STUDY OF GENETIC DIVERGENCE IN FINGER MILLET (*Eleusine coracana* (L.) Gaertn) GERMPLASM

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B.Sc. (Ag.)

MASTER OF SCIENCE IN AGRICULTURE
(GENETICS AND PLANT BREEDING)

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BY

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B.Sc. (Ag.)

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2014

DECLARATION

I, **MAHANTHESHA M** hereby declare that the thesis entitled "**STUDY OF GENETIC DIVERGENCE IN FINGER MILLET (*Eleusine coracana* (L.) Gaertn) GERMPLASM**" submitted to Acharya N.G. Ranga Agricultural University for the degree of **MASTER OF SCIENCE IN AGRICULTURE** is a result of the original research work done by me. I also declare that the thesis or part thereof has not been published earlier elsewhere in any manner.

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CERTIFICATE

Mr. MAHANTHESHA M has satisfactorily prosecuted the course of research and that the thesis entitled "**STUDY OF GENETIC DIVERGENCE IN FINGER MILLET (*Eleusine coracana* (L.) Gaertn) GERMPLASM**" submitted is the result of original research work and is of sufficiently high standard to warrant its presentation to the examination. I also certify that the thesis or part thereof has not been previously submitted by him for a degree of any University.

Date: **(Dr. M. Sujatha)**

Place: Hyderabad Chairperson

CERTIFICATE

This is to certify that the thesis entitled "**STUDY OF GENETIC DIVERGENCE IN FINGER MILLET (*Eleusine coracana* (L.) Gaertn) GERMPLASM**" submitted in partial fulfilment of the requirements for the degree of **MASTER OF SCIENCE IN AGRICULTURE** of the Acharya N.G. Ranga Agricultural University, Hyderabad is a record of the bonafide research work carried out by **MAHANTHESHA M** under my guidance and supervision. The subject of the thesis has been approved by the Student's Advisory Committee.

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

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LIST OF CONTENTS

LIST OF TABLES

LIST OF ILLUSTRATION

LIST OF SYMBOLS AND ABBREVIATIONS

%	per cent
<	less than
>	more than
ANOVA	Analysis of variance
C.D.	Critical difference
C.V.	Coefficient of variation
cm	centimeter
d.f.	degrees of freedom
et al.	and others
F_1	First filial generation
g	gram
Gca	general combing ability
ha	hectare
i.e.	that is
kg	kilogram
m	meter
MSS	Mean Sum of Squares
No.	Number
r	Correlation coefficient
RBD	Randomized Block Design
t	tonne
viz.	namely
Vs.	versus

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ABSTRACT

A field experiment was conducted to estimate the genetic variability and genetic divergence in finger millet and to carry out yield component analysis through correlation and path analysis. Forty eight germplasm lines were sown in a randomized block design with three replications, during *kharif* 2013 at National Bureau of Plant Genetic Resources, Regional station, Rajendranagar, Hyderabad. The objective of the experiment was to identify divergent genotypes to use as donor parents in hybridization programmes.

On the basis of the mean performance of the genotypes among traits studied, the following were identified as promising lines for further crop improvement. Genotype 13570 could be used as a promising donor for grain yield per plant and grain yield per plot. Genotype 13426 recorded highest mean value for maximum no. of leaves and finger width. Genotype 13433 recorded highest plant height and main ear length. Genotype 13632 recorded highest ear width, 13650 maximum no. of productive tillers, 13712 highest finger length, 13675 maximum no. of basal tillers and 13555 maximum no. of leaves. The above mentioned genotypes will be useful for increasing the productivity.

The analysis of variance revealed significant differences among genotypes for all the characters. Studies of genetic variability revealed high phenotypic and genotypic coefficients of variation, heritability and genetic advance as per cent of mean for the traits *viz*., no. of basal tillers per plant, no. of productive tillers per plant, main ear width, grain yield per plant and grain yield per plot indicating simple selection can be practiced for improvement of these characters.

The genotypic coefficient of variation for all the characters studied was lesser than the phenotypic coefficient of variation indicating the effect of environment. High GCV and PCV values were observed for grain yield per plot followed by grain yield per plant, no. of basal tillers per plant, productive tillers per plant, main ear width and finger length. High heritability coupled with high genetic advance as per cent of mean was observed for plant height, no. of basal tillers per plant, no. of productive tillers per plant, main ear length, main ear width, finger length, grain yield per plant and grain yield per plot. Thus, these traits are predominantly under the control of additive gene action and hence these characters can be improved by selection.

The correlation analysis revealed that grain yield per plant showed positive significant association with no. of basal tillers, no. of leaves on the main tiller, productive tillers per plant, main ear length, finger width, total no. of fingers on the main ear, grain yield per plot and plant height.

Path coefficient analysis revealed that grain yield per plot exhibited highest positive direct effect on grain yield per plant, followed by finger width, plant height and along with significant positive correlation for all the above mentioned characters. Therefore, it is emphasized to lay attention on traits like grain yield per plot, finger width and plant height in crop improvement programme of finger millet in future.

The D^2 analysis was carried out for eleven characters which partitioned the forty eight genotypes into eight clusters. Maximum divergence was observed between cluster VI and VIII, while minimum was between cluster I and V. The maximum intra cluster distance was shown by cluster VIII.

Higher grain yield per plant was recorded for clusters are VI, II and IV. Genotype included in cluster VI is having highest mean value for grain yield per plant, finger width and grain yield per plot. Cluster IV is having highest mean value for main ear width. The genotypes 13570, 13675 and 13528 (VI), 13569 and 13568 (II) were having high mean values for grain yield per plant may be directly used for adaptation or may be used as parents in future hybridization programme.

Among the 11 quantitative characters studied the most important character contributing to the divergence was grain yield per plant followed by main ear width, total no. of basal tillers per plant, total no. of fingers on the main ear, finger width, main ear length, plant height, no. of leaves on the main tiller, total productive tillers per plant, finger length and grain yield per plot. In order to select genetically diverse genotypes the material should be screened for the important traits *viz*., grain yield per plant, main ear width, total no. of basal tillers per plant, total no. of fingers on the main ear, main ear length and plant height.

Chapter I

Introduction

Chapter I

INTRODUCTION

Finger millet [*Eleusine coracana* (L.) Gaertn.] also known as African millet or Ragi belongs to family Graminae or Poaceae and common name 'Finger millet' is derived from the finger-like branching of the panicle. It is a self pollinated tetraploid (2n = 36) crop. The crop is native to the Ethiopian highlands of central Africa and was introduced into Indian subcontinent approximately 3000 years ago. The long history of cultivation of finger millet in India under diverse agro-climatic conditions and the associated human and natural selection has resulted in generation of large variability giving India the status of secondary centre of diversity.

It is the most important small millet cultivated in more than 25 countries in Africa and Asia. The major producers are Uganda, India, Nepal and China. India is the major producer in Asia. In India ragi is grown in an area of 2.0 M ha with a production of 2.15 M t, which accounts for 45 per cent of the world's cultivated area and 55 per cent of the world's production. Ragi is widely grown in the states of Karnataka, Tamil Nadu, Andhra Pradesh, Maharashtra, Orissa, Gujarat, Jharkhand, Uttar Pradesh, Madhya Pradesh and Uttarakhand (Ministry of Agriculture, 2012).

Finger millet is highly nutritious as its grain contains the high quality protein (7-10%). It is the richest source of calcium (344 mg/100 g), iron (3.9 mg/100 g) and other minerals. It is also rich in phosphorus (283 mg/100 g) and potassium (408 mg/100 g). It is highly valued as a reserve food in the times of famine. Despite all these merits, this crop has been neglected from the main stream of crop improvement programme. One of the means to boost its production and productivity is to enhance utilization of finger millet.

Exploitation of genetic variability existing in the working germplasm is the first principle in the improvement of any crop. Heritability measures the degree of resemblance between the parents and the off-springs and its magnitude indicates the heritability with which a genotype can be identified by its phenotypic expression, while genetic advance aids in exercising the necessary selection pressure.

The efficiency of selection in any breeding programme depends on the direction and magnitude of association between yield and its components. Thus, correlation enables to identify the characters or combination of characters which might be useful as indicator of high yield by way of evaluating relative influence of various characters on yield and among themselves as well. The original concept of correlation was given by Galton (1889) and later elaborated by Fisher (1967).

Path analysis is done with the main purpose of understanding the direct and indirect contribution of different characters towards grain yield. The direct contribution of each component to the yield and the indirect effects and its association with other characters cannot be differentiated by simple correlations. It was first developed and described by Wright (1921) as a tool in genetic analysis for deriving the direct and indirect effects of any set of variables themselves related to one another. Later it was employed for crop improvement by Dewey and Lu, (1959).

Genetic diversity is the basic for any crop improvement programme. The D^2 statistic is useful tool to assess the genetic divergence among population. It also provides a quantitative measure of association between geographic and genetic diversity based on generalized distance (Mahalanobis, 1936).

Analysis and utilization of available genetic diversity is a short-term strategy for developing improved cultivars for meeting immediate requirement of the farmers and the end users. The present study was undertaken with the following objectives to identify diverse genotypes with good yield potential.

1. To estimate the genetic variability, heritability and genetic advance in the germplasm of finger millet.
2. To study the association of various characters with yield and among themselves through correlation studies.
3. To estimate the direct and indirect effects of component characters on yield.
4. To estimate the genetic divergence in the available germplasm.

Chapter II

Review of Literature

Chapter II

REVIEW OF LITERATURE

The phenotype of quantitative traits, in principle, is the joint product of genotype and environment. Hence, the estimates of variability and its heritable components for the yield contributing characters in the available germplasm are pre-requisites for a breeding programme for high yield.

The success of any breeding programme depends on the quantum of genetic variability available for exploitation. The information on the type of variation in the available genetic material and the part played by the environment on the expression of plant characters is of prime importance for the appraisal of rate and magnitude of possible improvement. Several investigators have screened finger millet genotypes from different sources, which exhibited immense range of variation in morphological, physiological and biochemical traits that govern the performance.

A brief review of available literature in consonance with the objectives of the present investigation "Study of Genetic Divergence in Finger millet (*Eleusine coracana* (L.) Gaertn) Germplasm" are reviewed and presented under the following heads.

2.1 Genetic Variability, Heritability and Genetic Advance

2.2 Correlation Studies

2.3 Path Coefficient Analysis

2.4 Genetic Diversity

2.1 GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE

Improvement of economic characters like yield through selection is conditioned by the nature and magnitude of variability existing in such populations. However, the phenotypic expression of complex character like yield is a combination of genotype, environment and their interaction. This indicates the need for partition of overall variability into heritable and non-heritable components with the help of appropriate statistical techniques.

Possibility of achieving improvement in any crop plants depends heavily on the magnitude of genetic variability. Phenotypic variability expressed by a genotype or a group of genotypes in any species can be partitioned into genotypic and environmental components. The genotypic component being the heritable part of the total variability, its magnitude for yield and its component characters influences the selection strategies to be adopted by the breeders.

Thakur and Saini (1995*)* reported high heritability coupled with genetic advance for yield, days to flowering, plant height and days to maturity.

Gowda (1997) observed narrow difference between PCV and GCV for grain yield, while productive tillers and fingers per ear exhibited wide differences indicating high magnitude of environmental effect on these traits. However, grain yield exhibited high heritability and high genetic gain whereas, productive tillers registered moderate heritability and high genetic gain.

Vadivoo *et al.* (1998) observed that genotypic coefficients of variability were moderate and high for protein and calcium, respectively. High heritability coupled with high genetic advance indicated their governance by additive gene action.

Jain and Yadava (1999) concluded that genotypic and phenotypic coefficient of variation were moderate for grain yield, tillers per plant, harvest index and leaves per plant whereas ear length, vegetative period, number of stomata and harvest index, exhibited high heritability coupled with moderate to high genetic advance as a percentage of mean.

Bendale *et al.* (2002) observed that phenotypic variances were higher than genotypic variances. Phenotypic (PCV) and genotypic coefficients of variation (GCV) were high for number of tillers, number of effective tillers, grain yield per plant, straw yield per plant and weight of grains of main ear head.

Anand (2003) observed high GCV, heritability and expected genetic advance for grain weight of main ear followed by length of the main ear and number of productive tillers in a study comprising of F_2 population of ragi.

Tiwari *et al.* (2005) found a considerable level of intra and inter population variability for most quantitative and qualitative traits like plant height, leaf number, length of flag leaf, finger branching, finger type and size, and spikelet shattering.

Bedis *et al.* (2006a) studied that high PCV and GCV for plant height, productive tillers per plant and days to 50% flowering with high values of heritability and genetic advance as per cent of mean.

John (2006) concluded that the varietal improvement for grain yield is mainly dependent upon the extent of genetic variability present in the population. High genotypic and phenotypic coefficient of variation was observed for number of productive tillers per plant, number of fingers per ear and total dry matter production. Number of productive tillers per plant, number of fingers per ear, test weight, total dry matter production and harvest index possessed high heritability coupled with high estimates of genetic advance.

Sripichitt *et al*. (2006) found low PCV and high GCV for days to maturity and grain yield per plant, respectively. Finger width and length exhibited high heritability coupled with high genetic advance.

Sumathi *et al.* (2007) reported low GCV and PCV for plant height and days to fifty per cent of flowering whereas moderate values for productive tillers, grain yield per plant and finger length coupled with high heritability and genetic advance as per cent of mean.

Gowda *et al*. (2008) observed low GCV and PCV for plant height, days to fifty percent flowering and days to maturity, moderate for number of fingers per ear and high for grain yield per plant and also high GCV and moderate PCV for number of productive tillers per plant. In F_2 population they also observed high heritability for all the characters where as low genetic advance for days to fifty per cent flowering and days to maturity, moderate for plant height, number of productive tillers per plant and number of fingers per ear and high for finger length and grain yield per plant.

Prabhu *et al.* (2008) observed high heritability and high genetic advance for number of tillers and single plant yield, indicating the possibility of improvement for this trait by simple selection.

Sonnad *et al*. (2008) recorded that the trait grain yield per plant showed moderate genotypic and phenotypic coefficients of variability with high heritability and genetic advance as per cent of mean. Straw yield per plant had higher variability, heritability and genetic advance as per cent of mean while, the other characters under study had low variability, high heritability and moderate to high genetic advance.

Kadam *et al.* (2009) found that PCV and GCV were high for plant height, days to 50 % flowering, flag leaf blade length, inflorescence length and yield. Heritability and genetic advance was high for leaf blade length, basal tillers and plant height.

Krishnappa *et al.* (2009) revealed involvement of both additive and dominance genetic variation with a preponderance of the latter in the expression of time to 50% flowering, plant height and dry fodder weight per plant while only dominance genetic variation was operative in the expression of number of tillers per plant, number of fingers per ear and grain weight per plant.

Kumar and Gupta (2009) concluded that phenotypic variability was higher for all the traits except days to 50 % and 90% flowering, seed hardness and protein content, which showed similar magnitude of genotypic variability. Maximum difference between phenotypic and genotypic variability was observed for number of seeds per main ear.

Shet *et al*. (2010) observed high PCV and GCV values for grain yield per plant, finger width, plant height and days to 50% flowering whereas low to moderate for all other characters. High broad sense heritability accompanied with high genetic advance were observed for plant height, finger length, test weight and grain yield per plant reported.

Dhamdhere *et al.* (2011) concluded that genotypic coefficient of variation was the major component of total variation. However, PCV was invariably higher than GCV for most of the characters studied. Crude fiber content showed high PCV followed by ear weight, iron content, straw weight and grain yield while plant height showed lowest PCV. Ear weight, straw weight and total biomass showed high heritability and high genetic advance while grain yield exhibited moderate heritability and high genetic advance.

Ganapathy *et al.* (2011) studied two hundred and forty finger millet germplasm accessions. The coefficient of variation at phenotypic (PCV) and genotypic (GCV) levels were high for productive tillers per plant and moderate for the traits *viz*., days to 50 % flowering, plant height, finger numbers per ear, finger length and grain yield per plant. Low PCV and GCV were observed in the trait days to maturity. From the results, high heritability coupled with high genetic advance observed in days to 50 % flowering, plant height, productive tillers per plant, finger numbers per ear, finger length and seed yield per plant.

