity, thirty five lines of lentil were raised in the growing season of 2011-2012 at the field of Sher-e-Bangla Agricultural University, Dhaka. The data on days to 50% flowering, 100% flowering, number of primary and secondary branches/plant, days to maturity, plant height (cm), 100 seed weight (g), pods per plant, seeds per pod, seeds per plant, yield per plant (g) etc. were recorded, analyzed and presented in this chapter.

Genetic diversity was analyzed using GENSTAT software program. Genetic diversity analysis involves several steps, i.e., estimation of distance between the varieties, clustering and analysis of inter-cluster distance. Therefore, more than one multivariate techniques were required to represent the results more clearly and it was obvious from the results of many researchers (Bashar, 2002; Uddin, 2001; Juned *et al.*, 1988 and Ario, 1987). In the analysis of genetic diversity in lentil multivariate techniques were used.

4.1 Genetic parameters

The analysis of variance indicated the existence of highly significant variability for all the characters studied (Table 3). The mean sum of square, mean, range, variance components, coefficients of genotypic and phenotypic variations, heritability estimates, genetic advance and genetic advance in percent of mean (GAPM) are presented in Table 3.

The results are discussed character wise as follows:

4.1.1 Days of 50% flowering

The mean number of days of 50% flowering was 55.10 DAS. It had a range of 52 to 57 DAS (Table 3). The genotypes G-1 (BARI MASOOR-1) was the earliest to 50 % flowering at 52 days while G-32 (BD-3832) were late to flower (57 days) (Appendix IV). The PCV and GCV were 3.02 and 3.52 percent, respectively. There were very little differences between phenotypic and genotypic co-efficient of variation, indicating minor environmental influence on this character. The heritability (73.21 %) estimates for this trait was quite higher, genotypic advance (2.93) and genetic advance over percentage of mean (5.31) were found low (Table 3). Genotypic and phenotypic variability in lentil are show in Figure 2. Heritability and genetic advance over mean in lentil are show in Figure 3. Low genotypic and phenotypic coefficient of variability were observed for days to 50 per cent flowering which are in line with the earlier observation of Singh *et al.* (1973) Prasad and Prasad (1976).

Table 3: Estimation of genetic parameters in eleven characters of 35 genotypes in lentil

Parameters	Range	Mean	MS	$\sigma^2 p$	$\sigma^2 g$	$\sigma^2 e$	PCV	GCV	ECV	h^2_b	GA (5%)	GAPM
Days of 50% flowering	52.00-57.00	55.10	4.56**	3.77	2.76	1.01	3.02	3.52	1.82	73.21	2.93	5.31
Days of 100% flowering	59.67-63.00	61.42	1.50**	1.32	1.03	0.29	1.65	1.87	0.88	78.03	1.85	3.01
Primary branches/plant	2.00-3.11	2.58	0.20**	0.17	0.12	0.05	13.43	15.98	8.67	70.59	0.60	23.24
Secondary branches/plant	12.44-25.11	16.93	23.47**	18.94	12.64	6.3	21.00	25.71	14.83	66.74	5.98	35.34
Plant height (cm)	10.08-13.08	11.95	1.47*	0.93	0.27	0.65	4.35	8.07	6.75	29.03	0.58	4.83
Days to maturity	77-112.00	106.81	97.98**	97.35	65.87	31.48	7.60	9.24	5.25	67.66	13.75	12.88
Pods/plant	41.56-76.89	57.58	243.79**	221.76	187.97	33.79	23.81	25.86	10.10	84.76	26.00	45.16
Seeds/plant	54.78-137.67	101.06	776.67**	757.8	564.6	193.2	23.51	27.24	13.75	74.51	42.25	41.81
Seeds/pod	1.68-1.84	1.76	0.035*	0.03	0.02	0.01	8.04	9.84	5.68	66.67	0.24	13.52
100 seed weight (g)	1.47-2.07	1.67	0.02**	0.02	0.01	0.01	5.99	8.47	5.99	50.00	0.15	8.72
Yield/plant (g)	1.27-2.23	1.69	0.057**	0.03	0.02	0.01	8.37	10.25	5.92	66.67	0.24	14.08

Here, ** Mean square is significant at the 0.01 level, MS = Mean sum of square, σ^2 p = Phenotypic variance, σ^2g = Genotypic variance and σ^2 e = Environmental variance, PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation, ECV = Environmental coefficient of variation, h2b= Heritability, GA= Genetic advance, GAPM= Genetic advance in percent of mean and CV% = Coefficient of variation.

