GENETIC DIVERSITY STUDIES IN LITTLE MILLET (*Panicum sumatrense* L.)

THESIS

Submitted in partial fulfilment of the requirements for the Degree of

MASTER OF SCIENCE
IN
AGRICULTURE
(GENETICS AND PLANT BREEDING)

By

SARAK KOMAL SHIVAJI
(ADPM/20/2746)

DEPARTMENT OF AGRICULTURAL BOTANY
COLLEGE OF AGRICULTURE, DAPOLI

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NOVEMBER, 2022

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Under the Guidance of

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NOVEMBER, 2022

DECLARATION OF STUDENT

I hereby declare that the experimental work and its interpretation of the Thesis entitled **"Genetic diversity studies in Little millet (*Panicum sumatrense* L.)"** or part thereof has neither been submitted for any other degree or diploma of any University, nor the data have been derived from any thesis / publication of any University or scientific organization. The source of materials used and all assistance received during the course of investigation have been duly acknowledged and that no part of the thesis has been submitted for any other degree or diploma.

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CERTIFICATE

This is to certify that the thesis entitled, **"Genetic diversity studies in Little millet (*Panicum sumatrense* L.)"** submitted for the degree of M. Sc. (Agri.) in Genetics and Plant Breeding, of the College of Agriculture, Dr. Balasaheb Sawant Konkan Krishi Vidyapeeth, Dapoli, is a bonafide research work carried out by **Miss. Sarak Komal Shivaji (ADPM/20/2746)** under my supervision and that no part of this thesis has been submitted for any other degree. The student had completed all the Course and Research requirement as per the norms in regular mode and has submitted one research paper from her M.Sc.work.

The assistance and help received during the course of investigation have been fully acknowledged.

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Date: / /2022

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THESIS APPROVAL BY THE STUDENT'S ADVISORY COMMITTEE INCLUDING EXTERNAL EXAMINER

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Place: Dapoli

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LIST OF ABBREVIATIONS

%	:	Percentage
*	:	Significant at 5% level of significance
**	:	Significant at 1% level of significance
ha	:	hectare
i.e.	:	That is
cm	:	Centimeter
d.f.	:	Degree of freedom
Viz.,	:	Namely
°C	:	Degree Celsius
et al.	:	And others
Kg	:	Kilogram
g	:	Grams
N	:	Nitrogen
P_2O_5	:	Phosphorus
K	:	Potassium
RBD	:	Randomized block design
@	:	At the rate of
m	:	Meter
C.D.	:	Critical Difference
EMSS	:	Error mean sum of squares
MSS	:	Mean sum of squares
Err.	:	Error
S.E.	:	Standard error
Sig.	:	Significant
mg	:	Milligram
<	:	Less than
>	:	Greater than
=	:	Equal to
Fig.	:	Figure
GA	:	Genetic advance
G.A.M.	:	Genetic advance as per cent of mean
G.C.V.	:	Genotypic coefficient of variation
P.C.V.	:	Phenotypic coefficient of variation
h^2	:	Heritability
mm	:	millimeter
$\sigma^2 p$	:	Phenotypic variance
$\sigma^2 g$	:	Genotypic variance
$\sigma^2 e$	:	Environmental variance

GLOSSARY

Genetic variability: Genetic variability is either the presence of, or the generation of, genetic differences.

Heritability: Heritability is the amount of phenotypic (observable) variation in a population that is attributable to individual genetic differences.

Genotype: Genotype is the genetic makeup of an individual cell or organism that determines or contributes to its phenotype.

Genetic advance: Genetic advance is a measure of how much gain you may get from phenotypic selection for a trait.

Path analysis: Path analysis is a method to discern and assess the effects of a set of variables acting on a specified outcome via multiple causal pathways.

Genetic diversity: Genetic diversity is the biological variation that occurs within species.

Konkan: Konkan is the 700 km long rugged section of the western coastline of Arabian Sea which extends from Damon in the North to western side land of Maharashtra and Goa.

CHAPTER I : INTRODUCTION

1.1 Background Information

Little millet (*Panicum sumatrense* L.) is one of the most important millet. It belongs to the family poaceae and sub family panicoideae. In India it is commonly known as sama, samo, morai, vari and kutki. It is self-pollinated crop and having basic chromosome number 9 (tetraploid=2n=4x=36). Little millet is a cereal that is commonly grown in India, Nepal, Burma, Sri Lanka, Pakistan, Japan, China, Egypt, Arabia, Western Europe, and Southeast Asia. Little millet is fast growing, early maturing crop resistant to adverse agro climatic conditions. The crop is adapted to both dry and humid conditions and can be cultivated in drought-prone areas as well as water-logged conditions, as the crop matures early and withstands adverse conditions. It is an annual herbaceous plant that grows to a height of approximately 80 cm to 160 cm with straight or folded blades. The leaves have hairy laminae. The length of panicles ranged from 10 to 50 cm and have a 2 to 3.5 mm long awn. The grain is smooth and circular, measuring 1.8 to 1.9 mm in length. Grain shape is elliptical to oval shape and its colour vary from grey to straw white.

Small millets being cultivated in India on an area of 6,19,000 ha. with production of 4,41,000 tonnes (Gowari and Shivkumar, 2020). In Maharashtra small millets occupied an area of about 36,962 ha with a production of 16,720 tonnes and the productivity level is 452 kg/ha, while area under small millets in Konkan region is 8,431 ha with production of 4500 tonnes and productivity is 530 kg/ha (Anonymous, 2021). Though small millets are grown in almost every state/region, the distribution of individual millet is not uniform. Little millet is small seeded grain used as food, feed and fodder which is most popular as fasting food because of its high surplus value and better mineral composition. Value added products are developed by processing of seeds. Little millet contains carbohydrate (60-75 g), crude fiber (4-8 g), protein (7-10 g) calcium (12-30 mg) and iron (7-13 mg) per 100 g which is more nutritious as compare to other cereals. (Himanshu *et al.*, 2018). It has nearly 2.5 times minerals, nearly 38 times fiber and nearly 13 times iron than rice and has abundant quantities of Thiamin (vit-B1). In some countries it is also cultivated as green fodder crop. As like Sorghum, it does not contain HCN so it is more palatable as green fodder purpose.

1.2 Importance and need of the study

Little millet can be grown in tropical and subtropical climates and it is well known for its drought tolerance capacity. It is considered as one of the least water demanding crop and it is suitable for late sowing, rain fed condition, drought tolerant, multiple and contingent cropping system. Compared to other small millets and staple food crops like rice and wheat, little millet

contains fairly good amount of iron. It is an important dependable climate resistance small seeded crop grown by tribal and poor farmers for their own consumption. It is wonderful millet which is suitable for people of all age group. It helps to prevent constipation and heals all the problems related to stomach. Good source of energy, protein, fiber and minerals. It helps to prevent breast cancer, type 2 diabetes, helps to protect against heart disease. Effective in reducing blood pressure, aids in treating respiratory conditions such as asthma. Due to its nutritional value farmers will fetch high price in market.

Variability arises as a result of variances in the genetic makeup of people in a group or changes in the environment in which they are raised. Knowledge of genetic variability in respect of yield structure in any species is valuable in plant breeding programme. It helps in choice of the best yield attributes either for selection or hybridization. This may be achieved by estimating the genetic parameters *viz*; GCV, PCV heritability and genotypic advanced for grain yield and its component characters. Correlation studies are helpful in determine the components of complex traits like yield. But they do not provide direct & indirect influenced of each of component characters towards the yield. Although, path coefficient analysis is helpful to recognize direct and indirect causes of correlation and also enables us to compare the causal factors on the genetic basis of their contribution. While genetic diversity is the base for crop genetic enhancement and important for the conservation, evaluation, and utilization of crop germplasms. little millet is the least studied among the small millet species and only two reports are available on the genetic diversity of Indian little millet (*Panicum sumatrense*) on the basis of morphological traits (Arunachalam *et al*., 2003; Selvi *et al*., 2015). The choice of the parents plays a more significant role in breeding programmes. It is crucial to examine a significant number of germplasm samples for genetic diversity. It is key to choose a variety of genotypes while conducting a hybridization programme. Genetic diversity is an important factor and also an essential in any hybridization programme.

1.3 Objectives of study

Keeping in view the above important aspects, the present investigation will carried out following objectives.

1. To estimate genetic variability among different genotypes of little millet for yield and yield components.
2. To study magnitude of direct and indirect effects on important yield components through path analysis.
3. Measurement of divergence between different genotypes by D^2 statistics.

1.4 Hypothesis

The genetic diversity of this crop is very little because of its restricted cultivation in India, Sri Lanka, Nepal, and Myanmar, with India accounting for more than 98% of the area and production of little millet. This research will help to utilize information relative to genetic variability, heritability and genetic advance for different traits. Correlation and path analysis will serve path for future breeding programme by determining the interrelationship among yield and its contributing characters in little millet.

1.5 Scope and limitation

This crop received little research attention in the past years and continued to be an ignored and underutilized crop. The potentiality of little millet is not yet exploited properly in India. Genetic variability studies provide basic information regarding the genetic properties of the population based on which breeding methods are expressed for further improvement of the crop. (Shingane *et al*., 2016). Genetic diversity is another important parameter helps in development of genotypes and gives idea about genetically distance among the genotypes under study. The knowledge of characters influencing divergence is an important aspect for a plant breeder. Information on the nature and degree of divergence would help the plant breeder to choose right parents for breeding programs.

Being a minor millet, crop is totally ignored due to lack of awareness about their nutritional values. The yield potential of little millet is low due to lack of improved varieties. Land is not more under this crop because of negligence of farmer and among the society. The production of this crop is low mainly due to farmers not used improved package of practices and varieties. The land under this crop goes on decreasing.

Considering the growing awareness among the consumers regarding the health benefits of little millet, it was essential to study genetic diversity in little millet to develop a variety having good yield potential and nutrient content. Genetic diversity is an important factor and also a prerequisite in any hybridization programme. Therefore, the present study entitled **"Genetic diversity studies in Little millet (*Panicum sumatrense* L.)"** was undertaken at the Education and Research farm, Department of Agriculture Botany, College of Agriculture Dapoli, Dr. B.S. Konkan Krishi Vidyapeeth, Dapoli during the *Kharif* , 2021.

CHAPTER II : REVIEW OF LITERATURE

The present study had undertaken to evaluate variability, diversity, genotypic and phenotypic correlation coefficient, path analysis for yield and yield attributing characters in 44 genotypes of little millet. The relevant literatures related to various aspects of present study entitled "**Genetic diversity studies in Little millet (*Panicum sumatrense* L.)**" are reviewed under the following heads.

2.1. To estimate genetic variability among different genotypes of little millet for yield and yield components.

2.2. To study magnitude of direct and indirect effects on important yield components through path analysis.

2.3. Measurement of divergence between different genotypes by D^2 statistics.

2.1 To estimate genetic variability among different genotypes of little millet for yield and yield components.

The degree of improvement of a character would depend mainly on the amount of variability in the population where selection has to be made. Hence the study of inheritance of various developmental and productive characters through the estimation of different genetic parameters like components of variances, genotypic and phenotypic coefficient of variability, heritability and genetic advance is helpful for outlining the effective breeding programme.

Nirmalakumari *et al*. (2010) studied 109 Little millet germplasm. Grain yield, number of productive tillers per plant, flag leaf width and flag leaf sheath length all had high estimates of variability, high heritability and strong genetic advance, which suggested additive gene effects on these traits. For yield potential, phenotypic selection based on these traits may be useful.

Subramanian *et al.* (2010) evaluated 188 genotypes of kodo millet to calculate genetic variability, heritability and genetic advance for eight yield component traits. ANOVA was significant for all the characteristics, observed widest range of variance was for the number of productive tillers per plant (5.30 to 13.30). Heritability estimates were found to be high in general for the traits fodder yield (97%), plant height (95%), seed yield per plant (89%), inflorescence length (73%), and longest raceme length (69%).

Govindaraj *et al*. (2011) evaluated the local pearl millet germplasm accessions the phenotypic co-efficient of variation (PCV) was greater than genotypic co-efficient of variation (GCV) for all the characters studied; this shows the effect of environmental factors on the characters. The magnitudes of phenotypic and genotypic variances were low for the 1000 grain

weight whereas high estimates of genetic co-efficient of variation, heritability and genetic advance were presented by iron and crude fat content.

Patil *et al*. (2013) conducted an experiment to evaluate genetic variability for yield and yield contributing characters among 11 genotypes of finger millet. Reported that high GCV and PCV for number of productive tillers and fodder yield per plot and for the trait main ear length found high heritability (93.5%) estimates. Panicle weight, fodder yield per plot, and the number of productive tillers per plant all showed high heritability and strong genetic advance as a per cent of the mean, demonstrating additive gene action for these variables and the benefit of phenotypic selection based on these parameters.

Wolie *et al*. (2013) examined 88 finger millet genotypes. The high genotypic coefficient of variation (GCV) was recorded for number tillers per plant (71.93), number of ears per plant (96.55), number of fingers per ear (85.48), finger length (94.48), biomass yield (87.67), and grain yield (78.17), while high phenotypic coefficient of variation (PCV) was similarly recorded for number tillers per plant (30.42), number of ears per plant (45.55), number of fingers per ear (24.88), finger length (26.18), biomass yield (85.56), and grain yield (29.87).

Choudhary *et al*. (2014) studied 35 genotypes of finger millet found that the phenotypic and genotypic variability were high for days to 50 per cent flowering, days to maturity, plant height and straw yield whereas it is medium for the trait's total fingers per plant and grain yield. The low estimates were found for number of tillers per plant, number of productive tillers per plant, fingers per main ear, ear head length and test weight.

Selvi *et al*. (2014) studied 105 little millet genotypes. The results were showed that high genotypic and phenotypic coefficients of variation were detected for panicle length, straw yield per plant, culm branches per plant, flag leaf width, grain yield and number of tillers per plant. Hence, selection at phenotypic level for these characters would be effective.

Geethanjali *et al*. (2016) carried out an investigation in 51 genotypes of foxtail millet (*setaria italica* L.) observed that grain yield per plant had the greatest variance, with a CV of 22.5 per cent, whereas days to 50% flowering and plant height had the least variation, with CVs of 7.2 per cent and 9.3 per cent, respectively.

Jyothsna *et al*. (2016) studied 25 genotypes of little millet genotypes. Found that genotypic coefficient of variation was lesser than the corresponding phenotypic coefficient of variation which indicate that interaction of genotypes with environment. The characters grain yield per plant and straw yield per plant had high heritability coupled with high genetic advance.

Shingane *et al.* (2016) examined 44 genotypes of foxtail millet. They identified that genotypic and phenotypic coefficients of variation were high for number of productive tillers per plant, number of panicles per plant, grain yield per plant, straw yield per plant and iron content. High genetic advance as per cent of mean with high estimates of broad sense heritability showed that, the variation observed for most of the characters were heritable and selection would be productive for development of these characters.

Anuradha *et al*. (2017) study the genetic variability, heritability and correlation of grain yield and yield related traits of little millet. Significant variation was found for all the studied characteristics in the analysis of variance of 30 genotypes of little millet. There was evidence that the number of tillers per plant, panicle length, and fodder yield were all significantly and positively correlated with grain yield. The results were showed that yield and other associated parameters exhibit high heritability and considerable variability that may be used for little millet improvement.

Kavya *et al*. (2017) evaluated 40 genotypes of foxtail millet. In the present investigation, high heritability together with high genetic advance as per cent of mean was observed for no. of productive tillers, no. of culm branches, panicle length, ear length, ear width, 1000 seed weight, seed yield/plant, straw yield per plant and protein content.

Sao *et al*. (2017) conducted research on kodo millet genotypes. The coefficient of variation at phenotypic and genotypic levels were high for fodder and grain weight whereas moderate for number of tillers and length of panicles. The low estimates were of PCV and GCV were observed in the characters like days to maturity, number of panicles, days to 50% flowering and plant height.

Negi *et al*. (2017) studied morphological characterization and genetic analysis of 35 finger millet germplasm. All 35 genotypes showed highly significant differences in the analysis of variance, with a broad range of mean values for several characters. The biological yield per plant had the most genetic and phenotypic variation, followed by plant height, days to 50% flowering and harvest index. For all of the traits analysed, a high estimate of heritability in the broad sense was reported.

Thakur *et al*. (2018) analysed genetic parameters for yield and yield contributing characters of thirty three Kodo millet genotypes Maximum range of variation was recorded for Panicle length (4.55 cm to 8.50 cm). High genetic advance as per cent of mean was recorded for number of productive tillers per plant (56.05%). Results were showed that high heritability coupled with high genetic advance as per cent of mean was higher for tillers per plant followed

by panicle length (cm), plant height (cm), fodder yield (g) and test weight (g), these characters were directly selected because they were under the control of additive gene action.

Patel *et al*. (2018) evaluated thirty two genotypes of little millet. The result indicated that all the sixteen characters had a wide range of variability in the different little millet genotypes. High assessment of genotypic and phenotypic variance were observed for days to 50 per cent flowering, plant height at maturity, panicle length, straw yield per plant, 1000 seed weight, protein content, ash content, fat content, Ca content, Fe content & fibre content which suggested that these characters are largely control by additive genes and selection based on these characters help in the development of yield could be satisfying.

Savankumar *et al.* (2018) examined 32 little millet genotypes and recorded that number of productive tillers per plant (4.46 to 10.82) and grain yield per plant (2.33 to 8.55gm) found wide range of variation. Days to maturity showed low range of phenotypic and genotypic coefficient of variation. High heritability with high genetic advance was observed for number of productive tillers per plant, grain yield per plant, straw yield per plant, protein content, ash content, fat content, calcium content, iron content and fiber content.

Suryanarayana *et al*. (2018) studied twenty three little millet genotypes. The characters *viz*; plant height, no. of productive tillers, days to 50 per cent flowering, days to maturity and grain yield showing highly significant differences in twenty three genotypes which indicates sufficient amount of variability among genotypes.

Dhanalakshmi *et al*. (2019) studied genetic variability and association for different morphological and yield contributing traits in 99 barnyard millet genotypes. Plant height, ear width, lower raceme length, flag leaf length, flag leaf breadth, and grain yield per plant all had high phenotypic coefficients of variation, genotypic coefficients of variation, and heritability.

Anuradha *et al*. (2020) evaluated twenty eight little millet genotypes. High phenotypic coefficient of variation was detected for grain yield and straw yield per plant whereas the trait days to 50% flowering demonstrated high heritability and genetic advance as a percentage of the mean, indicating that additive gene action is the primary cause of this phenomenon.

Nagar *et al*. (2020) conducted experiment on twenty little millet genotypes and characters days to maturity, plant height, tillers/plant, flag leaf length, peduncle length, and 1000 grain weight showed a higher magnitude of PCV and GCV, whereas the characters days to maturity, plant height, tillers/plant, flag leaf length, peduncle length, and 1000 grain weight showed a moderate value of GCV and PCV.

2. To study magnitude of direct and indirect effects on important yield components through path analysis.

Yield is a complex dependent character and is funded by several component characters. Path analysis detects the yield components which directly and indirectly influence the yield. Hence help to find out strategies for better selection of quantitative traits for building up the ultimate yield.

Baghel and Maloo (2004) evaluated the thirty four diverse genotypes of proso millet (*Panicum miliaceum* L.). Reported that maximum direct effect were recorded for main panicle length followed by main panicle weight and 1000 seed weight.

Anuradha *et al*. (2013) calculated character association and path analysis in twenty finger millet accessions belonging to late maturity group. Path analysis showed that number of fingers per ear (-0.1983) exhibited negative indirect effects through ear length at both levels.

Kumar *et al*. (2014) analysed 140 genotypes of finger millet and observed direct effect on productive tillers per plant, biological yield, harvest index, and number of fingers per ear.

Jadhav *et al*. (2015) studied finger millet genotypes and recorded that the traits 1000 seed weight, number of fingers per ear, days to maturity, ear weight per plant, finger length and days to 50% flowering showed significant positive association and high positive direct effect.

Prakash *et al*. (2015) estimated 65 genotypes of barnyard millet and detected positive direct effect of ear head length (0.4777) and plant height (0.281) on the grain yield per plant.

Negi *et al.* (2016) studied path analysis of 34 genotypes of finger millet and discovered that characters like flag leaf area, number of productive tillers per plant, number of leaves per plant, thousand grain weight and number of grains per panicle (0.16) had high positive direct effect on grain yield.

Devaliya *et al*. (2017) evaluated 68 genotypes of finger millet (*Eleusine coracana* L.) and the results were showed that days to 50% flowering, straw yield per plant, thousand grain weight, and protein content had a positive direct effect on grain yield per plant.

Amaranath *et al*. (2018) examined that plant height (0.3455, 0.4585), panicle length (0.2388, 0.4606) and thousand seed weight (0.2577, 0.3021) had positive significant association with grain yield per plant at both phenotypic and genotypic levels.

Gohel *et al*. (2018) investigated 30 different genotypes of finger millet. The study revealed that grain weight per main ear (0.534) had the highest direct positive effect on grain yield followed by number of productive tillers per plant (0.353), panicle length (0.166), days to

flowering (0.133), harvest index (0.124), biological yield per plant (0.081), leaf blade length (0.011).

Suryanarayana *et al*. (2018) studied 23 genotypes of little millet. Productive tillers per plant show significant correlation with grain yield at both genotypic as well as phenotypic level. Number of productive tillers had the maximum effect on grain yield than plant height.

Shinde *et al*. (2018) carried out an experiment to study path analysis using sixty genotypes of little and found that grain yield per plant was significantly and positively correlated with ear head length, no. of ear heads per plant, no. of productive tillers per plant, thousand grain weight and fodder yield per plant.

Chavan *et al*. (2019) conducted experiments on thirteen genotypes of finger millet. The results were showed that path coefficient analysis was exerted by harvest index (%) followed by straw yield per plant (g), number of fingers per ear, number of tillers per plant, plant height which had highest direct effects on grain yield per plant at genotypic level and phenotypic level.

Venkataratnam *et al*. (2019) evaluated 50 little millet genotypes and recorded that harvest index, number of productive tillers per plant, leaf area index at panicle initiation, panicle weight, panicle length, thousand seed weight showed maximum positive effect on grain yield per plot.

Sneha *et al*. (2019) described positive significant correlation of number of productive tillers per plant (0.759, 0.831) with grain yield per plant at both phenotypic and genotypic levels, among 40 genotypes of finger millet.

Lad *et al.* (2020) tested 50 finger millet genotypes and reported that days to 50% flowering, days to maturity, productive tillers per plant, plant height, length of finger, 1000-seed weight, ear weight per plant, fingers per ear, fodder output per plant, and harvest index all had positive and significant correlation with grain yield per plant.

Nagar *et al*. (2020) identified 20 genotypes of little millet (*Panicum sumatrense*) indicated that grain yield/plant showed highly significant and positive phenotypic correlation with harvest index, length of inflorescence, biological yield/plant and peduncle length.

Laxmi *et al.* (2020) evaluated forty genotypes of foxtail millet and reported that days to 50% flowering, panicle length, peduncle length, biological yield, harvest index, and test weight showed positive direct effect on grain yield per plant at phenotypic level.

3. Measurment of divergence between different genotypes by D^2 statistics.

Many breeding efforts have been carried out to increase the yield of this crop. Genetic diversity is an important aspect and also an essential in any hybridization programme.

Shinde *et al.* (2013) studied 41 genotypes of finger millet were grouped into seven clusters. Clusters II, I, V, VI, and III, respectively, included 17, 10, 7, 3, and 2 genotypes. Clusters IV and VII were mono-genotypic, suggesting that they were very different from the others. Clusters II and VII had the greatest inter-cluster distance, followed by IV and VII, suggesting that genotypes from these clusters might be used as possible parents for hybridization.

Kumari *et al*. (2015) examined divergence among 35 genotypes of finger millet using Mahalanobis D^2statistics. The 35 genotypes were divided into six groups, with clusters IV and VI displaying the highest levels of genetic variety. Maximum genetic divergence was caused by days to 50% flowering and grain yield per plant.

Selvi *et al*. (2015) analysed thirty little millet genotypes established 20 definite clusters with high inter cluster distances. Cluster mean confirmed the result of divergence analysis. Genotypes in cluster XX had the highest mean value for all the desirable attributes. The intra cluster distance was the highest in cluster X (17.6). The highest inter cluster distance was noticed between clusters V and XX (210.5).

Ulaganathan *et al.* (2015) categorised the 305 finger millet genotypes using multivariate traits. 305 genotypes were divided into 16 clusters using multivariate hierarchical clustering in cluster analysis. Clusters VII, X, XIII, and XVI formed solitary clusters and showed that these accessions had a wide range of character variability.

Gangurde *et al*. (2016) studied 66 foxtail millet genotypes. Cluster I, with 36 genotypes, had the highest number of entries, followed by Cluster II, which had 15 genotypes Cluster II had the greatest intra-cluster distance, followed by Cluster III and Cluster I. Cluster IV and III had the greatest inter-cluster distance, followed by Cluster IV and V, Cluster IV and I.