Priyadharshini *et al*. (2011) observed values of phenotypic coefficients of variability were greater than genotypic coefficients of variability for all the traits studied. High PCV and GCV were recorded for number of productive tillers per plant and moderate PCV and GCV for longest finger length, seed protein content and harvest index indicated large extent of genetic variability for these traits in the material. High heritability along with high genetic advance (% of mean) observed for plant height, number of productive tillers per plant, number of fingers per ear head, longest finger length, seed protein content, harvest index and single plant grain yield.

Upadhyaya *et al.* (2011) found that finger millet core collection for grain nutrients and agronomic traits revealed a substantial genetic variability for grain Fe, Zn, calcium (Ca) and protein contents. Accessions rich in Zn content have significantly higher grain yield potential than those rich in Fe and protein content.

2.2 CORRELATION STUDIES

Grain yield in any crop depends on many component characters which influence yield either jointly or singly and either directly or indirectly through other related characters. Selection for yield on the basis of per-se performance alone may not be as effective as that based on the component characters associated with it, which is biometrically determined by correlation coefficient and path analysis.

The inter relationship of quantitative characters with yield determine the efficiency of selection in breeding programmes. It merely indicates the intensity of association. Phenotypic correlation reflects the observed relationship, while genotypic correlation underlines the true relationship among characters. Selection procedures could be varied depending on the relative contribution of each.

Thakur and Saini (1995) concluded that days to germination, heading and maturity showed high negative association with grain yield, whereas fingers per plant showed high positive association.

Gowda (1996) reported high positive and significant association of grain yield with plant height, number of productive tillers, fingers per ear and spikelet density.

Dawa *et al*. (1996) evaluated forty genotypes of ragi for productivity related traits and found that grain yield per plant was positively associated with all the measured traits except flowering days.

Ravindran *et al*. (1996) indicated that productive tillers and fingers per ear had highly significant and positive association with grain yield.

Gowda (1997) reported low positive association of grain yield with plant height, ear length, productive tillers and fingers per ear.

Marimuthu (1997) observed that grain yield had positive association with ear weight, number of productive tillers, fingers per ear, finger length, plant height and days to 50 per cent flowering.

Shanthakumar and Gowda (1997) found that grain yield was positively associated with ear weight per plant, productive tillers per plant, fingers per ear and grains per cm length of finger.

Jain and Yadava (1999) showed significant positive association of blast resistance with plant height, leaf angle, leaf area and number of stomata per unit area. These traits also exhibited comparatively higher estimates of correlated response and relative selection efficiency.

Mahto *et al*. (2000) concluded that seed yield per plant had a significant positive correlation with days to 50 % flowering and a highly significant positive association with number of tillers per plant, days to maturity where as plant height revealed a highly significant negative correlation with seed yield.

Bendale *et al*. (2002) observed that grain yield had significant positive correlation with days to emergence of finger, days to maturity, finger length, weight of grains of main ear head and straw yield per plant.

Satish (2003) observed that grain yield had positive and highly significant association with all the characters studied except plant height, days to 50 % flowering and days to maturity.

Anantharaju and Meenakshiganesan (2005) showed that grain yield has a positive and significant genotypic correlation with number of productive tillers and culm thickness.

Sharathbabu (2005) in a study comprising 19 genotypes of finger millet observed that at both genotypic and phenotypic levels, grain yield per plant exhibited highly significant positive association with finger number per ear and ear weight per plant.

Bedis *et al.* (2006b) reported that days to flowering, days to maturity, plant height, main ear length, number of fingers per ear and fodder yield were positively correlated with grain yield, suggesting that these are the major yield contributing traits in finger millet.

John (2006) concluded that total dry matter production showed a positive and highly significant association with test weight. Grain yield showed a positive and highly significantly correlated with test weight, total dry matter production and harvest index.

Sripichitt *et al.* (2006) observed positive association of culm thickness with leaf blade width while the strongest negative association was found between 1000-grain weight and finger number. Grain yield per plant associated positively with productive tillers, 1000-grain weight, number of grains per spikelet and finger number and negatively associated with days to heading and maturity.

Gowda (2008) in a study involving F_2 generations of three crosses of finger millet reported grain yield was positively correlated with culm thickness, days to maturity, finger length and test weight.

Sonnad *et al.* (2008) recorded that grain yield per plant had strong positive association with finger number per ear and ear weight per plant whereas ear head length and finger length had significant positive association with grain yield per plant.

Kadam *et al.* (2009) opined from the correlation analysis that there were highly significant positive association with yield and almost all the growth and yield contributing characters except flag leaf blade width and exertion.

Kumar and Gupta (2009) observed plant height, number of tillers per plant, number of panicles per main spike, length of main ear and number of seeds per main ear were significantly correlated with grain yield plant.

Nandini *et al.* (2010) indicated that grain yield has strong positive correlation with weight of main ear, 1000 seed weight and total tillers per plant in F_2 population.

Shet *et al.* (2010) concluded from the correlation studies that grain yield per plant exhibited highly significant positive association with finger width and test weight.

Shinde *et al.* (2010) indicated positive and highly significant correlation with straw yield per plant, harvest index and weight of grains on main ear head at phenotypic and genotypic level, while number of fingers on main ear head at genotypic level only.

Ganapathy *et al.* (2011) opined from the correlation analysis productive tillers per plant and finger length are the important yield contributing traits and due critical emphasis needs to be given to productive tillers per plant and finger length while selecting for grain yield improvement in finger millet.

Priyadharshini *et al.* (2011) found that grain yield had positive correlation with number of productive tillers, finger length and harvest index.

Wolie and Dessalegn (2011) observed that correlations among the traits and grain yield was significantly correlated with its component characters like plant height, number of ears per plant, number of fingers per ear, finger length, biomass yield, harvest index, and thousand kernel weight.

Muduli *et al.* (2012) performed correlation analysis in forty four micro-mutant lines of each of the two finger millet varieties VR 708 and GPU 26. Significant positive association of tillers per plant, fingers per ear and ear weight per plant with grain yield per plant and among themselves was observed in both sets of mutant lines.

2.3 PATH COEFFICIENT ANALYSIS

Assuming yield is a contribution of several characters which are correlated among themselves and to the yield, path coefficient analysis was developed (Wright, 1921; Dewey and Lu, 1959). Unlike the correlation coefficient which measures the extent of relationship, path coefficient measures, the magnitude of direct and indirect contribution of a component character to a complex character and it has been defined as a standardized regression coefficient which splits the correlation coefficient into direct and indirect effects.

Thakur and Saini (1995*)* opined from the path coefficient analysis that per-se selection for yield would be highly effective, with simultaneous selection for lower days to germination, heading and maturity and higher number of tillers and fingers per plant.

Dawa *et al.* (1996) observed positive and direct effect of biological yield, harvest index and maturity duration on grain yield from the path analysis studies.

Ravindran *et al.* (1996) reported that number of productive tillers per plant and number of fingers on main ear had high direct effect on grain yield. While plant height showed negative and indirect effect on yield. They suggested that, selection programme based on number of productive tillers per plant and number of fingers on main ear will be effective for grain yield improvement.

Gowda (1997) observed high effect of productive tillers and fingers per ear on grain yield and suggested that due weightage has to be given to the characters in breeding programme for high yield. Harvest index contributed maximum positive direct effect to grain yield and duration of grain filling registered largest negative direct effect.

Marimuthu (1997) through the path coefficient analysis revealed that ear weight, number of productive tillers and finger length showed positive direct effects on grain yield.

Shanthakumar and Gowda (1997) found that ear weight per plant had the greatest direct effect on grain yield in F_2 and F_3 generation of finger millet cross WR9 and U6.

Mahto *et al*. (2000) noticed that number of tillers per plant and days to maturity had high positive direct effect on grain yield.

Bendale *et al*. (2002) opined from association and path analysis, days to emergence of finger, days to 50% flowering, finger length, finger width, and weight of grains of main ear head had significant influence on grain yield per plant in finger millet.

Satish (2003) observed high direct effects of ear weight per plant, straw yield per plant and flag leaf length and suggested to lay stress on these characters in selection programme for increasing yield.

Anantharaju and Meenakshiganesan (2005) reported that number of productive tillers had a high positive direct effect and culm thickness and number of leaves had moderate direct effects on grain yield. Finger length had high indirect effect on grain yield through the number of leaves and days to 50 % flowering.

Anand *et al.* (2005) revealed high direct positive effect of biomass on grain yield along with ear weight and number of fingers per plant.

Bedis *et al*. (2006) indicated that the number of days to maturity, plant height, number of fingers per ear and fodder yield has direct positive contribution on grain yield. These traits deserve special emphasis in selection while selecting for improvement in grain yield of finger millet.

Jayarame Gowda *et al.* (2007) reported high positive effect of plant height, culm thickness, days to flowering and days to maturity on grain yield and they had suggested these could be used as indirect measure to select for high yield in finger millet.

Kadam *et al*. (2009) opined from the path analysis that indirect effect of yield had masked the direct or indirect effect in almost all the characters except inflorescence width. The traits like yield, flag leaf blade length, flag leaf sheath length, inflorescence length, inflorescence width and 1000 grain weight be given due emphasis in selection programme of genotypes for substantial high yield improvement of finger millet.

Kumar and Gupta (2009) opined from path coefficient analysis that days to 50% flowering contributed maximum direct effect on grain yield per plant, followed by number of tillers per plant and 1000-grain weight. However, the indirect effects were also equally important.

Nandini *et al*. (2010) revealed that weight of main ear, 1000 seed weight showed positive direct effect on grain yield of main ear.

Shet *et al*. (2010) concluded that productive tillers per plant had the highest positive direct effect followed by finger width and test weight on grain yield in these two crosses while finger number exerted low positive direct effect on grain yield.

Shinde *et al*. (2010) reported that finger length, harvest index, number of fingers on main ear head and straw yield per plant had direct positive effect on grain yield at genotypic level. Selection programme based on number of fingers on main ear head and straw yield per plant will be effective for grain yield improvement in finger millet.

Ganapathy *et al.* (2011) concluded that productive tillers per plant and finger length are the important yield contributing traits, since these traits had significant positive correlation with grain yield and positive inter-correlation also themselves.

Priyadharshini *et al.* (2011) reported that harvest index had high positive direct effect on grain yield and number of productive tillers and finger length had moderate direct effect and revealed true relationship of these traits with grain yield.

Wolie and Dessalegn (2011) showed that biomass yield and finger length, number of fingers per ear, and number of ears per plant to exert positive direct effects on grain yield, while plant height, days to heading and days to maturity exhibited negative direct effects.

Muduli *et al.* (2012) revealed that ear weight per plant had the highest direct effect on grain yield followed by days to flowering in VR 708, whereas, days to maturity followed by fingers/ear and ear weight/plant had the maximum direct contribution in GPU 26. As the direct effect of ear weight/plant in VR 708 was too high, its indirect effects via other traits were small or often negative and in GPU 26, it had low direct effect due to positive indirect effects via fingers/ear, tillers/plant and days to flowering.

2.4 GENETIC DIVERGENCE

The sum total of genes present in the genotypes is called germplasm. The study of genotype diversity and the information of core subsets are important activities in the conservation, evaluation and utilization of genetic resources (Brown, 1989).

Morphological similarity, eco-geographic diversity, phylogenetical relationship, Mahalanobis D^2 statistics etc were the few earlier methods used for discriminating divergent populations, which are reinforced by more scientific and advanced biometric techniques *viz.,* multivariate analysis based on principal component analysis, agglomerative cluster analysis.

Sheriff (1992) conducted study on nine metric traits in twenty ragi varieties grown under rainfed and irrigated conditions using Mahalanobis D^2 statistic. They were grouped into four clusters under rainfed and eleven under irrigated conditions. Genetic diversity is not related to geographic diversity. Days to flowering, days to maturity, plant height, ear length, ear weight and grain weight contributed maximum to genetic diversity in both environments.

Suryakumar (1998) studied forty nine finger millet genotypes grouped into 10 clusters. Cluster analysis revealed that geographical diversity was not related to genetic diversity. The genotypes from the clusters II, X, V and VII having moderate to high genetic divergence coupled with high mean performance may be selected for yield and its important components such as productive tillers and straw yield for better recombination.

Vadivoo *et al*. (1998) grouped thirty six genotypes into eight clusters. Based on inter cluster distances of the genotypes MS 1168, MS 174 and CO 13 were found to be suitable for use as parents in a hybridization program for improving yield.

Bedis *et al.* (2007) conducted an experiment on thirty seven finger millet strains to study the nature and magnitude of genetic divergence for seed yield and its components. D^2 values corresponding to the pairs of comparison between thirty seven cultivars indicated a considerable amount of genetic diversity among the strains studied. The thirty seven strains were grouped into seven clusters, the cluster means revealed that days to flowering, days to maturity, plant height, number of productive tillers per plant, main ear length, number of fingers per ear, and fodder and grain yield per plant are important characters towards maximum divergence.

Satish *et al.* (2007**)** conducted a study on finger millet to assess extent of genetic diversity involving 178 genotypes of finger millet for productivity traits. Study revealed that the genetic diversity did not relate to geographic origin. All the genotypes were grouped into ten different clusters. The inter cluster distance revealed that cluster 2 and 5 were found to be highly divergent. Florets number per spikelet contributed maximum to the divergence. Among all the clusters, cluster 7 showed highest cluster mean across the fifteen traits followed by cluster 5, 8 and 4 indicating presence of most promising genotypes in them. Selection of parents for hybridization to get desirable recombinants has been suggested.

Anantharaju and Meenakshiganesan (2008) conducted an experiment on fifty genotypes of finger millet for genetic divergence using cluster analysis for ten quantitative traits. The genotypes were grouped into fourteen clusters. Among the characters they studied, days to 50% flowering followed by number of leaves contributed more towards the total divergence.

Kadam (2008) grouped seventy genotypes in 8 clusters. The higher inter cluster distance was observed between cluster VIII and V followed by that between cluster VI and II, suggesting more variability in genetic makeup of genotypes included in these clusters. Cluster III had the highest mean values for grain yield/plant, 1000-grain weight, panicle branch number and flag leaf blade width. Cluster VIII was the second highest for grain yield plant (g) and for exertion peduncle length and basal tiller, plant height and days to 50% flowering followed by flag leaf blade length contributed maximum towards the total divergence. There were 4 solitary clusters and in the remaining clusters the genotypes varied from 2 to 4 numbers. Parallelism was observed between geographical diversity and genetic diversity.

Prabhu *et al*. (2008) grouped one hundred fifty finger millet germplasm into 18 cluster based on genetic distance. Fourteen solitary clusters were superior viz., II, III, V, VI, VIII, X, XI, XII, XIII, XIV, XV, XVI, XVII and XVIII. Intercrossing between genotypes of these diverse clusters would generate a broad spectrum of variability for effective selection in the segregating generations for the development of high yielding cultivars.

Kumar *et al*. (2010) grouped one hundred and forty diverse genotypes of finger millet into ten non-overlapping clusters. The inter-cluster distance varied from 16.85 between clusters X and I to 1.94 between clusters III and VIII. Genetic diversity was observed to be independent of the geographical origin of the genotypes.

Lule *et al.* (2012) concluded that the trend of quantitative trait diversity revealed that the highest genetic diversity were observed at the lowest level (among landrace populations) followed among the regions or countries of origin and least among altitude classes. This leads to suggest, taking more samples within a locality or population would be a better approach to capture the range of variation in finger millet population.

Sahu and Pradhan (2012) grouped thirty finger millet genotypes into 12 clusters out of which, cluster 1 had six genotypes, cluster II seven genotypes, clusters III and V three genotypes each, clusters IV, VI and VII two genotypes each and clusters VIII to XIII consisted of one genotype each. The inter cluster distance was highest between cluster IV and VII followed by cluster IV and XII. The highest means for grain yield were observed in cluster X (OEB 71) and cluster VI and for number of productive tillers/plant were observed in cluster VIII. Custer XII (VL 149) had the highest mean for plant height, fingers/ear and ear length. The genotypes of these superior clusters can be effectively used in breeding programs. Among the characters, days to maturity followed by days to flowering and plant height contributed more towards the total divergence.