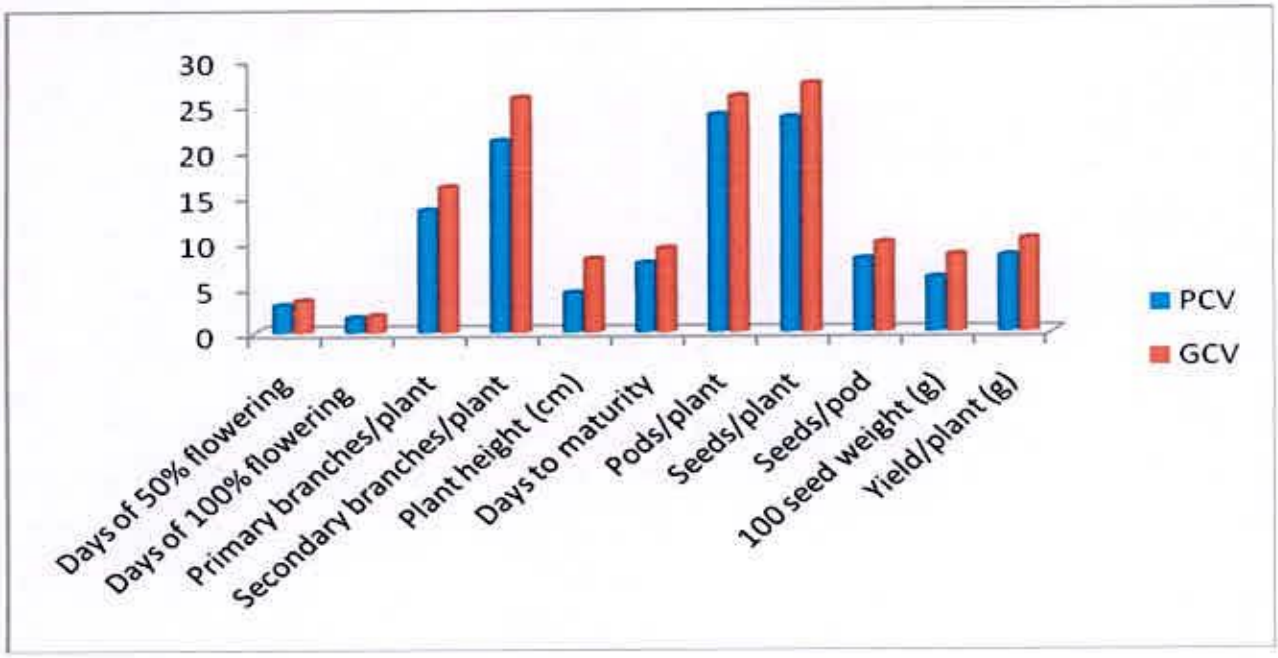


Figure 2: Genotypic and phenotypic variability in lentil

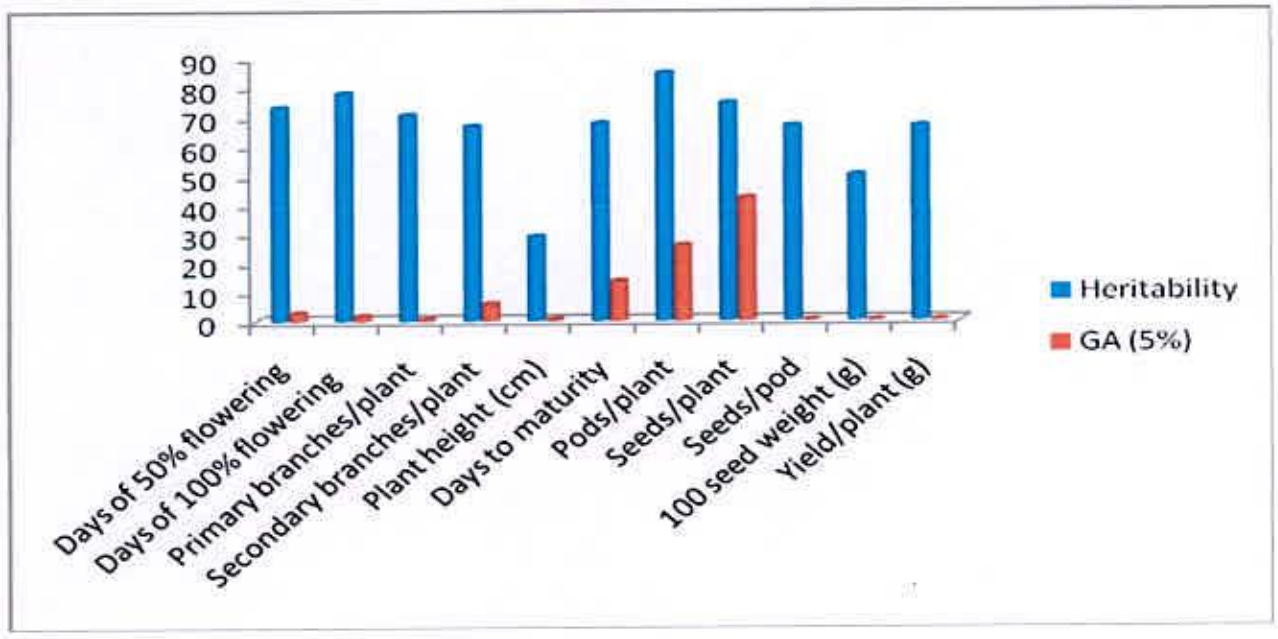


Figure 3: Heritability and genetic advance over mean in lentil

4.1.2 Days of 100% flowering

Significant differences were recorded among the entries with respect to days of 100% flowering (Table 3). The value ranged from 59.67 to 63.00 DAS, The genotypes G-19 (BD-3819) and G-31(BD-3831) were the earliest to 100 % flowering at 59.67 days while G-32 'BD-3832' was late to flower (63.00 days) (Appendix IV). The PCV and GCV were 1.65 and 1.87 percent with a overall mean of 61.42 days (Table 3). There was a very little difference between phenotypic and genotypic co-efficient of variation, indicating minor environmental influence on this character. The heritability (bs) estimates were moderate high (78.03 %) with an expected genetic advance over mean of 3.01 percent (Table 3). High heritability coupled with low genetic advance was observed for days to 100 per cent by Islam *et al.* (1995) and Ramanujam *et al.* (1974).

4.1.3 Primary branches

It ranged from 2.00 to 3.11 with a mean value of 2.58. Maximum number of primary branches was recorded in 'BD-3811' and 'BD-3822' genotype showed the minimum number of primary branches (Appendix IV). The PCV and GCV observed were 13.43 and 15.98 percent, respectively (Table 3). There was little difference between phenotypic and genotypic co-efficient of variation indicating little environmental influence in the expression of this character. Genotypic and phenotypic coefficients of variation for number of primary branches per plant were high. Heritability (bs) of 70.59 percent

coupled with low genetic advance over percentage of mean 23.24 percent were noticed (Table 3). This character also showed high heritability estimates. Such values of GCV with least difference were also observed by Malik *et al.* (1984) and Reddy and Reddy (1998).

4.1.4 Secondary branches

It ranged from 12.44 to 25.11 with a mean value of 16.93. Maximum number of secondary branches was recorded in 'BD-3826' and 'BARI MASOOR-3' genotype showed the minimum number of secondary branches (Appendix IV). The PCV and GCV observed were 21.00 and 25.71 percent, respectively (Table 3). There was little difference between phenotypic and genotypic co-efficient of variation indicating little environmental influence in the expression of this character. Genotypic and phenotypic coefficients of variability for number of branches per plant were high. Heritability (bs) of 66.74 percent coupled with low genetic advance over percentage of mean 35.34 percent were noticed (Table 2). This character also showed moderate high heritability estimates which was also found by Reddy and Reddy (1998).

4.1.5 Plant height (cm)

The grand mean plant height recorded was 11.95 cm. It ranged from 10.08 cm to 13.08 cm (Table 3). The analysis of variance revealed highly significant differences among the

genotypes with respect to plant height. The maximum plant height was recorded by the G-21 (BD-3821) and the lowest plant height was recorded by 'BARI MASOOR-6' (Appendix IV). The PCV and GCV were 4.35 and 8.07 percent, respectively (Table 3). There was little difference between phenotypic and genotypic co-efficient of variation indicating little environmental influence in the expression of this character. In the present study, the genotypic and phenotypic co-efficient of variability were moderate for plant height. The estimates of heritability was high at 29.03 per cent with an expected genetic advance (4.83 %) (Table 3). Low heritability and low genetic advance for this character was observed by Islam *et al.* (1995).

4.1.6 Days to maturity

Significant differences were recorded among the entries with respect to days to maturity. The value ranged from 77 to 112 DAS. The accession G-14 (BD-3811) showed minimum and the accession G-10 (BD-3806) showed maximum days to maturity, respectively (Appendix IV). The PCV and GCV were 7.60 and 9.24 percent with an overall mean of 106.81 days. The heritability (bs) estimates were moderate (67.66 %) with an expected genetic advance over mean of 12.88 percent. Moderate heritability and higher genetic advance for this character was observed by Gupta and Singh (1970).

4.1.7 Pods/plant

Wide variation of 41.56 to 76.89 pods per plant with a mean of 57.58 was observed in Table 3. The values of PCV and GCV were 23.81 and 25.86, respectively (Table 3). The difference between GCV and PCV indicated less influence of environment on this trait. The genotype BARI MASOOR-3 recorded the minimum number of pods per plant. Whereas, genotype 'BD-3827' showed the highest number of pod per plant (Appendix IV). A moderate value of genotypic coefficient of variation and phenotypic coefficient of variation were noticed for number of pods per plant (Table 3). Higher heritability estimate of 84.76 percent with high genetic advance as percent mean (45.16) were recorded for this trait (Table 3). This result is similar to the earlier findings by Muchlbauer (1974).

4.1.8 Seeds/plant

It was ranged from 54.78 to137.67 with a mean of 101.06. The coefficient of variability at phenotypic and genotypic levels were 23.51 and 27.24, respectively (Table 3). The difference between GCV and PCV indicated less influence of environment on this trait. The maximum seeds/plant was observed in the genotype 'BD-3827' and the minimum with the genotype BARI MASOOR-1 (Appendix IV). In the present study, the genotypic and phenotypic coefficients of variability were high for number of fruits per cluster. Moderate heritability of 74.51 percent was noticed with a genetic gain of 42.25 percent

(Table 3). High heritability and moderate genetic gain for this character were also observed by Muchlbauer (1974).