Geethanjali *et al*. (2016) evaluated 51 genotypes of foxtail millet and divided into four clusters. The most relevant variables in differentiating the primary clusters of foxtail millet genotypes at the morphological level were determined to be plant height, number of tillers, days to 50% flowering, grain production per plant, and 1000 seed weight.

Mahanthesha *et al*. (2017) divided the 48 finger millet germplasm lines into eight clusters to studied the 11 quantitative traits. Cluster I had the highest germplasm lines (24), followed by cluster II with twelve germplasm lines, cluster IV with five germplasm lines, cluster VI with three genotypes, and cluster III, V, VII, and VIII with one each. Cluster VI has the greatest intra-cluster distance. The greatest difference was found between clusters VI and VIII, whereas the smallest was found between clusters I and V.

Nirubana *et al*. (2017) was conducted experiment to evaluate genetic divergence among the 103 kodo millet germplasm using Mahalanobis D^2 statistic and grouped into 11 different clusters. Cluster I had a maximum of 63 genotypes, followed by clusters II and III with 14 each, cluster X with four genotypes and cluster VIII with two genotypes. Remaining clusters IV, V, VI, VII, IX and XI were mono-genotypic indicating wide divergence from other clusters.

Sarjansinh *et al.* (2017) examined sixty eight genotypes of finger millet for studying genetic divergence for yield and its traits. They are grouped into eight clusters among that maximum inter cluster distance was observed in cluster VIII and cluster III which suggest use of these distinct clusters for hybridization to increase the productivity of finger millet.

Patel *et al*. (2018) investigated genetic diversity in little millet genotypes. They grouped 32 genotypes into seven clusters and maximum diversity was observed in cluster II followed by cluster I, cluster III and cluster VII. Maximum inter cluster distance was recorded between cluster II and VI followed by cluster II and V. In their study grain yield and thousand seed weight contributed maximum to the genetic diversity.

Suryanarayana *et al*. (2018) studied twenty three genotypes of little millet for genetic diversity using Mahalanobis D^2 statistics. Considering the inter cluster distances, it was highest between cluster IV and V (163.09) followed by V and VI (145.69). Among the five-character grain yield (q/ha), days to 50 per cent flowering and plant height (cm) showed maximum total divergence and were found to be responsible for primary variation.

Thippeswamy *et al*. (2018) divided 149 germplasm of foxtail millets into 15 clusters and the maximum contribution to divergence was found for the traits 1000 seed weight (12.07%), followed by the number of productive tillers per plant (10.18%), days to maturity (8.68%), days to 50% flowering (7.03%), grain yield/hectare (6.80%), and plant height (5.74%).

Anteneh *et al*. (2019) estimated genetic diversity in 225 finger millet germplasm accessions. Five different clusters were formed from the 225 genotypes. They discovered a greater genetic distance between clusters II and III, indicating that a hybridization programme using accessions from these clusters would result in a high level of genetic diversity.

Ayesha *et al*. (2019) studied 50 foxtail millet genotypes were divided into eight groups using both D^2 analysis and Ward's technique. Cluster III, with 13 genotypes, is the biggest in D^2analysis, followed by clusters II, IV, I, VI, V, VII, and VIII.

Thakur *et al*. (2020) examined genetic divergence in kodo millet. Out of the nine characteristics studied, days to maturity contributed the most to diversity (66.29%), followed by days to 50% flowering (19.70%), fodder yield per plot (5.11%), tillers per plant (4.36%), test

weight (1.52%), and grain yield per plot (1.14%). A relatively small amount of variation was contributed by the characteristics of panicle length (0.95%), plant height (0.57%), and panicles per plant

Thakur *et al*. (2020) investigated 33 kodo millet genotypes were divided into six groups. Cluster V has the most genotypes (11), followed by Cluster IV (seven genotypes), Cluster II (six genotypes), Cluster III (four genotypes), and Cluster VI (one genotype). Cluster IV had the greatest intra-cluster difference, indicating that the genotypes present had a significant genetic distance between them. Cluster I and Cluster VI had the greatest inter-cluster difference, suggesting a significant degree of genetic diversity.

Suthediya *et al*. (2021) evaluated the genetic diversity of seventy kodo millet genotypes. Mahalanobis D2 analysis was used to arrange seventy genotypes into seven separate groups. Cluster I contained 51 genotypes, cluster II had 14, and clusters III, IV, V, VI, and VII were mono genotypic. Clusters II and III had a large inter-cluster distance, hence these genotypes should be used as parents for hybridization to generate possible segregants.

CHAPTER III: MATERIALS AND METHODS

The present investigation, entitled "**Genetic diversity studies in Little millet (*Panicum sumatrense* L.)**", was conducted at the Education and Research farm, Department of Agriculture Botany, Dapoli., Dist. Ratnagiri, during the *Kharif* , 2021. The details of the material used and the methodology adopted during the course of investigation are given in this chapter.

3.1 Materials Required

3.1.1. Inputs used

The material for the present investigation comprised of 44 genotype of little millet. The experimental material is given below in Table 3.1.

Table 3.1. Experimental material

Sr. No.	Genotype	Source
1	DPLV-1	Jawahar
2	DPLV-2	Jawahar
3	DPLV-3	Jawahar
4	DPLV-4	Jawahar
5	DPLV-5	Jawahar
6	DPLV-6	Jawahar
7	DPLV-7	Jawahar
8	DPLV-8	Jawahar
9	DPLV-9	Jawahar
10	DPLV-10	Vikramgad
11	DPLV-11	Vikramgad
12	DPLV-12	Vikramgad
13	DPLV-13	Vikramgad
14	DPLV-14	Vikramgad
15	DPLV-15	Thane
16	DPLV-16	Thane
17	DPLV-17	Talasari
18	DPLV-18	Mokhada
19	DPLV-19	Vikramgad
20	DPLV-20	Vikramgad
21	DPLV-21	Dapoli

Sr. No.	Genotype	Source
22	DPLV-22	Jawahar
23	DPLV-23	Jawahar
24	DPLV-24	Dapoli
25	DPLV-25	Dapoli
26	DPLV-26	Dapoli
27	DPLV-27	Dapoli
28	LM-1	Zonal Agricultural Research Station, Kolhapur
29	LM -2	
30	LM -3	
31	LM-4	
32	LM-5	
33	LM-6	
34	LM-7	
35	LM-8	
36	LM-9	
37	LM-10	
38	LM-11	
39	LM -12	
40	LM-13	
41	LM-14	
42	LM-15	
43	LM-16	
44	LM-17	

3.1.2 Machine and Equipment used

Machines used

- Mould bold plough
- Rotovator
- Clod crusher
- Power tiller/ tractor
- Land leveler
- Tractor and Trolley
- Kjeldahl apparatus
- Socs plus apparatus
- Atomic Absorption Spectrophotometer (AAS)
- Muffle furnace

Equipment used

- Vaibhav sickle
- Weighing balance
- Measuring scale
- Meter tape

3.2 Methodology Adopted

The experiment was conducted in the Randomized Block Design (RBD) with two replications for *Kharif,* 2021 at Education and Research farm, Department of Agricultural Botany, College of Agriculture, Dapoli, the experimental details were as below.

3.2.1 Experimental details

Table 3.2. Details of experimental plot

1	Crop	**:**	Little millet
2	Spacing	:	20 cm x 15 cm
3	Experimental design	:	Randomized Block Design (RBD)
4	No. of replications	:	2
5	No. of treatments	:	44
6	Plot size	:	0.40 X10.5 m^2
7	Row to row	:	20 cm
8	Plant to plant	:	15 cm
9	Gross row	:	2 Row
10	Row length	:	10.5 m
11	Recommended dose of fertilizer	:	40 kg N : 20 kg $P_2 O_5$
12	Season	:	*kharif* 2021
13	Date of sowing	:	23th June, 2021
14	Date of Transplanting	:	02nd Aug, 2021

3.2.2 Cultural practices

The experiment was conducted at the normal fertility level on lateritic soil. The preliminary tillage operations were carried out properly in order to bring the soil at fine tilth. The total fertilizer dose applied @40 Kg N 20 Kg P_2O_5 per hectare. Out of which half dose of nitrogen in the form of urea was applied at the time of transplanting and remaining dose nitrogen was applied one month after transplanting. The operation like gap filling was done 10 days after sowing so as to maintain one plant per hill and to maintain the plant population.

Package of practices were carried out as and when required so as to maintain good stand of crop as per the standard recommendations.

3.2.3 Observations recorded

The observations were recorded on five randomly selected plants for 16 quantitative characters and 8 qualitative characters. The mean of observation of the five plants were used for statistical analysis.

1. Days to 50 per cent flowering

Days to 50 per cent flowering were recorded on commencement of flowering in fifty per cent on plants in the plots from the date of sowing of the plot.

2. Days to maturity

The numbers of days were counted from the date of sowing to the date on which 90 per cent of the plants showed drying up, confined by the hardiness of the seeds.

3. Plant height (cm)

Plant height was measured in centimetre (cm) from base of the plant (at ground level) to the tip of the main panicle at maturity stage and calculated the average for randomly selected five plants.

4. Number of tillers plant^{-1}

At the time of maturity, number of tillers was counted from randomly selected five plants and calculated the average for those randomly selected five plants.

5. Length of panicle (cm)

The length of panicle was measured from base to the tip of panicle in centimetres at the time of maturity and calculated the average for randomly selected five plants.

6. Grain yield (kg/plot)

Grains obtained from each plot were weighed in kilograms and recorded as grain yield per plot.

7. Straw yield (kg/plot)

Straw obtained from each plot after harvest of seeds was weighed in kilograms and recorded as straw yield per plot.

8. Grain yield (q/ha)

Grain yield obtained from each plot weighed in kilograms and calculated as grain yield in quintal per hectare.

9.1000 seed weight (g)

The harvested fully filled, matured and clean dry seed of each treatment are collected. Then 1000 randomly selected grains weighted and recorded in grams.

10. Grain yield per plant (g)

Grains obtained from each selected plant were weighed in grams and recorded as grain yield per plant.

11. Straw yield per plant (g)

After harvesting of seeds straw obtained from each selected plant was weighed in grams and recorded as straw yield per plant.

12. Protein content (%)

The oven dried plant samples (0.5g each) were digested by using concentrated H2SO4 (15mL) and H2O2 (5mL). The volume was made by distilled water to 50 mL after digestion of the sample. A suitable aliquot was taken for distillation and nitrogen was determined by Kjelplus apparatus as described by Tandon (1993). The digested materials were distilled in alkaline medium (40% NaOH) and the liberated ammonia was trapped in 2 per cent boric acid solution containing mixed indicator. The trapped ammonia was titrated against standard sulphuric acid ((0.02 N). (Jackson, 1973).

$$N\ (\%) = \frac{\text{Sample reading-Blank reading x N of acid} \times 0.014 \times \text{Vol. of digested}}{\text{Wt. of sample} \times \text{Aliquot taken}} \text{ X100}$$

Protein (%) = %N X 6.25.

13. Calcium content (mg/100g)

The seeds were ground into flour and Calcium content was estimated as follows.

The 0.5 g of sample was taken into a digestion tube and 10 ml of Diacid (mixture of HNO_3 and $HCLO_4$ in the ratio 9:4) was added and allowed for overnight digestion. Again the samples were digested on hot plate till the sample was clear and reduced in volume. These samples were transferred to 50 ml volumetric flask and volume was made by distilled water. 5 ml of sample was pipette out in porcelain dish and to which added 10 ml distilled water, 0.2 gm Ammonium purpurate indicator and 3 ml NaOH. This solution was titrated with 0.01N EDTA solution till the colour of solution changed from pink to dark purple. (Barrows, 1962).

Formula for Calcium content (mEq/L) is as follows.

$$Ca(\%) = \frac{\text{A X N of EDTA X Vol. of digested sample X 1OO}}{\text{Wt. of sample} \times \text{Aliquot taken}}$$

$$\text{Calcium (mg/100g)} = \frac{\text{Calcium}}{1000}$$

14. Fiber content (%)

Two grams of powdered sample were used to extract the fiber using petroleum ether. Following ether extraction, 2g of dried material was boiled for 30 minutes with bumping chips in 200 ml of 1.25% sulphuric acid solution. It was then rinsed with hot water after being strained through muslin cloth. Following that, the sample was heated for 30 minutes in 200 ml of a 1.25% sodium hydroxide solution. After filtering it once again through muslin cloth, it was washed with 25 ml 0f 1.25% sulphuric acid, 50 ml of water, and 25 ml of alcohol. The residue was placed in an ashing dish (prewashed dish W1) and dried at 130^0c for two hours. It was the chilled in a desiccator and weighed (W2). After that it was ignited for 30 minutes at 600^0c $\pm$ 15^0c. It was cooled in desiccator and weighed (W3).

$$\text{Fibre (\%)} = \frac{\text{(W2-W1) - (W3-W1)}}{\text{Weight of sample}} \text{ X 100}$$

Where, W_1= Preweighed dish

W_2= Loss in weight on ignition

W_3= Loss in weight in desiccator

15. Fat content (%)

The estimation of crude fat or oil was determined by using method described in A.O.A.C. (1990) socs plus apparatus was used for fat estimation. The per cent fat was estimated by using formula.

$$\text{Fat (\%)} = \frac{\text{W2-W1}}{\text{X}} \text{ X 100}$$

W1= weight of empty flask

W2= weight of flask + fat

X= weight of sample taken

16. Iron content (mg/100g)

The procedure for determination of iron is same as content up to digestion and reading well taken using Atomic Absorption Spectrophotometer (AAS). Micronutrients i.e. Cu, Zn, Fe and Mn in the digested sample were estimated by using Atomic Absorption Spectrophotometer. (Mclaren and Crawford, 1950).

$$\textbf{Fe conc. (ppm)} = \frac{\text{Graph ppm x Vol. of extractant}}{\text{Weight of soil}}$$

$$\textbf{Fe (mg)} = \frac{\text{Fe conc.}}{10}$$

17. Plant growth habit

Plant growth habit was recorded as Erect, Decumbent, Prostrate, as per the guideline given for DUS test by PPV & FRA.

18. Plant pigmentation

Plant pigmentation at leaf sheath was recorded as Present or Absent, as per the guideline given for DUS test by PPV& FRA.

19. Inflorescence shape

Inflorescence shape was recorded as Arched, Diffused, Globose-eliptic, as per the guideline given for DUS test by PPV &FRA.

20. Culm- Branching

Number of lateral branches at nodes were recorded and the genotypes were classified based on degree of culm branching, according to the guidelines proposed for DUS test by PPV&FRA as given below,

< 3 : Low

3 – 7 : Medium

> 7 : High

21. Panicle-compactness

Panicle appearance was recorded as compact, semi-compact or open, as per the guidelines given for DUS test by PPV&FRA.

22. Leaf sheath: pubescence

Leaf sheath pubescence was recorded as Absent or Present, as per the guideline given for DUS test by PPV& FRA.

23. Ligule: pubescence

Ligule pubescence was recorded as Absent or Present, as per the guideline given for DUS test by PPV& FRA.

24. Leaf Blade: pubescence

Leaf blade pubescence was recorded as Absent or Present, as per the guideline given for DUS test by PPV& FRA.

3.3 Statistical analysis

The data collected on distinct characters where subjected to the method of analysis of variance usually applicable to the randomized block design (Panse and Sukhatme 1985). The analysis of variance was done as given below.

3.3.1 Analysis of variance (ANOVA)

Source of Variation	**D.F.**	**S.S.**	**M.S.S.**	**Expected M.S.S.**
Replication	(r-1)	RSS	RMS	$\sigma^2e + \sigma^2r$
Genotype	(g-1)	GSS	GMS	$\sigma^2e + \sigma^2g$
Error	(r-1) (g-1)	ESS	EMS	σ^2e
Total	(rg-1)	TSS		

Where,

r = Number of replications

g = Number of genotypes

MSS = Mean sum of squares

σ^2e = Environmental variance

σ^2g = Genotypic variance

σ^2r = Replication variance

The genotype mean sum of square (GMS) was tested against error mean sum of square (EMS) by 'F' test for n_1 = (g-1) and n_2 =(r-1) (g-1) degrees of freedom.

3.3.2 Estimation of mean and range

i. Mean

Mean value of each character was worked out by dividing the total by corresponding of observations.

$$\bar{X} = \frac{\Sigma X_i}{n}$$

Where,

$\bar{X}$ = Mean of character

ΣX_i = Total of the character

n = Number of observations

ii. Range

The lowest and highest values from the mean of each character were recorded as range of that character.

Coefficient of variation (C.V) $= \frac{S.D}{\bar{X}} \times 100$

Where,

Standard Deviation (S.D) $= \sqrt{\frac{1}{n}}(X-\bar{X})^2$

3.3.3 Estimation of components of variation

The environmental ($\sigma^2 e$), phenotypic ($\sigma^2 p$), genotypic ($\sigma^2 g$) variances were calculated as,

i. Environmental variance

$(\sigma^2 e)$ = EMS

ii. Genotypic variances

$$(\sigma^2 g) = \frac{GMS - EMS}{r}$$

iii. Phenotypic variances

$$(\sigma^2 p)=(\sigma^2 g)+(\sigma^2 e)$$

Where,

GMS = Genotypic mean sum of squares

EMS = Error mean square

r = Number of replications

3.3.4 Estimation of standard error of mean and standard error of difference

a. Standard error of mean

$$SEm \pm = \sqrt{\sigma^2 e/r}$$

b. Standard error of difference

Standard error of difference between two means was calculated as S.E. of difference of mean (SEd).

$$(SEd)= SE_m \times \sqrt{2}$$

c. Critical difference

The critical difference between any two means was calculated as SEd x 't' value at error degrees of freedom.

3.3.5 Estimation of Coefficient of Variation

The genotypic and phenotypic coefficient of variation were calculated as per the formula given by Burton and De Vane (1953).

1. Genotypic coefficient of variation (GCV)

$$GCV\ (\%) = \sqrt{\frac{\sigma^2 g}{\bar{X}}} \times 100$$

2. Phenotypic coefficient of variation (PCV)

$$PCV\ (\%) = \sqrt{\frac{\sigma^2 p}{\bar{X}}} \times 100$$

Where,

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

$\bar{X}$ = Mean of characters

Categorization of range of variation as proposed by Shivasubramanian and Menon (1973)

<10(%) : Low

10 – 20 (%) : Moderate

>20 (%) : High

3.3.6 Estimation of Heritability

Heritability in broad sense estimated for various characters by using the formulae suggested by Lush (1949). It is estimated from the total genetic variances.

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

Where,

$\sigma^2 g$ = Genotypic variances

$\sigma^2 p$ = Phenotypic variances

Heritability in broad sense was estimated by method suggested by Johnson et.al (1955), as given below

0 - 20(%) : Low

20 – 50 (%) : Medium

50 (%) & above : High

3.3.7 Estimation of genetic advance (GA)

Improvement in the mean genotypic value of selected plant over the parental population is known as genetic advance. The genetic variability is directly proportional to the genetic advance. The genetic advance is generally high with the characters having, high heritability and vice versa. It is calculated by the formula suggested by Johnson *et.al* (1955).

i. Genetic advance

$$G.A. = \frac{\sigma^2 g}{\sigma^2 p} \times \sigma p \times k$$

ii. GA as per cent of mean

$$GAM = \frac{GA}{\bar{X}} \times 100$$

Where,

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

σp = Phenotypic standard deviation

k = Selection differential at 5% selection intensity

$\bar{X}$ = Mean of character

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

<10(%) : Low

10 – 20 (%) : Moderate

>20 (%) : High

3.3.8 Estimation of correlation coefficient

Analysis of co-variance was carried out by taking two characters at a time and error was used as environmental co-variance. The phenotypic and genotypic co-variances were derived as detailed below.

ANOVA for phenotypic and genotypic co-variances

Source	d. f.	Mean products
Replication	(r-1)	-
Treatment	(t-1)	GMP
Error	(r-1)(t-1)	EMP
Total	(rt-1)	-

Where,

r = Number of replication

g = Number of treatments

GMP = Genotype mean sum of products

EMP = Error mean sum of products

The genotypic and phenotypic co-variances were worked out as per the formulae given by Singh and Chaudhary (1977).

Environmental co-variance = (CoVe1.2) =EMP

Genotypic co-variance = (CoVg 1.2) = $\frac{\text{GMP}-\text{EMP}}{r}$

Phenotypic co-variance= (CoVp 1.2) = (CoVg1.2) + (CoVe 1.2)

The appropriate variances and co-variances were used for calculating phenotypic and genotypic correlation coefficients (Johnson *et al.* 1955).

1. Phenotypic correlation coefficient (r_p)

Phenotypic correlation coefficient was derived as

$$r_p1.2 = \frac{\text{CoVp 1.2}}{\sqrt{(\sigma^2 p1)\,(\sigma^2 p2)}}$$

Where,

r_p1.2 = Phenotypic correlation between character 1 and 2

CoVp 1.2 = Phenotypic co-variance between character 1 and 2

σ^2p1 and σ^2p2 = Phenotypic variances of characters 1 and 2 respectively.

2. Genotypic correlation coefficient (r_g)

Genotypic correlation coefficient were obtained by the formula

$$r_g1.2=\frac{\text{CoVg 1.2}}{\sqrt{(\sigma^2 g1)\,(\sigma^2 g2)}}$$

Where,

r_g1.2 = Genotypic correlation between character 1 and 2

CoVg 1.2 = Genotypic co-variances between character 1 and 2

σ^2g1 and σ^2g2 =Genotypic variances of character 1 and 2 respectively.

The significance of genotypic and phenotypic correlation coefficient were tested by using 't' test

$$t = \sqrt[r]{\frac{n-2}{1-r^2}}$$

Where,

r = Correlation coefficient

n= Total number of observation

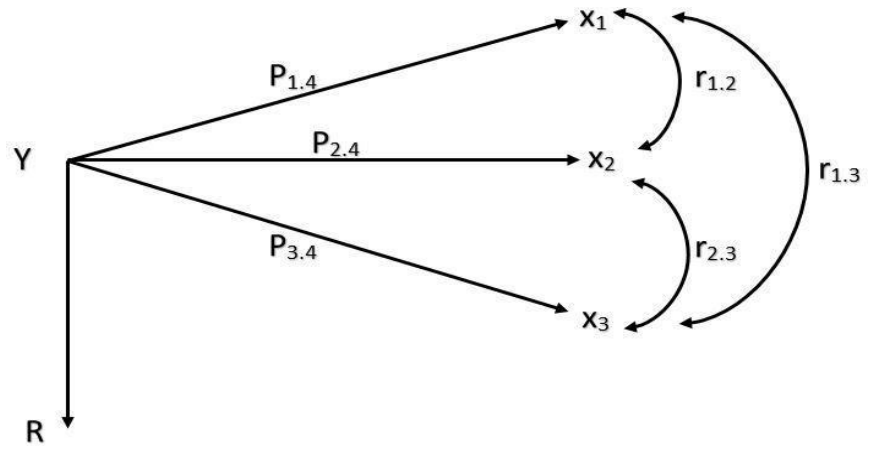
The calculated 't' value is tested with table 't' value for respective (n-2) degrees of freedom for significance.

3.3.9 Path Coefficient analysis

To establish a cause and effect relationship, the genotypic and phenotypic correlation coefficients were partitioned in direct and indirect effect by path analysis as suggested by Dewey and Lu (1959). The first step in path analysis is to prepare a path diagram based on cause and effect relationship.

Path coefficient analysis is simply a standardized partial regression coefficient which splits the correlation coefficient into the measures of direct and indirect effect.

The concept behind this is that yield is the function of various components like x_1, x_2, x_3 then these components show following type of association with one another.



From the above figure, it is clear that yield is the result of x_1, x_2 and x3 and some other undefined factors designated by 'R'. The double arrowed lines indicate mutual association as measured by correlation coefficients and the single arrowed line represented direct influence as measured by path coefficients Pij.

Path coefficients were obtained by solving a set of simultaneous equation of the form,

$r_{ny} = p_{ny} + r_{n2} + 4n_2p_y + 4n_3 + \ldots\ldots$

Where,

r_{ny} = represented correlation between one component and yield

p_{ny} = represented path coefficient between one component and the yield.

r_{n2} = represented correlation between that character and each of the other yield components in turn.

Matrix A Matrix B

$$\begin{pmatrix} r_{1Y} \\ r_{2Y} \\ r_{nY} \end{pmatrix} \qquad \begin{pmatrix} 1 & r_{1.2} & r_{1.3} \ldots\ldots\ldots\ldots & r_{1n} \\ r_{1.2} & 1 & r_{2.3} \ldots\ldots\ldots\ldots & r_{2n} \\ r_{n1} & r_{n2} & r_{n3} \ldots\ldots\ldots\ldots & 1 \end{pmatrix}$$

Where,

$r_{1.2} = r_{1.2}$ and so on.

r_{1y} = Correlation between one component character and yield

The 'B' matrix (P_{ij}) were obtained as

$$(P_{ij}) = A \times (B^{-1})$$

The indirect effect of a particular character through other characters was obtained by multiplication of direct path and particular correlation coefficients between these characters separately.