Chapter III

Material and Methods

Chapter III

MATERIAL AND METHODS

The present investigation entitled "Study of Genetic Divergence in Finger millet (*Eleusine coracana* (L.) Gaertn) Germplasm" was carried at Regional Station, National Bureau of Plant Genetic Resources, Hyderabad. The details of materials used and methodologies adopted during the course of the present investigation are elucidated under appropriate heads.

3.1 MATERIAL

The experimental material comprised of 48 germplasm lines of finger millet collected from National Bureau of Plant Genetic Resources, Regional station, Rajendranagar, Hyderabad-30. The details of the finger millet genotypes along with their source are furnished in Table 3.1.

3.2 METHODS

3.2.1 Experimental Design

The experiment was carried out during *kharif* 2013.The design adopted Randomized Block Design (RBD) with three replications. Each entry in each replication was sown in 2 rows spaced 25 cm apart and plant to plant distance of 15 cm was followed.

3.3 Morphological characterization

Observations on eleven different quantitative characters were recorded on three randomly selected plants for each genotype in various stages of the crop.

1. **Plant height (cm)**
   The height of the main tiller from the ground level to the top of the ear head was recorded in centimetres at maturity and mean was computed.

2. **No. of basal tillers per plant**
   Tiller number was counted from each tagged plants and the mean of three plants was computed as tillers per plant.

Table 3.1 Experimental material of 48 genotypes of finger millet

SL. No.	Genotypes	Source	SL. No	Genotypes	Source
1	**13426**	NBPGR Regional Research Station	25	**13651**	NBPGR Regional Research Station
2	**13433**	NBPGR Regional Research Station	26	**13652**	NBPGR Regional Research Station
3	**13434**	NBPGR Regional Research Station	27	**13660**	NBPGR Regional Research Station
4	**13484**	NBPGR Regional Research Station	28	**13661**	NBPGR Regional Research Station
5	**13486**	NBPGR Regional Research Station	29	**13665**	NBPGR Regional Research Station
6	**13487**	NBPGR Regional Research Station	30	**13672**	NBPGR Regional Research Station
7	**13489-1**	NBPGR Regional Research Station	31	**13673**	NBPGR Regional Research Station
8	**13492**	NBPGR Regional Research Station	32	**13674**	NBPGR Regional Research Station
9	**13502**	NBPGR Regional Research Station	33	**13675**	NBPGR Regional Research Station
10	**13517**	NBPGR Regional Research Station	34	**13676**	NBPGR Regional Research Station
11	**13523**	NBPGR Regional Research Station	35	**13677**	NBPGR Regional Research Station
12	**13528**	NBPGR Regional Research Station	36	**13678**	NBPGR Regional Research Station
13	**13539**	NBPGR Regional Research Station	37	**13689**	NBPGR Regional Research Station
14	**13542**	NBPGR Regional Research Station	38	**13690**	NBPGR Regional Research Station
15	**13555**	NBPGR Regional Research Station	39	**13691**	NBPGR Regional Research Station
16	**13565**	NBPGR Regional Research Station	40	**13700**	NBPGR Regional Research Station
17	**13567**	NBPGR Regional Research Station	41	**13710**	NBPGR Regional Research Station
18	**13568**	NBPGR Regional Research Station	42	**13712**	NBPGR Regional Research Station
19	**13569**	NBPGR Regional Research Station	43	**13713**	NBPGR Regional Research Station
20	**13570**	NBPGR Regional Research Station	44	**GPU-45**	NBPGR Regional Research Station
21	**13571**	NBPGR Regional Research Station	45	**GPU-67**	NBPGR Regional Research Station
22	**13631**	NBPGR Regional Research Station	46	**PR-202**	NBPGR Regional Research Station
23	**13632**	NBPGR Regional Research Station	47	**VL-149**	NBPGR Regional Research Station
24	**13650**	NBPGR Regional Research Station	48	**VR-708**	NBPGR Regional Research Station

3. **No. of leaves on the main tiller**

   Total no. of leaves on the main tiller was counted and mean was taken at the time of maturity.

4. **Productive tillers per plant**

   Number of basal tillers bearing the matured ears was counted from each of three tagged plants and average per plant was taken.

5. **Ear length (cm)**

   Length of main ear was measured in centimeter and mean was computed from three plants.

6. **Ear width(cm)**

   Width of main ear was measured in centimeter and mean was computed from three plants.

7. **Finger length (cm)**

   Length of the longest finger on main tiller was measured in centimeter and mean of three plants was computed.

8. **Finger Width (cm)**

   Width of each finger on main ear was taken and mean of three plants was computed.

9. **Total number of fingers on the main ear**

   The number of fingers on main ear of each tagged plant was counted and averaged per plant.

10. **Grain yield per plant (g)**

    Grains harvested from the three selected plants of each replication were dried and weighed. The average grain weight of three plants was expressed as grain yield per plant in grams.

11. **Grain yield per plot(g)**

    Grain harvested from each replication was threshed separately and weighed.

3.4 STATISTICAL ANALYSIS

The data collected for the above mentioned characters were subjected to the following statistical analysis with the help of appropriate standard statistical procedures:

3.4.1 Analysis of Variance

3.4.2 Estimation of Genetic Parameters

3.4.3 Estimation of correlation coefficients

3.4.4 Direct and indirect effects of characters using path coefficient analysis

3.4.5 Estimation of genetic divergence using Mahalanobis generalized distances (D^2)

3.4.1 Analysis of Variance

Before proceeding to the biometrical genetic analysis of the data, the genotypic differences among the entries were tested. Further analysis was carried out only when the mean squares due to genotypes were significant. Hence the data for different characters were statistically analyzed for significance by using analysis of variance technique described by Panse and Sukhatme (1985). The adopted design was Randomized Block Design (RBD) replicated thrice.

The linear mathematical model:

$$Y_{ij} = \mu + g_i + r_j + e_{ij}$$

Where,

Y_{ij} = phenotypic observation of i^{th} genotype in j^{th} replication

μ = general mean

g_i = effect of i^{th} genotype

r_j = effect of j^{th} replication

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

Source	**S.S.**	**Degrees of freedom**	**Mean sum of squares**	**F-ratio**
Replication	P	(r-1)	Mr’	Mr’/Me’
Treatment	Q	(t-1)	Mt’	Mt’/Me’
Error (e)	R	(r-1)(t-1)	Me’	
Total	S	(tr-1)	TMSS	

d.f. : degrees of freedom; SS : sum of squares; MSS : mean sum of squares

Where,

r = number of replications

t = number of treatments

P = Replications sum of squares

Q = Treatments sum of squares

R = Error sum of squares

S = Total sum of squares

Mr', Mt', Me' stands for mean sum of squares due to replications, treatments and error respectively. The significance of mean sum of squares for each character was tested against the corresponding error degrees of freedom using 'F' Test (Fisher and Yates, 1967).

3.4.2 Estimation of Genetic Parameters

3.4.2.1 Estimation of components of variances

From the analysis of variance table, the mean sum of squares between genotypes will consist of the variances (i) due to genotypic differences and (ii) due to the environmental variation among the individuals of each genotype. Therefore, the genotypic and phenotypic variances were calculated as per the formula given by Burton and DeVane (1953).

Environmental variance, $\sigma^2_e = Me'$

Genotypic variance, $\sigma^2_g = \dfrac{Mt' - Me'}{r}$

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

3.4.2.2 Phenotypic and genotypic co-efficient of variation

The components of variances were used to estimate genetic parameters like phenotypic and genotypic co-efficient of variation (PCV and GCV) as per the formulae given by Burton and DeVane (1953).

$$\text{GCV} = \frac{\sqrt{GV}}{\overline{X}} x100$$

$$\text{PCV} = \frac{\sqrt{PV}}{\overline{X}} x100$$

Where,

GCV = Genotypic coefficient of variation

PCV = Phenotypic coefficient of variation

GV = Genotypic variance

PV = Phenotypic variance

$\overline{X}$ = General mean of character

Categorization of the range of variation was followed as reported by Sivasubramanian and Menon (1973).

Low	:	Less than 10%
Moderate	:	10 to 20%
High	:	More than 20%

3.4.2.3 Heritability in broad sense [h^2 (b)]

Heritability in the broad sense refers to the proportion of genotypic variance to the total observed variance in the total population. Heritability [h^2 (b)] in the broad sense was calculated according to the formula given by Allard (1960) and expressed in percentage.

$$h^2\text{ (b)} = \frac{\text{Genotypic variance, }(\sigma^2 g)}{\text{Phenotypic variance, }(\sigma^2 p)} \text{ x } 100$$

As suggested by Johnson *et al.* (1955) the range of heritability estimates were categorized as:

Low	:	0-30%
Medium	:	above 30-60%

High : above 60%

3.4.2.4 Genetic advance (GA)

Genetic advance refers to the expected genetic gain or improvement in the next generation by selecting superior individuals under certain amount of selection pressure. From the heritability estimates the genetic advance was estimated by the following formula given by Burton (1953).

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

Where,

GA = Expected genetic advance

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

σ_p = Phenotypic standard deviation

h^2 (b) = Heritability in broad sense

In order to visualize the relative utility of genetic advance among the characters, genetic advance as per cent for mean (GAM) was computed.

$$GAM = \frac{GA}{\text{Grand mean, } (\overline{X})} \times 100$$

The range of genetic advance as per cent of mean was classified as suggested by Johnson *et al*. (1955).

Low : less than 10 %

Moderate : 10-20 %

High : more than 20 %

3.4.3 Estimation of correlation coefficients

Character association refers to the association of characters *i.e.*, a change in one character is accompanied by a change in the other character. The data on eleven quantitative characters were utilized for the computation of phenotypic and genotypic correlation co-efficient between grain yield and yield contributing traits of forty eight germplasm lines in finger millet.

Phenotypic and genotypic correlation co-efficient were calculated for the characters by working out the variance components of each character and the covariance components for each pair of characters using the formulae suggested by Al-Jibouri *et al.* (1958).

$$\text{Genotypic correlation coefficient, } (r_g) = \frac{\text{Cov } x\,y \text{ (genotypic)}}{\sqrt{(\text{Var } x).\ (\text{Var } y) \text{ (genotypic)}}}$$

Where,

$$\text{Genotypic variance} = \frac{\text{Treatment MS} - \text{Error MS}}{\text{Number of replication}}$$

Similarly,

$$\text{Genotypic covariance} = \frac{\text{Treatment Cov} - \text{Error Cov}}{\text{Number of replications}}$$

$$\text{Phenotypic correlation coefficient } (r_p) = \frac{\text{Cov } xy \text{ (phenotypic)}}{\sqrt{(\text{Var } x)\ (\text{Var } y) \text{ (phenotypic)}}}$$

The values of genotypic correlation exceeding unity should be considered as unit only (of same sign). To test the significance of correlation coefficients, the estimated values were compared with the table values of correlation coefficients (Fisher and Yates, 1967) at 5 per cent and 1 per cent levels of significance with (n-2) degrees of freedom, where ‘n’ is the number of pairs of observations used in the experiment.

3.4.4 Path coefficient analysis

The use of path coefficient analysis explains cause and effect relationship among the variables. It is a standardized partial regression coefficient and as such measures the direct influence of one variable upon another and permits the separation of the correlation coefficients into components of direct and indirect effects (Dewey and Lu, 1959). This method permits breeder to identify relatively important components of a variable, on the basis of their direct and indirect influences.

The direct and indirect effects both at genotypic and phenotypic level were estimated by taking grain yield per plant as dependent variable using path coefficient analysis suggested by Wright (1921) and Dewey and Lu (1959).

The following set of simultaneous equations were formed and solved for estimating various direct and indirect effects.

$r_{1y} = P_{1y} r_{11} + P_{2y} r_{12} + P_{3y} r_{13} \ldots\ldots\ldots\ldots + P_{ny} r_{1n}$

$r_{2y} = P_{1y} r_{21} + P_{2y} r_{22} + P_{3y} r_{23} \ldots\ldots\ldots\ldots + P_{ny} r_{2n}$

$r_{ny} = P_{1y} r_{n1} + P_{2y} r_{n2} + P_{3y} r_{n3} \ldots\ldots\ldots\ldots + P_{ny} r_{nn}$

Where,

$1, 2 \ldots\ldots\ldots n$ = Independent variable

y = Dependent variable (yield per plant)

$r_{1y}\, r_{2y} \ldots\ldots\ldots\ldots r_{ny}$ = Coefficient of correlation between causal factors ‘1’ to ‘n’ on dependent character 1

$P_{1y}\, P_{2y} \ldots\ldots P_{ny}$ = Direct effect of characters ‘1’ to ‘n’ on character Y

The above equations can be written in matrix form as:

$$\begin{array}{ccc} A & C & B \\ \begin{pmatrix} r_{1y} \\ r_{2y} \\ : \\ : \\ r_{ny} \end{pmatrix} & \begin{pmatrix} 1 & r_{12} & r_{13} & \ldots\ldots\, r_{1n} \\ r_{21} & 1 & r_{23} & \ldots\ldots\, r_{2n} \\ : & : & : & \\ : & : & : & \\ r_{n1} & r_{n2} & r_{n3} & \ldots\ldots\, 1 \end{pmatrix} & \begin{pmatrix} P_{1y} \\ P_{24} \\ : \\ : \\ P_{ny} \end{pmatrix} \end{array}$$

A and B vector values are known. Hence, to calculate C vector

$$B = [C]^{-1} A$$

Where,

$$C^{-1} = \begin{pmatrix} c_{11} & c_{12} & c_{13} \,.\,.\,.\,.\,.\, c_{1n} \\ c_{21} & c_{22} & c_{23} \,.\,.\,.\,.\,.\, c_{2n} \\ : & : & : \qquad\quad : \\ : & : & : \qquad\quad : \\ c_{n1} & c_{n2} & c_{n3} \,.\,.\,.\,.\,.\, c_{nn} \end{pmatrix}$$

Direct effects were as follows:

$$P_{1y} = \sum_{i=1}^{k} c_{1i}\; r_{iy}$$

$$P_{2y} = \sum_{i=1}^{k} c_{2i}\; r_{iy}$$

$$P_{ny} = \sum_{i=1}^{k} c_{nj} \; r_{iy}$$

Residual effect (PR_y), which measures the contribution of characters not considered, in the causal scheme was obtained as:

$$\text{Residual effect } (PR_y) = \sqrt{(1 - r^2)}$$

Where,

$r^2 = (P_{1y}\, r_{1y} + P_{2y}\; r_{2y} + \text{---------}\; P_{ny}\; r_{ny})$

P_{ny} = Direct effect of x_n on Y

r_{ny} = Correlation coefficient of x_n on y

3.4.5 Estimation of genetic divergence by Mahalanobis generalized distance (D²)

The genetic divergence between forty eight genotypes was estimated using Mahalanobis (1936) D^2 statistic technique.

D^2 value between i^{th} and j^{th} genotypes for 'p' characters was calculated as:

$$D^2_{ij} = \sum_{t=1}^{P} (\overline{Y}_{it} - \overline{Y}_{jt})^2$$

Where,

Y_{it} = Uncorrelated mean values of i^{th} genotype for't' character

Y_{jt} = Uncorrelated mean values of j^{th} genotype for 't' characters and

D^2_{ij} = D^2 between i^{th} and j^{th} genotype

3.4.5.1 Test of significance

After testing the differences between genotypes for each of the characters, a simultaneous test for significance for differences in the mean values of a number of correlated variations with regard to the pooled effect of characters was carried out by using `V` statistic which in turn utilizes Wilk`s 'Λ' criterion. The sum of squares and sum of product of *error* + *genotype* were used for this purpose. The estimation of 'Λ' (Wilk`s criterion) was done using the following relationship.

$$\wedge = \frac{|W|}{|S|}$$

Where,

$\wedge$ = Wilk's criterion

$|W|$ = Determinant of error matrix and

$|S|$ = Determinant of error + variety matrix

The significance of $\wedge$ was tested by V (stat.). The value of 'V' statistic was worked out using Wilk' s lambda criterion.

$$V\text{ (stat.)} = -m \log_e \wedge = -\left(n - \frac{p+q+1}{2}\right) \log_e \wedge$$

Where,

m = n - (p+q+1)/2

p = number of variables (or) characters

q = number of genotypes -1 (or degrees of freedom for population)

n = degrees of freedom for error + genotypes

e = 2.7183

or $\log_e \wedge = 2.3026 \log_{10} \Lambda$

V (stat.) is distributed as χ^2 with 'pq' degrees of freedom. The tabulated value of χ^2 for 'pq' degrees of freedom at 5 per cent level is used to compare with the above calculated value of χ^2 for testing the significance.