4.1.9 Seeds/pod

A wide variation was found among the germplasm genotypes for the number of seeds per pod. It varied from 1.68 to 1.84 significantly among the genotypes with an overall mean of 1.76 (Table 3). The genotype G-19 (BD-3819) and G-24 (BD-3824) showed highest number of seeds per pod and the lowest number of seeds per pod was recorded by the entry 'BARI MASOOR-2' (Appendix IV). The PCV and GCV were 8.04 and 9.84, respectively (Table 3). The moderate high heritability estimates of 66.67 percent with an expected genetic advance over mean of 13.52 percent were noticed for seeds per plant (Table 3). Similar findings were also obtained by Malik *et al.* (1984) and Muchlbauer (1974).

4.1.10. Hundred seed weight (g)

It ranged from 1.47 to 2.07 g with a mean of 1.67 g. The minimum 100 seed weight was recorded by the variety 'BARI MASOOR-2' and variety 'BD-3805' showed the maximum fruit weight (Appendix IV). The PCV and GCV obtained were 5.99 and 8.47 percent, respectively demonstrated that environment has little influence of the expression of this character (Table 3). Therefore selection based upon phenotypic expression of this

character would be effective for the improvement of this crop. The values of moderate heritability (50.00 %) along with low genetic advance as per cent mean (8.72 %) were observed for this trait (Table 3). Moderate heritability and low genetic advance for this character was observed by Nadaf *et al.* (1986).

4.1.11 Yield/plant (g)

The mean yield per plant noticed was 1.69 g with a range of 1.27-2.23 g in the genotype 'BARI MASOOR-3' and 'BD-3827', respectively (Appendix IV). Low phenotypic coefficient of variability (8.37 %) and genotype coefficient of variability (10.25%) were recorded for this character (Table 3). The high genotypic and phenotypic coefficient of variability were exhibited by fruit yield per plant, these findings are similar with earlier reports of Singh *et al.* (2006) and Manivannan *et al.* (2005). Moderate heritability (66.67 %) and low genetic advance as percent mean (14.08) were recorded for this character (Table 3). Moderate heritability and low genetic advance for this character was also observed by Shahi *et al.* (1986).

Plate 5a. Showing phenotypic variation in seeds among different genotypes of lentil (G_1-G_{12})

Plate 5b. Showing phenotypic variation in seeds among different genotypes of lentil (G_{13}-G_{24})

Plate 5c. Showing phenotypic variation in seeds among different genotypes of lentil (G_{25}-G_{35})

4.2 Multivariate Analysis

4.2.1 Principal Component Analysis (PCA)

Principal components were computed from the correlation matrix and genotype scores obtained from first components (which has the property of accounting for maximum variance) and succeeding components with latent roots greater than the unity (Jeger *et al.*, 1983). Contributions of the different morphological characters towards divergence were discussed from the latent vectors of the first two principal components.

The principal component analysis yielded Eigen values of each principal component axes of coordination of genotypes in which the first axes totally accounting for the variation among the genotypes, whereas four of these Eigen values above unity accounted for 77.4 %. The first two principal axes accounted for 55.49% of the total variation among the 11 characters describing in 35 lentil genotypes (Table 4). Based on principal component axes I and II, a two dimensional chart (Z_1-Z_2) of the genotypes are presented in Figure 4. The scattered diagram (Figure 4) represents that apparently there were mainly five clusters and the genotypes were distantly located from each other.

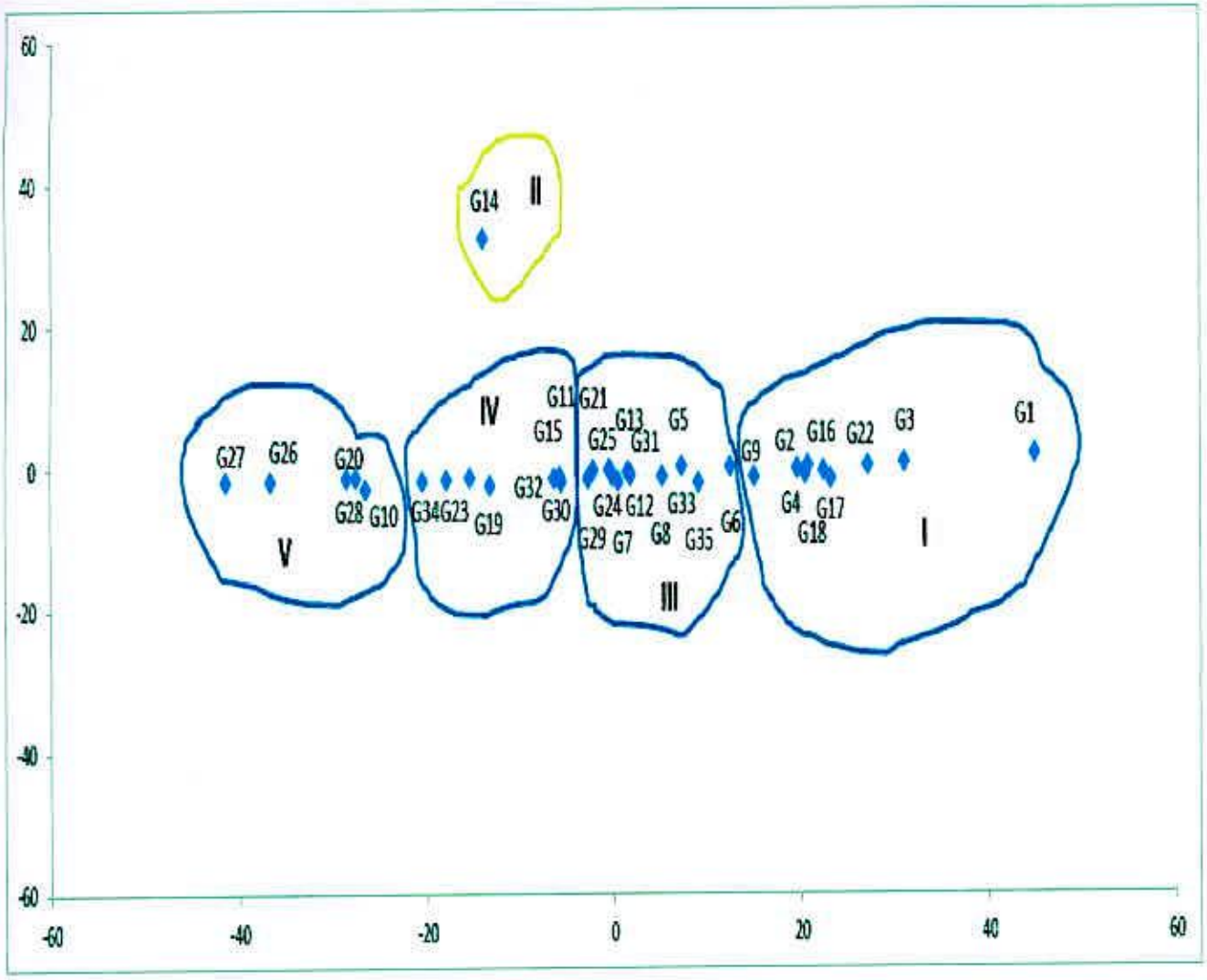


Figure 4: Scatter distribution of 35 lentil genotypes based on their principal component scores superimposed with clustering

Table 4. Eigen values and yield percent contribution of 11 characters of 35 lentil genotypes

Characters	Eigen values	Percent variation	Cumulative % of Percent variation
Days of 50% flowering	4.508	40.98	40.98
Days of 100% flowering	1.596	14.51	55.49
Primary branches/plant	1.483	13.48	68.97
Secondary branches/plant	0.928	8.43	77.4
Plant height (cm)	0.769	6.99	84.39
Days to maturity	0.688	6.26	90.65
Pods/plant	0.459	4.18	94.83
Seeds/plant	0.325	2.96	97.79
Seeds/pod	0.193	1.75	99.54
100 seed weight (gm)	0.043	0.39	99.93
Yield/plant (gm)	0.007	0.07	100.00

4.2. 2 Principal Coordinate Analysis (PCO)

Inter-genotypic distances obtained from principal coordinate analysis for selective combination, showed that the highest distance (86.400) was observed between the genotypes number G1 and G27, followed by G1 and G26 (81.647) and the lowest distance was observed between G25 and G33 (0.176) followed by G12 and G24 (0.217), G7 and G24 (0.373) (Table 5).