Indirect effect = $r_{ij} \times P_{ij}$

Where,

i = 1 to n

j = 1 to n

P_{ij} = P_1Y_1, P_2Y_2, ----P_nY_n

Path coefficient (P_{ij}), correlation coefficient (r_{ij}) and residual factor (s) were diagrammatically presented.

The residual factors i.e. variation in yield unaccounted for by these association was calculated from the following formula,

Residual factor (x) = $1 - R^2$

Where,

$R^2 = P_{1y}r_{1y} + P_{2y}r_{2y} + P_{3y}r_{3y}..... + P_{ny}r_{ny}$

Where,

P_{1y}, P_{2y}..... P_{ny} = Path values

r_{1y}, r_{2y}..... r_{ny} = Correlation coefficients

3.4 Estimation of Diversity and clustering by D^2 analysis

The genetic diversity in seventy genotypes for characters was estimated using Mahalanobi's (1936) D^2 statistic technique.

i. Estimation of D^2 values

The first step in the analysis was the evaluation of all D^2 values. The generalized distance between any two populations was defined as:

$\Delta 2 = \Sigma\Sigma\lambda y_{ij}\delta i\delta j$

Where,

Λy_{ij} = The reciprocal matrix to the common dispersion matrix and

δi = The difference between the two mean values of the two populations for ith character ($\mu i1 - \mu i2$).

This quantity was estimated by D^2 statistics as

$$D2 = \sum\sum^{ij} \delta i \delta j$$

Where,

Sij was the simple estimate of (λij) and i.

Since this formula for computation required the inversion of eleventh order determinant and then evaluation of 11(11-1)/2, terms whose sum was D^2, transformation of the original correlated, unstandardized character mean to standardized un-correlated variables was done.

ii. Determination of popular constellation

No formal rules could be laid down for finding the clusters, because a cluster is not well defined term. The only criterion appeared to be that any group belonging to the same cluster should at least on the average showed a smaller D^2 value, than those belonging to two different clusters. A simple device suggested by Tocher (Rao, 1952) was to start with two closely associated groups and find third group which had smaller average D^2 values from the first two. Similarly the fourth was chosen to have smallest average D^2 value of a group from the first three and so on. If at any stage the average D^2 value of group from those already listed, appeared to be high, then this group did not fit in with the former groups and was therefore, taken to be outside the former cluster. The group of the first cluster was then omitted and rests were treated similarly. It was also useful to calculate the change in average D^2 within a cluster due to inclusion of an additional group. If the change was appreciable, then the newly added group had to be considered as outside the cluster.

a. Average intra cluster distances

$$\text{Intra distance} = \sum_{i=1}^{n} Di^2 / n$$

Where,

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

b. Average inter cluster distances

The average inter cluster distances were calculated as

$$\text{Average inter cluster } D^2 = \sum Di^2 / n\, i \times nj$$

Where,

ni and nj = Number of population in clusters *i* and *j*

c. Cluster means

The cluster means for individual characters were calculated on basis of mean performance of the genotypes included in the cluster.

d. Cluster diagram

With the help of D^2 values between the clusters, the diagram showing the relationship between difference populations was drawn.

3.5 Place / duration / seasons of experiment.

The field experiment was carried out during *Kharif*, 2021 at the Education and Research Farm, Department of Agricultural Botany, College of Agriculture, Dapoli.

Geographically, Dapoli is situated in the sub-tropical region on the $17^0 45'$ North latitude and $73^0 12'$ East longitude having an elevation of 250 meters above the mean sea level with warm and humid conditions throughout the year. The soil of the experimental plot was lateritic in nature, the mean annual rainfall of this region ranges from 3500 to 4000 mm which is generally received from June to October.

CHAPTER IV : RESULTS AND DISCUSSION

The present research entitled, "Genetic diversity studies in Little millet (*Panicum sumatrense* L.)" was undertaken at the Education and Research farm, Department of Agricultural Botany, College of Agriculture, Dapoli during *Kharif*, 2021. The results of the experiment are presented in this chapter under the following headings.

4.1 Genetic variability

4.2 Correlation

4.3 Path analysis

4.4 Genetic diversity

4.1 Genetic variability

4.1.1 Analysis of variances

The analysis of variances shown significant differences among the treatments. The differences between the treatment's means were tested by 't' test at about 5 and 1 percent level of significance. The results of analysis of variances are presented in table 4.1.

The mean sum of squares due to the genotypes was significant for all the character under study. This showed substantial variation for all the characters among the population.

4.1.2 Mean performance and range of variability

The mean performance, general means, range of variation, standard error and critical difference of forty four genotypes for 16 quantitative characters studied are presented in Table 4.1

Table 4.1 Analysis of variance for yield and yield contributing traits in little millet

Sr. No.	Characters	Mean sum of squares		
		Replication (1)	Genotype (43)	Error (43)
1	Days to 50% flowering	7.102	45.348**	4.335
2	Days to maturity	1.375	45.13**	9.375
3	Plant height(cm)	4.590	350.43**	20.080
4	Number of productive tillers per plant	0.382	0.357**	0.153
5	Panicle length(cm)	0.241	8.164*	4.058
6	Thousand seed weight(g)	0.003	0.012**	0.001
7	Grain Yield (kg/plot)	0.002	0.015**	0.004
8	Grain yield (q/ha)	1.005	8.388**	2.206
9	Straw Yield(kg/plot)	0.069	0.278**	0.124
10	Grain yield per plant (g)	0.003	1.603**	0.194
11	Straw yield per plant(g)	0.046	3.419**	0.488
12	Protein content (%)	0.001	1.221**	0.013
13	Calcium content (mg)	0.046	30.287**	1.627
14	Fiber content (%)	1.182	7.182**	0.619
15	Iron content (mg)	0.016	8.461**	0.133
16	Fat content (%)	0.005	3.124**	0.003

*Significant at 5% level. **Significant at 1% level

(Figures in parenthesis denotes degrees of freedom)

Table 4.2 Mean performance of Forty four genotypes of Little millet for various yield attributing characters.

Sr. No	Genotype	DF	DM	PH	NT	PL	TW	GY (kg/pl)	GY (q/ha)	SY (kg/pl)	GYPP	SYPP	PC	CC	Fibre C	Fe C	Fat C
1	**DPLV-1**	93	121.00	143.90	3.20	40.60	1.66	0.53	12.62	2.56	5.85	3.95	7.11	16.00	7.00	8.70	6.11
2	**DPLV-2**	93	122.50	149.50	3.30	38.70	1.63	0.62	14.76	2.38	7.28	4.85	7.44	12.00	7.53	9.85	4.30
3	**DPLV-3**	101	131.00	151.90	3.20	40.00	1.67	0.55	13.10	2.18	6.13	4.10	6.24	14.00	3.55	8.55	3.42
4	**DPLV-4**	96.5	128.50	148.00	3.30	40.20	1.64	0.62	14.65	2.23	7.30	4.85	6.56	18.00	10.00	5.20	2.81
5	**DPLV-5**	107	135.50	144.40	2.90	37.40	1.60	0.59	13.93	2.13	7.35	4.90	6.78	8.00	10.20	3.10	1.84
6	**DPLV-6**	109	138.00	161.00	2.30	37.90	1.76	0.48	11.31	2.21	4.78	3.20	5.14	10.00	9.85	5.40	3.34
7	**DPLV-7**	97	127.00	150.80	2.90	39.10	1.70	0.51	12.15	2.01	5.83	3.90	5.69	10.00	4.40	8.10	4.12
8	**DPLV-8**	93	122.00	143.80	3.00	38.30	1.74	0.49	11.55	1.87	5.28	3.50	5.80	12.00	6.55	2.95	5.01
9	**DPLV-9**	96	126.00	131.80	3.30	40.00	1.66	0.51	12.03	2.15	5.88	3.85	5.58	14.00	5.60	7.60	3.48
10	**DPLV-10**	102	130.50	139.60	3.40	39.90	1.75	0.50	11.91	2.15	7.63	5.10	7.88	16.00	8.33	10.50	2.83
11	**DPLV-11**	101	127.50	145.70	2.90	40.30	1.73	0.55	12.98	2.33	7.98	5.30	5.47	15.00	7.53	4.45	1.61
12	**DPLV-12**	91	122.00	134.90	3.50	42.00	1.71	0.63	15.00	2.86	7.35	4.90	5.14	12.00	9.88	10.35	1.99
13	**DPLV-13**	95	126.00	147.40	2.60	33.90	1.66	0.50	11.79	1.79	6.43	4.30	5.69	12.00	8.63	6.90	5.12
14	**DPLV-14**	94	122.50	149.70	2.90	38.10	1.61	0.51	12.15	2.25	6.03	4.05	5.47	16.00	9.33	8.65	4.39
15	**DPLV-15**	92	122.00	146.15	2.50	40.30	1.43	0.46	10.95	1.59	5.33	3.55	5.31	8.00	8.05	9.75	1.88
16	**DPLV-16**	101	132.00	151.80	3.30	41.10	1.61	0.65	15.36	2.23	8.70	5.50	5.97	16.00	7.40	9.00	2.83
17	**DPLV-17**	94.5	126.00	151.40	2.80	40.40	1.76	0.46	10.95	2.10	5.90	3.85	5.09	8.00	9.75	9.20	5.23

DF- Days to 50% flowering	**DM- Days to maturity**	**PH- Plant Height (cm)**	**NT- Number of tillers per plant**
PL- Panicle Length (cm)	**TW- Thousand seed weight (g)**	**GY(Kg/pl)- Grain yield**	**GY(q/ha)- Grain yield**
SY(Kg/pl)- Straw yield	**GYPP- Grain yield per plant**	**SYPP- Straw yield per plant**	**PC- Protein content**
CC- Calcium content	**Fibre C- Fiber content**	**Fe C- Iron content**	**Fat C- Fat content**

Sr. No	Genotype	DF	DM	PH	NT	PL	TW	GY (kg/pl)	GY (q/ha)	SY (kg/pl)	GYPP	SYPP	PC	CC	Fibre C	Fe C	Fat C
18	**DPLV-18**	98	129.00	155.40	2.30	39.30	1.60	0.49	11.67	1.94	6.35	3.85	5.58	10.00	9.03	9.05	3.26
19	**DPLV-19**	102	133.00	158.70	2.90	40.30	1.66	0.45	10.72	1.87	4.45	2.95	5.69	4.00	8.40	9.50	4.29
20	**DPLV-20**	96	121.00	160.20	3.00	39.80	1.71	0.53	12.50	2.71	6.73	4.25	5.25	6.00	8.30	7.90	1.78
21	**DPLV-21**	94.5	123.00	151.90	2.80	40.90	1.69	0.46	10.95	1.78	6.20	3.80	5.75	8.00	8.70	4.05	2.12
22	**DPLV-22**	98	127.00	144.10	2.30	41.50	1.63	0.45	10.72	2.17	4.78	3.10	5.69	10.00	3.43	4.60	1.31
23	**DPLV-23**	98.5	122.50	151.70	2.00	40.70	1.65	0.48	11.31	1.77	4.55	2.95	6.02	12.00	7.20	6.10	3.17
24	**DPLV-24**	103	133.50	142.10	3.00	40.30	1.70	0.54	12.86	2.36	6.85	4.55	5.20	10.00	9.35	5.70	4.01
25	**DPLV-25**	106	137.00	137.10	3.70	39.70	1.71	0.44	10.48	2.86	4.75	3.15	5.25	12.00	10.05	4.85	1.96
26	**DPLV-26**	104	136.50	140.20	3.80	42.60	1.74	0.71	16.98	3.14	8.75	6.25	7.88	17.00	9.05	8.45	4.76
27	**DPLV-27**	97	121.50	139.50	3.90	42.10	1.56	0.81	19.29	3.25	11.03	7.15	8.09	18.00	7.50	8.45	4.43
28	**LM-1**	96.5	131.00	123.60	2.80	38.90	1.77	0.46	10.83	2.43	6.12	4.00	5.58	14.00	9.20	7.70	2.35
29	**LM-2**	96	130.00	151.30	3.60	43.30	1.71	0.60	14.29	2.65	6.73	4.30	5.14	4.00	9.70	8.35	3.19
30	**LM-3**	92	123.50	134.40	3.10	40.70	1.74	0.44	10.48	1.97	5.25	3.45	5.20	8.00	9.25	6.40	4.11
31	**LM-4**	84	123.00	147.70	3.40	39.30	1.69	0.51	12.15	2.37	5.78	4.25	5.25	10.00	8.50	7.20	1.51
32	**LM-5**	97	131.50	134.00	3.10	41.50	1.68	0.45	10.72	2.38	5.95	3.90	5.47	12.00	5.95	3.70	1.42
33	**LM-6**	97	133.00	161.40	3.30	42.30	1.78	0.62	14.64	2.71	7.65	5.05	5.58	10.00	9.35	5.65	1.40
34	**LM-7**	93.5	131.50	124.70	3.20	41.60	1.59	0.53	12.50	2.60	6.53	3.95	5.47	12.00	9.83	6.45	2.88

DF- Days to 50% flowering	**DM- Days to maturity**	**PH- Plant Height (cm)**	**NT- Number of tillers per plant**
PL- Panicle Length (cm)	**TW- Thousand seed weight (g)**	**GY(Kg/pl)- Grain yield**	**GY(q/ha)- Grain yield**
SY(Kg/pl)- Straw yield	**GYPP- Grain yield per plant**	**SYPP- Straw yield per plant**	**PC- Protein content**
CC- Calcium content	**Fibre C- Fiber content**	**Fe C- Iron content**	**Fat C- Fat content**

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Sr. No	Genotype	DF	DM	PH	NT	PL	TW	GY (kg/pl)	GY (q/ha)	SY (kg/pl)	GYPP	SYPP	PC	CC	Fibre C	Fe C	Fat C
35	**LM-8**	92.5	128.50	145.50	3.20	42.10	1.73	0.53	12.50	2.37	6.75	4.50	5.31	16.00	8.73	7.60	2.59
36	**LM-9**	95.5	128.50	136.60	2.60	40.40	1.67	0.47	11.19	2.86	5.93	3.90	5.36	16.00	10.20	8.80	3.46
37	**LM-10**	95.5	123.50	142.90	2.30	42.10	1.76	0.41	9.76	2.63	4.65	2.80	5.25	8.00	4.00	4.55	3.14
38	**LM-11**	94.5	123.00	113.00	3.00	40.70	1.79	0.47	11.19	2.10	6.50	4.20	5.20	14.00	9.05	6.10	4.79
39	**LM-12**	94.5	127.00	123.30	3.20	45.40	1.78	0.51	12.03	2.21	6.35	4.25	5.36	17.00	10.05	5.25	3.12
40	**LM-13**	95	129.50	107.10	3.60	43.40	1.59	0.65	15.48	2.69	6.78	5.10	5.47	18.00	10.15	7.30	2.88
41	**LM-14**	96	130.00	126.60	2.90	41.30	1.46	0.38	8.93	2.00	4.95	3.20	5.31	12.00	8.45	3.80	1.95
42	**LM-15**	95	129.00	139.40	2.90	43.40	1.74	0.39	9.17	2.52	5.15	3.45	5.91	8.00	5.05	7.20	1.80
43	**LM-16**	93	126.00	119.80	3.30	44.80	1.67	0.51	12.03	2.12	4.75	3.05	5.69	6.00	7.20	8.55	1.19
44	**LM-17**	89	122.00	110.50	3.20	42.50	1.62	0.46	10.83	1.98	5.15	3.40	5.47	6.00	10.25	8.20	2.19
General mean		**96.5**	**127.60**	**141.25**	**3.04**	**40.66**	**1.67**	**0.52**	**12.35**	**2.30**	**4.15**	**6.28**	**5.79**	**11.70**	**8.17**	**7.04**	**3.07**
Range	**Low**	**84**	**121**	**107.1**	**2**	**33.9**	**1.43**	**0.38**	**8.93**	**1.59**	**4.45**	**2.8**	**5.09**	**4**	**3.43**	**2.95**	**1.19**
	High	**109**	**138**	**161.4**	**3.9**	**45.4**	**1.79**	**0.81**	**19.29**	**3.25**	**11.03**	**7.15**	**8.09**	**18**	**10.25**	**10.5**	**6.11**
C.D. at 5%		**4.20**	**6.17**	**9.04**	**0.79**	**4.06**	**0.04**	**0.126**	**3.00**	**0.71**	**0.89**	**1.41**	**0.23**	**2.57**	**1.198**	**0.74**	**0.11**
S.E.		**1.47**	**2.17**	**3.17**	**0.28**	**1.42**	**0.01**	**0.04**	**1.05**	**0.24**	**0.31**	**0.49**	**0.08**	**0.90**	**0.56**	**0.26**	**0.04**
C.V. %		**2.15**	**2.40**	**3.17**	**12.85**	**4.95**	**1.18**	**12.01**	**12.02**	**15.31**	**11.11**	**10.63**	**1.96**	**10.89**	**9.63**	**5.17**	**1.74**

DF- Days to 50% flowering	**DM- Days to maturity**	**PH- Plant Height (cm)**	**NT- Number of tillers per plant**
PL- Panicle Length (cm)	**TW- Thousand seed weight (g)**	**GY(Kg/pl)- Grain yield**	**GY(q/ha)- Grain yield**
SY(Kg/pl)- Straw yield	**GYPP- Grain yield per plant**	**SYPP- Straw yield per plant**	**PC- Protein content**
CC- Calcium content	**Fibre C- Fiber content**	**Fe C- Iron content**	**Fat C- Fat content**

1. Days to 50 per cent flowering

The character days to 50 per cent flowering ranged from 84 days (LM-4) to 109 days (DPLV-6) with general mean of the 96.58 days. In all 44 genotypes 27 genotypes flowered earlier than general mean, while 17 genotypes flowered late than general mean. LM -4 (84 days) showed earliest flowering followed by LM-17 (89 days) and late flowering was observed in DPLV-6 (109 days) followed by DPLV-25 (106 days) and DPLV-26 (104 days).

2. Days to maturity

Days to maturity ranged from 121 days to 138 days among the 44 genotypes with general mean 127.6 days. Twenty three genotypes matured earlier than general mean while twenty one genotypes matured late than general mean. DPLV-1 (121 days), DPLV-20 (121 days) and DPLV-27 (121.50 days) was the earliest maturing than general mean, while DPLV-6 (138 days) followed by DPLV-25 (137 days), DPLV-26 (136.5 days) and DPLV-24 (133.5 days) matured late than general mean.

3. Plant height (cm)

The variation for plant height was 107.1 cm to 161.4 cm with the general mean of 141.25 cm. Eighteen genotypes observed tall height than the general mean, while twenty six genotypes observed dwarf height than the general mean. Among the genotypes LM-6 (161.4 cm) was the tallest followed by DPLV-6 (161 cm) and DPLV- 20 (160.20 cm). Minimum height was observed in LM-13 (107.1 cm) followed by LM- 17 (110.50 cm).

4. Number of productive tillers per plant

Number of productive tillers per plant ranged from 2 to 3.9. The average number of productive tillers per plant was 3.04. Twenty two genotypes had less and twenty two genotypes had more productive tillers than average. The minimum number of productive tillers per plant was recorded in DPLV-23 (2) followed by DPLV-6, DPLV-18, DPLV-22 and LM-10 (2.3), While maximum number of productive tillers per plant were recorded in DPLV-27 (3.9) followed by DPLV-26 (3.8), DPLV-25 (3.7) and LM-2 (3.6).

5. Panicle length (cm)

Length of panicle varied from 33.9 cm to 45.4 cm with the general mean of 40.66 cm. The lowest panicle length was observed in DPLV-13 (33.9 cm) followed by DPLV-5 (37.40 cm) and DPLV-6 (37.90 cm). LM-12 (45.4 cm) followed by LM-16 (44.8 cm) showed highest panicle length.

6. Thousand seed weight (g)

The weight of thousand seeds ranged from 1.43g to 1.79g with an average of 1.67g. Among the 44 genotypes, 18 genotypes had less seed weight, while 26 genotypes had more seed

weight than general mean. LM-11 (1.79 g) recorded maximum seed weight followed by LM-12 (1.78 g) and LM-6 (1.78g). The minimum 1000 seed weight was observed in DPLV-15 (1.43 g).

7. Grain yield (kg/plot)

The range of variation for grain yield per plot was 0.38 kg/plot to 0.81 kg/plot with a general mean of 0.52 kg/pot. Among 44 genotypes, 27 genotypes recorded lower grain yield per plot than average while 16 genotypes recorded higher grain yield per plot than the average. The maximum grain yield was recorded by DPLV-27 (0.81 kg/plot), while the LM-14 (0.38 kg/plot) recorded minimum grain yield per plot.

8. Grain yield (qt/ha)

The range of variation for grain yield per hectare was 8.93qt to 19.29qt with a general mean of 12.35qt/ha. Among the 44 genotype, 28 genotypes recorded lower grain yield (qt/ha) and 16 genotypes recorded higher grain yield (qt/ha). LM-14 (8.93 qt/ha) recorded low grain yield followed by LM-15 (9.17 qt/ha) and LM-10 (9.76 qt/ha). The higher grain yield was recorded by DPLV-27 (19.29 qt/ha).

9. Straw yield per plot (kg/plot)

The genotypes varied substantially for this character from 1.59 kg/plot to 3.25 kg/plot. The mean straw yield was 2.30 kg/plot. 24 genotypes showed higher straw yield over the mean value, whereas 20 genotypes showed lower straw yield than average. DPLV-15 (1.59 kg/plot) was recorded lowest straw yield per plant followed by DPLV-23 (1.77kg/plot) and DPLV-21 (1.78 kg/plot), while DPLV-27 (3.25 kg/plot) and DPLV-26 (3.14 kg/plot) recorded highest straw yield per plot.

10. Grain yield per plant (g)

The range of variation for grain yield was 4.45g to 11.03g with a general mean 4.15 g. Among genotype, 24 genotypes recorded lower grain yield per plant and 20 genotypes recorded higher grain yield per plant. DPLV 19 (4.45 g) showed lowest grain yield per plant followed by DPLV-23 (4.55g), DPLV-25 (4.75g) and LM-16 (4.75 g) whereas DPLV-27 (11.03g) recorded higher grain yield per plant.

11. Straw yield per plant (g)

The straw yield per plant varied from 2.8g to 7.15g with general mean 6.28 g. 43 genotypes recorded lower straw yield per plant and 1 genotypes recorded higher straw yield per plant. DPLV-27 (7.15g) recorded highest straw yield per plant. The genotype LM-10 (2.8 g)

recorded lowest straw yield per plant followed by DPLV-23 (2.95 g) and DPLV-19 (2.95 g).

12. Protein content (%)

The protein content varied from 5.09% to 8.09 %. The average of protein content was 5.79%. 32 genotypes had minimum and 12 genotypes had maximum protein content than average. DPLV-27 (8.09 %) and DPLV-26 (7.88%) recorded highest per cent protein whereas DPLV-17(5.09%) recorded lowest per cent protein followed by DPLV-6(5.14%), DPLV-12 (5.14%) and LM-2 (5.14 %).

13. Calcium content (mg)

The calcium content varied from 4mg to 18mg. The average of calcium content was 11.7mg. Nineteen genotypes had minimum and twenty five genotypes had maximum calcium content than average. The maximum calcium content was recorded in DPLV- 27(18mg), DPLV-4 (18 mg) and LM-13 (18 mg) while minimum calcium content was recorded in LM-2 (4mg) and DPLV-19 (4 mg).

14. Fiber content (%)

The variation for fiber content ranged between 3.43% to 10.25% with general mean 8.17%. Twenty eight genotypes produced highest fiber content than the general mean whereas sixteen genotypes showed lower fiber content than the general mean. LM-17 (10.25%) showed higher fiber content followed by DPLV-5 (10.20) and LM-9 (10.20%). The genotype DPLV-22 (3.43%) and DPLV-3 (3.55%) showed lowest fiber content as compared to other genotypes.

15. Iron content (mg)

The value of Iron content ranged between 2.95mg/100g to 10.5mg/100g. Among 44 genotypes, twenty five genotypes had greater value of iron content than the general mean (7.04mg/100g). The highest number iron content was observed in DPLV-10 (10.5mg/100g) and DPLV-12 (10.35mg/100g). The minimum number of iron content was DPLV-8 (2.95mg/100g) followed by DPLV-5 (3.10mg/100g) and LM-5 (3.7mg/100g).

16. Fat content (%)

Out of 44 genotypes studied 22 genotypes recorded higher value of fat content and remaining 22 genotypes show lower value of fat content than the general mean (3.07%). The range for variation in fat content was 1.19% (LM-16) to 6.11% (DPLV-1).

4.3 The mean performance of eight qualitative characters are given in table 4.3(i) and (ii)

Table 4.3 (i) Qualitative characters in Little millet.