When *d.f.* were beyond 100, then the tabulated χ^2 value is calculated by the formula as given by Singh and Chaudhary (1977).

$$Z = \sqrt{2\chi^2} - \sqrt{2n-1}$$

Where, Z = Tabulated χ^2 value

n = number of degrees freedom

3.4.5.2 Transformation of correlated variables

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

3.4.5.3 Computation of D^2 values

For a given combination of 'i' and 'j' genotype, the mean deviation *viz.*, Y_{it} - Y_{jt} for t = 1, 2 …….. 'p' variables were computed and the D^2 values were calculated as sum of squares of deviations *i.e.,*

$$D^2_{ij} = \sum_{t=1}^{P} (\overline{Y}_{it} - \overline{Y}_{jt})^2$$

Where,

Y_{it} = Uncorrelated mean values of i^{th} genotype for't' character

Y_{jt} = Uncorrelated mean values of j^{th} genotype for't' character

D^2_{ij} = D^2 between i^{th} and j^{th} genotype

3.4.5.4 Testing the significance of D^2 values

The D^2 values obtained for a pair of genotypes was taken as the calculated value of χ^2 and was tested against the tabulated value of χ^2 for ‘p’ degrees of freedom, where ‘p’ was the number of characters considered.

3.4.5.5 Contribution of individual characters towards divergence

In all the combinations each character was ranked on the basis of their contribution towards divergence between two entries ($d_i = Y_{it}-Y_{jt}$). Rank 1 was given to the highest mean difference and rank ‘p’ to the lowest difference, where ‘p’ is the total number of characters considered.

Percentage contribution of each character (X) towards genetic divergence was calculated using the formula:

$$\text{Percentage contribution of character, } X = \frac{N}{M} \times 100$$

Where,

N = Number of genotype contributions where the character was ranked first

M = All possible combinations of genotypes considered

3.4.5.6 Grouping of genotypes into various clusters

Grouping of genotypes into different clusters was done using Tocher’s method as described by Rao (1952). The criterion used in clustering by this method is that any two genotypes belonging to the same cluster should show at least on an average smaller D^2 value among themselves than those belonging to different clusters.

The first step in grouping the genotypes into different clusters was to arrange the genotypes in the order of their relative distance from each other. For this purpose, D^2 values of all combinations of each genotype were arranged in increasing order of their magnitude in a tabular form as described by Singh and Chaudhary (1977). To start with the two genotypes having the smallest distance from each other were considered first to which a third population having the smallest average D^2 value from the first two genotypes was added. Similarly, next nearest fourth genotype was considered and this procedure was continued. At certain stage where it was felt that after adding a particular genotype, there was abrupt increase in the average D^2 value, that population was not considered for including in that cluster. The group of the first cluster was then omitted and the rest was treated in a similar way. This process was continued till all the genotypes were included into one or other clusters.

3.4.5.7 Average intra cluster distance

For the measurement of intra cluster distance, the formula used was $\Sigma D^2_i / n$. Where,

ΣD^2_i = Sum of distances between all possible combinations (n) of the population included in a cluster

n = Number of genotypes included in a cluster

3.4.5.8 Average inter-cluster distance

Clusters were taken one by one and their distance from other clusters was calculated. The distance between two clusters was the sum of D^2 values between the members of one cluster to each of the member of other cluster divided by the product of number of genotypes in both the clusters under consideration.

The square root of the average D^2 value gave the genetic distance 'D' between the clusters. Based on D values (inter cluster distance) the scale given by Rao (1952) for rating of the distance was adopted and the cluster diagram was prepared.

$$\text{Average intercluster distance} = \frac{D^2}{n_1 \times n_2}$$

Where,

n_1 and n_2 are the number of genotypes in cluster 1 and cluster 2, respectively.

Category	**‘D’ values**
Closely related	Below 22
Moderately divergent	Between 22 and 30
Highly divergent	Above 30

Chapter IV

Results and Discussion

Chapter IV

RESULTS AND DISCUSSION

The present investigation was intended to address the variation present in forty eight germplasm lines of finger millet. Genetic diversity was assessed at morphological level for facilitating their effective utilization in future hybridization programmes. The results of the analysis are presented here under the following heads.

4.1 Mean performance of genotypes
4.2 Analysis of variance
4.3 Genetic variability, heritability and genetic advance
4.4 Character association
4.5 Path coefficient analysis
4.6 Genetic divergence

4.1 Mean performance of genotypes

The mean performance of 48 finger millet genotypes for 11 quantitative characters is presented in Table 4.1.

4.1.1 Plant height (cm)

Plant height ranged from 28.33 cm to 90.00 cm with a general mean of 69.14 cm. The shortest genotype was 13660 (28.33 cm) while the tallest genotype was 13433 (90.00 cm).

4.1.2 No. of basal tillers per plant

The mean basal tillers per plant ranged from 6.33 tillers (13489-1) to 17 tillers (13675) with a general mean of 10.72 tillers per plant.

4.1.3 No. of leaves on the main tiller

The average number of leaves on the main tiller ranges from 5.66 to 11.66 with a general mean of 8.28. The data revealed that 13426 (5.66) recorded minimum no. of leaves and maximum no. of leaves was found in genotype 13709 (11.66).

Table 4.1. Mean values of the eleven quantitative characters in finger millet germplasm

S. No	Plant Height(cm)	No. of basal tillers/plant	No. of leaves on the main tiller	Productive tillers/Plant	Main ear length (cm)	Main ear width (cm)	Finger length (cm)	Finger width(cm)	Total fingers on the main ear	Grain yield /plant (g)	Grain yield/plot(g)
13426	84.33	9.66	11.66	8.00	8.33	4.50	6.66	0.96	8.66	48.00	1383.00
13433	90.00	6.66	10.66	6.33	13.33	10.33	10.66	0.93	10.00	9.33	320.00
13434	79.33	8.00	10.33	8.00	8.83	7.00	6.33	0.89	8.00	28.33	910.00
13484	72.66	7.33	8.00	7.00	7.00	5.00	5.66	1.00	8.00	22.00	660.00
13486	68.00	6.66	8.00	6.66	7.00	5.33	5.33	0.97	8.33	20.66	540.00
13487	62.00	8.33	8.33	8.00	5.00	4.33	4.33	0.93	10.00	9.66	340.00
13489-1	73.66	6.33	8.33	6.33	8.00	8.00	5.66	0.96	10.00	27.66	845.00
13492	72.00	7.00	7.66	6.00	6.00	5.66	4.66	0.94	8.00	22.00	626.00
13502	74.00	11.66	7.66	10.66	7.66	7.00	6.33	0.94	6.66	36.66	1100.00
13517	86.00	7.66	9.00	8.33	7.33	7.33	5.33	0.97	7.66	59.00	1806.00
13523	88.33	6.66	8.33	7.33	8.00	9.00	5.66	0.93	10.00	40.00	1213.00
13528	82.66	8.00	9.33	7.00	9.00	7.00	7.00	0.92	7.00	78.00	2560.00
13539	83.66	6.66	8.66	6.66	5.33	5.33	5.00	1.04	9.00	57.33	1766.00
13542	86.00	7.00	8.66	7.00	7.66	7.00	5.66	0.96	8.00	50.00	1500.00
13555	70.66	9.33	9.00	10.00	8.33	8.33	6.33	0.95	13.66	27.00	810.00
13565	80.66	8.66	6.66	8.00	8.00	9.00	6.66	0.95	12.00	56.33	1650.00
13567	69.66	13.33	8.33	12.33	7.33	8.00	6.33	0.96	13.33	25.00	750.00
13568	68.66	13.00	9.00	12.33	8.00	8.33	5.33	0.89	11.33	71.00	2180.00
13569	77.66	12.66	9.00	12.33	10.00	8.66	7.66	0.91	12.33	71.66	2316.00
13570	58.33	14.00	9.00	15.00	6.33	5.33	5.00	1.04	9.00	92.33	2780.00
13571	70.00	11.00	7.66	11.00	10.33	9.00	8.33	0.88	9.33	53.00	1590.00
13631	74.00	11.66	9.66	11.66	7.33	14.00	9.66	0.91	8.00	33.66	1070.00
13632	66.00	13.66	9.00	13.66	9.66	17.00	9.00	0.92	8.00	28.33	850.00
13650	54.66	16.00	9.00	17.66	11.00	14.00	8.66	0.82	6.33	8.33	250.00
13651	64.66	13.33	8.66	13.33	6.33	5.33	5.00	0.80	8.66	12.00	360.00
13652	60.66	13.00	7.33	10.66	8.00	7.66	6.33	1.04	7.33	30.33	910.00

S. No	Plant Height(cm)	No. of basal tillers/plant	No. of leaves on the main tiller	Productive tillers/Plant	Main ear length (cm)	Main ear width (cm)	Finger length(cm)	Finger width (cm)	Total fingers on the main ear	Grain yield /plant (g)	Grain yield/plot (g)
13660	28.33	11.00	8.00	7.66	7.66	7.00	6.00	0.85	7.33	12.00	360.00
13661	66.00	13.00	8.66	12.66	8.33	10.00	7.33	0.87	7.33	26.33	790.00
13665	57.66	11.00	7.66	11.00	7.66	6.00	6.33	1.03	9.66	21.00	593.00
13672	59.00	12.00	7.00	9.33	7.00	6.66	6.00	1.04	9.00	18.00	636.00
13673	71.66	13.33	8.33	13.33	7.66	7.33	7.00	0.98	10.00	35.66	1100.00
13674	62.66	11.00	7.33	10.00	7.66	7.33	7.33	0.99	8.33	36.00	1066.00
13675	80.00	17.00	8.66	17.00	8.66	9.00	7.66	1.04	8.00	88.33	2620.00
13676	60.33	12.33	8.00	11.66	7.00	6.33	6.00	0.98	7.66	35.00	1050.00
13677	55.00	11.00	8.00	12.00	8.11	6.44	6.00	0.99	8.00	42.66	1280.00
13678	52.66	7.66	6.00	5.66	9.00	9.00	8.00	0.92	7.33	14.33	443.00
13689	56.00	13.33	9.00	13.00	7.33	6.33	6.33	0.92	9.00	20.66	660.00
13690	54.00	12.66	7.66	12.66	6.33	6.33	5.33	0.99	9.33	30.00	886.00
13691	60.33	13.33	8.33	13.33	6.33	5.66	5.66	1.01	9.00	49.33	1480.00
13709	57.33	11.66	5.66	10.33	8.33	11.33	8.33	0.96	9.33	14.00	420.00
13710	60.66	11.66	7.00	11.00	9.33	11.00	7.66	1.06	8.00	51.66	1550.00
13712	77.33	15.66	6.66	15.66	12.66	16.00	11.00	0.88	8.33	48.00	1466.00
13713	73.33	13.00	7.33	13.66	12.33	16.66	10.00	1.04	8.00	34.66	1050.00
GPU45	77.66	8.00	8.00	7.00	7.33	7.00	5.33	1.05	9.66	41.00	1230.00
GPU67	70.66	9.00	8.33	9.00	6.66	6.00	4.00	1.13	9.00	47.00	1383.00
PR-202	64.66	11.66	8.66	8.66	6.33	5.33	4.66	1.02	6.66	19.66	660.00
VL-149	78.00	9.00	8.66	10.00	7.33	9.00	6.00	0.96	9.00	55.00	1650.00
VR-708	77.33	9.00	7.66	8.00	6.66	5.33	5.33	0.90	6.66	50.66	1626.00
Mean	69.14	10.72	8.28	10.29	8.03	8.09	6.58	0.95	8.81	37.68	1147.77
C.V	12.48	12.28	12.85	13.66	14.57	13.61	13.70	6.09	14.68	9.38	9.83
S.E	4.98	0.76	0.61	0.81	0.67	0.63	0.52	0.03	0.74	2.04	65.14
C.D 5%	13.99	2.13	1.72	2.27	1.89	1.78	1.46	0.09	2.09	5.73	182.92
C.D 1%	18.52	2.82	2.28	3.01	2.51	2.36	1.93	0.12	2.77	7.58	242.21

4.1.4 Productive tillers per plant

The mean productive tillers per plant ranged from 5.66 tillers (13678) to 17.66 tillers (13650) with a general mean of 10.29 tillers per plant.

4.1.5 Main ear length (cm)

The average ear length recorded was 8.03 cm, with a range of 5.00 cm to 13.33 cm. The genotype 13487 (5.00 cm) recorded the lowest length whereas, genotype 13433 (13.33 cm) had the highest ear length.

4.1.6 Main ear width (cm)

Ear width ranged from 4.33 cm to 17.00 cm with a general mean of 8.09 cm. The highest ear width was recorded for the genotype 13632 (17.00 cm) while the lowest was recorded for the genotype 13487 (4.33 cm).

4.1.7 Finger length (cm)

The average length of finger recorded was 6.58 cm, with a range of 4.00 cm to 11.00 cm. The genotypes GPU-67 (4.00 cm) recorded the lowest length whereas 13712 (11.00 cm) had the highest finger length.

4.1.8 Finger width (cm)

Finger width ranged from 0.80 cm to 1.13 cm with a general mean of 0.95 cm. The highest finger width was recorded for the genotype GPU-67 (1.13 cm) while the lowest was recorded for the genotype 13651 (0.80 cm).

4.1.9 Total fingers on the main ear

The mean values for number of fingers ranged from 6.33 (13650) to 13.66 (13555) with general mean of 8.81.

4.1.10 Grain yield per plant (g)

The mean for grain yield per plant was 37.68 g and the mean value ranged from 8.33g to 92.33 g. The genotype 13650 recorded lowest grain yield per plant where as the genotype 13570 exhibited highest grain yield per plant.

4.1.11 Grain yield per plot (g)

The mean grain yield per plot recorded 1147.77 g and the mean values ranged from 250 g (13650) to 2780 g (13570). Among the genotypes tested 13570 recorded the highest grain yield per plot and 13650 recorded the lowest grain yield per plot.

Among the 48 genotypes, 13570 which recorded highest mean grain yield per plant also exhibited the maximum mean value for grain yield per plot, thus 13570 could be used as a promising donor for these two characters. Genotype 13426 recorded highest mean value for maximum no. of leaves and finger width. 13433 recorded highest plant height and main ear length. Genotype 13632 recorded highest ear width, 13650 for maximum no. of productive tillers, 13712 for highest finger length, 13675 for maximum no. of basal tillers and 13555 for maximum no. of leaves. The above mentioned genotypes will be useful for increasing the productivity, when used in appropriate breeding programs.

4.2 ANALYSIS OF VARIANCE

Analysis of variance for the experiment involving a set of 48 finger millet genotypes for 11 quantitative characters *viz.,* plant height (cm), no. of basal tillers per plant, no. of leaves on the main tiller, productive tillers per plant, main ear length (cm), main ear width (cm), finger length (cm), finger width (cm), total no. of fingers on the main ear, grain yield per plant (g) and grain yield per plot (g), revealed that the mean sum of squares were highly significant for all the characters indicating greater diversity among the 48 finger millet genotypes studied. The results of ANOVA are prescribed in the Table 4.2.

4.3 GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE

The genotypic and phenotypic coefficients of variation, heritability and genetic advance as per cent of mean were estimated for 48 genotypes and the results are furnished in Table 4.3 for PCV, GCV and heritability, genetic advance as per cent of mean respectively. The characters studied in the present investigation exhibited low, moderate and high PCV and GCV values.