By using these inter-genotypic distances intra-cluster genotypic distances were calculated (Table 8) as suggested by Sinha and Chowdhary (1984). The highest intra-cluster distance (0.025) found in cluster V composed of five genotypes (Table 6) and cluster II showed the lowest intra-cluster distance (0.00) composed of one genotype (Table 6), which indicated within group diversity of the genotypes, was maximum in cluster V and minimum in cluster II, Intra-cluster distances between II (0.2311) to IV (0.2412) and III (0.1371) to V (0.1502) were more or less similar.

4.2.3 Non -hierarchical Clustering

The computation from covariance matrix gave non hierarchical clustering among 35 genotypes. By application of non- hierarchical clustering and using covariance matrix, the 35 lentil genotypes were grouped into five different clusters. Mishra *et al.* (1985) reported similar number of clustering in 75 soybean genotypes. Shunmugam *et al.* (1982)

Table 5. Ten highest and ten lowest inter genotypic distance among the 35 lentil genotypes

Highest distance		
Sl No.	**Genotype**	**Distance**
01	G1-G27	86.400
02	G1-G26	81.647
03	G1-G20	73.525
04	G1-G28	72.570
05	G3-G27	72.454
06	G1-G10	71.624
07	G22-G27	68.535
08	G3-G26	67.700
09	G1-G14	66.305
10	G1-G34	65.507
Lowest distance		
Sl No.	**Genotype**	**Distance**
01	G25-G33	0.176
02	G12-G24	0.217
03	G7-G24	0.373
04	G7-G12	0.512
05	G13-G33	0.697
06	G15-G30	0.698
07	G11-G30	0.754
08	G13-G25	0.874
09	G11-G15	0.879
10	G20-G28	0.955

Table 6. Distribution of 35 genotypes in different clusters

Cluster no.	Symbol of Genotypes	Number of member	Genotypes
I	G1, G2, G3, G4, G9, G16, G17, G18, G22	9	BARI MASOOR-1, BARI MASOOR-2, BARI MASOOR-3, BARI MASOOR-4, BD-3805, BD-3815, BD-3817, BD-3818, BD-3822
II	G14	1	BD-3811
III	G5, G6, G7, G8, G12, G13, G21, G24, G25, G29, G31, G33, G35	13	BARI MASOOR-5, BARI MASOOR-6, BINA MASOOR-2, BD-3804, BD-3808, BD-3810, BD-3821, BD-3824, BD-3825, BD-3829, BD-3831, BD-3833, LAND RACE
IV	G11, G15, G19, G23, G30, G32, G34	7	BD-3807, BD-3812, BD-3819, BD-3823, BD-3830, BD-3832, BD-3824
V	G10, G20, G26, G27, G28	5	BD-3806, BD-3820, BD-3826, BD-3827, BD-3828

reported ten clusters; Nadaf *et al.* (1986) nine clusters, Golakia and Make (1992) seven clusters; Reddy *et al.* (1987) six clusters in groundnut. These results confirmed the clustering pattern of the cultivars according to the Principal Component Analysis. So, the results obtained through PCA were confirmed by non-hierarchical clustering. Compositions of different clusters with their corresponding genotypes including the clusters are presented in Table 6. Cluster III had maximum thirteen genotypes followed by cluster I, IV, V and II, which had nine, seven, five and one genotypes, respectively. Cluster I composed of nine genotypes namely BARI MASOOR-1, BARI MASOOR-2, BARI MASOOR-3, BARI MASOOR-4, BD-3805, BD-3815, BD-3817, BD-3818, BD-3822. Cluster I showed highest mean values for 100 seed weight. Cluster II contains only one genotype namely BD-3811. Cluster II showed highest mean values for three characters and those were days of 100 % flowering, primary branches and plant height. Cluster III was constituted of thirteen genotypes namely BARI MASOOR-5, BARI MASOOR-6, BINA MASOOR-2, BD-3804, BD-3808, BD-3810, BD-3821, BD-3824, BD-3825, BD-3829, BD-3831, BD-3833, LAND RACE. Cluster IV constituted of seven genotypes namely BD-3807, BD-3812, BD-3819, BD-3823, BD-3830, BD-3832, BD-3824. Cluster IV showed highest mean values for two characters and those were days to maturity and seeds/pod. Cluster V consisted of five genotypes namely BD-3806, BD-3820, BD-3826, BD-3827, BD-3828. Cluster V showed highest mean values for five characters and those were days of 50 % flowering, primary branches/plant, pods/plant, seeds/plant (g) and yield/plant (g).

4.2.4. Cluster means

Days to 50% flowering: It is observed that minimum days required in the cluster group I (54.07 days). It reveals 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 (56.13 days) (Table 7).

Days to 100% flowering: It was observed that minimum days required in the cluster group I (61.04 days). It revealed that most of the early flowering materials were laying in this group. On the other hand late flowering materials were present in the cluster group II (61.67 days) (Table 7).

Days to maturity: In this experiment days to maturity varied significantly from each other. The highest days to maturity were found in the cluster group IV (110.95) and the lowest value was observed in the cluster II (77 days) (Table 7).

Pods per plant: The highest pods per plant was found in the cluster group V (72.71) and the lowest value was observed in the cluster I (46.61) (Table 7). This is an important character that contributes towards yield.

Seeds per pod: This is also a yield contributing character. The highest value was observed in the cluster IV (1.78) and the lowest value was found in the cluster group II (1.71) (Table 7). It revealed that small seeds were laying in the cluster group II.

Seeds per plant: The highest number of seeds was found in the cluster V (129.16) and the lowest value was observed in the cluster I (78.80) (Table 7).

Table 7. Cluster means for 11 characters in 35 genotypes of lentil

Characters	I	II	III	IV	V
Days of 50% flowering	54.07	55.33	55.08	55.67	56.13
Days of 100% flowering	61.04	61.67	61.26	61.62	62.20
Primary branches/plant	2.49	3.11	2.51	2.60	2.75
Secondary branches/plant	14.39	17.44	16.22	18.86	20.56
Plant height (cm)	11.93	12.26	11.83	12.05	12.11
Days to maturity	110.56	77.00	110.51	110.95	110.60
Pods/plant	46.61	65.44	55.91	62.86	72.71
Seeds/plant	78.80	111.56	99.08	111.80	129.16
Seeds/pod	1.73	1.71	1.76	1.78	1.77
100 seed weight (gm)	1.71	1.60	1.68	1.64	1.64
Yield/plant (gm)	1.39	1.82	1.65	1.84	2.12

100 Seed weight: The highest 100 seed weight was observed in the cluster group I (1.71 g) and the lowest mean was found in the cluster II (1.60 g) (Table 7). It means that most of the bold seeded genotypes were present in cluster I.