Sr. No.	Genotype	Plant growth habit	Inflorescence shape	Plant pigmentation	Panicle compactness
1	DPLV-1	Erect	Arched	Present	Compact
2	DPLV-2	Erect	Arched	Present	Compact
3	DPLV-3	Decumbent	Arched	Present	Intermediate
4	DPLV-4	Erect	Diffused	Present	Compact
5	DPLV-5	Erect	Arched	Present	Compact
6	DPLV-6	Erect	Arched	Present	Compact
7	DPLV-7	Erect	Arched	Present	Compact
8	DPLV-8	Erect	Arched	Absent	Compact
9	DPLV-9	Erect	Arched	Present	Compact
10	DPLV-10	Erect	Arched	Present	Compact
11	DPLV-11	Erect	Arched	Present	Compact
12	DPLV-12	Erect	Arched	Absent	Compact
13	DPLV-13	Erect	Diffused	Present	Open
14	DPLV-14	Erect	Arched	Present	Compact
15	DPLV-15	Erect	Arched	Absent	Compact
16	DPLV-16	Erect	Arched	Absent	Compact
17	DPLV-17	Erect	Arched	Present	Intermediate
18	DPLV-18	Erect	Arched	Present	Open
19	DPLV-19	Erect	Arched	Absent	Compact
20	DPLV-20	Erect	Arched	Present	Compact
21	DPLV-21	Erect	Arched	Present	Compact
22	DPLV-22	Erect	Arched	Present	Compact
23	DPLV-23	Erect	Arched	Absent	Compact
24	DPLV-24	Erect	Arched	Absent	Compact
25	DPLV-25	Decumbent	Arched	Present	Compact
26	DPLV-26	Erect	Arched	Absent	Compact
27	DPLV-27	Erect	Arched	Absent	Compact
28	LM-1	Erect	Arched	Absent	Intermediate
29	LM-2	Decumbent	Arched	Present	Intermediate
30	LM-3	Erect	Arched	Absent	Intermediate
31	LM-4	Erect	Arched	Absent	Compact
32	LM-5	Decumbent	Arched	Present	Compact
33	LM-6	Erect	Arched	Present	Compact
34	LM-7	Erect	Arched	Present	Compact
35	LM-8	Erect	Arched	Present	Compact
36	LM-9	Erect	Arched	Present	Compact
37	LM-10	Erect	Arched	Absent	Compact
38	LM-11	Erect	Arched	Absent	Intermediate
39	LM-12	Erect	Diffused	Absent	Intermediate
40	LM-13	Decumbent	Arched	Absent	Compact
41	LM-14	Erect	Arched	Absent	Compact
42	LM-15	Decumbent	Arched	Present	Compact
43	LM-16	Erect	Arched	Present	Compact
44	LM-17	Decumbent	Diffused	Absent	Intermediate

Table 4.3 (ii) Qualitative characters in Little millet.

Sr. No.	Genotype	Culm branching	Leaf sheath : pubescence	Ligule : pubescence	Leaf blade : pubescence
1	DPLV-1	Absent	Absent	Absent	Absent
2	DPLV-2	Absent	Absent	Absent	Absent
3	DPLV-3	Absent	Absent	Absent	Absent
4	DPLV-4	Absent	Absent	Absent	Absent
5	DPLV-5	Absent	Absent	Absent	Absent
6	DPLV-6	Absent	Absent	Absent	Absent
7	DPLV-7	Absent	Absent	Absent	Absent
8	DPLV-8	Absent	Absent	Absent	Absent
9	DPLV-9	Absent	Absent	Absent	Absent
10	DPLV-10	Absent	Absent	Absent	Absent
11	DPLV-11	Absent	Absent	Absent	Absent
12	DPLV-12	Absent	Absent	Absent	Absent
13	DPLV-13	Absent	Absent	Absent	Absent
14	DPLV-14	Absent	Absent	Absent	Absent
15	DPLV-15	Absent	Absent	Absent	Absent
16	DPLV-16	Absent	Absent	Absent	Absent
17	DPLV-17	Absent	Absent	Absent	Absent
18	DPLV-18	Absent	Absent	Absent	Absent
19	DPLV-19	Absent	Absent	Absent	Absent
20	DPLV-20	Absent	Absent	Absent	Absent
21	DPLV-21	Absent	Absent	Absent	Absent
22	DPLV-22	Absent	Absent	Absent	Absent
23	DPLV-23	Absent	Absent	Absent	Absent
24	DPLV-24	Absent	Absent	Absent	Absent
25	DPLV-25	Absent	Absent	Absent	Absent
26	DPLV-26	Absent	Absent	Absent	Present
27	DPLV-27	Absent	Absent	Absent	Present
28	LM-1	Absent	Absent	Absent	Absent
29	LM-2	Absent	Absent	Absent	Absent
30	LM-3	Absent	Absent	Absent	Absent
31	LM-4	Absent	Absent	Absent	Absent
32	LM-5	Absent	Absent	Absent	Absent
33	LM-6	Absent	Absent	Absent	Absent
34	LM-7	Absent	Absent	Absent	Absent
35	LM-8	Absent	Absent	Absent	Absent
36	LM-9	Absent	Absent	Absent	Absent
37	LM-10	Absent	Absent	Absent	Absent
38	LM-11	Absent	Absent	Absent	Absent
39	LM-12	Absent	Absent	Absent	Absent
40	LM-13	Absent	Absent	Absent	Absent
41	LM-14	Absent	Absent	Absent	Absent
42	LM-15	Absent	Absent	Absent	Absent
43	LM-16	Absent	Absent	Absent	Absent
44	LM-17	Absent	Absent	Absent	Absent

1. Plant growth habit

Two types of plant growth habit were observed in Little millet i.e. Erect and decumbent. Out of 44 genotypes of Little millet, 37 genotypes had erect type plant growth habit whereas 7 genotypes had decumbent plant growth habit. Genotypes having erect type growth habit constituted about 84.09% and genotypes having decumbent growth habit constituted about 15.90% of total number of genotypes.

2. Inflorescence shape

Two types of inflorescence shape were observed in Little millet.one is arched type and another is diffused type inflorescence. Out of 44 genotypes, 40 genotypes had arched inflorescence shape and only 4 genotypes having diffused type inflorescence. Genotypes having arched inflorescence shape constituted about 90.90% and genotypes having diffused type inflorescence constituted about 9.09% of total number of genotypes**.**

3. Plant pigmentation

Out of 44 genotypes of little millet, 27 genotypes showing plant pigmentation whereas plant pigmentation is absent in remaining 17 genotypes. Genotypes having presence of plant pigmentation which constitute about 61.36% and genotypes having no pigmentation constituted about 38.63% of total number of genotypes.

4. Panicle compactness

Three types of panicle appearances were observed in little millet i.e. open, intermediate and compact. Out of 44 genotypes of little millet, 2 genotypes had open type panicle, 8 had intermediate type panicle and 34 had compact type panicle. Genotypes having compact type panicle constituted about77.27 %, genotypes having open type panicle constituted about 4.54% and genotypes having intermediate type panicle constituted about 18.18% of total number of genotypes.

5. Culm branching

Culm branching is absent in all little millet genotypes.

6. Leaf sheath: pubescence

Leaf sheath: pubescence is absent in little millet genotypes.

7. Ligule: pubescence

Ligule: pubescence is absent in little millet genotypes.

8. Leaf blade: pubescence

Out of 44 genotypes of little millet only 2 genotypes showing pubescence on leaf blade whereas 42 genotypes having no pubescence on leaf blade. Genotypes having pubescence on leaf blade constituted about only 4.54% and genotypes having no pubescence on leaf blade constituted about 95.45% of total number of genotypes.

4.1.3 Components of variation

The total variation among the population was divided into three components etc., Genotypic, phenotypic and environmental variance. The estimates of variances due to these three components for 16 characters given in Table 4.4.

The phenotypic variances ranged between 0.01 (Thousand seed weight and Grain yield per plot) to 185.26 (Plant height). The genotypic variances ranged between 0.01 (Thousand seed weight and Grain yield per plot) to 165.17 (Plant height). The environmental variance ranged between 0.00% (Thousand seed weight and Grain yield per plot) to 20.08 (plant height).

In general, for all character's phenotypic variances were higher magnitude than genotypic variance. Phenotypic variance was found to be high for plant height (185.26) whereas days to maturity (27.25), days to 50% flowering (24.84) and calcium content (15.96) showed moderate magnitude of phenotypic variance. The traits straw yield per plot (0.20), number of productive tillers per plant (0.26), protein content (0.62), grain yield per plant (0.90), fat content (1.56), straw yield per plant (1.95), fiber content (3.90), iron content (4.30), grain yield (5.29) and panicle length (6.11) showed lower estimate of phenotypic variance.

The genotypic variances were greater in magnitude over respective environmental variances for all the characters. Plant height (165.17) indicated higher variance while days to 50% flowering (20.51), days to maturity (17.88) and calcium content (14.33) recorded moderate estimates of genotypic variance. Lowest magnitude of genotypic variances were recorded for thousand seed weight (0.01), grain yield per plot (0.01), straw yield per plot (0.08), number of productive tillers per plant (0.10), protein content (0.60), grain yield per plant (0.70), straw yield per plant (1.47), fat content (1.56), panicle length (2.05), grain yield per hectare 3.09), fiber content (3.28) and iron content (4.16).

In general, environmental variances were lower in magnitude over the respective phenotypic and genotypic variances for the diverse characters.

4.1.4 Coefficient of variation

The estimates of phenotypic and genotypic coefficient of variation are presented in table 4.5.

In general, phenotypic coefficient of variation (PCV) was greater in magnitude over respective genotypic coefficient of variation (GCV). The character fat content (40.67%), calcium content (34.13%), iron content (29.45%), fiber content (24.18%), grain yield per plant (22.87%) and straw yield per plant (22.25%) shows maximum magnitude of phenotypic coefficient of variation, while straw yield per plot (19.48%), grain yield per plot (18.70%), grain yield per hectare (18.63%), productive tillers per plant (16.62%) and protein content (13.57%) indicated comparatively moderate estimations of phenotypic coefficient of variation. Lower magnitude of phenotypic coefficient of variation were recorded for the characters days to maturity (4.09%), thousand seed weight (4.78%), days to 50% flowering (5.16%), panicle length (6.08%) and plant height (9.64%).

Table 4.4 Estimates of phenotypic ($\sigma^2 p$), genotypic ($\sigma^2 g$) and environmental ($\sigma^2 e$) variance for little millet genotypes.

Sr. No.	Characters	Phenotypic variance	Genotypic variance	Environmental variance
1	**Days to 50% flowering**	24.84	20.51	4.33
2	**Days to maturity**	27.25	17.88	9.38
3	**Plant height(cm)**	185.26	165.17	20.08
4	**Number of productive tillers per plant**	0.26	0.10	0.15
5	**Panicle length(cm)**	6.11	2.05	4.06
6	**Thousand seed weight(g)**	0.01	0.01	0.00
7	**Grain Yield (kg/plot)**	0.01	0.01	0.00
8	**Grain yield (q/ha)**	5.29	3.09	2.20
9	**Straw Yield(kg/plot)**	0.20	0.08	0.12
10	**Grain yield per plant (g)**	0.90	0.70	0.19
11	**Straw yield per plant(g)**	1.95	1.47	0.49
12	**Protein content (%)**	0.62	0.60	0.01
13	**Calcium content (mg)**	15.96	14.33	1.63
14	**Fiber content (%)**	3.90	3.28	0.62
15	**Iron content (mg)**	4.30	4.16	0.13
16	**Fat content (%)**	1.56	1.56	0.00

The extent of genetic variation present in these genotypes was worked out in terms of genotypic coefficient of variation (GCV). The characters fat content (40.63%), calcium content (32.34%), iron content (28.99%), fiber content (22.17%) and grain yield per plant (20.25%) recorded highest amount of genotypic coefficient of variation, while straw yield per plant (19.28%), grain yield per plot (14.30%), grain yield per hectare (14.24), protein content (13.43%) and straw yield per plot (12.05%) noted comparatively moderate value of GCV. The minimum GCV was shown by characters days to maturity (3.31%), panicle length (3.52%), thousand seed weight (4.63%), days to 50% flowering (4.69%), plant height (9.10%) and number of productive tillers per plant (10.54%).

4.1.5 Heritability and genetic advance

All the characters studied exhibited high estimates of heritability in broad sense. Heritability ranged from 33.59 per cent for panicle length to 99.81 per cent for fat content. The high heritability recorded by the characters fat content (99.81%), protein content (97.91%), iron content (96.91%), thousand seed weight (93.75%), calcium content (89.80%), plant height (89.16%), fiber content (84.13%) and days to 50% flowering (82.55%) while grain yield per plant (78.39%), straw yield per plant (75.04%) and days to maturity (65.60%) showed moderate range of heritability. The characters grain yield per plot (58.51%), grain yield per hectare (58.39%), number of productive tillers per plant (40.20%), straw yield per plot (38.25%) and panicle length (33.59%) recorded lowest estimates of heritability. The estimation of heritability and genetic advance was presented in the Table 4.5.

Plant height (25) recorded the high estimate of genetic advance followed by days to 50% flowering (8.48), calcium content (7.39), days to maturity (7.05), iron content (4.14), fiber content (3.42), grain yield per hectare (2.77), fat content (2.57), straw yield per plant (2.16), panicle length (1.71), protein content (1.58), grain yield per plant (1.53), productive tillers (0.42), straw yield per plot (0.35), thousand seed weight (0.15) and grain yield per plot (0.12).

Genetic advance as per cent of mean ranged from 4.21% (panicle length) to 83.63% (fat content). Fat content (83.63%), calcium content(63.14%), iron content(58.79%), fiber content (41.90%), grain yield per plant (36.93%), straw yield per plant (34.40%) and protein content (27.37%) exhibited higher estimates of genetic advance as per cent of mean, while grain yield per plot (22.54%), grain yield per hectare (22.41%), plant height (17.70%), straw yield per plot (15.35%) and number of productive tillers per plant (13.76%) showed moderate estimates of genetic advance as per cent of mean. Thousand seed weight (9.23%), days to 50 % flowering (8.78%), days to maturity (5.53%) and panicle length (4.21%) exhibited minimum estimates of genetic advance as percent mean.

Table 4.5 Estimates of genetic parameters of various characters of little millet genotypes.

Sr. No.	Characters	PCV (%)	GCV (%)	ECV (%)	H(^{2}bs) (%)	GA	GAM (%)
1	**Days to 50% flowering**	5.16	4.69	2.16	82.55	8.48	8.78
2	**Days to maturity**	4.09	3.31	2.40	65.60	7.05	5.53
3	**Plant height(cm)**	9.64	9.10	3.17	89.16	25.00	17.70
4	**Number of productive tillers per plant**	16.62	10.54	12.85	40.20	0.42	13.76
5	**Panicle length(cm)**	6.08	3.52	4.95	33.59	1.71	4.21
6	**Thousand seed weight(g)**	4.78	4.63	1.18	93.75	0.15	9.23
7	**Grain Yield (kg/plot)**	18.70	14.30	12.02	58.51	0.12	22.54
8	**Grain yield (q/ha)**	18.63	14.24	12.02	58.39	2.77	22.41
9	**Straw Yield(kg/plot)**	19.48	12.05	15.31	38.25	0.35	15.35
10	**Grain yield per plant (g)**	22.87	20.25	10.63	78.39	1.53	36.93
11	**Straw yield per plant(g)**	22.25	19.28	11.12	75.04	2.16	34.40
12	**Protein content (%)**	13.57	13.43	1.96	97.91	1.58	27.37
13	**Calcium content (mg)**	34.13	32.34	10.90	89.80	7.39	63.14
14	**Fiber content (%)**	24.18	22.17	9.63	84.13	3.42	41.90
15	**Iron content (mg)**	29.45	28.99	5.18	96.91	4.14	58.79
16	**Fat content (%)**	40.67	40.63	1.74	99.81	2.57	83.63

4.2 Correlation between yield per plant and other yield contributing characters

The seed yield is composite character which depends on different independent characters and hence, it is essential to know the relationship between the yield and its constituent characters. In order to acquire knowledge of interrelation between yield contributing characters, correlation coefficient was worked out for all the possible combinations among characters under study at phenotypic and genotypic level and existing in table 4.6 and 4.7 respectively.

4.2.1 Phenotypic correlation coefficient

The results existing in table 4.6 shown that grain yield per plant indicated positive highly significant correlation with number of productive tillers per plant (0.4937), protein content (0.5469), calcium content (0.5016), and straw yield per plant (0.9674), while positive significant correlation were recorded for fiber content (0.228) and iron content (0.2194). However remaining characters had either positive or negative non-significant correlation with grain yield per plant.

Days to 50% flowering showed positive highly significant correlation with days to maturity (0.7237) and plant height (0.282) and exhibited positive significant correlation with protein content (0.2365) and negative significant with panicle length (-0.2271) whereas it showed positive non-significant correlation with thousand seed weight (0.1035), calcium content (0.075), fiber content (0.0208), fat content (0.0241), straw yield per plant (0.1248) and grain yield per plant (0.1156). It had negative non-significant correlation with number of productive tillers per plant (-0.0417) and iron content (-0.1878).

Plant height had negative highly significant correlation with panicle length (-0.3644). It had negative significant correlation with number of productive tillers per plant (-0.2404) and calcium content (-0.2268). While positive non-significant correlation with days to maturity (0.0743), thousand seed weight (0.0737), iron content (0.0741), fat content (0.1031), straw yield per plant (0.057) and grain yield per plant (0.0139). It had negative non-significant correlation with fiber content (-0.1633).

Number of productive tillers per plant had positive highly significant correlation with, protein content (0.3036), straw yield per plant (0.4618) and grain yield per plant (0.4937). It had positive significant correlation with panicle length (0.2419) and calcium content (0.2425). It had positive non-significant correlation with days to maturity (0.1292), thousand seed weight (0.0436), fiber content (0.1864), iron content (0.1941) and fat content (0.0211).

Panicle length had negative significant correlation with fat content (-0.2578). It had positive non-significant correlation with thousand seed weight (0.0358), iron content (0.0306), straw yield per plant (0.0769) and grain yield per plant (0.0782). It had negative non-significant correlation with days to maturity (-0.0484), protein content (-0.043) and fiber content (-0.0207).

Days to maturity had positive non-significant correlation with thousand seed weight (0.1172), protein content (0.0179), calcium content (0.0334), fiber content (0.1776), straw yield per plant (0.0691) and grain yield per plant (0.0853). It had negative non-significant correlation with iron content (-0.1727) and fat content (-0.1614).

Table 4.6 Estimation of phenotypic correlation coefficient between different characters in little millet.

	DF	PH	NT	PL	DM	TW	PC	CC	Fiber C	Fe C	Fat C	SY	GY
DF	**1****	0.282**	-0.0417	-0.2271*	0.7237**	0.1035	0.2365*	0.075	0.0208	-0.1878	0.0241	0.1248	0.1156
PH		**1****	-0.2404*	-0.3644**	0.0743	0.0737	0.0973	-0.2268*	-0.1633	0.0741	0.1031	0.057	0.0139
NT			**1****	0.2419*	0.1292	0.0436	0.3036**	0.2425*	0.1864	0.1941	0.0211	0.4618**	0.4937**
PL				**1****	-0.0484	0.0358	-0.043	-0.0298	-0.0207	0.0306	-0.2578*	0.0769	0.0782
DM					**1****	0.1172	0.0179	0.0334	0.1776	-0.1727	-0.1614	0.0691	0.0853
TW						**1****	-0.1218	-0.026	0.0006	-0.1104	0.1311	-0.029	-0.0191
PC							**1****	0.4013**	-0.1304	0.2363*	0.2874**	0.5245**	0.5469**
CC								**1****	0.0699	0.034	0.2444*	0.4643**	0.5016**
FIC									**1****	0.0734	0.0258	0.2042	0.228*
FEC										**1****	0.26*	0.199	0.2194*
FAC											**1****	0.1116	0.1252
SY												**1****	0.9674**
GY													**1****

*Significant at 5 per cent **Significant at 1 per cent

DF- Days to 50% flowering	**PH- Plant Height (cm)**	**NT- Number of tillers per plant**	**PL- Panicle Length (cm)**
DM- Days to maturity	**TW- Thousand seed weight (g)**	**PC- Protein content**	**CC- Calcium content**
Fiber C- Fiber content	**Fe C- Iron content**	**Fat C- Fat content**	**SY- Straw yield per plant**
GY- Grain yield per plant			

Thousand seed weight had positive non-significant correlation with fiber content (0.0006) and fat content (0.1311). It had negative non-significant correlation with protein content (-0.1218), calcium content (-0.026), iron content (-0.1104), straw yield per plant (-0.029) and grain yield per plant (-0.0191).

Protein content had positive highly significant correlation with calcium content (0.4013), fat content (0.2874) straw yield per plant (0.5245) and grain yield per plant (0.5469). It showed positively significant correlation with iron content (0.2363), while it had negative non-significant correlation with fiber content (-0.1304).

Calcium content had positive highly significant correlation with straw yield per plant (0.4643) and grain yield per plant (0.5016) while it had positive significant with fat content (0.2444). Fiber content (0.0699) and iron content (0.034) recorded positive non-significant correlation with calcium content.

Fiber content had positive significant correlation with grain yield per plant (0.228) whereas positive non-significant with iron content (0.0734), fat content (0.0258) and straw yield per plant (0.2042).

Iron content had positive significant correlation with fat content (0.26), and grain yield per plant (0.2194), while positive non- significant correlation with straw yield per plant (0.199).

Fat content had positive non- significant correlation with straw yield per plant (0.1116) and grain yield per plant (0.1252).

Straw yield per plant had positive highly significant correlation with grain yield per plant (0.9674).

4.2.2 Genotypic correlation coefficient

In general, genotypic correlation coefficients were greater in magnitude over the respective phenotypic correlation coefficients.

The results summarized in table 4.7 presented that grain yield per plant had positively highly significant correlation with number of productive tillers per plant (0.8441), protein content (0.629), calcium content (0.6315) and straw yield per plant (0.9948). It had positive non-significant correlation with days to 50% flowering (0.1526), plant height (0.0391), panicle length (0.0185), days to maturity (0.0956) fiber content (0.2254) iron content (0.2379) and fat content (0.1421). It had negative non-significant correlation with thousand seed weight (-0.091).

Table 4.7 Estimation of genotypic correlation coefficient between different characters in Little millet genotypes.

	DF	PH	NT	PL	DM	TW	PC	CC	Fiber C	Fe C	Fat C	SY	GY
DF	**1****	0.3319*	-0.1775	-0.1972	0.8206**	0.1116	0.2545	0.0866	0.0009	-0.241	0.0218	0.1686	0.1526
PH		**1****	-0.4033**	-0.5594**	0.1225	0.0677	0.0976	-0.2464	-0.2088	0.0732	0.1083	0.0804	0.0391
NT			**1****	0.6565**	0.0827	0.104	0.4779**	0.4332**	0.3378*	0.3092*	0.0264	0.7539**	0.8441**
PL				**1****	0.0449	0.1948	-0.0744	0.0551	-0.0303	0.1123	-0.4505**	0.0208	0.0185
DM					**1****	0.1545	0.0362	0.0751	0.2352	-0.2298	-0.1992	0.0569	0.0956
TW						**1****	-0.1243	-0.0305	0.0087	-0.1208	0.1361	-0.0253	-0.0091
PC							**1****	0.421**	-0.1561	0.243	0.2905	0.6184**	0.629**
CC								**1****	0.0673	0.0409	0.2602	0.5706**	0.6315**
FIC									**1****	0.0752	0.0285	0.2099	0.2254
FEC										**1****	0.2647	0.2328	0.2379
FAC											**1****	0.1286	0.1421
SY												**1****	0.9948**
GY													**1****

*Significant at 5 percent **Significant at 1 percent

DF- Days to 50% flowering	**PH- Plant Height (cm)**	**NT- Number of tillers per plant**	**PL- Panicle Length (cm)**
DM- Days to maturity	**TW- Thousand seed weight (g)**	**PC- Protein content**	**CC- Calcium content**
Fiber C- Fiber content	**Fe C- Iron content**	**Fat C- Fat content**	**SY- Straw yield per plant**
GY- Grain yield per plant			

Days to 50% flowering had highly positive correlation with days to maturity (0.8206) and it showed positive significant correlation with plant height (0.3319). It had positive non-significant correlation with thousand seed weight (0.1116), protein content (0.2545), calcium content (0.0866), fiber content (0.0009), fat content (0.0218), straw yield per plant (0.1686) and grain yield per plant (0.1526). However remaining characters had negative but non- significant correlation with days to 50% flowering.

Plant height had negative highly significant correlation with number of productive tillers per plant (-0.4033) and panicle length (-0.5594). It showed positive non-significant correlation with days to maturity (0.1225), thousand seed weight (0.0677), protein content (0.0976), iron content (0.0732), fat content (0.1083), straw yield per plant (0.0804) and grain yield per plant (0.0391). It had negative non-significant correlation with fiber content (-0.2088) and calcium content (-0.2464).