4.3.1 Plant height (cm)

The genotypic and phenotypic coefficients of variation estimates observed for this trait were moderate i.e., 15.43 and 19.84, respectively. The observed heritability estimate for this character was high (60.40) with high genetic advance as per cent of mean (24.71). Similar results were reported by John (2006) for high GCV and PCV, high heritability and high genetic advance as per cent of mean, Prabhu *et al*. (2008) for moderate PCV, GCV and high heritability.

4.3.2 No. of basal tillers per plant

The genotypic and phenotypic coefficients of variation for this trait were high i.e., 25.17 and 28.01 respectively. The observed heritability estimate was high (80.80) and with high genetic advance as per cent of mean (46.60). Similar results were reported by Anand *et al*. (2005) for high heritability coupled with genetic advance as per cent of mean, Kumar (1995) for moderate PCV and GCV.

4.3.3 No. of leaves on the main tiller

The genotypic and phenotypic coefficients of variation for this trait were medium i.e., 10.82 and 16.80 respectively. The observed heritability estimate was medium (41.50) and with medium genetic advance as per cent of mean (14.30). Similar results were reported by Anand *et al.* (2005) for moderate PCV, GCV, medium heritability and moderate genetic advance as per cent of mean.

4.3.4 Productive tillers per plant

A high GCV (28.40) and PCV (31.51) were observed for this trait. The heritability estimates for this trait was high (81.20) coupled with moderate genetic advance as per cent of mean (52.72). Similar results were observed by Sonnad *et al.* (2008) and Priyadharshini *et al*. (2011) for high heritability coupled with moderate genetic advance as per cent of mean, Kumar (1995) reported for moderate PCV and GCV.

4.3.5 Main ear length (cm)

A moderate GCV (19.86) and high PCV (24.63) were recorded for this trait. The heritability observed for this trait was high (65.00). This character recorded high

Table: 4.2 The mean sum of squares for all the 11 characters in finger millet germplasm

S.No.	Characters	Replication df:2	Genotypes df:47	Error df:94
1	**Plant height(cm)**	46.583	416.112 **	74.505
2	**No. of basal tillers/plant**	0.465	23.593 **	1.735
3	**No. of leaves on the main tiller**	0.007	3.546 **	1.135
4	**Productive tillers/Plant**	0.083	27.612 **	1.977
5	**Main ear length(cm)**	1.785	9.002 **	1.371
6	**Main ear width(cm)**	0.107	28.348 **	1.214
7	**Finger length(cm)**	0.750	7.851 **	0.814
8	**Finger width(cm)**	0.181**	0.015 **	0.003
9	**Total no. of fingers on the main ear**	0.194	7.943 **	1.677
10	**Grain yield/plant(g)**	1.861	1271.928 **	12.499
11	**Grain yield/plot(g)**	329.861	98283.000 **	12731.280

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

Table: 4.3 Estimation of variability, heritability and genetic advance as

S.No.	Character	Variance		GCV (%)	PCV (%)	h^2 (%) (Broad sense)	GA	GA as percent of mean (5%)
		Genotypic	Phenotypic					
1	**Plant height(cm)**	113.86	188.37	15.43	19.84	60.40	17.09	24.71
2	**No. of basal tillers/plant**	7.28	9.02	25.17	28.01	80.80	4.99	46.60
3	**No. of leaves on the main tiller**	0.80	1.93	10.82	16.80	41.50	1.18	14.35
4	**Productive tillers/Plant**	8.54	10.52	28.40	31.51	81.20	5.42	52.72
5	**Main ear length(cm)**	2.54	3.91	19.86	24.63	65.00	2.64	32.98
6	**Main ear width(cm)**	9.04	10.25	37.14	39.56	88.20	5.81	71.85
7	**Finger length(cm)**	2.34	3.16	23.26	27.00	74.20	2.71	41.29
8	**Finger width(cm)**	0.004	0.007	6.48	8.89	53.10	0.09	9.73
9	**Total no. of fingers on the main ear**	2.08	3.76	16.38	22.00	55.50	2.21	25.14
10	**Grain yield/plant (g)**	419.80	432.30	54.37	55.18	97.10	41.59	110.38
11	**Grain yield/plot (g)**	395183.80	407915.10	54.77	55.64	96.90	1274.62	111.05

percentof mean for eleven characters in 48 genotypes genetic advance as per cent of mean (32.98). Similar results were observed by Jain and Yadava (1999) and Kumar (1995) for high heritability and genetic advance as per cent of mean.

4.3.6 Main ear width (cm)

The GCV and PCV for this trait were high i.e., 37.14 and 39.56, respectively. The heritability observed for this trait was high (88.20). This character recorded high genetic advance as per cent of mean (71.85).

4.3.7 Finger length (cm)

A high GCV (23.26) and high PCV (27) were observed for this trait. The heritability estimate for this trait was high (74.20) with high genetic advance as per cent of mean (41.29). Similar results were observed by Lal *et al.* (1996) for high PCV, heritability and genetic advance as per cent of mean. Sonnad *et al*. (2008) for moderate GCV.

4.3.8 Finger width (cm)

A medium GCV (6.48) and moderate PCV (8.89) were observed for this trait. The heritability estimate for this trait was moderate (53.10) with moderate genetic advance as per cent of mean (9.73). Similar results were observed by Bendale *et al.* (2002) for low GCV.

4.3.9 Total no. of fingers on the main ear

A medium GCV (16.38) and high PCV (22) were observed for this trait. The heritability estimate for this trait was moderate (55.50) with high genetic advance as per cent of mean (24.14). Similar results were observed by Prabhu *et al*. (2008) and Anand *et al*. (2005) for medium PCV, high GCV and high heritability coupled with high genetic advance as percent of mean.

4.3.10 Grain yield per plant (g)

A high genotypic coefficient of variation (54.37) and phenotypic coefficient of variation (55.18) were observed for this trait. A high heritability estimate (97.10) coupled with high genetic advance as per cent of mean (110.38) recorded for this character. The results are in conformity with the findings of Lal *et al.* (1996), Prabhu *et al.* (2008) and Anand *et al.* (2005) for high GCV and PCV and high heritability coupled with high genetic advance as per cent of mean.

4.3.11 Grain yield per plot (g)

A high genotypic coefficient of variation (54.77) and phenotypic coefficient of variation (55.64) were observed for this trait. A high heritability estimate (96.90) coupled with high genetic advance as per cent of mean (111.05) was recorded for this trait.

The knowledge of genetic variability present in a given crop species for the character under improvement is of paramount importance for the success of any plant breeding programme. Information on coefficient of variation is useful in measuring the range of variability present in the characters. Heritability and genetic advance are important selection parameters. Genotypic coefficient of variation (GCV) along with heritability estimates would provide a better picture of the amount of genetic advance to be expected by phenotypic selection (Burton, 1952). It is suggested that genetic gain should be considered in conjunction with heritability estimates (Johnson *et al*., 1955). Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone.

Coefficients of variation studies indicated that the estimates of PCV were slightly higher than the corresponding GCV estimates for all the characters, indicating that the characters were less influenced by the environment. Therefore, selection on the basis of phenotype alone can be effective for the improvement of these traits.

The estimates of heritability act as predictive instrument in expressing the reliability of phenotypic value. Therefore, high heritability helps in effective selection for a particular character. Heritability in broad sense is the ratio of genotypic variance to the phenotypic variance and is expressed in percentage. In the present study all quantitative characters show high heritability (broad sense). High heritability for quantitative characters indicates the scope of genetic improvement of these characters through selection.

If the value of heritability in broad sense is high, it indicates that though the character is least influenced by the environmental effects, the selection for improvement of such character sometimes may not be useful, because broad sense heritability is based on total genetic variance which includes both fixable (additive) and non-fixable (dominance and epistasis) variances. On the other hand if the value of genetic advance is high, it shows that the character is governed by additive genes and selection will be rewarding for improvement of such trait.

So high heritability accompanied with high genetic advance indicates most likely the heritability is due to additive gene effect and selection may be effective.

In the present investigation, high heritability coupled with high genetic advance as percent of mean was observed for plant height, no. of basal tillers per plant, no. of productive tillers per plant, main ear length, main ear width, finger length, grain yield per plant and grain yield per plot. Thus, these traits are predominantly under the control of additive gene action and hence these characters can be improved by selection.

Moderate heritability with High genetic advance was recorded for total no. of fingers on the main ear and moderate heritability with moderate genetic advance was recorded for total no. of leaves on main tiller and finger width. These traits appear to be under the control of both additive and non-additive gene actions.

4.4 CHARACTER ASSOCIATION

Crop yield is the end product of the interaction of a number of other, often interrelated attributes. A thorough understanding of the interaction of characters among themselves had been of great use in plant breeding. The efficiency of selection for yield mainly depends on the direction and magnitude of association between yield and its component characters and also among themselves. Character association provides information on the nature and extent of association between pairs of metric traits and helps in selection for the improvement of the character. Phenotypic and genotypic correlations were worked out on yield and yield contributing characters in 48 genotypes. In general, most of genotypic correlations were found to be higher than phenotypic correlations, which indicate that though there is strong inherent association between characters studied, its expression is lessened due to influence of environment (Table 4.4).

Character association provides information on the nature and extent of association between pairs of metric traits and helps in selection for the improvement of the character. Phenotypic and genotypic correlations were worked out on yield and yield contributing characters in 48 genotypes. In general, most of genotypic correlations were found to be higher than phenotypic correlations, which indicate that though there is strong inherent association between characters studied, its expression is lessened due to influence of environment. The results are furnished in the Table 4.4.

4.4.1 Plant height (cm)

Plant height recorded a positive and non-significant correlation with main ear width (0.0735P, 0.0532G), finger length (0.1192P, 0.0847G), finger width (0.1379P, 0.1329G), total fingers on the main ear (0.1434P, 0.2170G) and grain yield per plant (0.3587P, 0.4525G) at both phenotypic and genotypic levels. Significant positive correlation with no. of leaves on the main tiller (0.3357P), main ear length (0.2228P) and grain yield per plot (0.3617P) at phenotypic level, non-significant positive correlation with no. of leaves on the main tiller (0.4636G), main ear length (0.1850G) and grain yield per plot (0.4610G) at genotypic level, significant negative correlation with no. of basal tillers per plant (-0.2976P) and productive tillers per plant (-0.1939P) at phenotypic level, non-significant negative correlation with no. of basal tillers per plant (-0.4887G) and productive tillers per plant (-0.3291G) at genotypic level,

Similar results were reported by Ravikumar and Seetharam (1993) for basal tillers per plant, productive tillers per plant, grain yield per plant, Sonnad *et al.* (2008) for positive main ear length and finger width, Bedis *et al.* (2006b) for grain yield per plot, positive non-significant with main ear width, Bendale *et al.* (2002) for finger length.

Table: 4.4 Phenotypic (P) and genotypic (G) correlation coefficients among yield and yield attributes in forty eight genotypes

S.NO	**Character**		**Plant height (cm)**	**No of basal tillers/ plant**	**No of leaves on the main tiller**	**Productive tillers/plant**	**Main ear length (cm)**	**Main ear width(cm)**	**Finger length (cm)**	**Finger width (cm)**	**Total fingers on the main ear**	**Grain yield /plot(g)**	**Grain yield/plant (g)**
1	**PH**	***P***	**1.0000**	-0.2976 * *	0.3357**	-0.1939 *	0.2228 * *	0.0735	0.1192	0.1379	0.1434	0.3617 **	0.3587
		G	**1.0000**	-0.4887	0.4636	-0.3291	0.1850	0.0532	0.0847	0.1329	0.2170	0.4610	0.4525
2	**NBT**	***P***		**1.0000**	-0.0076	0.9126 **	0.1977 *	0.3402 **	0.2939 **	-0.0835	-0.0725	0.1254	0.1273
		G		**1.0000**	-0.1749	0.9592	0.2343	0.4085	0.3858	-0.1952	-0.0592	0.1157	0.1235
3	**NL**	***P***			**1.0000**	0.0597	0.0980	-0.1058	-0.0030	-0.0480	0.0275	0.1353	0.1351
		G			**1.0000**	-0.0662	0.0353	-0.1707	-0.0741	-0.0799	0.1006	0.2017	0.1817
4	**PT**	***P***				**1.0000**	0.2338 **	0.3990 **	0.3226 **	-0.0382	-0.0206	0.1954 *	0.2064
		G				**1.0000**	0.2781	0.4657	0.3899	-0.0721	0.0118	0.1908	0.2024
5	**EL**	***P***					**1.0000**	0.6533 **	0.8233 **	-0.1180	0.0435	0.0149	0.0072
		G					**1.0000**	0.7916	0.8996	-0.2082	-0.0541	0.0113	0.0043
6	**EW**	***P***						**1.0000**	0.7748 **	-0.1047	-0.0233	-0.0398	-0.0419
		G						**1.0000**	0.8821	-0.1658	-0.0747	-0.0484	-0.0503
7	**FL**	***P***							**1.0000**	-0.1588	-0.0372	-0.0495	-0.0560
		G							**1.0000**	-0.2441	-0.0856	-0.0664	-0.0758
8	**FW**	***P***								**1.0000**	0.0511	0.2294 **	0.2507
		G								**1.0000**	0.0591	0.3055	0.3415
9	**TF**	***P***									**1.0000**	0.0664	0.0678
		G									**1.0000**	0.1065	0.1127
10	**GYP**	***P***										**1.0000**	0.9927
		G										**1.0000**	0.9990
11	**GYPP**	***P***											**1.0000**
		G											**1.0000**

PH- Plant height (cm), NBT- No. of basal tillers per plant, NL- No. of leaves on the main tiller, PT- Productive tillers per plant, EL-Main ear length, EW-Main ear width, FL- Finger length , FW- Finger width, TF-Total fingers on the main ear, GYP-Grain yield per plot, GYPP-Grain yield per plant

4.4.2 No. of basal tillers per plant

No. of basal tillers per plant recorded a non-significant and positive correlation with grain yield per plant (0.1254P, 0.1157G) and grain yield per plot at both phenotypic and genotypic levels. Significant and positive correlation with productive tillers per plant (0.9126P), main ear length (0.1977P), main ear width (0.3402P) and finger length (0.2939P) at phenotypic level, non-significant and positive correlation with productive tillers per plant (0.2343G), main ear length (0.2343G), main ear width (0.4085G) and finger length (0.3858G) at genotypic level, non-significant negative correlation with no. of leaves on the main tiller (-0.0076P, -0.1749G), finger width (-0.0835P, -0.1952G) and total fingers on the main ear (-0.0725P, -0.0592G) at both phenotypic and genotypic levels. Similar results were reported by Sonnad *et al.* (2005) for finger length and ear length, Ravikumar and Seetharam (1993) for productive tillers per plant, Kumar (1995) for grain yield per plant, Bendale *et al.* (2002) for finger width.

4.4.3 No. of leaves on the main tiller

No. of leaves on the main tiller recorded a non-significant positive correlation with main ear length (0.0980P, 0.0353G), total fingers on the main ear (0.0275P, 0.1006G) grain yield per plant (0.1353P, 0.2017G) and grain yield per plot (0.1351P, 0.1817G) at both phenotypic and genotypic levels, finger length (0.3072P, 0.3078G) at phenotypic and genotypic levels, non-significant negative correlation with main ear width (-0.1058P, -0.1707G), finger length (-0.0030P, -0.0741G) and finger width (-0.0480P, -0.0799G) at both levels, , non-significant positive correlation with productive tillers per plant (0.0597P) at phenotypic level and non-significant negative correlation with productive tillers per plant (-0.0662G) at genotypic level.

Similar results were reported by Anantharaju and Meenakshiganesan (2005) for productive tillers per plant and finger length.