Yield per plant: The highest mean yield was observed in the cluster group V (2.12 g) and the lowest value was found in the cluster group I (1.39 g) (Table 7). It revealed that the high yielding genotypes were belonging to this cluster group.

According to the above discussion it could be recommended that the materials preset in the cluster I and III were early maturing and simultaneously high yielding as other yield contributing characters were also high in this group.

From the class mean values it was observed that all the cluster mean values for days to 50% flowering, days to maturity, plant height, seed per pod, no. of primary branches, no. of secondary branches, 100 seed weight, dry matter weight, yield per plant and harvest index were more or less similar. The maximum range of variability was observed for the character seed per plant (78.80 to 137.67) and days to maturity (77.00 to 110.95) among all the characters in five clusters.

Cluster II and V included mainly late flowering and late maturing genotypes with low yield, but they were highly heterogeneous in nature. The high yielding lines belonged to early flowering and early maturing groups, I and IV. Bartual *et al.* (1985) also reported

similar relationship in soybean. To develop high yielding varieties/lines, genotypes of these groups could be used in hybridization program.

4.2.5. Canonical Variate Analysis (CVA)

Canonical Variate Analysis was performed to compute the inter-cluster Mahalanobis's values. Statistical distances represent the index of genetic diversity among the clusters. The average intra and inter-cluster distance (D^2) values are presented in Table 8. Results indicated that the highest inter-cluster distance was observed between II and IV (62.20), followed by I and II (61.40) and II and III (61.40), then I and V (11.79) and IV and I (7.87). The lowest inter-cluster distance was observed between the cluster III and IV (3.58) followed by IV and V (4.22), III and I (4.42) and V and III (7.51), suggesting a close relationship among those clusters. The inter-cluster distances were larger than the intra-cluster distances suggesting wider genetic diversity among the genotypes of different groups (Table 8 and Figure 5). Islam (1995) obtained larger inter-cluster distances than the intra-cluster distances in a multivariate analysis.

However, the maximum inter-cluster distance was recorded between cluster II and IV followed by between I and II. Genotypes from these clusters can use in hybridization program.

The intra-cluster divergence varied from 0.00 to 0.025, maximum for cluster V, which was comprised of five genotypes of diverse origin, while the minimum distance was observed in cluster II that comprised one genotype.

Table 8: Intra (Bold) and inter cluster distances (D^2) for 35 genotypes

Cluster	I	II	III	IV	V
I	**0.016**	61.40	4.42	7.87	11.79
II		**0.00**	61.40	62.20	61.68
III			**0.006**	3.58	7.51
IV				**0.012**	4.22
V					**0.025**

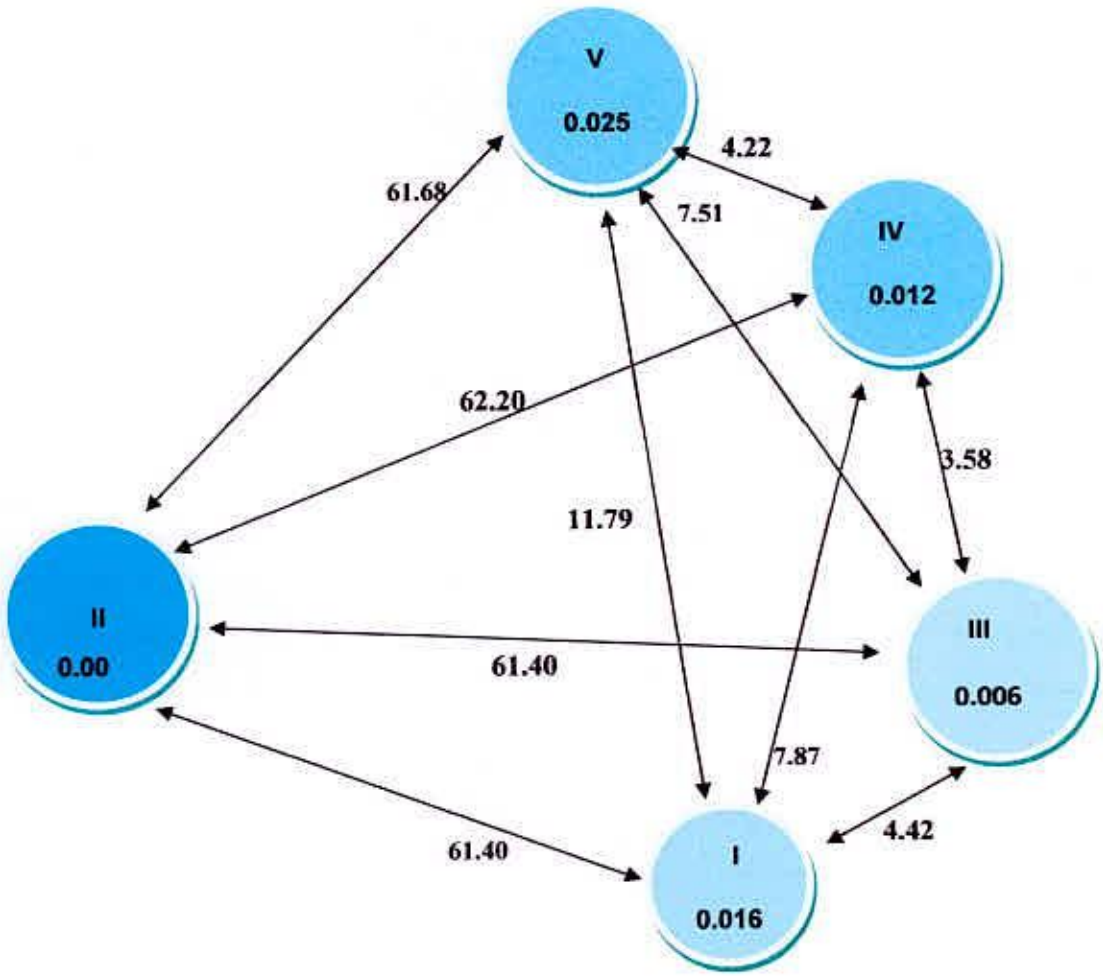


Figure 5. Diagram showing intra and inter -cluster distances (D^2) of thirty five genotypes in lentil

The clustering pattern of the genotypes revealed that varieties/lines originating from the same places did not form a single cluster because of direct selection pressure. This indicated that geographic diversity was not related to genetic diversity that might be due to continuous exchange of genetic materials among the countries of the world. Same results have been reported by Shewe *et al.* (1972) in groundnut; Verma (1970) in groundnut and soybean; Murty and Anand (1966); Anand and Rawat (1984) in brown mustard; Das and Gupta (1984) in black gram; Natarajan *et al.* (1988) green gram, Patel *et al.* (1989) in sunflower; Mian and Bhal (1989) in chickpea.

It had been observed that geographic diversity is not always related to genetic diversity and therefore, it is not adequate as an index of genetic diversity. Murty and Arunachalam (1966) studied that genetic drift and selection in different environment could cause greater diversity than geographic distance.

Furthermore, there is a free exchange of seed material among different region, as a consequence, the characters constellation that might be associated with particular region in nature, loose their individuality under human interference, and however, in some cases effect of geographic origin influenced clustering that is why geographic distribution was not the sole criterion of genetic diversity.