Number of productive tillers per plant indicated positive highly significant correlation with panicle length (0.6565), protein content (0.4779), calcium content (0.4332), straw yield per plant (0.7539) and grain yield per plant (0.8441). It showed positive significant correlation with fiber content (0.3378) and iron content (0.3392). It had positive non-significant correlation with days to maturity (0.0827), thousand seed weight (0.104) and fat content (0.0264).

Panicle length had negative highly significant correlation with fat content (-0.4504). It showed positive non-significant correlation with days to maturity (0.0449), thousand seed weight (0.1948), calcium content (0.0551), iron content (0.1123), straw yield per plant (0.0208) and grain yield per plant (0.0185). It showed negative non-significant correlation with protein content (-0.0744) and fiber content (-0.0303).

Days to maturity had positive non-significant correlation with thousand seed weight (0.1545), protein content (0.0362), calcium content (0.0751), fiber content (0.2352), straw yield per plant (0.0569) and grain yield per plant (0.0956). It showed negative non-significant correlation with iron content (-0.2298) and fat content (-0.1992).

Thousand seed weight had positive non-significant correlation with fiber content (0.0087) and fat content (0.1361). It had negative non-significant correlation with protein content (-0.1243), calcium content (-0.0305), iron content (-0.1208), straw yield per plant (-0.0253) and grain yield per plant (-0.0091).

Protein content had positive highly significant correlation with calcium content (0.421), straw yield per plant (0.6184) and grain yield per plant (0.629). It showed positive non-significant correlation with iron content (0.243) and fat content (0.2905), whereas it shows negative non-significant correlation with fiber content (-0.1561).

Calcium content had positive highly significant correlation with straw yield per plant (0.5706) and grain yield per plant (0.6315). It showed positive non-significant correlation with fiber content (0.0673), iron content (0.0409) and fat content (0.2602).

Fiber content had positive non-significant correlation with iron content (0.0752), fat content (0.0285) straw yield per plant (0.2099) and grain yield per plant (0.2254).

Iron content had positive non-significant correlation with fat content (0.2647), straw yield per plant (0.2328) and grain yield per plant (0.2379).

Fat content had positive non-significant correlation with straw yield per plant (0.1286) and grain yield per plant (0.1421).

Straw yield per plant had positive highly significant correlation with grain yield per plant (0.9948).

4.3 Path coefficient analysis

The correlation was further divided in order to calculate the direct and indirect effects of various characters on grain yield per plant.

4.3.1. Phenotypic correlation coefficient partitioned for path coefficient analysis

The phenotypic correlation coefficients were divided into direct and indirect effects are presented in table 4.8.

The results specify that, the character days to 50% flowering had negative direct effect (-0.035) on grain yield per plant. It had positive indirect effect via panicle length, days to maturity, thousand seed weigh, protein content, calcium content, fiber content, fat content and straw yield per plant. It had negative indirect effect via plant height and number of productive tillers per plant. The character had positive non-significant phenotypic correlation (0.116) with grain yield per plant.

The character plant height had negative direct effect (-0.014) on grain yield per plant. Its indirect effect via panicle length, days to maturity, thousand seed weight, protein content, iron content and straw yield per plant were positive. Its indirect effect via days to 50% flowering, number of productive tillers per plant calcium content, fiber content and fat content were negative. The character had positive non-significant correlation (0.014) with grain yield per plant.

The character number of productive tillers per plant had positive direct effect (0.034) on grain yield per plant. It had positive indirect effect via days to 50% flowering, plant height, days to maturity, thousand seed weight, protein content, calcium content, fiber content, iron content

fat content and straw yield per plant. It had negative indirect effect through panicle length. The character had positive highly significant phenotypic correlation (0.4937) with grain yield per plant.

The direct effect of panicle length on grain yield per plant was negative (-0.008). The indirect effect through days to 50% flowering, plant height, number of productive tillers per plant, thousand seed weight, iron content, fat content and straw yield per plant were positive. Its indirect effect through days to maturity, protein content, calcium content and fiber content were negative. The character had positive non-significant correlation (0.078) with grain yield per plant.

Days to maturity had positive direct effect (0.037) on grain yield per plant. Its positive indirect effect via number of productive tillers per plant, panicle length, thousand seed weight, protein content, calcium content, fiber content, fat content and straw yield per plant. It had negative indirect effect via days to 50% flowering, plant height and iron content. However, this character had positive non-significant correlation (0.085) with grain yield per plant.

Thousand seed weight showed positive direct effect (0.016) on grain yield per plant. It had positive indirect effect through number of productive tillers per plant, panicle length, days to maturity and fiber content. Its indirect effect via days to 50% flowering, plant height, protein content, calcium content, iron content, fat content and straw yield per plant were negative. The character had negative non-significant correlation (-0.019) with grain yield per plant.

Protein content had positive direct effect (0.064) on grain yield per plant. Its indirect effect through number of productive tillers per plant, panicle length, days to maturity, calcium content, iron content and straw yield per plant were positive. Its indirect effect via days to 50% flowering, plant height, thousand seed weight, fiber content, and fat content were negative. The character had positive highly significant correlation (0.5469) with grain yield per plant.

The character calcium content had positive direct effect (0.054) on grain yield per plant. Its indirect effect through plant height, number of productive tillers per plant, panicle length, days to maturity, thousand seed weight, protein content, fiber content, iron content and straw yield per plant were positive. Whereas its negative and negligible indirect effect through days to 50% flowering and fat content. The resulting phenotypic correlation with grain yield per plant was positive (0.5016) and highly significant.

The direct effect of fiber content on the grain yield per plant was positive (0.035). The indirect effect via plant height, number of productive tillers per plant, panicle length, days to maturity, calcium content, iron content and straw yield per plant were positive. The negative and low indirect effect via days to 50% flowering and protein content. The character had positive significant correlation (0.228) with grain yield per plant.

Table 4.8 Path analysis for different characters at phenotypic levels in little millet genotypes.

	DF	PH	NT	PL	DM	TW	PC	CC	Fiber C	Fe C	Fat C	SY	GY
DF	**-0.035**	-0.004	-0.001	0.002	0.027	0.002	0.015	0.004	0.001	-0.004	0.000	0.111	**0.116**
PH	-0.010	**-0.014**	-0.008	0.003	0.003	0.001	0.006	-0.012	-0.006	0.002	-0.001	0.050	**0.014**
NT	0.001	0.003	**0.034**	-0.002	0.005	0.001	0.019	0.013	0.007	0.004	0.000	0.409	**0.4937****
PL	0.008	0.005	0.008	**-0.008**	-0.002	0.001	-0.003	-0.002	-0.001	0.001	0.002	0.068	**0.078**
DM	-0.026	-0.001	0.004	0.000	**0.037**	0.002	0.001	0.002	0.006	-0.004	0.001	0.061	**0.085**
TW	-0.004	-0.001	0.002	0.000	0.004	**0.016**	-0.007	-0.001	0.000	-0.002	-0.001	-0.032	**-0.019**
PC	-0.008	-0.001	0.010	0.000	0.001	-0.002	**0.064**	0.022	-0.005	0.005	-0.003	0.465	**0.5469****
CC	-0.003	0.003	0.008	0.000	0.001	0.000	0.026	**0.054**	0.002	0.001	-0.002	0.412	**0.5016****
FIC	-0.001	0.002	0.006	0.000	0.007	0.000	-0.008	0.004	**0.035**	0.002	0.000	0.181	**0.228***
FEC	0.007	-0.001	0.007	0.000	-0.006	-0.002	0.015	0.002	0.003	**0.023**	-0.002	0.177	**0.2194***
FAC	-0.001	-0.001	0.001	0.002	-0.006	0.002	0.018	0.013	0.001	0.006	**-0.009**	0.099	**0.125**
SY	-0.004	-0.001	0.016	-0.001	0.003	-0.001	0.033	0.025	0.007	0.004	-0.001	**0.887**	**0.9674****

*Significant at 5 percent **Significant at 1 percent

DF- Days to 50% flowering	**PH- Plant Height (cm)**	**NT- Number of tillers per plant**	**PL- Panicle Length (cm)**
DM- Days to maturity	**TW- Thousand seed weight (g)**	**PC- Protein content**	**CC- Calcium content**
Fiber C- Fiber content	**Fe C- Iron content**	**Fat C- Fat content**	**SY- Straw yield per plant**
GY- Grain yield per plant			

The character iron content had positive direct effect (0.023) on grain yield per plant. It shows positive indirect effect via days to 50% flowering, number of productive tillers per plant, panicle length, protein content, calcium content, fiber content and straw yield per plant. Its indirect effect via plant height, days to maturity, thousand seed weight and fat content were negative. The character had positive significant correlation (0.2194) with grain yield per plant.

The character fat content expressed low negative direct effect (-0.009) on grain yield per plant. However, it had positive indirect effect via number of productive tillers per plant, panicle length, thousand seed weight, protein content, calcium content, fiber content, iron content and straw yield per plant. It had negative indirect effect via days to 50% flowering, plant height and days to maturity. The resulting phenotypic correlation with grain yield per plant was positive (0.125) and non-significant.

The direct effect of straw yield per plant on grain yield per plant was positive (0.887). Its indirect effect through number of productive tillers per plant, days to maturity, protein content, calcium content fiber content and iron content were positive. However, it had low and negative indirect effect via days to 50% flowering, plant height, panicle length thousand seed weight and fat content. This character had positive highly significant correlation (0.9674) with grain yield per plant.

4.3.2 Genotypic correlation coefficient partitioned for path coefficient analysis

The genotypic correlation coefficient was subdivided into direct and indirect effect and presented in table 4.9.

The results specify that, the characters days to 50% flowering had negative direct effect (-0.415) on grain yield per plant. It had moderate positive indirect effect via number of productive tillers per plant, days to maturity, thousand seed weight, protein content, calcium content, fiber content, iron content, fat content and straw yield per plant. It had negligible negative indirect effect through plant height and panicle length. The resulting genotypic correlation was positive and non-significant (0.1526) with grain yield per plant.

Plant height had negative direct effect (-0.045) on grain yield per plant. It had positive indirect effect via number of productive tillers per plant, days to maturity, thousand seed weight, protein content, fiber content, fat content and straw yield per plant. Its indirect effect through days to 50% flowering, panicle length, calcium content and iron content were negative. The resulting genotypic correlation with grain yield per plant was positive and non-significant (0.0391).

Number of productive tillers per plant had negative direct effect (-0.188) on grain yield per plant. Its indirect effect through days to 50% flowering, plant height, panicle length, days to maturity, thousand seed weight, protein content, calcium content, fat content and straw yield per plant were positive. Its indirect effect through fiber content and iron content was negative. Over all this character had highly significant positive correlation (0.8441) with grain yield per plant.

Panicle length had positive direct effect (0.038) on grain yield per plant. However, it had positive indirect effect via days to first flowering, plant height, days to maturity, thousand seed weight, fiber content, and straw yield per plant. Its indirect effect *via* number of productive tillers per plant, protein content, iron content and fat content were negative. The character showed positive non-significant correlation (0.0185) with grain yield per plant.

Days to maturity showed positive direct effect (0.410) on grain yield per plant. It expresses positive indirect effect *via* panicle length, thousand seed weight, protein content, iron content and straw yield per plant. It shows low negative indirect effect *via* days to 50% flowering, plant height, number of productive tillers per plant, fiber content and fat content. The character had positive non-significant correlation (0.0956) with grain yield per plant.

Thousand seed weight had positive direct effect (0.015) on grain yield per plant. Its indirect effect through panicle length, days to maturity, iron content and fat content were positive. It had negative indirect effect *via* days to 50% flowering, plant height, number of productive tillers per plant, protein content and straw yield per plant. The character with grain yield per plant had negative non-significant correlation (-0.091).

The direct effect of protein content on grain yield per plant was positive (0.090). The indirect effect via days to 50% flowering, plant height, number of productive tillers per plant, panicle length, thousand seed weight and iron content were negative. Its indirect effect through days to maturity, calcium content, fiber content, fat content and straw yield per plant were positive. The character had positive highly significant correlation (0.629) with grain yield per plant.

The calcium content had positive direct effect (0.003) on grain yield per plant. Its indirect effect *via* days to 50% flowering, number of productive tillers per plant, fiber content and iron content were negative. It had positive indirect effect through plant height panicle length, days to maturity, protein content, fat content and straw yield per plant The resulting genotypic correlation was positive and highly significant (0.6315) with grain yield per plant.

Table 4.9 Path analysis for different characters at genotypic levels in Little millet genotypes.

	DF	PH	NT	PL	DM	TW	PC	CC	Fiber C	Fe C	Fat C	SY	GY
DF	**-0.415**	-0.015	0.033	-0.007	0.336	0.002	0.023	0.000	0.000	0.004	0.002	0.190	0.1526
PH	-0.138	**-0.045**	0.076	-0.021	0.050	0.001	0.009	-0.001	0.008	-0.001	0.010	0.091	0.0391
NT	0.074	0.018	**-0.188**	0.025	0.034	0.002	0.043	0.001	-0.014	-0.005	0.002	0.851	0.8441**
PL	0.082	0.025	-0.123	**0.038**	0.018	0.003	-0.007	0.000	0.001	-0.002	-0.041	0.023	0.0185
DM	-0.341	-0.005	-0.016	0.002	**0.410**	0.002	0.003	0.000	-0.009	0.003	-0.018	0.064	0.0956
TW	-0.046	-0.003	-0.020	0.007	0.063	**0.015**	-0.011	0.000	0.000	0.002	0.012	-0.029	-0.0091
PC	-0.106	-0.004	-0.090	-0.003	0.015	-0.002	**0.090**	0.001	0.006	-0.004	0.026	0.698	0.629**
CC	-0.036	0.011	-0.081	0.002	0.031	0.000	0.038	**0.003**	-0.003	-0.001	0.024	0.644	0.6315**
FIC	0.000	0.009	-0.063	-0.001	0.096	0.000	-0.014	0.000	**-0.040**	-0.001	0.003	0.237	0.2254
FEC	0.100	-0.003	-0.058	0.004	-0.094	-0.002	0.022	0.000	-0.003	**-0.015**	0.024	0.263	0.2379
FAC	-0.009	-0.005	-0.005	-0.017	-0.082	0.002	0.026	0.001	-0.001	-0.004	**0.090**	0.145	0.1421
SY	-0.070	-0.004	-0.141	0.001	0.023	0.000	0.056	0.002	-0.008	-0.004	0.012	**1.129**	0.9948**

*Significant at 5 percent **Significant at 1 percent

DF- Days to 50% flowering	**PH- Plant Height (cm)**	**NT- Number of tillers per plant**	**PL- Panicle Length (cm)**
DM- Days to maturity	**TW- Thousand seed weight (g)**	**PC- Protein content**	**CC- Calcium content**
Fiber C- Fiber content	**Fe C- Iron content**	**Fat C- Fat content**	**SY- Straw yield per plant**
GY- Grain yield per plant			

The character fiber content showed negative direct effect (-0.040) on grain yield per plant. Its indirect effect *via* number of productive tillers per plant, panicle length, protein content and iron content were negative. Its indirect effect *via* plant height, days to maturity, fat content and straw yield per plant were positive. The character had positive non-significant genotypic correlation (0.2254) with grain yield per plant.

Iron content had negative direct effect (-0.015) on grain yield per plant. The indirect effect through days to 50% flowering, panicle length, protein content fat content and straw yield per plant were positive. The negative indirect effect *via* plant height, number of productive tillers per plant, days to maturity, thousand seed weight and fiber content. The resulting genotypic correlation with grain yield per plant was positive and non-significant (0.2379).

The character fat content had positive direct effect (0.090) on grain yield per plant. Its indirect effect through days to 50% flowering, days to maturity, plant height number of productive tillers per plant, panicle length, fiber content and iron content were negative. Its indirect effect via thousand seed weight, protein content, calcium content and straw yield per plant were positive. The character had positive non-significant genotypic correlation (0.1421) with grain yield per plant.

The direct effect of straw yield per plant on grain yield per plant was positive (1.129). The indirect effect is positive and negligible through panicle length, days to maturity, protein content, calcium content and fat content. Days to 50% flowering, plant height number of productive tillers per plant fiber content and iron content had negative but negligible indirect effect. The resulting genotypic correlation was positive (0.9948) and highly significant with grain yield per plant.

4.4 Genetic divergence (D^2 analysis)

Between all possible traits of 44 genotypes D^2 values estimated by Mahalonobis D^2 statistics.

4.4.1 Clustering pattern of genotypes

The cluster formation was done by following Tocher method suggested by Rao (1952). The distribution of 44 genotypes in different clusters were presented in table 4.10.

On the basis of magnitude of D^2 values, the forty for genotypes were grouped in 5 clusters. Cluster I with 16 genotypes emerged as the largest clusters followed by cluster III with 9 genotypes, whereas the cluster II with 8 genotypes, cluster V with 8 and IV with 3 genotypes were solitary.

Table 4.10 Grouping of Little millet genotypes into different clusters by Tocher method.

Cluster	Number of genotypes	Name of the genotypes
I	16	LM-13, LM-7, LM-1, LM-9, LM-11, LM-12, LM-16, LM-17, LM-4, DPLV-12, LM-8, DPLV-20, DPLV-21, LM-2, DPLV-17, LM-3
II	8	DPLV-9, DPLV-3, DPLV-7, DPLV-1, DPLV-2, DPLV-8, DPLV-13, DPLV-14
III	9	DPLV-22, LM-10, LM-15, LM-5, DPLV-19, DPLV-18, DPLV-23, DPLV-15, LM-14
IV	3	DPLV-27, DPLV-10, DPLV-26
V	8	DPLV-16, DPLV-4, DPLV-24, DPLV-11, LM-6, DPLV-5, DPLV-25, DPLV-6

4.4.2 Average Inter and Intra cluster divergence

The average inter and intra cluster D^2 values are presented in table among five clusters. The highest inter cluster divergence was observed between cluster II and III (105.59) followed by cluster II and cluster V (98.2), cluster II and cluster IV (89.16), cluster I and II (83.07), cluster III and IV (78.88), cluster I and III (73.28), cluster I and IV (73.11) cluster IV and V (71.93), cluster III and V (71.7) and cluster I and V (63.75). In intra cluster distance, highest divergence was recorded in cluster III (63.55) followed by cluster IV (62.57), cluster V (56.33), II (53.46) and cluster I (49.5).

The cluster I was most diverse from cluster II (D= 9.12) followed by cluster III (D=8.56), cluster IV (D=8.55), cluster V (7.98) and cluster I (7.03). The cluster II had maximum divergence from cluster III (D=10.28), followed by cluster V (D=9.90), cluster IV (D=9.45) and cluster II (D=7.32). The cluster III had maximum distance from cluster IV (D=8.89) followed by cluster V (D=8.47) and cluster III (D=7.98). The cluster IV had maximum distance from cluster V (D=8.48) followed by cluster IV (D=7.94). The cluster V had distance from cluster V (D=7.50).

Table 4.11 Average inter and intra cluster values in 5 clusters (D^2) in Little millet genotypes.

Cluster	I	II	III	IV	V
I	49.5	83.07	73.28	73.11	63.75
II		53.46	105.59	89.16	98.2
III			63.55	78.88	71.7
IV				62.57	71.93
V					56.33

Table 4.12 Average inter and intra cluster values in 5 clusters (D) = ($\sqrt{D2}$) in Little millet genotypes.

Cluster	I	II	III	IV	V
I	7.03	9.12	8.56	8.55	7.98
II		7.32	10.28	9.45	9.90
III			7.98	8.89	8.47
IV				7.94	8.48
V					7.50

4.4.3 Cluster mean for different characters

Cluster mean for the 13 characters among 44 genotypes are presented in table 4.13.

1. Days to 50% flowering

The value of cluster mean for this character varied from 91.63 days to 99.4days with population mean of 96.55 days. The genotype in cluster II (91.63 days) were early for the days to 50% flowering followed by cluster V (96.36 days), cluster IV (97.5 days), cluster I (97.88 days) and cluster III (99.4 days).

5. Days to maturity

The value of cluster mean for this character varied from 123.69 days to 130.31 days with population mean of 127.33 days. The genotype in cluster II (123.69 days) were early for the days to maturity followed by cluster V (126.64 days), cluster IV (127.41 days), cluster III (128.6days) and cluster I (130.31 days).

3. Plant height

The cluster mean for this character varied between 134.81 cm to 149.62 cm with population mean of 141.63. Higher cluster mean values were recorded for cluster IV (149.62 cm) followed by cluster III (144.12 cm), cluster V (141.51 cm), cluster II (138.12 cm) and cluster I (134.81 cm).

4. Number of productive tillers per plant

The cluster mean for this character ranged between 2.61 to 3.54 with population mean of 3.06. High cluster mean values were recorded by cluster III (3.54) followed by cluster II (3.2), cluster I (3.13), cluster IV (2.85) and cluster V (2.61).

5. Panicle length

The cluster mean for this character ranged between 38.9cm to 41.63 cm with population mean of 40.79 cm. The highest cluster mean was recorded for cluster V (41.63 cm) followed by cluster II (41.59 cm), cluster I (40.98 cm), cluster III (40.88 cm) and cluster IV (38.9 cm).

6. Thousand Seed Weight

Cluster mean for this character ranged between 1.66 g to 1.7 g with the population mean of 1.67 g. The highest cluster mean was recorded for cluster I (1.7 g) followed by cluster IV (1.68 g), cluster II, III and V (1.66 g).

7. Protein content

Cluster mean for this character varied from 5.3% to 5.73% with the population mean of 5.93%. The highest cluster mean was recorded for cluster III (7.45 %) followed by cluster IV (5.73 %) cluster V (5.63 %) cluster I (5.58 %), and cluster II (5.3 %).

8. Calcium content

A wide range was noticed for this character and cluster mean ranged between 7.5 mg to 15.8 mg. The highest cluster mean was recorded for cluster III (15.8 mg) followed by cluster I (13.85 mg), cluster IV (111.45 mg), cluster V (10.mg) and cluster II (7.5 mg).

9. Fiber content

Cluster mean for this character varied from 6.11% to 9.51 % with the population mean of 7.98%. The highest cluster mean was recorded for cluster I (9.51 %) followed by cluster II (8.89 %) cluster III (7.96 %) cluster II (7.46 %), and cluster V (6.11 %).

10. Iron content

A wide range was noticed for this character and cluster mean ranged between 4.86 mg to 9.25 mg. The highest cluster mean was recorded for cluster III (9.25 mg) followed by cluster II (8.34 mg), cluster IV (7.69 mg), cluster I (6.01.mg) and cluster V (4.86 mg).

11. Fat content

Cluster mean for this character varied from 2.13% to 4.34 % with the population mean of 3.05%. The highest cluster mean was recorded for cluster IV (4.34 %) followed by cluster III (3.83 %) cluster I (2.74 %) cluster II (2.23 %), and cluster I (2.13 %).

12. Grain yield per plant

Cluster mean for this character ranged between 5.18 g to 8.68 g with the population mean of 6.42 g. The highest cluster mean was recorded for cluster III (8.68 g) followed by cluster I (6.68 g), cluster II (5.88 g), cluster IV (5.72 g) and cluster V (5.18 g).

13. Straw yield per plant

Cluster mean for this character ranged between 3.31 g to 5.77 g with the population mean of 4.23 g. The highest cluster mean was recorded for cluster III (5.77 g) followed by cluster I (4.44 g), cluster II (3.89 g), cluster IV (3.77 g) and cluster V (3.31 g).

Table 4.13 Cluster mean performance of 13 characters in 44 genotypes of little millet.

Sr. No.	Characters	Clusters					Population mean
		I	II	III	IV	V	
1	**Days to 50% flowering**	97.88	91.63	99.4	97.5	96.36	96.55
2	**Days to maturity**	130.31	123.69	128.6	127.41	126.64	127.33
3	**Plant height(cm)**	134.81	138.12	144.12	149.62	141.51	141.63
4	**Number of productive tillers per plant**	3.13	3.2	3.54	2.85	2.61	3.06
5	**Panicle length(cm)**	40.98	41.59	40.88	38.9	41.63	40.79
6	**Thousand seed weight(g)**	1.7	1.66	1.66	1.68	1.66	1.67
7	**Protein content (%)**	5.58	5.3	7.45	5.73	5.63	5.93
8	**Calcium content (mg)**	13.85	7.5	15.8	11.45	10	11.72
9	**Fiber content (%)**	9.51	8.89	7.96	7.46	6.11	7.98
10	**Iron content (mg)**	6.01	8.34	9.25	7.69	4.86	7.23
11	**Fat content (%)**	2.74	2.23	3.83	4.34	2.13	3.05
12	**Grain yield per plant (g)**	6.68	5.88	8.68	5.72	5.18	6.42
13	**Straw yield per plant(g)**	4.44	3.89	5.77	3.77	3.31	4.23

4.4.4 Character contribution towards divergence

The contribution of different characters in per cent to total divergence is presented in Table 4.14. Highest contribution was reported in fat content (34.00%) followed by fiber content (15.13%), grain yield per plant (12.77%), calcium content (10.53%), thousand seed weight (7.38%), number of productive tillers per plant (5.78%), protein content (5.40%), iron content

(3.77%), straw yield per plant (3.11%) and plant height (1.37%). However, the contribution of days to 50% flowering (0.74%) and days to maturity (0.02) recorded lowest contribution towards divergence.