4.4.4 Productive tillers per plant

Productive tillers per plant recorded a non-significant positive correlation yield per plant (0.2064P, 0.02024G) at both phenotypic and genotypic levels, significant positive correlation with main ear length (0.2338P), main ear width

(0.3990P), finger length (0.3226P) and grain yield per plot (0.1954P) at phenotypic level, non-significant positive correlation with main ear length (0.2781G), main ear width (0.4657G), finger length (0.3899G) and grain yield per plot (0.1908G) at genotypic level, negative non-significant correlation with total fingers on the main ear (-0.0206P) at phenotypic level, positive non-significant correlation with total fingers on the main ear (0.0118G) at genotypic level, negative non-significant correlation with finger width (-0.0382P, -0.0721G) at both levels.

Similar results were reported by Priyadharshini *et al*. (2011), Anantharaju Meenakshiganesan (2005) and Kumar (1995) for grain yield per plant, Kumar (1995) ear length, Priyadharshini *et al*. (2011) for finger length, total finger on the main ear, Sonnad (2005) for finger length.

4.4.5 Main ear length (cm)

Main ear length recorded a non-significant positive correlation with yield per plant (0.0149P, 0.0113G) and yield per plot (0.0072P, 0.0043G) at both phenotypic and genotypic levels, non-significant negative correlation with finger width (-0.1180P, -0.2082G) at both phenotypic and genotypic levels, significant positive correlation with main ear width (0.6550P) and finger length (0.8233P) at phenotypic level, non-significant positive correlation with main ear width (0.7916G), finger length (0.8996G) at genotypic level, non-significant positive correlation with total finger on the main ear (0.0435P) at phenotypic level, non-significant negative correlation with total finger on the main ear (-0.0541G) at genotypic level. Similar results were reported by Sonnad *et al.* (2008) for finger length and finger no. John (2006) for grain yield per plant.

4.4.6 Main ear width (cm)

Main ear width recorded significant positive correlation with finger length (0.7748P), at phenotypic level, non-significant positive correlation with finger length (0.8821G), at genotypic level, non-significant negative correlation with finger width (-0.1047P, -0.8821G), total fingers on the main ear (-0.0233P, -0.0747G), grain yield per plant (-0.0398P, -0.0484G) and grain yield per plot (-0.0419P, -0.0503G) at both levels.

4.4.7 Finger length (cm)

Finger length recorded a non-significant negative correlation with finger width (-0.1588P, -0.2441G), total no. of fingers on the main ear (-0.0372P, -0.0856G), grain yield per plant (-0.0495P, -0.0664G) and grain yield per plot (-0.0560P, -0.0758G) at both phenotypic and genotypic levels.

Similar results were reported by Sonnad *et al.* (2008) and Lal (1996) for grain yield per plant. Sonnad *et al.* (2008) also reported negative correlation with finger no. at genotypic level, negative and non-significant correlation with finger width but here correlation with finger width is significantly negative.

4.4.8 Finger width (cm)

Finger width recorded a significant positive correlation with grain yield per plot (0.2294P), at phenotypic level, non-significant positive correlation with grain yield per plot (0.3055G), at genotypic level, positive and non-significant correlation with total finger on the main ear (0.0511P, 0.0591G) and grain yield per plant (0.2507P, 0.3415G) at both levels. Similar results were reported by Bendale *et al.* (2002) for grain yield per plot.

4.4.9 Total no of fingers on the main ear

Total fingers on the main ear recorded a non-significant positive correlation with grain yield per plant (0.0664P, 0.1065G) and grain yield per plot (0.0678P, 0.1127G) at both levels. Similar results were reported by Ravikumar and Seetharam (1993) and Ravindran *et al*. (1996) at both levels.

4.4.10 Grain yield per plot (g)

Grain yield per plot recorded a significant positive correlation with the grain yield per plant (0.9927P, 0.9990G) at both phenotypic and genotypic levels.

4.4.11 Grain yield per plant (g)

Grain yield per plant recorded a non-significant positive correlation with no. of basal tillers per plant (0.1273P, 0.1235G), no. of leaves on the main tiller (0.1351P, 0.1817G), no. of productive tillers per plant (0.2064P, 0.2024G), main ear length (0.0072P, 0.0043G) finger width (0.2507P, 0.3415G), total fingers on the main ear

(0.0678P, 0.1127G), grain yield per plot (0.9927P, 0.9990G) and plant height (0.3587P, 0.4525G) at both levels, Positive and non-significant correlation with main ear width (-0.0419P, -0.0503G) and finger length (-0.0560P, -0.0758G) at both levels.

Grain yield per plant showed positive non-significant association with no. of leaves on the main tiller, main ear length and total fingers on the main ear. Similar kind of association was revealed by Kumar (1995) for no. of basal tillers per plant, productive tillers, Sonnad *et al.* (2008) and Lal *et al.* (1996) for finger length, Ravindran *et al.* (1996) and Bedis *et al.* (2006b) for total no. of fingers on the main ear, finger width has been found positively non-significant in this experiment where as Bendale *et al.* (2002) recorded negative and non-significant correlation.

The result obtained indicated that, yield was increased whenever there was increase in no. of basal tillers per plant, no. of leaves on the main tiller, no. of productive tillers per plant, main ear length, finger width, total fingers on the main ear, grain yield per plot and plant height. Hence, these characters could be considered as criteria for selection for higher yield as these were mutually and directly associated with grain yield.

Grain yield per plant shows positive and non-significant correlation with Plant height and negative non-significant correlation with main ear width and finger length. Similar kind of association was revealed by Priyadarshini *et al.* (2011), Sonnad *et al.* (2008), Anantharaju and Meenakshiganesan (2005) for plant height, whereas Bedis *et al.* (2006b) recorded significant positive correlation with plant height, John (2006) for ear length, where as Sonnad *et al.* (2005) and Kumar (1995) recorded positive and non-significant correlation with main ear length. As plant height positively associated with grain yield it may consider for selection criteria for increase in grain yield.

4.5 PATH COEFFICIENT ANALYSIS

Correlation gives only the relation between two variables whereas path coefficient analysis allows separation of the direct effect and their indirect effects through other attributes by partitioning the correlations (Wright, 1921). Hence, this objective was undertaken in the present investigation.

Based on the data recorded on the genotypes in the present investigation, the genotypic and phenotypic correlations were estimated to determine direct and indirect effects of yield and yield contributing characters.

As discussed in character association based on the importance of phenotypic effects the present results of phenotypic and genotypic path coefficient of yield and yield contributing characters discussed here under which were presented in the table 4.5 and Fig 4.2 and 4.3.

4.5.1 Plant height (cm)

Plant height had positive direct effect (0.0010P, 0.0421G) on grain yield per plant at both phenotypic and genotypic levels, while the correlation of plant height with grain yield per plant was positive and non-significant. The correlation with yield was positive due to negative indirect contribution through no. of basal tillers per plant (-0.0003P, -0.0206G) and productive tillers per plant (-0.0002P, -0.0139G) at both levels. Similar results reported by Priyadarshini *et al.* (2011) and Bendale *et al.* (2002), Ravindran *et al.* (1996), Anantharaju and Meenakshiganesan (2005) positive direct effect of plant height on grain yield.

4.5.2 No. of basal tillers per plant

No. of basal tillers had positive phenotypic direct effect (0.0147P) and negative genotypic effect (-0.0575G) on grain yield per plant, while the correlation of no. of basal tillers with grain yield per plant was positive and non-significant at both levels. The correlation was negative and non-significant at phenotypic level due to negative indirect effect by Productive tillers per plant (-0.0450P), main ear length (-0.0097P), main ear width (-0.0168P), finger length (-0.0145P), and grain yield per plot (-0.0062P), the correlation was positive and non-significant at genotypic level due to positive indirect effect by productive tillers per plant (0.1129G), main ear length (0.0276G), main ear width (0.0481G), finger length (0.0454G), and grain yield per plot (0.0136G). Similar results reported by Lal *et al.* (1996), Sonnad *et al.* (2005) for positive phenotypic and negative genotypic effect on grain yield per plant.

4.5.3 No. of leaves on the main tiller

No. of leaves on the main tiller had negative direct effect (-0.0011P, -0.0166G) on grain yield per plant at both levels while the correlation between no. of leaves on the main tiller and grain yield per plant was positive and non-significant. This positive effect mainly due to positive indirect effect through no. of basal tillers

Table: 4.5 Phenotypic (P) and genotypic (G) path coefficient analysis indicating direct (bold and diagonal) and indirect effects of components characters on grain yield

S.NO	Character		Plant height (cm)	No of basal tillers/ plant	No of leaves on the main tiller	Productive tillers/ plant	Main ear length (cm)	Main ear width(cm)	Finger length (cm)	Finger width (cm)	Total fingers on the main ear	Grain yield /plot(g)	Correlation
1	PH	P	**0.0010**	-0.0003	0.0003	-0.0002	0.0002	0.0001	0.0001	0.0001	0.0001	0.0004	0.3587
		G	**0.0421**	-0.0206	0.0195	-0.0139	0.0078	0.0022	0.0036	0.0056	0.0091	0.0194	0.4525
2	NBT	P	0.0147	**-0.0493**	0.0004	-0.0450	-0.0097	-0.0168	-0.0145	0.0041	0.0036	-0.0062	0.1273
		G	-0.0575	**0.1177**	-0.0206	0.1129	0.0276	0.0481	0.0454	-0.0230	-0.0070	0.0136	0.1235
3	NL	P	-0.0004	0.0000	**-0.0011**	-0.0001	-0.0001	0.0001	0.0000	0.0001	0.0000	-0.0001	0.1351
		G	-0.0077	0.0029	**-0.0166**	0.0011	-0.0006	0.0028	0.0012	0.0013	-0.0017	-0.0034	0.1817
4	PT	P	-0.0125	0.0590	0.0039	**0.0647**	0.0151	0.0258	0.0209	-0.0025	-0.0013	0.0126	0.2064
		G	0.0220	-0.0642	0.0044	**-0.0669**	-0.0186	-0.0312	-0.0261	0.0048	-0.0008	-0.0128	0.2024
5	EL	P	-0.0011	-0.0010	-0.0005	-0.0011	**-0.0049**	-0.0032	-0.0040	0.0006	-0.0002	-0.0001	0.0072
		G	0.0088	0.0112	0.0017	0.0133	**0.0477**	0.0378	0.0429	-0.0099	-0.0026	0.0005	0.0043
6	EW	P	-0.0003	-0.0014	0.0004	-0.0017	-0.0027	**-0.0041**	-0.0032	0.0004	0.0001	0.0002	-0.0419
		G	0.0009	0.0067	-0.0028	0.0077	0.0130	**0.0165**	0.0145	-0.0027	-0.0012	-0.0008	-0.0503
7	FL	P	-0.0004	-0.0009	0.0000	-0.0010	-0.0026	-0.0025	**-0.0032**	0.0005	0.0001	0.0002	-0.0560
		G	-0.0068	-0.0311	0.0060	-0.0314	-0.0724	-0.0710	**-0.0805**	0.0197	0.0069	0.0053	-0.0758
8	FW	P	0.0031	-0.0019	-0.0011	-0.0009	-0.0026	-0.0023	-0.0036	**0.0224**	0.0011	0.0051	0.2507
		G	0.0069	-0.0102	-0.0042	-0.0038	-0.0108	-0.0086	-0.0127	**0.0520**	0.0031	0.0159	0.3415
9	TF	P	-0.0001	0.0001	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	**-0.0008**	-0.0001	0.0678
		G	0.0010	-0.0003	0.0005	0.0001	-0.0002	-0.0003	-0.0004	0.0003	**0.0045**	0.0005	0.1127
10	GYP	P	0.3547	0.1229	0.1327	0.1916	0.0146	-0.0390	-0.0485	0.2249	0.0651	**0.9807**	0.9927
		G	0.4428	0.1112	0.1938	0.1833	0.0109	-0.0465	-0.0638	0.2934	0.1023	**0.9606**	0.9990

PH- Plant height (cm), NBT- No. of basal tillers per plant, NL- No. of leaves on the main tiller, PT- Productive tillers per plant, EL-Main ear length, EW-Main ear width, FL- Finger length , FW- Finger width, TF-Total fingers on the main ear, GYP-Grain yield per plot