The free clustering of the genotypes suggested dependence upon the directional selection pressure applied for realizing maximum yield in different regions; the nicely evolved homeostatic devices will favor constancy of the associated characters will thus

indiscriminate clustering. This would be suggested that it was not necessary to choose diverse parents for diverse geographic regions for hybridization.

4.2.6 Contribution of characters towards divergence of the cultivars

The values of Vector I and Vector II are presented in Table 9. Vector I obtained from PCA expressed that days of 100% flowering (0.133), plant height (0.684), primary branches/plant (1.052), secondary branches/plant (0.023), pods/plant (0.053), seeds/plant (0.031) and 100 seed weight (2.098) were major characters that contribute to the genetic divergence. It was the reflection of first axis of differentiation. In vector II; days to 50% flowering (0.016), plant height (0.255 cm), 100 seed weight (0.892 g), yield per plant (0.042 g) showed their important role toward genetic divergence. The value of Vector I and Vector II revealed that both Vectors had positive values for plant height (cm), 100 seed weight (g) indicating the highest contribution of these traits towards the divergence among 35 genotypes of lentil. Negative values in both vectors for days to maturity and seeds/pod had lower contribution towards the divergence.

Table 9: Relative contributions of the eleven characters of 35 varieties to the total divergence

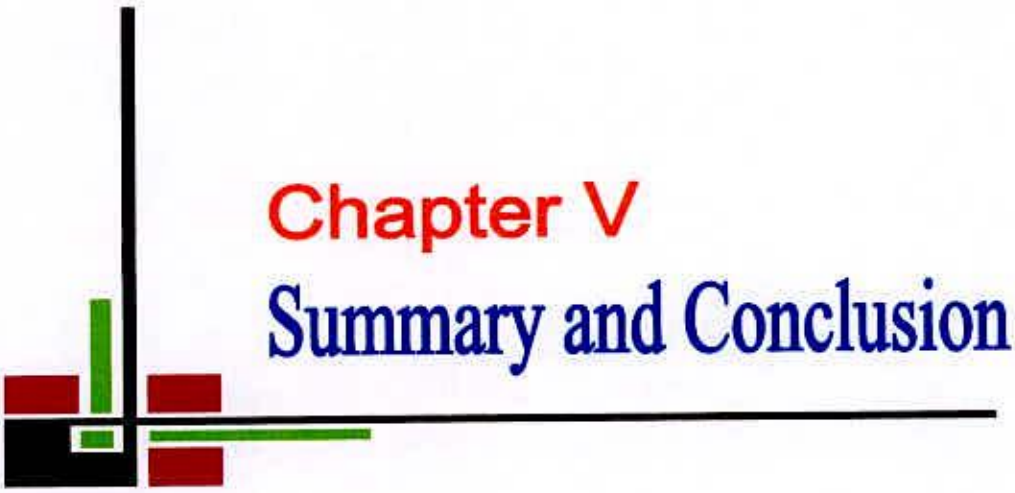
Characters	Vector-1	Vector-2
Days of 50% flowering	-0.099	0.016
Days of 100% flowering	0.133	-0.374
Primary branches/plant	1.052	-0.128
Secondary branches/plant	0.023	-0.215
Plant height (cm)	0.684	0.255
Days to maturity	-1.794	-0.063
Pods/plant	0.053	-0.258
Seeds/plant	0.031	-0.058
Seeds/pod	-6.144	-9.528
100 seed weight (g)	2.098	0.892
Yield/plant (g)	-4.292	0.042

4.2.7 Selection of cultivars for future hybridization

Genotypically distant parents are able to produce higher heterosis (Falconer, 1960; Moll *et al.*, 1962; Ramanujam *et al.*, 1974; Chauhan and Singh, 1982; Arunachalam *et al.*, 1981; Ghaderi *et al.*, 1984; Mian and Bhal, 1989). Beside this, Arunachalam *et al.* (1981) reported in groundnut that the higher heterosis for yield and its components could be obtained from the crosses between the intermediate divergent parents than extreme ones. Mian and Bhal (1989) also reported the same in chickpea that medium divergent genotypes showed higher heterosis in crosses for different yield contributing characters. Srivastava and Arunachalam (1977) reported in triticale that very high or very low parental divergent failed to result in heterosis. Mian and Bhal (1989) also reported the same concept in chickpea that medium divergent genotypes showed higher heterosis in crosses for different yield contributing characters.

Considering the magnitude of cluster mean and agronomic performance the genotype G1 (BARI MASOOR-1) for minimum days to 50 % flowering from cluster I; G27 (BD-3827) for maximum number of pod per plant and maximum number of seed per plant from cluster II; G9 (BD-3805) for maximum 100 seed weight from cluster I; G27 (BD-3827) for maximum yield per plant from cluster II; G3 (BARI MASOOR-3) and G14 (BD-3811) for maximum primary and secondary branches respectively from cluster I and cluster II were found promising. Therefore considering group distance and other agronomic performance the inter genotypic crosses between G1 (BARI MASOOR-1) and G27 (BD-3827); G1 (BARI MASOOR-1) and G9 (BD-3805); G1 (BARI MASOOR-1)

and G3 (BARI MASOOR-3); G1 (BARI MASOOR-1) and G14 (BD-3811); G27 (BD-3827) and G9 (BD-3805); G27 (BD-3827) and G3 (BARI MASOOR-3); G27 (BD-3827) and G14 (BD-3811); G9 (BD-3805) and G3 (BARI MASOOR-3); G9 (BD-3805) and G14 (BD-3811); G3 (BARI MASOOR-3) and G14 (BD-3811) may be suggested for future hybridization program.



Chapter V

Summary and Conclusion

CHAPTER 5

SUMMARY AND CONCLUSION

An experiment with 35 lentil genotypes was conducted in the field of Sher-e-Bangla Agricultural University, Dhaka to study diversity pattern based on 11 characters during November 2010 to March 2011. Seeds were sown in the main field in the month of November 2010 in RCBD with three replications. Data on plant height, days to 50% flowering, days to 100% flowering, days to maturity, primary branches/plant, secondary branches/plant, pods/plant, seeds/pod, seeds/plant, 100 seed weight, yield/plant were recorded on plant basis.

The highest mean value was observed for days to maturity. This character exhibited the second highest range of variation (77-112.00) indicated that all the genotypes showed wide range of variation in respect of this character. This character showed moderate heritability (67.66 %) accompanied with low genetic advance in percentage of mean and the phenotypic variance (97.35) was higher than the genotypic variance (65.87). Among these characters, days to 50% flowering, days of 100% flowering, seeds/pod, pods/plant and yield/plant showed least difference between phenotypic and genotypic variance, which indicated additive gene action for the expression of this characters. These entire characters showed moderate to high phenotypic and genotypic co-efficient of variation except days of 100% flowering, days to 50% flowering and plant height. Among the

characters the highest genotypic co-efficient of variation was recorded for seeds/plant (27.24), pods/plant (25.86) followed by secondary branches/plant (25.71), primary branches/plant (15.98), yield/plant (10.25), seeds/pod (9.84), days to maturity (9.24). Heritability in broad sense was low to high for all the characters studied and it ranged from 29.03 % to 84.76 % which indicated that selection based on phenotypic expression of any character for breeding could be effective. The genetic advance was very low to moderate. These findings revealed that it was indicative of non-additive gene action. The high heritability was being exhibited due to favorable influence of environment rather than genotypes. Thus, the genotypes which performed well in various characters were due to genetic reasons and have a possibility for improvement through selection in the subsequent generations.