Table 4.14 Character contribution towards divergence

Sr. No.	Character	Per cent contribution
1	Days to 50% flowering	0.74
2	Days to maturity	0.02
3	Plant height(cm)	1.37
4	Number of productive tillers per plant	5.78
5	Panicle length(cm)	0.00
6	Thousand seed weight(g)	7.38
7	Protein content (%)	5.40
8	Calcium content (mg)	10.53
9	Fiber content (%)	15.13
10	Iron content (mg)	3.77
11	Fat content (%)	34.00
12	Grain yield per plant (g)	12.77
13	Straw yield per plant(g)	3.11

DISCUSSION

Little millet (*Panicum sumatrense* L.) is one of the minor millets grown in India. Similar to other small millets, little millet is a good source of calcium and iron. They are nutritionally rich comparable to rice, wheat, and other staple cereals. Since seed yield is a very complex trait that depends on numerous genetic factors that interact with the environment, it is always advisable to determine how the yield component relates to highly heritable characters and apply selection pressure to these traits, which accounts for indirect selection. Understanding the relationship between different characteristics and path coefficients is essential for accumulating the maximum yield contribution of contributing characters. In addition to this, genetic diversity knowledge is a worthy addition for crop improvement strategies.

In the present examination, entitled "Genetic diversity studies in little millet (*Panicum sumatrense* L.)" attempts were made to study the variability for different quantitative, qualitative and biochemical characters amongst the 44 genotypes, the correlation between the dependent and independent variables along with their direct and indirect effects on yield and genetic diversity between all genotypes. The results on various characteristics are discussed in this chapter, under the following sub headings.

4.5 Genetic variability

Any breeding programme for genetic improvement must start with the fundamental knowledge of the genetic variability present in the crop. If selection is solely based on yield, it won't be very effective unless and until sufficient variability information is available to set the selection programme for further improvement.

Analysis of variance exposed significant differences among the genotypes for all the quantitative characters *viz.,* days to 50% flowering, days to maturity, number of productive tillers per plant, plant height, panicle length, thousand seed weight, grain yield (kg/plot), grain yield (q/ha), straw yield (kg/plot), protein content (%), calcium content (mg), fiber content (%), iron content (mg), fat content (%), straw yield per plant (g) and grain yield per plant (g) representing the presence of extensive genetic variation in the experimental material. Similar results were observed by Nirmalakumari *et al.* (2010), Selvi *et al.* (2014) and Anuradha *et al*. (2017).

The wide range of variation was observed for the characters days to 50% flowering (84 to 109 days), plant height (107.1 to 161.4cm), grain yield per plot (0.38 to 0.81 kg/plot) and grain yield per hectare (8.93 to 19.29 q/ha). Similar range of variation in these characters was reported by Choudhary *et al*. (2014), Patel *et al*. (2018), Suryanarayana *et al*. (2018).

Moderate range of variation was given by characters like panicle length (33.9 to 45.4cm), days to maturity (121 to 138 days), thousand seed weight (1.43 to 1.79g) and calcium content (4 to 18mg). Similar findings were reported by Savankumar *et al.* (2018).

Narrow range of variation was observed for the characters number of productive tillers per plant (2 to 3.9), straw yield per plot (1.59 to 3.25kg/plot), protein content (5.09 to 8.09 %), fiber content (3.43 to 10.25 %), iron content (2.95 to 10.5mg), fat content (1.19 to 6.11%), straw yield per plant (2.8 to 7.15g) and grain yield per plant (4.45 to 11.03g). These results are in contradictory with results obtained by Baghel *et al*. (2004) in proso millet.

The genotypes LM-4 (84 days), LM-17 (89 days), DPLV-12 (91 days), DPLV-15 (92 days) and LM-8 (92.5 days) were found to be earliest type for days to 50% flowering and having good performance. Early flowering and early maturing are required for evolving early maturity or short duration little millet crop.

The characters number of productive tillers and length of panicle are found to be the important yield contributing traits *i.e.* more the number of productive tillers and more the length of panicle, which result into more yields. Hence the variation for these traits can be exploited for yield improvement in breeding programme. Subramanian *et al.* (2010), Anuradha *et al.* (2017), Nirubanav *et al.* (2017), Suryanarayana *et al.* (2018) and Savankumar *et al.* (2018) reported similar results for number of productive tillers per plant and Jyoti *et al*. (2018) establish similar results for length of panicle.

The genotype DPLV-27 (Number of productive tillers, panicle length, protein content, calcium content, straw yield per plant and grain yield per plant) produced high performance for the individual characters.

Based on 8 qualitative characters the 44 genotypes of little millet were classified into different classes. The genotypes DPLV-27, DPLV-26 and DPLV-12 indicated erect plant growth habit, arched inflorescence as well as compact panicle which are also high yielding genotypes. Out of 44 genotypes of little millet, 37genotypes had erect growth, 7 had decumbent type plant growth. 34 showed compact panicle, 8 had intermediate type while 2 had open type panicle.40 genotypes had arched type inflorescence shape while 4 had diffused shape. Plant pigmentation is present in 27 genotypes while absent in 17 genotypes, leaf blade pubescence is present in only two genotypes, while culm branching, leaf sheath pubescence, ligule pubescence were absent in all 44 genotypes.

4.5.1 Components of variation

The total variability in each of the sixteen characters could be divided into three components *viz*., phenotypic, genotypic and environmental variation. Out of these, the genotypic variation is of prime importance which helps to determine the heritable and non-heritable portion of variation with respect to characters under study. The result showed that magnitude of phenotypic variance was higher than genotypic variance denoting the influence of environment. Similar finding were observed by Govindaraj *et al*. (2011)

The phenotypic variance was maximum for plant height (185.26) followed by days to maturity (27.25), days to 50% flowering (24.84), calcium content (15.96), panicle length (6.11), grain yield per hectare (5.29), iron content (4.30), fiber content (3.90), straw yield per plant (1.95), fat content (1.56), grain yield per plant (0.90), protein content (0.62), number of productive tillers per plant (0.26), straw yield per plot (0.20), thousand seed weight and grain yield per plot (0.01). These results are in confirmation with those of Patel *et al*. (2018) for days to 50% flowering, panicle length, protein content, straw yield per plant, fat content, iron content and fiber content.

The genotypic variance was maximum for plant height (165.17) followed by days to 50% flowering (20.51), days to maturity (17.88), calcium content (14.33), iron content (4.16), fiber content (3.28), grain yield per hectare (3.09), panicle length (2.05), fat content (1.56), straw yield per plant (1.47), grain yield per plant (0.70), protein content (0.60), number of productive tillers per plant (0.10), straw yield per plot (0.08), thousand seed weight and grain yield per plot (0.01). These results are in confirmation with those of Patel *et al*. (2018) for days to 50% flowering, panicle length, protein content, straw yield per plant, fat content, iron content and fiber content.

4.5.2 Coefficient of variation

The variability contained in the investigated genotypes may be estimated using the genotypic and phenotypic coefficients of variation. It is a fundamental evaluation tool that does not require units and is used to compare characteristics assessed in various ways. Gene expression and environmental factors combine to form phenotypic values. It may be incorrect to base a decision exclusively on external factors. As a result, the genotypic coefficient of variation is a more accurate and genuine estimate of the level of genetic diversity in a population than its phenotypic equivalent.

The variability of phenotypes was often higher than the variability of their corresponding genotypes. The genotypic coefficient of variation allows for comparison of the degree of

variation and aids in determining the genetic stability of various features. According to estimations of PCV the genotypes were extremely varied for fat content (40.67%), followed by calcium content (34.13%), iron content (29.45%), fiber content (24.18%), grain yield per plant (22.87%), straw yield per plant (22.25), straw yield per plot (19.48%), grain yield per plot (18.70%), grain yield per ha (18.63%), number of productive tillers per plant (16.62%), protein content (13.57%). These results are in agreement with Shingane *et al.* (2016) for number of productive tillers per plant, iron content, grain yield per plant and straw yield per plant. Also Kavya *et al*. (2017) observed similar results for PCV often higher than GCV.

Least degree of phenotypic coefficient of variation recorded in days to maturity (4.09%), thousand seed weight (4.78%), days to 50 % flowering (5.16), panicle length (6.08%) and plant height (9.64%). Sao *et al*. (2017) recorded similar results for days to 50% flowering and days to maturity while Monika *et al*. (2021) recorded similar results for days to maturity.

Maximum value of genotypic coefficient of variation was recorded for fat content (40.63%), followed by calcium content (32.34%), iron content (28.99%), fiber content (22.17%), grain yield per plant (20.25%), straw yield per plant (19.28%), grain yield per plot (14.30%), grain yield per ha (14.24%), protein content (13.43%), straw yield per plot (12.05%), number of productive tillers per plant (10.54%). These results are in agreement with Nagar *et al*. (2020) for number of productive tillers per plant and grain yield per plant.

Least degree of genotypic coefficient of variation recorded in days to maturity (3.31%), panicle length (3.52%), thousand seed weight (4.63%), days to 50 % flowering (4.69%) and plant height (9.10%). Sao *et al*. (2017) noted similar results for days to 50% flowering and days to maturity.

4.5.3 Heritability and genetic advance

The environment has a stronger impact on quantitative qualities. There will be partial transmission of the observed phenotype to subsequent generations. The heritable component of variability must thus be studied. Heritability is a useful metric for measuring how traits are passed down from one generation to the next and serves as a tool for us to choose superior genotypes from a wide range of genetic populations. It provides an accurate indication of the heritable part of variability. The base population can be improved to a significant extent through genetic advancement through selection. That is heredity, and genetic progress aids in identifying the impact of the environment on the manifestation of traits and the scope of improvement following selection.

In the present investigation, high evaluation of heritability in broad sense was observed for the characters fat content (99.81%), followed by protein content (97.91%), iron content (96.91%), thousand seed weight (93.75%), calcium content (89.80%), plant height (89.16%), fiber content (84.13%), days to 50% flowering (82.55%), grain yield per plant (78.39%) and straw yield per plant (75.04%) showing that these characters may serve as effective selection parameters during breeding programme for the improvement of Little millet productivity. Similar results were reported by Anuradha *et al*. (2017) and Kavya *et al*. (2017) for grain yield per plant and straw yield per plant. While moderate heritability assessment was observed for character days to maturity (65.60%), grain yield per plot (58.51%) and grain yield per ha. (58.39%). Whereas Number of productive tillers per plant (40.20%), straw yield per plot (38.25%) and panicle length (33.59%) recorded low estimates of heritability. These findings are in conformity with Subramanian *et al.* (2010), Patil *et al.* (2013), Sao *et al*. (2017) and Shivangi *et al*. (2017).

Genetic advancement forecasts the genetic improvement under selection. Because heritability, phenotypic standard deviation, and selection intensity all play a role in determining its estimated value, genetic advance expressed as a percentage of the mean provides a more accurate indicator of how well selection has worked to improve a characteristic. The genetic advance ranged from grain yield per plot (0.12) to plant height (25.00). The estimate of genetic advance as per cent of mean ranged from panicle length (4.21%) to fat content (83.63%). Fat content (83.63%) followed by calcium content (63.14%), iron content (58.79%), fiber content (41.90%), grain yield per plant (36.93%), Straw yield per plant (34.40%), protein content (27.37%), grain yield per plot (22.54%), and grain yield per ha (22.41) revealed higher estimate of genetic advance as per cent mean, which clearly specified that highest priority should be given for these characters while formulating selection strategies and selection of these characters may be effective. Panicle length (4.21%) and days to maturity (5.53%) showed minimum genetic advance as per cent of mean. Similar results were observed by Savankumar *et al.* (2018) for days to maturity.

However, estimation of heritability along with genetic advance is more useful in predicting the resultant effect from selecting the best individual. In the present study, high heritability coupled with high genetic advance as per cent of mean was noticed in fat content (99.81, 83.63), iron content (96.91, 58.79), calcium content (89.80, 63.14), fiber content (84.13, 41.90,), grain yield per plant (78.39, 36.93), straw yield per plant (75.04, 34.40) and protein content (97.91, 27.37). It showed the presence of minor environmental impact and dominance of additive gene action in their expression. High heritability along with low genetic advance were detected for and thousand seed weight (93.75, 9.23), plant height (89.16, 17.70), days to 50 %

flowering (82.55, 8.78), days to maturity (65.60, 5.53), grain yield per plot (58.51, 22.54), grain yield per ha (58.39, 22.41), number of productive tillers per plant (40.20, 13.76), straw yield per plot (38.25, 15.35), and panicle length (33.59, 4.21) specifying these traits may be controlled by non-additive gene action. Similar results were recorded by Shivangi *et al*. (2017). While Sao *et al*. (2017) also recorded similar results for grain yield per plant and straw yield per plant.

4.6 Correlation

In plant breeding, an understanding of how characteristics interact with one another and with the environment is very helpful. By choosing the other of a pair of traits, it would be possible to improve the genetic makeup of one trait. Correlation studies provide information on the kind and degree of correlation between any two quantitative traits. In the current examination, a study of the relationships between the thirteen traits and the forty-four genotypes was conducted.

In the current study, the findings showed that all of the characteristics had phenotypic correlations that were generally higher than their genotypic counterparts. As a result, phenotypic correlations naturally link two factors; this linkage may be used to enhance crops in subsequent generations.

The characters grain yield per plant had positive highly significant correlation with number of productive tillers per plant, protein content, calcium content and straw yield per plant at both genotypic and phenotypic level indicating that these four traits could be important for improving the seed yield in little millet. Similar positive and significant correlation of grain yield with different quantitative traits were reported by Anuradha *et al.* (2017), Amarnath *et al.* (2018), Suryanarayana *et al.* (2018), Ayesha *et al.* (2019) and Sneha *et al.* (2019).

Days to 50% flowering exhibited positive highly significant correlation with days to maturity at both levels and with plant height at phenotypic level. It exhibited positive significant correlation with protein content at phenotypic level. But positive non-significant with the traits thousand seed weight, calcium content, fiber content, fat content, straw yield per plant and grain yield per plant, while it was negative and non-significantly associated with number of productive tillers per plant and iron content. Days to maturity recorded positive and non-significant association with thousand seed weight, protein content, calcium content, fiber content, straw yield per plant and grain yield per plant at both genotypic and phenotypic level. Whereas iron content and fat content showed negative non-significant with days to maturity. Lad *et al*. (2020) recorded highly significant association of days to 50% flowering with days to maturity and plant height.

Number of productive tillers per plant had positive highly significant correlation with protein content, straw yield per plant and grain yield per plant at both levels. Panicle length and calcium content was positive and highly significant at genotypic level whereas positive and significant at phenotypic level. Whereas it was positively and non-significantly correlated with days to maturity, thousand seed weight and fat content at both genotypic and phenotypic level. Jyothsna *et al*. (2016), Suryanarayana *et al*. (2018) and Shinde *et al*. (2018) reported similar results.

The character panicle length showed positive non-significant correlation with thousand seed weight, straw yield per plant and grain yield per plant at both genotypic and phenotypic levels. It indicated that increase in length of panicle and might give to high yields in little millet. This situation meant to select high yielding genotypes of little millet, it was essential to consider the above characters with their increasing magnitude. It helped in simultaneous improvement of all the positively correlated characters. Similar kind of highly significant positive association of panicle length with grain yield was reported earlier by Amarnath *et al*. (2018), and Ayesha *et al*. (2019).

At both genotypic and phenotypic levels thousand seed weight showed positive non-significant correlation with fiber content and fat content. While it had negative non-significant correlation with protein content, iron content, calcium content, straw yield per plant and grain yield per plant at phenotypic and genotypic level. Protein content had positive highly significant correlation with calcium content, straw yield and grain yield per plant at both levels. It showed negative non-significant correlation with fiber content at genotypic and phenotypic level. Calcium content had positive highly significant correlation with straw yield per plant and grain yield per plant at both level, while positive non-significant correlation with fiber content and iron content at genotypic and phenotypic level. Devaliya *et al*. (2017) reported that protein had positive and highly significant correlation with grain yield per plant at genotypic level.

Fiber content, fat content and iron content had positive but non-significant correlation with grain yield at both level. Straw yield per plant showed positive highly significant correlation with grain yield per plant at both level. Nagar *et al*. (2020), Chavan *et al*. (2019) reported the similar results for straw yield per plant.

4.7 Path analysis

The relationship between two trait pairs is measured by the correlation. However, a dependent characteristic is an interaction between a numbers of parts that are associated with one another. The path analysis considers the relationship of cause and effect between the variables by

dividing the association into direct and indirect effects through other independent variables to produce any such dependent variable.

Path coefficient analysis results revealed that days to 50% flowering had negative direct effect on grain yield per plant both at genotypic and phenotypic level. Its indirect effects through days to maturity, thousand seed weight, protein content, straw yield per plant and grain yield per plant were positive, while it had negative indirect effect for plant height at both phenotypic and genotypic levels. Lad *et al.* (2020) recorded similar results for days to maturity.

Plant height exhibited direct negative effect on grain yield per plant at both phenotypic and genotypic level. It had positive indirect effects via days to maturity, thousand seed weight, protein content, straw yield per plant and grain yield per plant at both level and indirect negative effects on days to 50% flowering and calcium content at both level. Andualem *et al.* (2011) and Anuradha *et al.* (2013) reported that plant height showed direct negative effect on grain yield per plant at genotypic level.

The character number of productive tillers per plant had positive direct effect on grain yield per plant at the phenotypic level and negative direct effect at genotypic level. Its positive indirect effect for grain yield per plant was highly significant, while traits like days to 50% flowering, plant height, days to maturity, thousand seed weight, protein content, calcium content and straw yield per plant were positive at both level and its indirect effect via fiber content and iron content were negative at genotypic level. Similar results were obtained by Jyothsna *et al*. (2016).

Days to maturity showed positive direct effect on grain yield per plant at both level. It had positive indirect effects via thousand seed weight, protein content, straw yield per plant and grain yield per plant, while it had negative indirect effects through days to 50% flowering and plant height at both phenotypic and genotypic levels. Similar results were reported by Jadhav *et al*. (2015), Lad *et al.* (2020).

The character panicle length revealed direct positive effect on grain yield per plant at genotypic level and negative effect at phenotypic level. It had positive indirect effect via days to 50% flowering, plant height, thousand seed weight, straw yield per plant and grain yield per plant at both genotypic and phenotypic level. It showed negative indirect effect with protein content at both level. Prakash *et al.* (2015), Amarnath *et al.* (2018), Ayesha *et al.* (2019) and Laxmi pallavi *et al.* (2020) stated that length of panicle showed direct positive effect on grain yield per plant.

The character thousand seed weight showed positive direct effect on grain yield per plant at both genotypic and phenotypic level. It had positive indirect effect through panicle length and days to maturity at both level and negative indirect effect via days to 50% flowering, protein content, straw yield per plant and grain yield per plant at both level. These results are in agreement with Jadhav *et al*. (2015) Negi *et al.* (2016), laxmi pallavi *et al.* (2020)

Protein content indicates low positive direct effect on grain yield per plant at both levels. It showed positive indirect effect on days to maturity, calcium content, straw yield per plant and grain yield per plant at phenotypic and genotypic level, while negative indirect effect via days to 50% flowering, plant height and thousand seed weight at both level. Devaliya *et al*. (2017) reported that protein content had positive direct effect on grain yield per plant at genotypic level.

Calcium content had negligible positive direct effect on grain yield per plant at the phenotypic and genotypic level. Its negative indirect effect on grain yield through days to50% flowering and number of productive tillers per plant at genotypic level and positive indirect effect *via* plant height, days to maturity, protein content, straw yield per plant and grain yield per plant at both level. Devaliya *et al*. (2017) recorded similar results in association with grain yield per plant.

Fiber content had positive direct effect on grain yield per plant at phenotypic level and negative at genotypic level. It showed negative indirect effects through number of productive tillers per plant, panicle length, protein content and iron content at genotypic level whereas positive effect at phenotypic level. It showed positive indirect effect on straw yield and grain yield per plant at both levels.

The trait iron content indicated positive direct effect on grain yield per plant at phenotypic level and negative direct effect at genotypic level. It had positive indirect effects through days to 50% flowering, protein content, calcium content, straw yield per plant and grain yield per plant at both level where they showed negative indirect effects via plant height, days to maturity and thousand seed weight at both level.

Fat content had negative direct effect on grain yield per plant at phenotypic level while positive effect at genotypic level. Its negative indirect effect through days to 50% flowering, plant height, days to maturity at both level, while positive effect on thousand seed weight, protein content, calcium content, straw yield and grain yield per plant at both level.

The trait straw yield per plant had highest positive direct effect on grain yield per plant at phenotypic level and genotypic level. It had positive indirect effects through days to maturity, protein content calcium content and grain yield per plant at both level. It showed negative

indirect effect via days to 50% flowering, plant height, number of productive tillers per plant, fiber content and iron content at genotypic level. Devaliya *et al*. (2017), Chavan *et al*. (2019) reported that straw yield per plant had positive direct effect on grain yield per plant at genotypic level.

4.8 Genetic divergence

The significant extent of variability in the quantitative characters appears to lead the wide range of genetic diversity among the biological genotypes under study. Therefore, D^2 statistics (Mahalanobis, 1936) was done to measure the degree of divergence among the little millet (*Panicum sumatrense* L.) genotypes to calculate the relative contribution of different components to the total divergence at inter and intra cluster levels.

Thus, the forty four genotypes were grouped into five clusters, which directed a wide range of variation among the genotypes studied. The Cluster I was the largest which consisted of 16 genotypes, followed by clusters III with 9 genotypes, cluster II and V with 8 genotypes and cluster IV with 3 genotypes. From the clustering pattern, it was found that the genotypes collected from different regions were independent of their genetic region. Hence, the genotypes studied are reliable enough for hybridization and selection.

Based on the divergence Selvi *et al.* (2015) grouped 110 little millet genotypes into five distinct clusters, Kumari *et al.* (2015) grouped 35 genotypes of finger millet into six clusters, Ulaganathan *et al.* (2015) grouped 305 finger millet genotypes into sixteen clusters, Mahanthesha *et al.* (2017) grouped 48 genotypes of finger millet into eight clusters, Nirubana *et al.* (2017) studied 103 genotypes of kodo millet and were grouped into eleven different clusters, Sarjansinh *et al.* (2017) grouped 68 genotypes of finger millet into eight clusters, Negi *et al.* (2018) grouped 35 genotypes of finger millet into six clusters, Suryanarayana et al. (2018) grouped 23 genotypes of little millet into six clusters, Thippeswamy *et al.* (2018) grouped 149 genotypes of foxtail millet into fifteen clusters, Anteneh *et al.* (2019) grouped 225 genotypes of finger millet into five distinct clusters, Jyoti *et al.* (2020) studied 33 genotypes of Little millet which were grouped into five clusters.

The cluster I was covered sixteen genotypes. These genotypes were better average for days to 50% flowering, number of productive tillers per plant, panicle length, thousand seed weight, calcium content, fiber content, grain yield per plant and straw yield per plant .

The cluster II consists of eight genotypes. These genotypes were better average for number of productive tillers per plant and fiber content.

The cluster III included nine genotypes which had better average for the characters days to 50% flowering, plant height, number of productive tillers per plant, panicle length, days to maturity, protein content, calcium content, fat content, straw yield per plant and grain yield per plant.

The cluster IV contained of only three genotypes, which had better average for the characters days to 50% flowering, plant height, days to maturity, thousand seed weight, iron content and fat content.

The cluster V consists of eight genotypes. This cluster had only one genotype that has better average for the trait panicle length than the population mean.

In addition to the cluster mean for a certain characteristic, another measure called intra-cluster distance was used to determine how variable the genotypes in a given cluster were.

High intra-cluster distance inside a cluster suggests a high degree of diversity within the cluster and gives opportunity for development through various selection techniques. The highest intra cluster distance was detected for cluster III (D=7.98) followed by cluster IV (D=7.94), cluster V (D=7.50), cluster II (D=7.32) and cluster I (D=7.03). The inter-cluster studies directed magnitude of genetic divergence between the clusters. It revealed that, how much this clusters were genetically diverse from each other. In present analysis, the maximum inter cluster distance was observed between cluster II and III (D=10.28) followed by cluster II and V (D=9.90), cluster II and IV (D=9.45), cluster I and II (D=9.12), cluster III and IV (D=8.89), cluster I and III (D=8.56) and cluster I and IV (D=8.55), cluster IV and V (8.48) and cluster III and V (8.47), while inter cluster distance between cluster I and V (D=7.98) noted moderate inter cluster distance.

The genotypes which involved in genetically diverse clusters i.e. cluster II and III (D=10.28) followed by cluster II and V (D=9.90), cluster II and IV (D=9.45), cluster I and II (D=9.12) might be used in hybridization programme for further crop improvement in little millet.