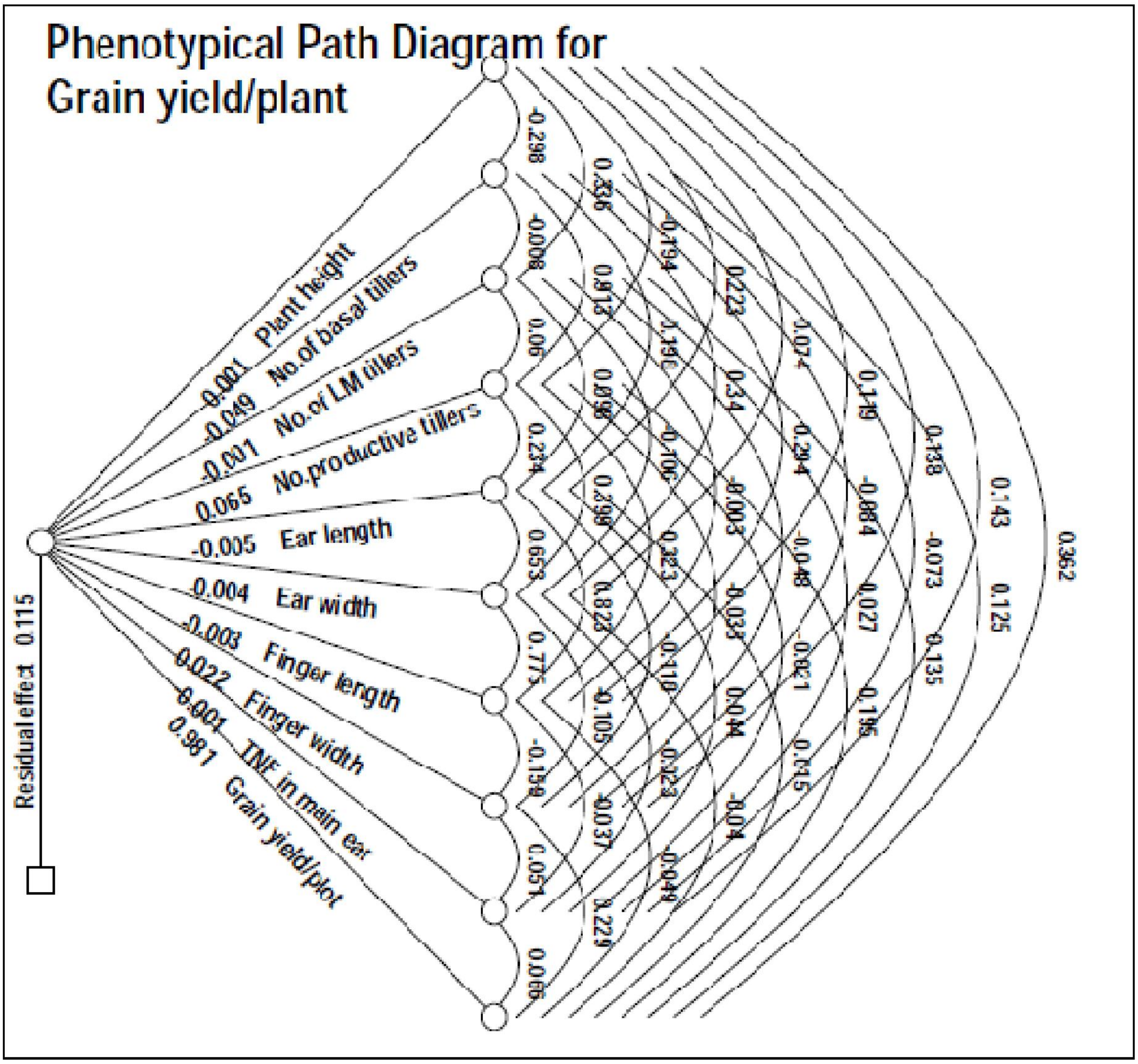

Fig: 4.2 Phenotypical Path Diagram for grain yield /plant

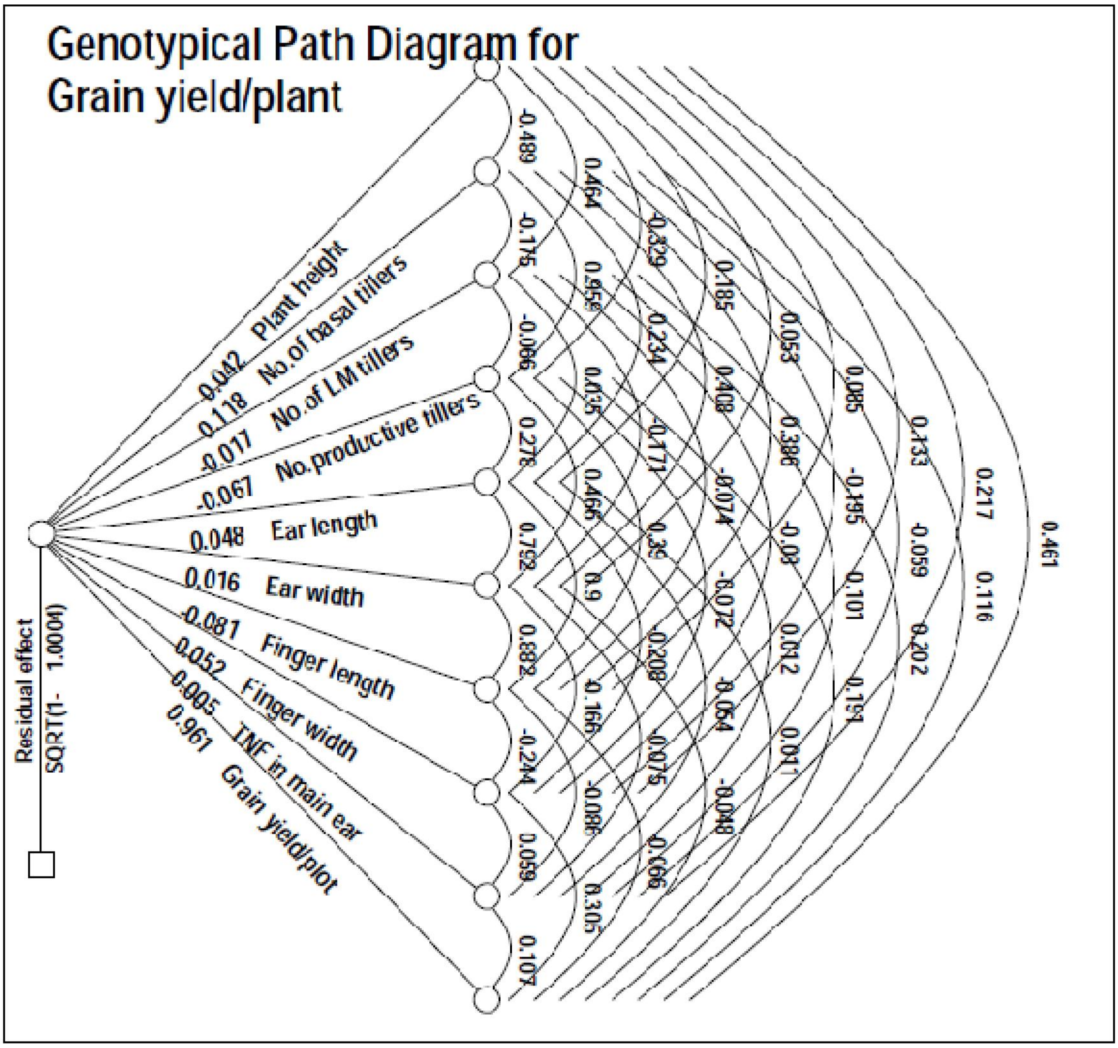

Fig: 4.3 Genotypical Path Diagram for grain yield /plant per plant (0.0000P, 0.0029G), main ear width (0.0001P, 0.0028G), finger length (0.0000P, 0.0012G) and finger width (0.0001P, 0.0013G) at both levels. Similar results reported by Anantharaju and Meenakshiganesan (2005) and Dhanakod and Chandrasekharan (1989) for genotypic effects.

4.5.4 Productive tillers per plant

No. of productive tillers per plant had positive phenotypic direct effect (0.0647P) and negative genotypic effect (-0.0669G) on grain yield per plant, on the other side productive tillers had positive and non-significant correlation with grain yield per plant. The correlation with grain yield per plant was positive due to positive phenotypic indirect effect through no. of basal tillers per plant (0.0590P), main ear length (0.0151P), main ear width (0.0258P), finger length (0.0209P) and grain yield per plot (0.0126P), the correlation was negative and non-significant at genotypic level due to negative indirect effect through no. of basal tillers per plant (-0.0642G), main ear length (-0.0186G), main ear width (-0.0312G), finger length (-0.0261G) and grain yield per plot (-0.0128G). Similar results were reported by Kumar (1995), Ravikumar and Seetharam (1993), Bedis *et al.* (2006b), Priyadarshini *et al.* (2011) and Anantharaju and Meenakshiganesan (2005) for positive direct effect on grain yield per plant.

4.5.5 Main ear length (cm)

Main ear length had negative phenotypic direct effect (-0.0049P) and positive genotypic effect (0.0477G) on grain yield per plant while correlation between main ear length and grain yield per plant was positive and non-significant at both levels. The correlation was negative and non-significant at phenotypic level due to negative indirect effect through plant height (-0.0011P), no. of basal tillers per plant (-0.0010P), no. of leaves on the main tiller (-0.0005P), productive tillers per plant (-0.0011P), finger length (-0.0032P) and finger width (-0.0040P), the correlation was positive and non-significant at genotypic level due to positive indirect effect through plant height (0.0088G), no. of basal tillers per plant (0.0112G), no. of leaves on the main tiller (0.0017G), productive tillers per plant (0.0133G), finger length (0.0378G) and finger width (0.0429G). Similar results were reported by Kumar (1995) and Bedis *et al.* (2006) is negative direct effect of main ear length on grain yield per plant.

4.5.6 Main ear width (cm)

Main ear width had negative phenotypic direct effect (-0.0041P) and positive genotypic effect (0.0165G) on grain yield per plant while correlation between main ear length and grain yield per plant was negative and non-significant at both levels. The correlation was negative and non-significant at phenotypic level due to negative indirect effect through plant height (-0.0003P), no. of basal tillers per plant (-0.0014P), productive tillers per plant (-0.0017P), ear length (-0.0027P) and finger length (-0.0032P), the correlation was positive and non-significant at genotypic level due to positive indirect effect through plant height (0.0009G), no. of basal tillers per plant (0.0067G), productive tillers per plant (0.0077G), ear length (0.0130G) and finger width (0.0145G).

4.5.7 Finger length (cm)

Finger length had negative direct effect (-0.0032P, -0.0805G) on grain yield per plant at both phenotypic and genotypic levels, while correlation between finger length and grain yield per plant was non-significantly negative. The correlation with grain yield per plant was negative due to positive indirect effect through no. of leaves on the main tiller (0.0000P, 0.0060G), main ear width (0.0005P, 0.0197G), total fingers on the main ear (0.0001P, 0.0069G) and grain yield per plot (0.0002P, 0.0053G). Same results were reported by Sonnad *et al.* (2008), Anantharaju and Meenakshiganesan (2005), Lal *et al.* (1996) and Bendale *et al.* (2002) negative direct effect of finger length on grain yield per plant.

4.5.8 Finger width (cm)

Finger width had positive direct effect (0.0224P, 0.0520G) on grain yield per plant while correlation between finger width and grain yield per plant was significantly positive. The correlation with grain yield per plant was positive and non-significant due to the indirect positive effect through total fingers on the main ear (0.0011P, 0.0031G) and grain yield per plot (0.0051P, 0.0159G). Same result reported by Bendale *et al.* (2002) positive direct effect of finger width on grain yield per plant.

4.5.9 Total fingers on the main ear

Total fingers had phenotypic negative direct effect (-0.0008P) and genotypic positive direct effect (0.0045G) on grain yield per plant while the correlation between total fingers on the main ear and grain yield was non-significantly positive. The correlation with grain yield per plant was negative and non-significant due to negative phenotypic direct effect through plant height (-0.0001P) and grain yield per plot (-0.0001P), The correlation with grain yield per plant was positive and non-significant due to negative genotypic direct effect through plant height (0.0010G) and grain yield per plot (0.0005G). Same result reported by Thakur and Saini (1995), Marimuthu (1997), Bendale *et al.* (2002) and Bedis *et al*. (2006) with grain yield per plant.

4.5.10 Grain yield per plot (g)

Grain yield per plot had positive direct effect (0.9807P, 0.9606G) on grain yield per plant while the correlation between grain yield per plot and grain yield per plant was positively non-significant. The correlation with grain yield per plant was positive and non-significant due to indirect positive effect through plant height (0.3547P, 0.4428G), no. of basal tillers per plant (0.1229P, 0.1112G), no. of leaves on the main tiller (0.1327P, 0.1938G), productive tillers per plant (0.1916P, 0.1833G), main ear length (0.0146P, 0.0109G), finger width (0.2249P, 0.2934G) and total fingers on the main ear (0.0651P, 0.1023G) at both phenotypic and genotypic levels.

The association of different component characters among themselves and with yield is quite important for devising an efficient selection criterion for yield. The total correlation between yield and component characters may be some times misleading, as it might be an over-estimate or under-estimate because of its association with other characters. Hence, indirect selection by correlated response may not be some times fruitful. When many characters are affecting a given character, splitting the total correlation into direct and indirect effects of cause as devised by Wright (1921) would give more meaningful interpretation to the cause of association between the dependent variable like yield and independent variables like yield components. This kind of information will be helpful in formulating the selection criteria. Indicating the selection for these characters is likely to bring about an overall improvement in single plant yield directly.

As a guideline for interpretation of results of path analysis the following broad points may be kept in view (Singh and Chaudhary, 1977).

If the correlation coefficient between a causal factor and the effect is almost equal to its direct effect, then correlation explains the true relationship and a direct selection through this trait will be effective.

If the correlation coefficient is positive, but the direct effect is negative or negligible, the indirect effects seem to be the cause of positive correlation. In such situations, the indirect causal factors are to be considered simultaneously for selection.

Correlation coefficient may be negative but the direct effect is positive and high. Under these circumstances, a restricted simultaneous selection model is to be followed *i.e.* restrictions are to be imposed to nullify the undesirable indirect effects in order to make use of the direct effect.

If correlation coefficient is negative and direct effect is also negative, then the selection based on that character has to be dropped.

The residual effect determines how best the causal factors account for the variability of the dependent factor. If the residual effect is high, some other factors which have not been considered here need to be included in this analysis to account fully for the variation in yield.

Path coefficient analysis revealed that grain yield per plant exerted the highest positive direct effect on grain yield per plot, followed by finger width, plant height and along with significant positive correlation for all the above mentioned characters.

These characters also exhibited indirect positive effect viz., Productive tillers per plant exhibited indirect positive effect on grain yield through plant height, no. of basal tillers per plant, no. of leaves on the main tiller, productive tillers per plant, main ear length, finger width and total fingers on the main ear, finger width exhibited indirect positive effect through plant height, total fingers on the main ear and grain yield per plot, plant height exhibited indirect positive effect through no. of leaves on the main tiller, main ear length main ear width, finger length, finger width, total no. of fingers on the main ear and grain yield per plot. Similar results were conformity with Ravindran *et al*. (1996) and Ravikumar and Seetharam (1993) for positive direct effect of productive tillers, Anantharaju and Meenakshiganesan (2005), Lal *et al*. (1996) for finger length, Bendale *et al.* (2002) for finger width.

No. of leaves on the main tiller had negative direct effect on grain yield per plant. No. of leaves on the main tiller exhibited indirect positive effect on grain yield through no. of basal tillers per plant, main ear width, finger length and finger width. Similar results were conformity with Bendale *et al.* (2002), Ravindran *et al.* (1996).

Finger length had negative direct effect on grain yield per plant. Finger length recorded negative and non-significant correlation with grain yield per plant through no. of leaves on the main tiller, finger width, total finger on the main ear and grain yield per plot. Similar results were conformity with Kumar (1995) and Bedis *et al.* (2006a) negative direct effect of finger length on grain yield per plant.

Path analysis revealed that plant height, finger width and grain yield per plot are the most important characters which could be used as selection criteria for effective improvement of grain yield.

4.6 GENETIC DIVERGENCE

The quantitative assessment of genetic divergence was made by adopting Mahalanobis D^2 statistic for yield and its contributing characters. Genetic divergence was estimated for 48 finger millet germplasm lines and the results obtained from the study are presented below.

4.6.1 Wilk’s ‘V’ criterion test

Wilk's 'V’ (statistic) criterion was used to test the significant differences between the groups based on the pooled effects of all the characters. The significance of 'V’ (statistic) value was tested by % at 517 degrees of freedom. The 'V’ statistic value was highly significant indicating that the genotypes differed significantly when all the characters were considered simultaneously.

The significance of 48 genotypes in the analysis of variance of dispersion clearly indicated the significant pooled effect of all the characters studied between different genotypes. Hence, further analysis was made to estimate D^2 analysis.

4.6.2 Mahalanobis generalized distance D^2 values

The correlated unstandardized means of eleven quantitative characters studied were transformed to standardized uncorrelated set of variables by using pivotal condensation method. The statistical distance (Mahalanobis D^2 value) between a pair of genotypes was obtained as sum of squares of differences between pairs of corresponding uncorrelated values of any two genotypes. These values were considered at a time and these were used for final grouping of genotypes.

4.6.3 Grouping of genotypes into various clusters

Forty eight genotypes were grouped into eight clusters based on D^2 values using Tocher's method (Rao, 1952) such that the genotypes belonging to same cluster had an average smaller D^2 values than those belonging to different clusters. The distribution of genotypes into various clusters is shown in Table 4.6 and Fig 4.1. Out of eight clusters, cluster I was the largest comprising of twenty four genotypes followed by clusters II with twelve genotypes, cluster IV with five genotypes, cluster VI with three genotypes and clusters III, V, VII, and VIII with one genotype each. The clusters III, V, VII and VIII were represented by single genotype indicating high degree of heterogeneity among the genotypes.

4.6.4 Average inter and intra cluster distances

Intra cluster D^2 values ranged from zero (cluster III, V, VII, VIII) to 24.20 (cluster VI). Maximum intra cluster distance was observed in cluster VI (24.20), followed by cluster IV (19.80), cluster II (15.60) and cluster I (14.82). The intra cluster distance varied from a maximum 24.20 for cluster VI to minimum 14.82 for cluster I having 4 genotypes though it was zero for solitary clusters (III, V, VII, and VIII) (Table 4.7). This reveals that genotypes occupying the same cluster have low level of diversity and selection of parents with in the cluster may not be considered promising as has been reported by Kumar *et al*. (2010).