Multivariate analysis was carried out through principal component analysis (PCA), principal coordinate analysis (PCO), cluster analysis, and canonical vector analysis (CVA) using GENSTAT software program. The first four principal characters with Eigen values were greater than unity contributed 77.4 % variation toward divergence. As per as PCA, D^2 and cluster analysis using the genotypes were grouped into five different clusters. Cluster I, II, III, IV and V comprised nine, one, thirteen, seven and five genotypes, respectively.

The maximum cluster distance was observed between cluster II and IV (62.20) followed by the distance between clusters V and II (61.68), I and II (61.40), II and III (61.40). The

lowest inter-cluster distance was observed between cluster III and IV (3.58), followed by IV and V (4.22).

The highest intra-cluster distance was identified in cluster V (0.025) and the lowest intra-cluster distance was observed in cluster II (0). Genotypes included in cluster I showed highest cluster mean for 100 seed weight (1.71 g). Cluster II had the highest mean for days of 100% flowering (61.67 days), primary branches/plant (3.11) and plant height (12.26). Cluster IV had the highest mean for days to maturity (110.95 days), seeds/pod (1.78) and. Cluster V had the highest cluster mean value was achieved for five character viz. days to 50 % flowering (56.13), secondary branches/plant (20.56), pods/plant (72.71), seeds/plant (129.16) and yield/plant (2.12 g).

Findings of the present study indicated significant variation among the genotypes for all the character studied. Considering the magnitude of cluster mean and agronomic performance the genotype G1 (BARI MASOOR-1) for minimum days to 50 % flowering from cluster I; G27 (BD-3827) for maximum number of pods per plant and maximum number of seeds per plant from cluster II; G9 (BD-3805) for maximum 100 seed weight from cluster I; G27 (BD-3827) for maximum yield per plant from cluster II; G3 (BARI MASOOR-3) and G14 (BD-3811) for maximum primary and secondary branches /plantrespectively from cluster I and cluster II were found promising. Therefore considering group distance and other agronomic performance the inter genotypic crosses between G1 (BARI MASOOR-1) and G27 (BD-3827); G1 (BARI MASOOR-1) and G9 (BD-3805); G1 (BARI MASOOR-1) and G3 (BARI MASOOR-3); G1 (BARI

MASOOR-1) and G14 (BD-3811); G27 (BD-3827) and G9 (BD-3805); G27 (BD-3827) and G3 (BARI MASOOR-3); G27 (BD-3827) and G14 (BD-3811); G9 (BD-3805) and G3 (BARI MASOOR-3); G9 (BD-3805) and G14 (BD-3811); G3 (BARI MASOOR-3) and G14 (BD-3811) may be suggested for future hybridization program.

The result of the present study revealed that a wide variability exists among the collected lentil genotypes. In addition, there was also genotypic variability of different yield contributing characters with yield of lentil. From the findings of the present study, the following conclusions could be drawn:

i. Wide range of genetic diversity existed among the lentil genotypes. That variability could be used for future breeding program of lentil in Bangladesh.

ii. Selection procedure would be applied for desired characters such as lowest days to 50% flowering and increase number of pods/plant, seeds/plant, seeds/pod, seed weight, yield/plant to develop high yielding varieties.

iii. Relatively higher value and lower differences between genotypic co-efficient of variation and phenotypic coefficient of variation of different yield contributing characters like pods/plant, seeds/plant, seeds/pod, yield per plant were observed which indicates high potentiality to select these traits in future which were less affected by environmental influence.

iv. Further collection of lentil germplasm would be continued for getting more variability and desired traits in lentil.

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CHAPTER 6

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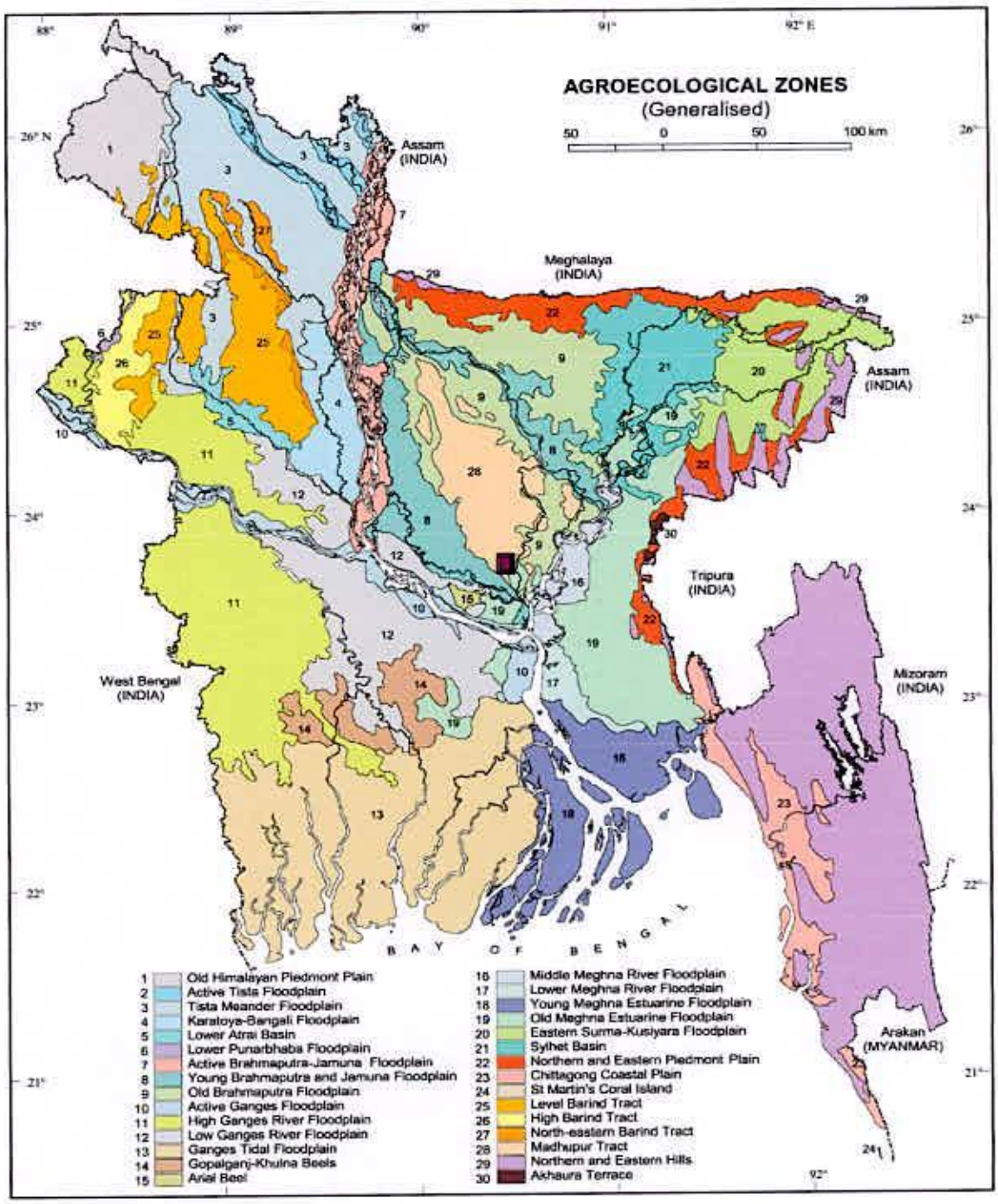
Appendices

APPENDICES

Appendix I. Map showing the experimental site under the study



The experimental site under study

Appendix II. Monthly average Temperature, Relative Humidity and Total Rainfall and sunshine of the experimental site during the period from October, 2010 to March, 2011