4.8.1 Contribution of each character towards total divergence

We can determine the degree of divergence between two clusters by using D2 values. Which traits are responsible for the genotype divergence? That is the ensuing question. Breeders can learn about the characteristics that are mostly responsible for the overall divergence by examining the contributions of various characters to it. This is important when choosing the parents for a breeding programme.

Out of 13 character studied highest contribution was reported in fat content (34.00%) followed by fiber content (15.13%), grain yield per plant (12.77%), calcium content (10.53%),

thousand seed weight (7.38%), number of productive tillers per plant (5.78%), protein content (5.40%), iron content (3.77%), straw yield per plant (3.11%) and plant height (1.37%). It is clear that the yield is the dependent character controlled by a number of other yield-contributing characteristics, each of which is influenced by a specific environment at a unique place. As a result, it is not possible to adjust the character variability across genotypes for breeding only on the basis of yield potential. In order to enhance it, selection must be made taking into account factors such as fat content, fiber content, grain yield and per plant, calcium content, thousand seed weight, number of productive tillers per plant, protein content and straw production per plant because these factors contribute more to total divergence.

4.8.2 Ranking and Selection

The variety seen in the little millet genotypes indicates that the selection process will be successful in increasing seed output. No isolated group could have all the ideal traits at once. Isolating the genotypes with the greatest number of desired features would be preferable. However, genotypes can be chosen for study based on yield performance and significant yield-attributing features. Characters with high variability, substantial economic significance, and a strong correlation to seed output per plant were chosen for future exploitation. The number of productive tillers, days to maturity, panicle length, protein content, calcium content, iron content, straw yield per plant and other traits should be given higher priority when choosing little millet genotypes for breeding strategies because they have high variability, heritability, highly significant correlation, and high positive direct effects on seed yield per plant.

The following genotypes are chosen for further study in the current investigation based on yield and significant yield attributing characters which are given in table 4.15.

Table 4.15 Promising genotypes with important yield contributing characters.

Genotypes	Grain yield per plant	Plant height	Number of productive tillers per plant	Length of panicle	Rank
DPLV-27	11.03	139.50	3.90	42.10	I
DPLV-26	8.75	140.20	3.80	42.60	II
DPLV-16	8.70	151.80	3.30	41.10	III
DPLV-11	7.98	145.70	2.90	40.30	IV
LM-6	7.65	161.40	3.30	42.30	V
DPLV-10	7.63	139.60	3.40	39.90	VI
DPLV-5	7.35	144.40	2.90	37.40	VII
DPLV-12	7.35	134.90	3.50	42.00	VIII
DPLV-4	7.30	148.00	3.30	40.20	IX

CHAPTER V: SUMMARY AND CONCLUSION

The present investigation entitled, "Genetic diversity studies in Little millet (*Panicum sumatrense* L.)" was undertaken with the following objectives

1) To estimate genetic variability among different genotypes of Little millet for yield and yield components.

2) To study of magnitude of direct and indirect effects on important yield components through path analysis.

3) Measurement of divergence between different genotypes by D^2 statistics.

The present study comprises of forty four genotypes out of which twenty seven genotypes collected from local area of konkan region while remaining seventeen genotypes were collected from zonal agriculture research station Kolhapur. These genotypes were cultivated in a randomised block design with two replications during the *Kharif* 2021. Sixteen quantitative and eight qualitative characters were observed, including the days to 50% flowering, plant height, number of productive tillers per plant, panicle length, days to maturity, thousand seed weight, grain yield per plot, grain yield per ha, straw yield per plot, protein content, calcium content, fiber content, iron content, fat content, straw yield per plant and grain yield per plant. Whereas qualitative characters comprises of plant growth habit, plant pigmentation, inflorescence shape, panicle compactness, culm branching, leaf sheath: pubescence, ligule: pubescence and leaf blade: pubescence.

The analysis of variance indicated a considerable variation in genotypes for each of the investigated characteristics. For almost all of the features under study, the estimations of the mean sum of squares revealed a comparably broad range of variance. The parameters with the greatest range of variance were plant height (cm), days to 50% flowering, days to maturity, calcium content, panicle length, and grain yield per hectare. The grain yield per plot, thousand seed weight, straw yield per plot and number of productive tillers per plant showed less variation.

Among the genotypes, LM-4 and DPLV-12 were earliest in days to 50% flowering and days to maturity. Maximum number of productive tillers per plant was noted in DPLV-27. LM-13 was the shortest in height. Among the genotypes maximum panicle length recorded in LM-12. LM-11 and LM-6 showed highest thousand seed weight. Out of 44 genotypes, 40 genotypes had arched inflorescence shape and only 4 genotypes having diffused type inflorescence, while 27 genotypes showing plant pigmentation whereas plant pigmentation is absent in remaining 17

genotypes. Out of 44 genotypes of Little millet, 37 genotypes had erect type plant growth habit whereas 7 genotypes had decumbent plant growth habit. Out of 44 genotypes of little millet only 2 genotypes showing pubescence on leaf blade whereas 42 genotypes having no pubescence on leaf blade. Culm branching, Ligule: pubescence and Leaf sheath: pubescence were absent in Little millet genotypes. The maximum protein content was recorded in DPLV-27 while maximum calcium content was recorded in DPLV-27. Maximum fiber content was recorded in LM-17 whereas DPLV-10 showed maximum value of iron content. DPLV-1 had maximum fat content. DPLV-27 had maximum grain yield per plant, DPLV-27 had maximum straw yield per plant.

Estimates of phenotypic, genotypic, and environmental variations revealed that for all the investigated traits, phenotypic variances were greater than genotypic variances. For the majority of the traits, the phenotypic and genotypic variations were smaller and closer together, indicating a less important role for the environment in the expression of these components. However, days to maturity and plant height, however, showed comparably greater estimates of environmental variation, showing the effect of the environment on these characters. In general, for all the traits, the phenotypic coefficient of variance was larger than the corresponding genotypic coefficient of variation. At both the phenotypic and genotypic levels, different traits show varied coefficients of variation. Fat content, calcium content, iron content, fiber content, grain yield per plant and straw yield per plant all had high genotypic and phenotypic coefficients of variation. However, days to 50% flowering, thousand seed weight and days to maturity had low genotypic and phenotypic coefficients of variation. High heritability was detected for the characters fat content, protein content, iron content, thousand seed weight, calcium content, plant height, fiber content, days to 50% flowering, grain yield per plant and straw yield per plant. While low heritability was observed in number of productive tillers per plant and panicle length. Genetic advance found to be highest for plant height followed by days to 50% flowering. While fat content showed comparatively higher estimates of genetic advance as per cent of mean.

The heritability estimates along with genetic advance as percent of mean were recorded high for fat content, calcium content, iron content, fiber content, grain yield per plant and straw yield per plant. It indicates that the role of additive gene action in the appearance of these characters and can be upgraded by selection.

In the current study, the phenotypic correlation coefficients were higher than their respective genotypic correlation coefficients. The correlation studies showed that number of productive tillers per plant, protein content, calcium content and straw yield per plant revealed highly significant positive correlation with grain yield per plant at both phenotypic and genotypic levels. Fiber content and iron content showed positive and significant correlation with grain yield

at genotypic level and positive but non-significant correlation at phenotypic level. Among the remaining characters *viz*., days to 50% flowering, plant height, panicle length, days to maturity and fat content had positive non- significant correlation with grain yield per plant at both level. Thousand seed weight had negative non-significant correlation with grain yield per plant at both phenotypic and genotypic level.

Path coefficient analysis shown that the characters *viz*., days to maturity, thousand seed weight, protein content, calcium content and straw yield per plant had positive direct effect on grain yield at both level while, days to 50% flowering and plant height exhibited negative direct effect on seed yield per plant at both phenotypic and genotypic levels. The character panicle length and fat content had positive direct effect on grain yield per plant at phenotypic level and negative direct effect at genotypic level. The character number of productive tillers per plant, fiber content and iron content had positive direct effect on grain yield per plant at phenotypic level and negative direct effect at genotypic level.

Genotypes were subdivided into various groups in the conservation of genetic resources and their utilization. Forty four genotypes were grouped into 5 different clusters on the basis of magnitude of D^2 values estimated by Mahalanobis D^2 analysis. Among forty four genotypes, 16 genotypes were clustered into first cluster followed by cluster II having 8 genotypes, cluster III having 9 genotypes, cluster IV concluding 3 genotypes and cluster V contain 8 genotypes. The maximum intra–cluster distance was observed in cluster III (D= 7.98), thus signifying that different genotypes included in this cluster might have different genetic construction. However, the lowest intra–cluster distance found in cluster I (D = 7.03) designated that the genotypes resembled one another genetically and seemed to have developed from a common gene pool. The inter–cluster distance was high between cluster II and III (D=10.28) and cluster II and V (D=9.90), there by displayed wide range of variation among the clusters formed. Hence, the genotypes underlying in these clusters could be selected and nominated for hybridization to obtain potential segregates. On the other hand, the lowermost inter–cluster distance (Between cluster I and V) proposed that the genetic constitution of the genotypes in both the clusters were in close proximity. Out of 13 character studied highest contribution was reported in fat content in %(76.00%) followed by iron content in mg (8.77%), protein content (7.40%), thousand seed weight in g (3.38), plant height in cm (1.37), fiber content in % (1.27) and grain yield per plant in g (0.74). Hence, these characters may be considered during selection of genotypes for further improvement.

CONCLUSION

As a result of the current investigation, it is clear that a wide range of variability exists for various traits, along with high heritability and high genetic advance as percentage of the mean for significant yield traits like plant height, days to 50% flowering, days to maturity, thousand seed weight, protein content, calcium content, iron content, fat content and grain yield per plant. Therefore, selections based on the traits could directly increase productivity in little millet. Four of the thirteen quantitative characteristics the number of productive tillers per plant, protein content, calcium content, and the straw yield per plant were highly significant and positively correlated with grain yield at both the phenotypic and genotypic levels. Days to maturity, panicle length, thousand seed weight, protein content, calcium content, fat content had a favourable direct impact on the grain yield. Therefore, these features might be used in direct selection in order to increase little millet's grain output. The current analysis also showed that clusters II and III were the most diverse among themselves. Based on the findings, the genotypes DPLV-27, DPLV-26, DPLV-16, and DPLV-11 are best performer having good genetic diversity used as a parent in a future hybridization programme.

CHAPTER VI : LITERATURE CITED

Amarnath, K., Durga Prasad, A.V. and Reddy, C. M. 2018. Character association and path analysis in foxtail millet genetic resources [*Setaria italica* (L.) Beauv]. Int. J. Chem. Stud. 6(5): 3174-3178.

Anteneh, D., Mekbib, F., Tadesse, T. and Dessalegn, Y. 2019. Genetic diversity among low land finger millet [*Eleusine coracana* (L.) Gaertn.] accessions. Ethiop. J. Agric. Sci. 29(2): 93-108.

Anuradha N., Udaya, B. K., Patro T.S.S.K. and Sharma N.D.R.K. 2013. Character association and path analysis in finger millet [*Eleusine coracana* (L.) Gaertn.] accessions belongs to mate maturity group. Int. j. food agric. Vet. Sci. ISSN: 2277-209X.

Anuradha, N., Patro, T.S.S.K., Divya, M., Sandhya Rani, Y., and Triveni, U. 2017. Genetic variability heritability and correlation of quantitative traits in little millet genotypes. J. pharmacogn.phytochem. 6(6): 489-492.

Anuradha, N., Kranthi, P. P., Patro, T.S.S.K. Sandhya Rani, Y. and Triveni, U. 2020. Association studies in little millet (*Panicum sumatrense* L.) for yield and other important traits. Int.J.Microbiol.App.Sci. Special Issue-11: 1465-1472.

Arunachalam, V., Rengalakshmi, R. and Kubera, M.S. 2003. Ecological stability of genetic diversity among landraces of little millet (*Panicum sumatrense*) in south India. *Genet Resour Crop Evol* 52, 15–19.

Ayesha, M. D. and Ratna, B. D. 2019. Genetic divergence studies in foxtail millet [*Setaria italica* (L.) Beauv.]. EJPB 10(1):18-29.

Baghel B.R.S. and Maloo, S.R. 2004. Character Association and Path Coefficient Analysis in Proso Millet (Panicum miliaceum L.). Agric. Sci. Digest. 24(1).

Barrows, H. L., and Simpson, E. C.1962. An EDTA method for the direct routine determination of calcium and magnesium in soils and plant tissue. Soil Science Society of America Journal 26.5 :443-445.

Burton, G.W. and De Vane, E.H. 1953. Estimating heritability in tall Fescue (*Festuca arundinaceae*) from replicated clonal material. J. Agron., 45 (2): 478-481.

Chavan, B. R., Jawale, L. N., and Shinde, A. V. 2019. Correlation and path analysis studies in finger millet for yield and yield contributing traits (*Eleusine coracana* L. Gaertn). Int. J. Chem. Stud.; 8(1): 2911-2914.

Choudhary, D .R., Chaudhary, P. P., Narwade, A. V., Pandya, M. M., and Patel, J. V. 2014. Studies on phenotypic and genotypic variation in finger millet (*Eleusine coracana* L.) Trends in Biosciences 7(3): 180-182.

Devaliya, S. D., Singh, M. and Visat, J. V. 2017. Character Association and Path Analysis in Finger Millet (*Eleusine coracana* (L.) Gaertn.). Trends in Biosciences 10 (31).

Dewey, O.R. and Lu, K.H. 1959. A correlation and path coefficient analysis of components of crested wheatgrass seed production. J. Agron., 57(1): 515-518.

Dhanalakshmi, R., Subramanian, A., Thirumurugan, T., Elangovan, M. and Kalaimagal, T. 2019. Genetic variability and association studies in barnyard millet (*Echinochloa*

frumentacea (Roxb.) Link) germplasm under sodic soil condition. Electron. J. Plant Breed. 10 (2): 430-439.

Gangurde, S. S., Moharil, M. P., Jadhav, P. V., Wandhare, Gawai, M. S., Dikshit, D., Suprasanna, N. P. and Dani, R. G. 2016. Genetic divergence studies in foxtail millet (*Setaria italica* L.). EJPB 7(3): 514-519.

Geethanjali, S. and Jegadeeswaran, M. 2016. Genetic diversity and variability in Foxtail millet [*Setaria italica* (L.)] germplasm based on morphological traits. EJPB ISSN 0975-928X.

Gohel, D. S. and Chaudhari, S. B. 2018. Study of correlation and path analysis of finger millet genotypes (*Eleusine coracana* L. Gaertn*)* J. pharmacogn. Phytochem. 7(6): 1283-1288.

Govindaraj, M., Selvi, B., Rajarathinam, S. and Sumathi, P. 2011. Genetic variability and heritability of grain yield components and grain mineral concentration in india's pearl millet (*pennisetum glaucum* (l) r. br.) accessions. African J. Food, Agric. Nutr. Dev. 11(3).

Gowri, U.M. and Shivankumar, K. M. 2020. Agric Econ AGR (TNAU), Coimbtore,Tamil Nadu, India.

Himanshu, C.M., Sonawane, S. K. and Arya S. S. 2018. "Nutritional and nutraceutical properties of millets: a review." Clinical Journal of Nutrition and Dietetics 1.1 (2018): 1-10.

Jackson, M. I. L. 1973. Soil chemical analysis: Prentice Hall of India Pvt. Ltd., New Delhi.

Jadhav, R., Ratna B. D., Lal, A. M. and Srinivasa Rao, V. 2015. Character association and path coefficient analysis for grain yield and yield components in finger millet (*Eleusine coracana* (L.) Gaertn.). EJPB 6(2): 535-539.

Johanson, H.W., Robinson, H.F. and Comstock, R. F.1955. Estimation of genetic environmental variability in soybean. J. Agron. 47(1): 314-318.

Jyothsna, S., Patro, T.S.S.K, Rani, S. Y., Neeraja, B., Ashok, S. and Triveni, U. 2016. Studies on genetic parameters, character association and path analysis of yield and its components in little millet (*Panicum sumatrense*). Int.J.Agric.Sci. 8(6):1018-1020.

Kavya, P., Sujatha, M., Pandravada, S. R., and Hymavathi, T. V.2017. Variability Studies in Foxtail Millet [*Setaria italica* (L.) P. Beauv] Int.J.Curr.Microbiol.App.Sci 6(9): 955-960.

Kumar, D., Tyagi,V. and Ramesh, B. 2014. Path Coefficient Analysis for Yield and its Contributing Traits in Finger Millet. J. Adv. Res.Volume 2, Issue 8, 235-240.

Kumari, S. and Singh, S.K. 2015. Assesment of genetic diversity in promising finger millet [*Eleusine coracan*a (L.) Gaertn.] genotypes. The Bioscan, 10(2): 825-830.

Lad, B. D., Mahalle, S. P. and Bade, B.A. 2020. Association of characters and path coefficient analysis for yield and its components in finger millet (*Eleusine coracana* (L.) Gaertn.) genotypes. J.pharmacogn.phytochem. 9(5): 599-602.

Lakshmi, N., Pallavi, R., Venkatesh, B, Jalandar Ram and Suresh, B. G. 2020. Studies on correlation and path coefficient analysis in foxtail millet [*Setaria italica* (L.) BEAUV]. IJCS; 8(6): 1941-1946.

Lush, J.C. (1949). Heritability of quantitative characters in farm animals. Proceeding of 8th Congress hereditas, 28 (3): 356-375.

Mahalanobis, P.C. 1936. On the Generalized Distance in statistics. Proc. Indian National Sci.Inst. 2(2): 49-55.

Mahanthesha, M., Sujatha, M., Pandravada, S. R. and Kumar, A. M. 2017. Study of Genetic Divergence in Finger Millet (*Eleusine coracana* (L.) Gaertn) Germplasm. Int. J. Pure App. Biosci. 5 (3): 373-377.

McLaren, R. G., and Crawford, D. V. 1950. Studies on soil copper: II. The specific adsorption of copper by soils. J. Soil Sci. 24.4: 443-452.

Nagar, J., Kumar, B., Sahu, B., Kumar, S. and Joshi, R. P. 2020. Studies on character association and path coefficient analysis for grain yield and its influencing traits in little millet (*Panicum sumatrense*). J.pharmacogn.phytochem. 9(3): 1899-1900.

Negi, A. S., Pandey, P. K. and Shrotria, P. K. 2017. Correlation and Path Coefficient Analysis of Component Attributes in Finger Millet [*Eleusine Coracana* (L.) Gaertn.] Environ. Ecol. 34 (4C) : 1852—1856.

Nirmalakumari, A., Salini, K. and Veerabadhiran, P. 2010. Morphological characterization and Evaluation of little millet (*Panicum sumatrense* Roth.ex.Roem. and Schultz.) Germplasm. Electron. J.Plant Breed.1(2) : 148-155.

Nirubanav, V., Ganesamurthy, K., Ravikesavan, R., and Chitdeshwari, T. 2017. Genetic Diversity studies in Kodo millet (*Paspalum scrobiculatum* L,) Germplasm Accessions Based on Based on Biometrical and Nutritional Quality Traits. Int.J.Curr. Microbiol. App. Sci. 6(10): 832-839.

Panse, V. G. and Sukhatme, P. V. 1985. In Statistical Methods of Agricultural Workers. ICAR publications, New Delhi, 327-340.

Patel, S. N., Patil, H. E., Modi, M. and singh, T.J. 2018. Genetic variability study in little millet (*Panicum miliare* L.). Genotypes in relation to yield and quality traits. Int J Curr Microbiol Appl Sci. 7(6): 2712- 2725.

Patel, S. N., Patil, H. E., Patel, S. P. and Patel, U. M. 2018. Genetic diversity studied in relation to yield and quality traits in little millet (*Panicum miliare* L.). Int J Curr Microbiol Appl Sci. 7(6): 2702-2711.

Patil, A.S and Mane, V.A. 2013. Studies on the genetic variation of yield and contributing traits in finger millet (*Eleusine coracana* L. Gaertn). Progress. Res. J. 8: 526-528.

Prakash, R. and Vanniarajan, C. 2015. Path analysis for grain yield in barnyard millet (*Echinochloa frumentacea* Roxb. Link). Bangladesh J. Bot. 44(1): 147-150.

Rao, C.R. 1952. Advanced statistical methods in biometrical research. John Wiley and Sons Inc., New York.

Sao, A., Singh, P., Kumar, P. and Pradhan, A. 2017. Estimates of Genetic Parameters for Yield and Contributing Traits in Kodo Millet (*Paspalum scrobiculatum* L.). Res.J.Agric.Sci. 8(1): 120-122.

Sarjansinh, D. Devaliya, M. S. and Intawal, C. G. 2017. Genetic Divergence Studies in Finger Millet [*Eleusine coracana* (L.) Gaertn.]. Int.J.Curr.Microbiol.App.Sci . 6(11): 2017-2022.

Savankumar, N. P., Patil, H.E.,. Modi, H. M and singh, T. J. 2018. Genetic variability study in little millet (*Panicum miliarie* L.) Genotypes in relation to yield and quality traits. Int.J.Curr.Microbiol.App.Sci , 7(6): 2712-2725.

Selvi, V. M., Nirmalakumari, A. and Subramanian, A. 2014. Genetics and interrelationships of yield traits for enhancing productivity of little millet. Electron. J. Plant Breed. 5(1): 82-86.

Selvi, V. M., Nirmalakumari, A. and Subramanian, A. 2015. Assessment of Genetic Diversity using Morphometric traits Little millet (*Panicum sumatrense*). Biosci Trends 8(1), Print : ISSN 0974-8.

Shinde, S. R., Desai, S. V. and Pawar, R. M. 2013. Genetic diversity pattern in finger millet [*Eleusine coracana* (L.) Gaertn]. EJPB, 4(3): 1242-1245.

Shinde, S. S., Karad, S. R. and Kadake, D. S. 2018. Correlation and path analysis studies on little millet (*Panicum sumatrense* L.). Int.J. Appl.Agric.Sci. 9(1): 21-23.

Shingane, S., Gomashe, S., Ganapathy, K. N. and Patil, J.V. 2016. Genetic variability and association analysis for Grain yield and Nutritional Quality in Foxtail millet. Int. j. bioresour. Stress manag. 7(6):1239-1243.

Sivasubramanian, S. and Menon, P.M. 1973. Genotypic and phenotypic variability in rice.Madras Agric. J. 60:1093-1096.

Sneha, R., Sapkal, V.V., Bhavsar., K.K. and Sarika, N. 2019. Correlation and path analysis for different characteristics in germplasm of finger millet [*Eleusine coracana* (L.) Gaertn]. Int. J. curr. Microbial. 8(1): 1020-1027.

Stansfield, W. D. 1969. Theory and practices of genetics.McGraw Hill, New York pp. 461.

Subramanian, A., Nirmalakumari, A. and Veerabadhiran, A. 2010. Trait based selection of superior kodo millet (*Paspalum scrobiculatum* L.) genotypes. EJPB 1(4): 852-855.

Suryanarayana, L. and Sekhar, D. 2018. Studies on genetic variability, character association and path analysis in little millet (*Panicum sumatrense* L.) genotypes. J.Pharm. Innv.7(7) : 908-910.

Suthediya, V. R., Desai, S. S., Pethe, U. B., Naik, K. V., Mahadik, S. G. and Pendyala, G. 2020. Genetic variability studies for yield and nutritional traits in foxtail millet (*Setaria italica* (L.) Beauv.). J.pharmacogn. phytochem. 9(6): 596-600.

Tandom, H. L. S. 1993. Methods of analysis of soils, plants, water and fertilizers. FDCO, New Delhi, India.

Thakur, J., Kanwar, R.R. Prafull Kumar, J.L. and Salam, S. K.2018. Studies of Genetic Parameters for Yield and Yield Attributing Traits of Kodo Millet (*Paspalum scrobiculatum* L.). Int. J. curr. Microbial. 7(9): 278-287.

Thakur, J., Kumar, V and R.R. Kanwar 2020. Genetic divergence studies in Kodo millet (*Paspalum scrobiculatum* L.). J. pharmacogn. Phytochem. 9(6): 1373-1377.

Thakur, J., Kumar, V. and Kanwar, R. R. 2020. Genetic divergence studies in kodo millet (*Paspalum scrobiculatum* L.). J.pharmacogn. phytochem. 9(6): 1373-1377.

Thippeswamy, V., Sajjanar, G.M. and Prabhakar. 2018. Genetic diversity analysis for yield and yield components in foxtail millet [*Setaria italica* (L.) Beauv.]. Int. J. Plant Sci. 13(1): 82-89.

Ulaganathan,V. and Nirmalakumari, A.2015. Finger millet germplasm characterization evalution using principal component analysis. SABRAO J Breed Genet. 47 (2) 79- 88.

Uma, G. M. and Shivakumar, K.M. 2020. Millet Scenario in India. Economic Affairs, Vol. 65, No. 3, pp. 363-370.

Venkataratnam, T., Latha, L. M., Sekhar, M. R. and Kumar, A. N. 2019. Studies on correlation and path analysis in little millet (*Panicum sumatrense*) Green farming Vol. 10 No.6 pp.679-682.