Table 4.6. Cluster classification of finger millet germplasm (Tocher's method)

Cluster	Number of genotypes	Germplasms
I	**24**	13434, 13484, 13486, 13487, 13489-1, 13492, 13502, 13523, 13555, 13567, 13652, 13661, 13665, 13672, 13673, 13674, 13676, 13677, 13678, 13689, 13690, 13691, GPU-45, PR-202
II	**12**	13426, 13517, 13539, 13542, 13565, 13568, 13569, 13571, 13710, GPU-67, VL-149, VR-708
III	**1**	13651
IV	**5**	13631, 13632, 13709, 13712, 13713
V	**1**	13660
VI	**3**	13528, 13570, 13675
VII	**1**	13433
VIII	**1**	13650

Table: 4.7 Intra (diagonal) and inter clusters D value D^2 value and extent of diversity among the clusters

Clusters	I	II	III	IV	V	VI	VII	VIII
I	3.85 **(14.82)**	6.44 **(41.47)**	4.98 **(24.80)**	6.13 **(37.57)**	5.10 **(26.01)**	10.96 **(120.12)**	5.92 **(35.04)**	8.12 **(65.93)**
II		3.95 **(15.60)**	9.45 **(89.30)**	8.23 **(67.73)**	9.17 **(84.08)**	6.60 **(43.56)**	9.42 **(88.73)**	12.21 **(149.08)**
III			0.00 **(0.00)**	6.95 **(48.30)**	4.16 **(17.30)**	14.07 **(197.96)**	6.00 **(36.00)**	5.98 **(35.76)**
IV				4.45 **(19.80)**	6.49 **(42.12)**	12.04 **(144.96)**	6.80 **(46.24)**	6.40 **(40.96)**
V					0.00 **(0.00)**	13.69 **(187.41)**	5.74 **(32.94)**	6.29 **(39.56)**
VI						4.92 **(24.20)**	14.32 **(205.06)**	16.44 **(270.27)**
VII							0.00 **(0.00)**	7.24 **(52.41)**
VIII								0.00 **(0.00)**

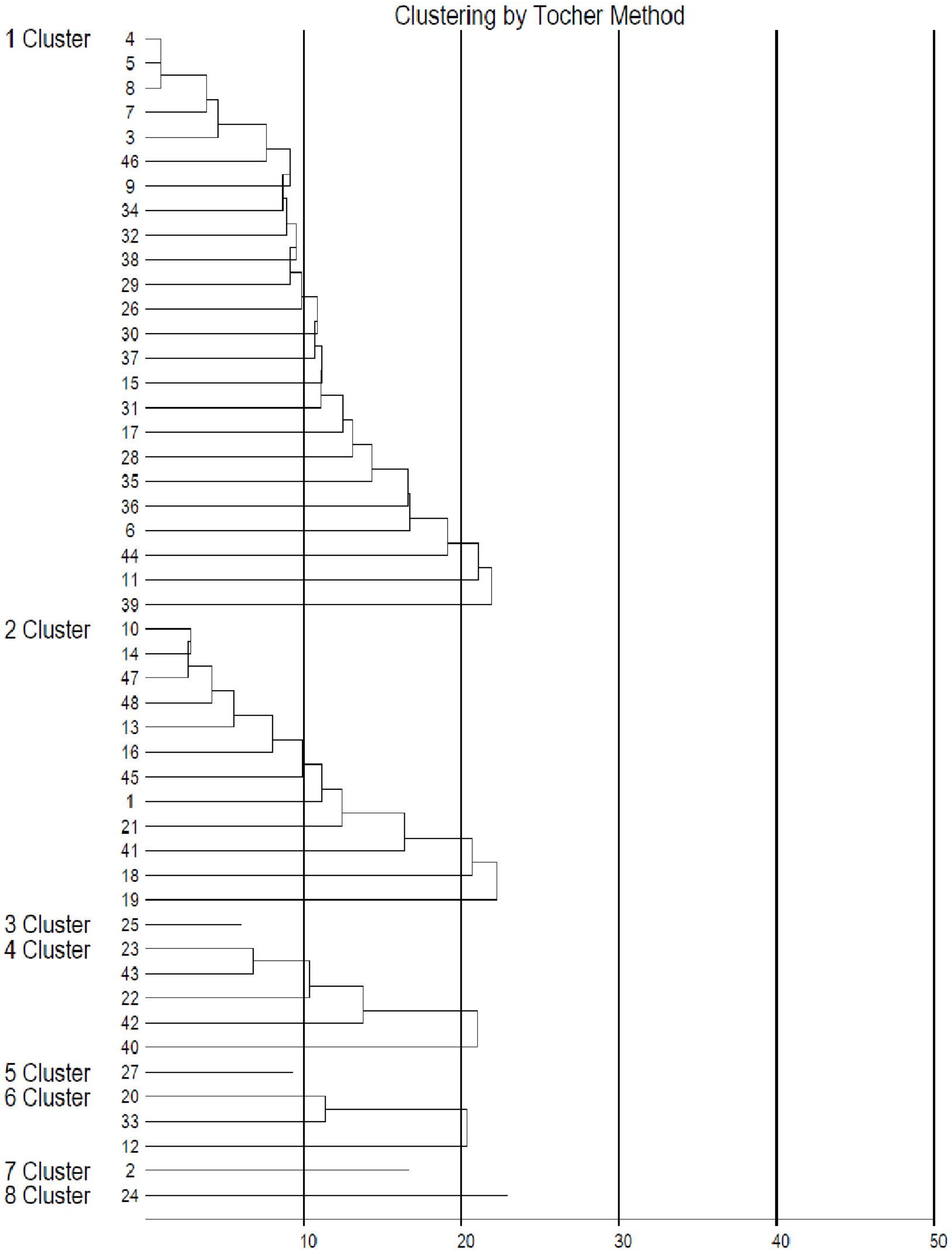

Fig.4.1 Grouping of genotypes into various clusters

From the inter cluster D^2 values of the eight clusters, it can be seen that the highest divergence occurred between cluster VI and VIII (270.27), followed by cluster II and VIII (149.08), cluster I and VIII (65.93), cluster VII and VIII (52.41), cluster IV and VIII (40.96), cluster V and VIII (39.56) and cluster III and VIII (35.76).

The inter-cluster D^2 values ranged widely with minimum value of 14.82 between clusters I and V and maximum value of 270.27 between clusters VI and VIII indicating high diversity among the genotypes of these clusters. The maximum amount of heterosis is expected from the crosses with parents belonging to the most divergent clusters has been reported by Kumar *et al.* (2010), Anantharaju and Meenakshiganesan (2008), and Kadam (2008). Hence, it is desirable to select the genotypes from the cluster showing high inter-cluster distance in breeding programme for obtaining the desirable segregants.

The inter-cluster distances were higher than the intra-cluster distances indicating the presence of wider genetic diversity between the clusters rather than within the clusters.

4.6.5 Cluster means of the characters

The cluster means for each of eleven characters are presented in Table 4.8. From the data it can be seen that considerable differences existed for all the characters under study. The data indicated that the cluster mean for plant height was highest in cluster VII (90 cm) and the lowest in cluster V (28.33 cm). No. of basal tillers per plant was highest in cluster VIII (16) and lowest in cluster VII (6.67). No. of leaves on the main tiller was highest in cluster VII (10.67) and lowest in cluster IV (7.67). A productive tiller per plant was highest in cluster VIII (17.67) and lowest in cluster VII (6.33). Cluster VII recorded the highest main ear length (13.33 cm) and the lowest was recorded in the cluster III (6.33 cm). Main ear width was highest in cluster IV (15.00 cm) and lowest in cluster III (5.33 cm). Finger length was recorded highest in cluster VII (10.67 cm) and lowest in cluster III (5.00 cm). Cluster VI recorded highest finger width (1.00 cm) and the lowest was recorded in the cluster III (0.81 cm). Total finger on the main ear was highest in cluster VII (10.00) and lowest in cluster VIII (6.33). Grain yield per plant was highest in cluster VI (86.22) and lowest in cluster

VIII (8.33). Grain yield per plot was highest in cluster VI (2653.33) and lowest in cluster VIII (250). The result indicates that selection of genotypes having high values for particular trait could be made and used in the hybridization programme for improvement of that character.

It is observed that no cluster contained at least one genotype with all the desirable traits, which ruled out the possibility of selecting directly one genotype for immediate use. Therefore, hybridization between the selected genotypes from divergent clusters is essential to judiciously combine all the targeted traits.

Genotype groups into cluster VIII were low yielder for grain yields per plant associated with very low grain yield per plot. Genotype groups in cluster III were low grain yielder, main ear length, main ear width, finger length and finger width. These results have been reported by Kumar *et al.* (2010) and Reddy *et al*. (1993).

4.6.6 Relative contribution of characters towards genetic divergence

The number of times that each of the eleven characters appeared in first rank and its respective per cent contribution towards genetic divergence is presented in Table 4.9. The results showed that the contribution of grain yield per plant was highest towards genetic divergence (61.88%) by taking 698 times ranking first, followed by main ear width (14.54%) by 164 times, total no. of basal tillers per plant (10.28%) by 116 times, total fingers on the main ear (3.63%) by 41 times, finger width (3.10%) by 35 times, main ear length (1.95%) by 22 times, plant height (1.42%) by 16 times, no. of leaves on the main tiller (1.24%) by 14 times, productive tillers per plant (0.89%) by 10 times, finger length (0.71%) by 8 times and grain yield per plot (0.35%) by 4 times, respectively to the genetic divergence in decreasing order.

Among the 11 quantitative characters studied the most important character contributing to the divergence was grain yield per plant followed by main ear width, total no. of basal tillers per plant, total no. of fingers on the main ear, finger width, main ear length, plant height, no. of leaves on the main tiller, total productive tillers per plant, finger length, grain yield per plot. These results are having conformity with the findings of Jylal and Haider (1994), Kumar (1995), Anantharaju and Meenakshiganesan (2008).

In order to select genetically diverse genotypes the material should be screened for the important traits *viz*., grain yield per plant, main ear width, total no. of basal tillers per plant, total no. of fingers on the main ear, main ear length and plant height.

TABLE: 4.8 Mean values of clusters for 11 characters in 48 finger millet germplasm (Tocher's method)

Cluster	Plant height (cm)	No. of basal tillers/ plant	No. of leaves on the main tiller	Productive tillers /Plant	Main ear length (cm)	Main ear width (cm)	Finger length (cm)	Finger width (cm)	Total fingers on the main ear	Grain yield/ plant (g)	Grain yield/plot (g)
I	66.19	10.33	8.08	9.72	7.39	6.88	6.01	0.95	8.93	28.29	857.64
II	76.97	9.58	8.50	9.31	7.96	7.54	6.14	0.97	9.25	55.89	1700.28
III	64.67	13.33	8.67	13.33	**6.33**	**5.33**	**5.00**	**0.81**	8.67	12.00	360.00
IV	69.60	13.13	**7.67**	13.00	10.07	**15.00**	9.60	0.95	8.33	31.73	971.33
V	**28.33**	11.00	8.00	7.67	7.67	7.00	6.00	0.82	7.33	12.00	360.00
VI	73.67	13.00	9.00	13.00	8.00	7.11	6.56	**1.00**	8.00	**86.22**	**2653.33**
VII	**90.00**	**6.67**	**10.67**	**6.33**	**13.33**	10.33	**10.67**	0.94	**10.00**	9.33	320.00
VIII	54.67	**16.00**	9.00	**17.67**	11.00	14.00	8.67	0.92	**6.33**	**8.33**	**250.00**

Table: 4.9 Contribution of each 11 quantitative characters to the divergence

S.NO	CHARACTER	TIMES RANKED	CONTRIBUTION %
1	**Plant height(cm)**	16	1.42
2	**No. of basal tillers/plant**	116	10.28
3	**No. of leaves on the main tiller**	14	1.24
4	**Productive tillers/ Plant**	10	0.89
5	**Main ear length(cm)**	22	1.95
6	**Main ear width(cm)**	164	14.54
7	**Finger length(cm)**	8	0.71
8	**Finger width(cm)**	35	3.10
9	**Total no. of fingers on the main ear**	41	3.63
10	**Grain yield/plant(g)**	698	61.88
11	**Grain yield/plot(g)**	4	0.35

Chapter V

Summary and Conclusions

Chapter V

SUMMARY AND CONCLUSIONS

The present investigation was carried out at National Bureau of Plant Genetic Resources, Regional station, Rajendranagar during *kharif* 2013 with 48 finger millet germplasm lines to study the genetic variability, heritability, genetic advance as per cent of mean, character association path coefficient analysis and genetic divergence. The data was recorded on 11 characters *viz.,* plant height (cm), no. of basal tillers per plant, no. of leaves on the main tiller, no. of productive tillers per plant, main ear length (cm), main ear width (cm), finger length (cm), finger width (cm), total fingers on the main ear, grain yield per plant (g) and grain yield per plot (g) and subjected to statistical analysis for drawing valid conclusions.

The material chosen differed in their genotypic make up as evidenced by the significant differences among them in respect of all the quantitative characters studied. Phenotypic coefficient of variation estimates were slightly higher than the genotypic coefficient of variation for all the traits indicating low environmental influence on the expression of all the traits. High GCV and PCV values were observed for grain yield per plot followed by grain yield per plant, no. of basal tillers per plant, productive tillers per plant, main ear width and finger length. High heritability coupled with high genetic advance as per cent of mean was observed for plant height, no. of basal tillers per plant, no. of productive tillers per plant, main ear length, main ear width, finger length, grain yield per plant and grain yield per plot. Thus, these traits are predominantly under the control of additive gene action and hence these characters can be improved by simple selection. Moderate heritability with high genetic advance was recorded for total no. of fingers on the main ear and moderate heritability with moderate genetic advance was recorded for total no. of leaves on main tiller and finger width. These traits appear to be under the control of both additive and non-additive gene actions.

Character association studies revealed that the characters grain yield per plant showed significant positive association with no. of basal tillers per plant, no. of leaves on the main tiller, productive tillers per plant, main ear length, finger width, total fingers on the main ear grain yield per plot and plant height. This indicated that simultaneous selection of all these characters was important for yield improvement.

Path coefficient analysis revealed that grain yield per plot exerted the highest positive direct effect on grain yield per plant, followed by finger width, plant height and along with significant positive correlation for all the above mentioned characters. A critical analysis of correlation and path analysis indicated that emphasis should be directed towards selection of parents having highest grain yield per plot, finger width, and plant height.

Among the 11 quantitative characters studied the most important character contributing to the divergence was grain yield per plant followed by main ear width, total no. of basal tillers per plant, total no. of fingers on the main ear, finger width, main ear length, plant height, no. of leaves on the main tiller, total productive tillers per plant, finger length and grain yield per plot. In order to select genetically diverse genotypes the material should be screened for the important traits *viz*., grain yield per plant, main ear width, total no. of basal tillers per plant, total no. of fingers on the main ear, main ear length and plant height.

Divergence studies through D^2 statistic indicated the presence of substantial diversity by forming large number of clusters with wide range of inter-cluster distances. The multivariate analysis revealed that forty eight genotypes were distributed into 8 clusters. Out of eight clusters, cluster I was the largest comprising of twenty four genotypes followed by clusters II with twelve genotypes, cluster IV with five genotypes, cluster VI with three genotypes and clusters III, V, VII, and VIII with one genotype each. The clusters III, V, VII and VIII were represented by single genotype indicating high degree of heterogeneity among the genotypes.

Intra cluster D^2 values ranged from zero (cluster III, V, VII, VIII) to 24.20 (cluster VI). Maximum intra cluster distance was observed in cluster VI (24.20), followed by cluster IV (19.80), cluster II (15.60) and cluster I (14.82). The intra cluster distance varied from a maximum 24.20 for cluster VI to minimum 14.82 for cluster I having 4 genotypes though it was zero for solitary clusters (III, V, VII, and VIII) (Table 4.9). This reveals that genotypes occupying the same cluster have low level of diversity and selection of parents with in the cluster may not be considered promising. From the inter cluster D^2 values of the eight clusters, it can be seen that the highest divergence occurred between cluster VI and VIII (270.27), followed by cluster II and VIII (149.08), cluster I and VIII (65.93), cluster VII and VIII (52.41), cluster IV and VIII (40.96), cluster V and VIII (39.56) and cluster III and VIII (35.76).

The inter-cluster D^2 values ranged widely with minimum value of 14.82 between clusters I and V and maximum value of 270.27 between clusters VI and VIII indicating high diversity among the genotypes of these clusters. The maximum amount of heterosis is expected from the crosses with parents belonging to the most divergent clusters.

The data indicated that, the cluster mean for finger width, grain yield per plant and grain yield per plot was highest in cluster VI. Plant height, no. of leaves on the main tiller, main ear length, finger length and total fingers on the main ear are highest in cluster VII. No. of basal tillers per plant and no. of productive tillers per plant was recorded highest in cluster VIII. Cluster IV recorded the highest main ear width.

High grain yield per plant is recorded in the clusters of VI, II and IV. Genotype included in cluster VI is having highest mean value for grain yield per plant, finger width and grain yield per plot. Cluster IV is having highest mean value for main ear width. The genotypes 13570, 13675 and 13528 (VI), 13569 and 13568 (II) were having high mean values for grain yield per plant may be directly used for adaptation or may be used as parents in future hybridization programme.

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