Month	Air temperature (°c)		Relative humidity (%)	Rainfall (mm) (total)	Sunshine (hr)
	Maximum	Minimum			
October, 2010	34.8	18.0	77	227	5.8
November, 2010	32.3	16.3	69	0	7.9
December, 2010	29.0	13.0	79	0	3.9
January, 2011	28.1	11.1	72	1	5.7
February, 2011	33.9	12.2	55	1	8.7
March, 2011	34.6	16.5	67	45	7.3

Source: Bangladesh Meteorological Department (Climate & Weather Division), Agargoan, Dhaka - 1212

Appendix III. Physical characteristics and chemical composition of soil of the experimental plot

Soil characteristics	Analytical results
Agrological Zone	Madhupur Tract
P^H	6.00 – 6.63
Organic matter	0.84
Total N (%)	0.46
Available phosphorous	21 ppm
Exchangeable K	0.41 meq / 100 g soil

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

Appendix IV. Mean performance of eleven different yield and yield contributing characters of 35 lentil genotypes

G	D50%F	D100%F	PB	SB	PH	DM	PP	SPP	SP	HSW	YPP
1	52.00	60.33	2.78	16.56	11.81	110.33	49.56	54.78	1.73	1.53	1.34
2	53.00	60.00	2.44	14.44	10.94	110.33	48.11	84.11	1.68	1.47	1.29
3	53.67	60.67	2.44	12.44	11.94	109.67	41.56	74.67	1.77	1.78	1.27
4	52.67	61.67	2.44	13.22	10.63	110.00	48.00	83.00	1.70	1.60	1.36
5	54.00	60.67	2.33	15.33	10.52	109.67	53.78	95.00	1.75	1.75	1.63
6	55.33	62.00	2.22	18.56	10.08	109.67	50.11	90.56	1.80	1.90	1.69
7	54.33	61.33	2.56	16.56	12.77	110.33	57.33	99.56	1.71	1.72	1.66
8	55.67	61.00	2.89	16.67	12.27	111.00	55.22	96.44	1.71	1.63	1.58
9	56.33	61.67	2.44	13.78	12.89	111.33	50.33	88.11	1.71	2.07	1.70
10	56.33	62.67	2.56	19.78	13.00	112.00	71.56	123.56	1.69	1.57	1.94
11	55.00	60.67	2.78	22.00	12.42	111.33	59.33	106.00	1.78	1.63	1.77
12	55.33	61.33	3.00	15.33	11.91	110.67	55.89	100.11	1.77	1.70	1.67
13	55.00	61.33	2.44	13.33	11.88	110.67	57.11	101.89	1.76	1.67	1.70
14	55.33	61.67	3.11	17.44	12.26	77.00	65.44	111.56	1.71	1.60	1.82
15	55.00	62.67	2.78	16.44	12.47	111.00	60.56	106.78	1.75	1.73	1.85
16	55.33	61.33	2.56	14.33	12.48	110.67	46.67	81.56	1.75	1.75	1.40
17	54.00	61.67	2.78	16.33	11.57	111.67	44.67	81.56	1.75	1.65	1.30
18	55.00	61.00	2.56	13.22	12.69	111.00	46.67	83.89	1.75	1.70	1.43

D50%F = Days of 50% flowering, D100%F = Days of 100% flowering, PB = Primary branches, SB = Secondary branches, PH = Plant height, DM = Days to maturity, PP = Pod/plant, SPP = Seed/plant, SP = Seed/pod, HSW = 100 seed weight (g), YPP = Yield/plant (g))

Appendix IV. Mean performance of eleven different yield and yield contributing characters of 35 lentil genotypes (Cont'd)

G	D50%F	D100%F	PB	SB	PH	DM	PP	SPP	SP	HSW	YPP
19	54.00	59.67	2.11	19.22	11.26	110.33	62.78	115.56	1.84	1.68	1.95
20	55.00	61.00	2.86	21.00	11.76	110.00	68.89	127.00	1.83	1.73	2.20
21	55.67	61.33	2.33	17.78	13.08	111.00	58.33	103.67	1.77	1.82	1.88
22	54.67	61.00	2.00	15.22	12.39	110.00	43.89	77.56	1.74	1.80	1.40
23	56.67	61.67	2.89	21.89	11.81	110.67	65.56	116.56	1.79	1.73	2.02
24	56.00	61.33	2.67	14.33	12.19	110.33	54.56	100.78	1.84	1.57	1.58
25	55.00	61.33	2.44	18.44	12.00	109.67	56.33	102.00	1.80	1.72	1.75
26	56.33	62.33	2.56	25.11	12.49	110.33	74.33	132.89	1.78	1.63	2.17
27	56.67	62.33	2.78	18.56	12.20	110.33	76.89	137.67	1.79	1.62	2.23
28	56.33	62.67	3.00	18.33	11.11	110.33	71.89	124.67	1.76	1.67	2.08
29	56.33	62.00	2.44	15.22	11.94	110.00	59.11	102.89	1.69	1.60	1.65
30	56.67	61.33	2.33	18.56	12.18	110.67	60.11	106.00	1.76	1.53	1.63
31	53.00	59.67	2.22	16.11	11.33	11.67	58.56	100.33	1.73	1.63	1.64
32	57.00	63.00	2.56	16.78	12.60	111.67	63.56	112.89	1.78	1.67	1.88
33	54.67	60.67	2.44	17.78	11.92	110.00	57.78	101.33	1.76	1.57	1.59
34	55.33	62.33	2.78	17.11	11.61	111.00	68.11	118.78	1.75	1.50	1.78
35	55.67	62.33	2.67	15.44	11.86	112.00	52.78	93.44	1.76	1.53	1.43
Mean	55.10	61.42	2.58	16.93	11.95	106.81	57.58	101.06	1.76	1.67	1.69
Min	52.00	59.67	2.00	12.44	10.08	11.67	41.56	54.78	1.68	1.47	1.27
Max	57.00	63.00	3.11	25.11	13.08	112.00	76.89	137.67	1.84	2.07	2.23

D50%F = Days of 50% flowering, D100%F = Days of 100% flowering, PB = Primary branches, SB = Secondary branches, PH = Plant height, DM = Days to maturity, PP = Pod/plant, SPP = Seed/plant, SP = Seed/pod, HSW = 100 seed weight (g), YPP = Yield/plant (g)

Appendix V. Principal component score thirty five genotypes of lentil

Genotypes	Z_1	Z_2
1	44.987	1.868
2	19.653	-0.108
3	31.074	0.752
4	20.782	0.31
5	7.295	0.184
6	12.474	0.127
7	1.534	-0.558
8	5.208	-1.182
9	15.032	-1.256
10	-26.477	-2.926
11	-5.599	-1.959
12	1.77	-1.013
13	-0.142	-1.007
14	-13.897	32.348
15	-6.341	-1.487
16	22.454	-0.413
17	23.217	-1.565
18	20.512	-0.863
19	-15.332	-1.284
20	-28.469	-1.336
21	-2.723	-1.475
22	27.167	0.31
23	-17.842	-1.596
24	1.818	-0.801
25	-0.43	-0.181
26	-36.578	-1.797
27	-41.336	-1.797
28	-27.515	-1.279
29	-2.181	-0.334
30	-5.699	-1.211
31	0.486	-1.829
32	-13.201	-2.391
33	-0.366	-0.346
34	-20.419	-1.777
35	9.084	-2.129