Wolie, A. and Tadesse, D. 2011. Correlation and path coefficient analyses of some yield related traits in finger millet [*Eleusine coracana* (L.) Gaertn.] germplasms in northwest Ethiopia. Afr. J. Agric. Res. 6(22): 5099-5105.

Wolie, A., Dessalegn, T. and Belete, K. 2013. Heritability, variance components and genetic advance of some yield and yield related traits in Ethiopian collections of finger millet (*Eleusine coracana* (L.) Gaertn.) genotypes. Afr. J. Biotechnol.Vol. 12(36), pp. 5529-5534.

Plate I: General view of the plot

Plate II: Variation in panicle length

1. LM-12
2. LM-16
3. LM-13
4. LM-15
5. DPLV-1
6. DPLV-3
7. DPLV-20
8. LM-1
9. DPLV-7
10. DPLV-8
11. DPLV-6
12. DPLV-5
13. DPLV-13

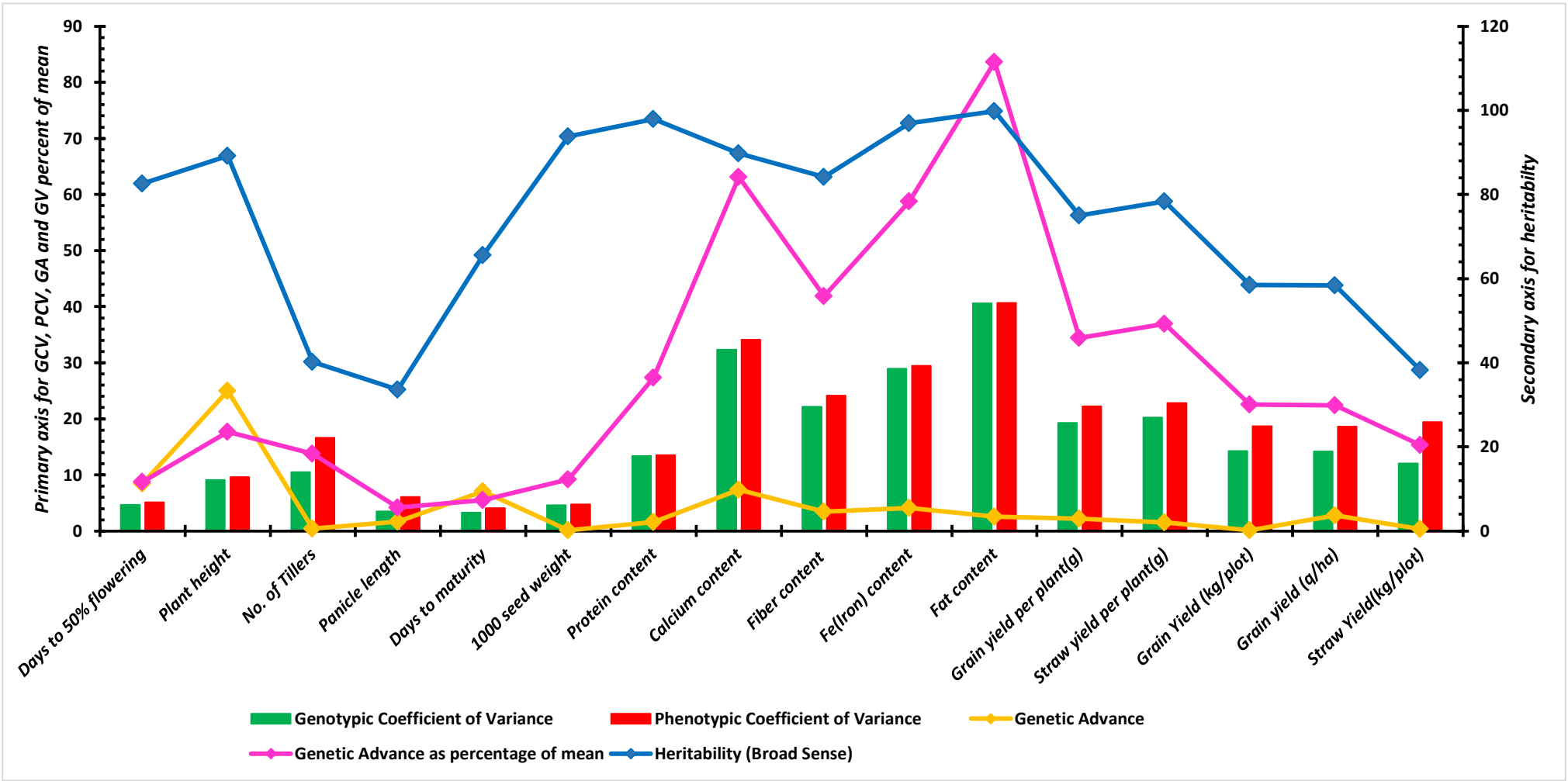

Fig. 4.1 Shows a graphical representation of genotypic and phenotypic coefficient of variation, heritability and genetic advance as per cent of mean.

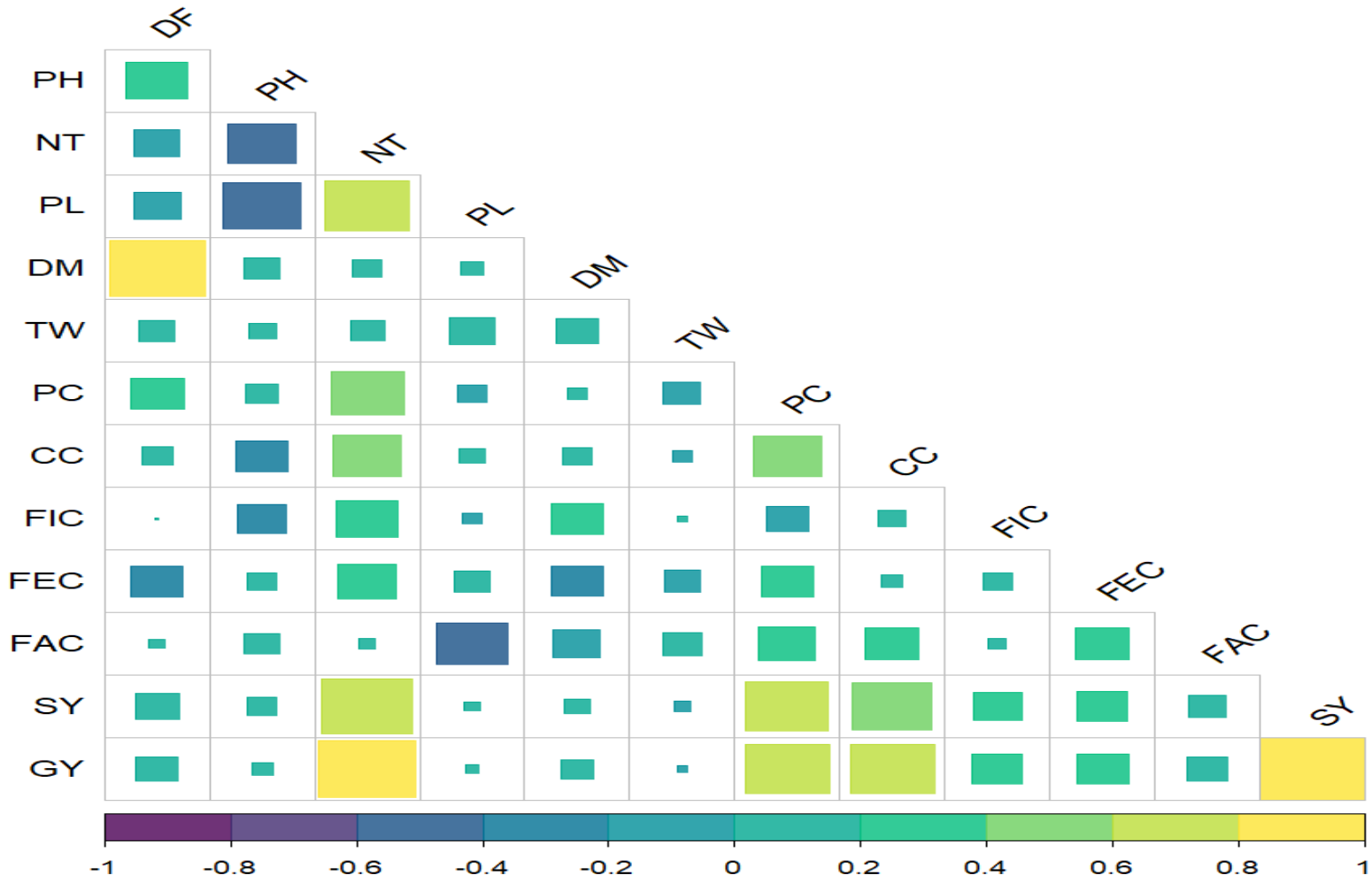

Fig.4.2 Phenotypic corplot

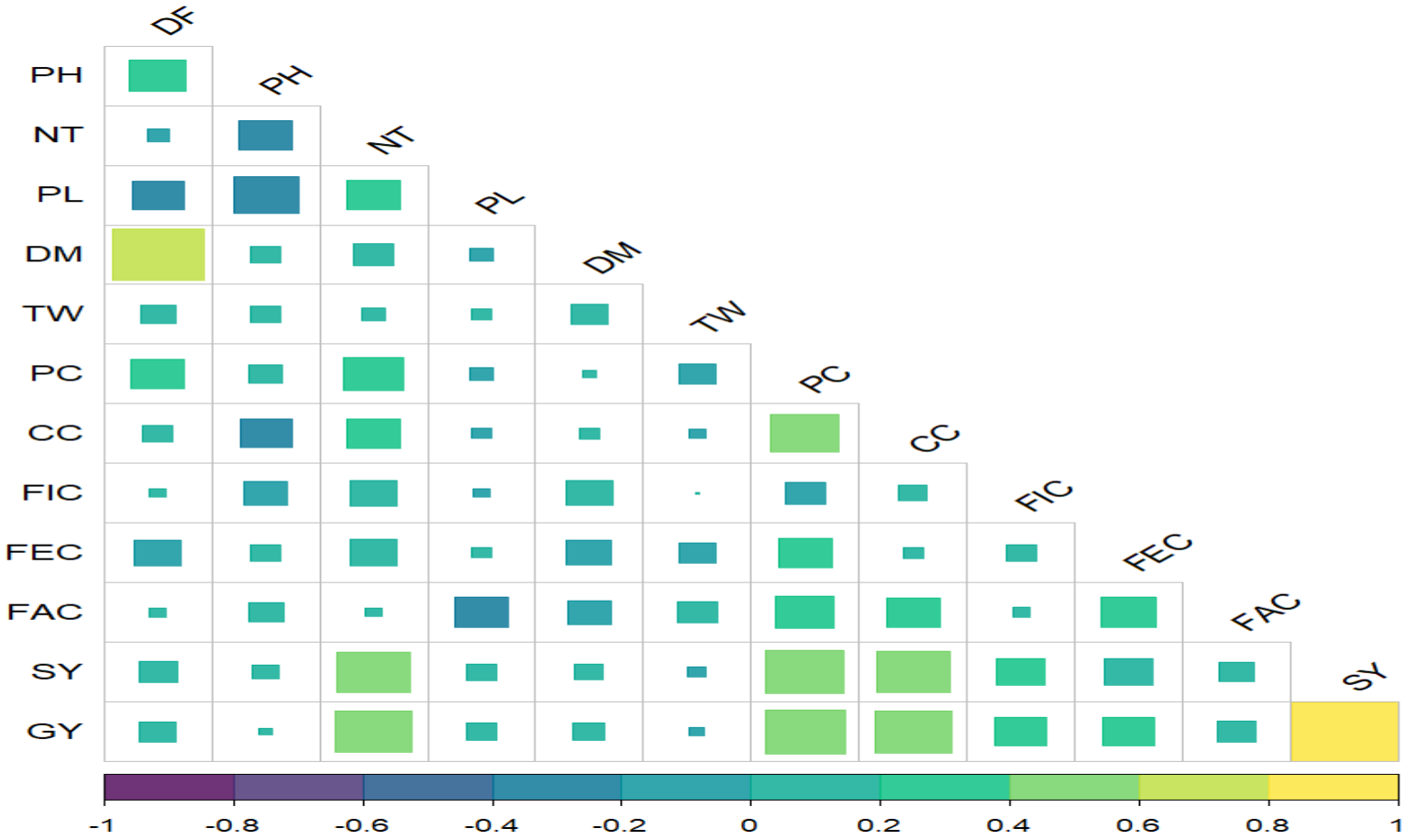

Fig 4.3 Genotypic corplot

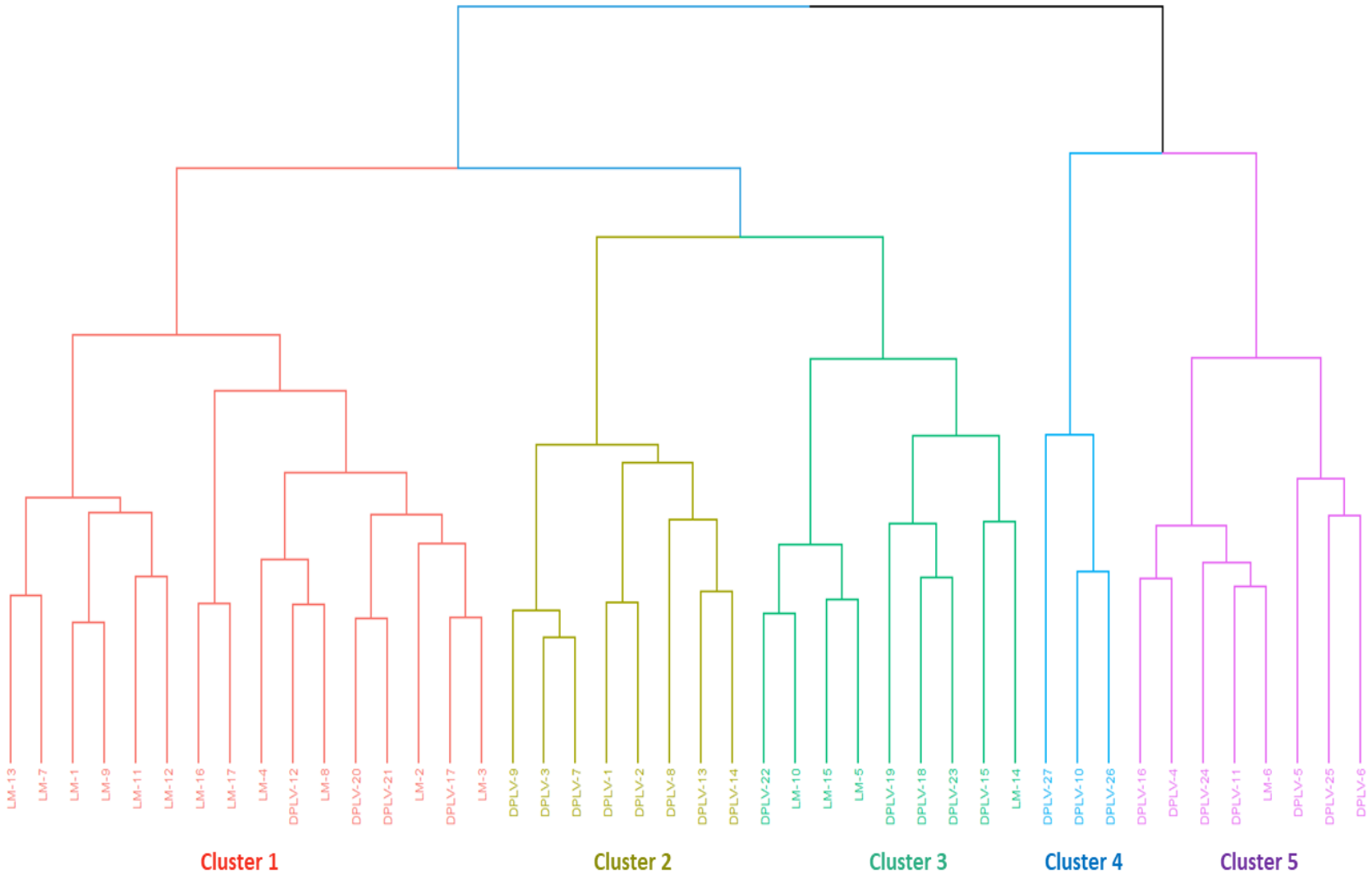

Fig 4.4 Clustering by Tocher method (Dendogram)

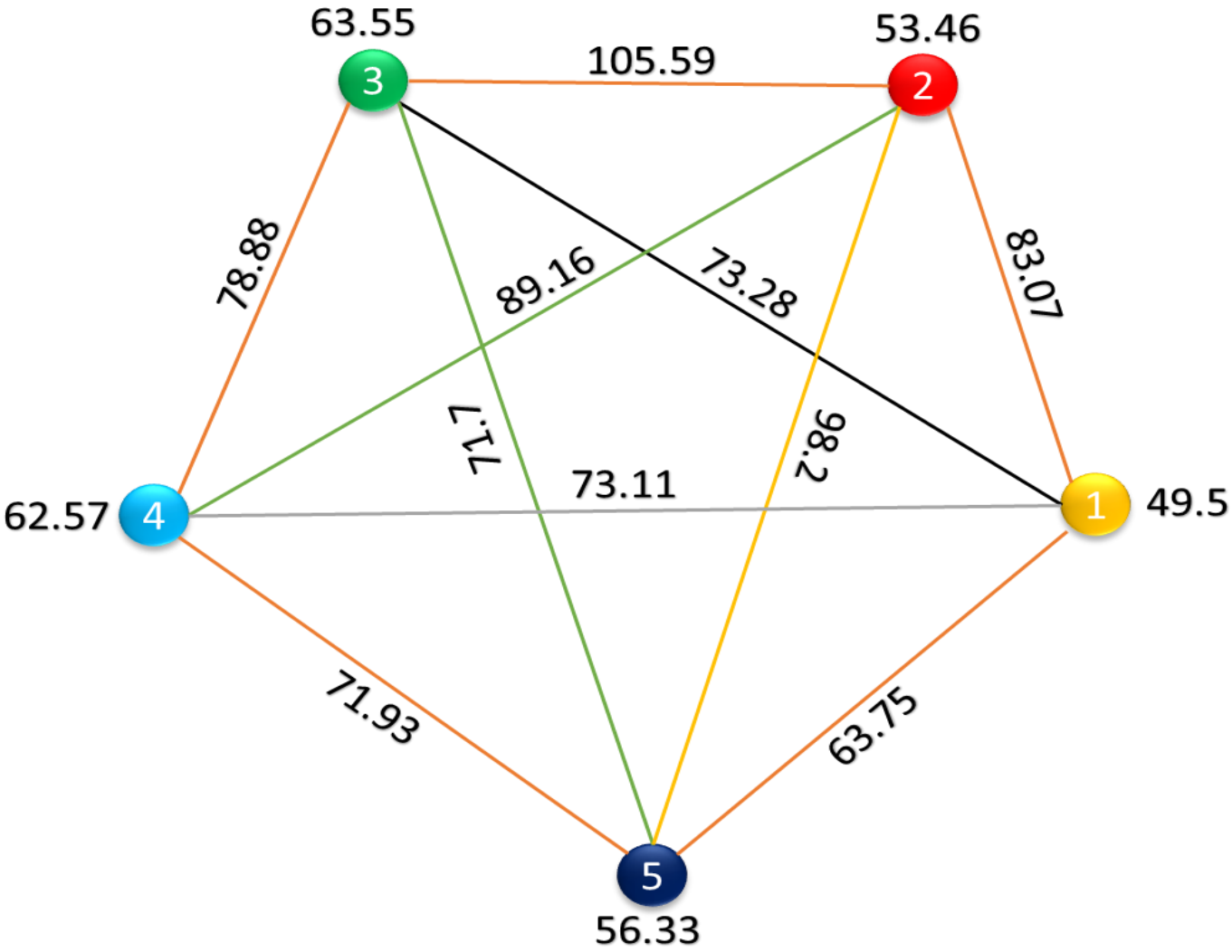

Fig 4.5 Cluster Diagram (Tocher method)

Weather data (*Kharif*-2021)

Date	Metero-logical Week	Rainfall (m.m.)	No. of Rainy days	Temperature (^{0}C.)		Humidity (%)	
				Max	Min	Mor.	Even.
14/05/21 to 20/05/21	20	205.6	5	33.2	23.6	84	66
21/05/21 to 27/05/21	21	0.0	0	32.6	23.7	84	65
28/05/21 to 03/06/21	22	92.6	2	32.9	23.9	89	70
04/06/21 to 10/06/21	23	279.8	5	30.8	22.4	95	80
11/06/21 to 17/06/21	24	581.6	7	28.3	22.3	96	88
18/06/21 to 24/06/21	25	332.6	7	29.7	22.6	93	86
25/06/21 to 01/07/21	26	197.0	7	29.1	22.6	96	86
02/07/21 to 08/07/21	27	57.4	3	30.9	24.0	92	81
09/07/21 to 15/07/21	28	695.0	7	27.6	22.5	98	96
16/07/21 to 22/07/21	29	970.2	7	27.1	22.4	98	97
23/07/21 to 29/07/21	30	164.8	7	28.4	23.4	93	89
30/07/21 to 05/08/21	31	89.8	7	28.3	23.2	94	86
06/08/21 to 12/08/21	32	73.3	5	29.5	22.8	96	82
13/08/21 to 19/08/21	33	178.8	7	28.4	21.7	95	86
20/08/21 to 26/08/21	34	109.8	3	29.1	21.8	96	79
27/08/21 to 02/09/21	35	74.2	6	28.8	21.9	96	83
03/09/21 to 09/09/21	36	598.2	7	28.5	22.1	98	89
10/09/21 to 16/09/21	37	238.4	6	28.5	23.0	96	86
17/09/21 to 23/09/21	38	224.9	6	28.8	22.3	96	88
24/09/21 to 30/09/21	39	120.6	6	29.1	22.0	96	83
01/10/21 to 07/10/21	40	14.4	2	31.7	22.4	94	74
08/10/21 to 14/10/21	41	13.0	2	31.6	22.0	93	76
15/10/21 to 21/10/21	42	0.0	0	31.7	20.1	92	70
22/10/21 to 28/10/21	43	0.0	0	32.4	17.5	89	62
29/10/21 to 04/11/21	44	0.0	0	33.0	18.6	85	63
05/11/21 to 11/11/21	45	10.2	1	32.5	17.9	90	62
12/11/21 to 18/11/21	46	25.0	2	33.4	19.2	93	60
19/11/21 to 25/11/21	47	4.4	0	31.9	21.6	94	65
26/11/21 to 02/12/21	48	33.0	1	31.1	18.1	92	62
03/12/21 to 09/12/21	49	20.0	2	29.8	17.1	94	67
10/12/21 to 16/12/21	50	0.0	0	32.5	16.2	94	52
17/12/21 to 23/12/21	51	0.0	0	31.2	13.5	95	54
24/12/21 to 31/12/21	52	0.0	0	30.4	13.2	95	62
		5404.6	**120.0**				

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This letter confirms that manuscript titled **"Genetic variability and path analysis in little millet (*Panicum sumatrense* L.)"** authored by **KS Sarak, SS Desai, RL Kunkerkar, Dr. SG Mahadik, Dr. PS Sawant and SA Chendake** has been accepted for publication.

Yours Sincerely,

Akhil Gupta

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THESIS ABSTRACT

a)	Title of the thesis	: **GENETIC DIVERSITY STUDIES IN LITTLE MILLET (*Panicum sumatrense* L.)**
b)	Full name of the student	: Sarak Komal Shivaji
c)	Name and address of the major advisor	: Dr. (Mrs) S. S. Desai Senior scientist, AICRP Agroforestry, College of Foresrty, Dapoli
d)	Degree to be awarded	: M.Sc. (Agri.)
e)	Year of award of degree	: 2022
f)	Major subject	: Genetics and Plant Breeding
g)	Total number of pages in the thesis	: 83
h)	Number of words in the abstract	: 181
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j)	Signature, Name and address of forwarding authority	:

The present study comprises of forty four genotypes out of which twenty seven genotypes collected from local area of konkan region while remaining seventeen genotypes were collected from zonal agriculture research station Kolhapur. These genotypes were cultivated in a Randomized Block Design with two replications at Education and Research Farm Department of Agricultural Botany, College of Agriculture, Dapoli during the *Kharif* 2021. As a result of the current investigation, it is clear that a wide range of variability exists for various traits, along with high heritability and high genetic advance as percentage of the mean for significant yield traits. Four of the thirteen quantitative characteristics the number of productive tillers per plant, protein content, calcium content, and the straw yield per plant, were highly significant and positively correlated with grain yield at both the phenotypic and genotypic levels. The current analysis also showed that clusters II and III had the most diversity among themselves. Based on the findings, the genotypes DPLV-27, DPLV-26, DPLV-16, and DPLV-11 are best performer having good genetic diversity used as a parent in a future hybridization programme.

Key words: Genotype, Variability, heritability, Genetic advance, Diversity

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Date: / / **Signature of Student**