ASSESSMENT OF GENETIC VARIABILITY AND DIVERSITY IN FINGER MILLET (*Eleusine coracana* (L.) Gaertn) GENOTYPES

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CERTIFICATE

This is to certify that the thesis entitled **'ASSESSMENT OF GENETIC VARIABILITY AND DIVERSITY IN FINGER MILLET (*Eleusine coracana* (L.) Gaertn) GENOTYPES'** submitted in partial fulfillment of the requirements for the award of the degree of **MASTER OF SCIENCE (AGRICULTURE) in GENETICS AND PLANT BREEDING** to the College of Agriculture, Shivamogga, University of Agricultural and Horticultural Sciences, Shivamogga is a bonafide record of research work carried out by **Mr. PRASHANTHA, B. N., ID No. MA1TAF0180** (prashanthbn143@gmail.com) during the period of study in this university under my guidance and supervision and no part of this thesis has previously formed the basis for the award of any other degree, diploma, associateship, fellowship or any other similar titles.

Shivamogga
July, 2018

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Prashantha B.N

SHIVAMOGGA ***(PRASHANTHA, B. N.)***

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Assessment of genetic variability and diversity in finger millet (*Eleusine coracana* (L.) Gaertn) genotypes

(Prashantha, B. N.)

Abstract

The aim of present investigation was to assess the extent of genetic variability, divergence, nature of association and micronutrient content in sixty genotypes of finger millet which was carried out at the Zonal Agricultural and Horticultural Research Station, Shivamogga during *kharif* 2017. The analysis of variance revealed the existence of highly significant differences among the genotypes for all the traits studied. A wide range of variability and high heritability coupled with high genetic advance was recorded for most of the yield, yield contributing and quality traits. Grain yield plant^{-1}possessed significant positive correlation with days to 50 per cent flowering, days to maturity and earhead weight plant^{-1}. Path analysis revealed that, the characters like days to maturity, earhead weight plant^{-1}and straw yield plant^{-1} had direct positive effect on grain yield plant^{-1}. The maximum inter cluster distances for grain yield and quality traits were recorded between cluster IV and cluster VIII and cluster IV and cluster I respectively.Genotypes from these clusters can be selected for hybridization programme to get desirable recombinants to improve further grain yield with quality.Plant height and calcium content had maximum contribution towards genetic diversity, indicates the presence of wide diversity among the genotypes under study for the traits. Two genotypes, Malali (25.30 g/plant) and IC-473155 (25.20 g/plant) recorded significantly higher yield than varietal check, GPU-28 (21.35 g/plant). Genotype, IC-474959 was superior for calcium (398.62 mg/100g), magnesium (167.77 mg/100g) and copper content (0.95 mg/100g). The higher iron and zinc content was exhibited by the genotypes, IC-473388 (14.19, 5.45mg/100g), IC-473143 (13.85, 5.65mg/100g) and Jeenumundaga Ragi (7.05, 5.65 mg/100g). These identified potential genotypes with high calcium, magnesium, iron, copper and zinc content can be further utilized as donor parents to transfer these traits to genotypes which are high yielding and well adapted.

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ರಾಗಿಯ (ಎಲುಸಿನ ಕೊರಾಕಾನ (ಎಲ್.) ಗಾರ್ಟ್ನೆನ್) ವಂಶವಾಹಿರೂಪಕಗಳಲ್ಲಿ ಅನುವಂಶಿಯ ಏರಿಳಿತ ಮತ್ತು ವೈವಿಧ್ಯತೆಯ ಮೌಲ್ಯಮಾಪನ

(ಪ್ರಶಾಂತ, ಬಿ. ಎನ್.)

ಸಾರಾಂಶ

ರಾಗಿಯ ಅರವತ್ತು ವಂಶವಾಹಿರೂಪಗಳಲ್ಲಿ ಅನುವಂಶೀಯ ಏರಿಳಿತ, ವೈವಿಧ್ಯತೆ, ಗುಣಸಂಯೋಜನೆ ಹಾಗೂ ಸೂಕ್ಷ್ಮಪೋಷಕಾಂಶಗಳ ಅಂಶದ ಮೌಲ್ಯಮಾಪನ ಕುರಿತು ಪ್ರಸ್ತುತ ಅನುವಂಶೀಯ ಅಧ್ಯಯನವನ್ನು ವಲಯ ಕೃಷಿ ಮತ್ತು ತೋಟಗಾರಿಕೆ ಸಂಶೋಧನಾ ಕೇಂದ್ರ, ನವಿಲೆ, ಶಿವಮೊಗ್ಗದಲ್ಲಿ ೨೦೧೭ ರ ಮುಂಗಾರಿನಲ್ಲಿ ಕೈಗೊಳ್ಳಲಾಯಿತು. ಅನುವಂಶೀಯ ಗುಣಗಳ ಏರಿಳಿತದ ವಿಶ್ಲೇಷಣೆಯಿಂದ ದಾಖಲಾದ ಎಲ್ಲಾ ಗುಣಲಕ್ಷಣಗಳಿಗೆ ಸಂಬಂಧಿಸಿದಂತೆ ವಂಶವಾಹಿರೂಪಗಳ ನಡುವೆ ಹೆಚ್ಚು ಮಹತ್ವಪೂರ್ಣ ವ್ಯತ್ಯಾಸ ಇರುವಿಕೆಯನ್ನು ಗಮನಿಸಲಾಯಿತು. ಇಳುವರಿ, ಗುಣಮಟ್ಟ ಹಾಗೂ ಇಳುವರಿಗೆ ಸಂಬಂಧಿಸಿದ ಬಹುತೇಕ ಗುಣಲಕ್ಷಣಗಳಿಗೆ ಅತ್ಯಧಿಕ ಅನುವಂಶೀಯ ಏರಿಳಿತ, ಹೆಚ್ಚಿನ ಅನುವಂಶೀಯ ಸಾಮರ್ಥ್ಯದ ಜೊತೆಗೆ ಹೆಚ್ಚಿನ ಸರಾಸರಿ ಮುಂಗಡ ಅನುವಂಶೀಯತೆಯನ್ನು ಗಮನಿಸಲಾಯಿತು. ಗುಣ ಸಂಯೋಜನೆ ಅಧ್ಯಯನದಿಂದ ಪ್ರತಿ ಗಿಡದ ಇಳುವರಿಯು, ಪ್ರತಿಶತ ೫೦ ಹೂ ಬಿಡುವಿಕೆಗೆ ಬೇಕಾಗುವ ದಿನಗಳು, ಬೆಳೆ ಪ್ರಬುದ್ಧತೆಗೆ ಬೇಕಾಗುವ ದಿನಗಳು ಹಾಗೂ ರಾಗಿಯ ತೆನೆಯ ತೂಕದ ಜೊತೆ ಗಮನಾರ್ಹ ಧನಾತ್ಮಕ ಗುಣಸಂಯೋಜನೆ ಹೊಂದಿರುವುದು ಕಂಡುಬಂದಿರುತ್ತದೆ. ಪಥ ವಿಶ್ಲೇಷಣೆಯ ಫಲಿತಾಂಶದಿಂದ ಬೆಳೆ ಪ್ರಬುದ್ಧತೆಗೆ ಬೇಕಾಗುವ ದಿನಗಳು, ಪ್ರತಿ ಗಿಡದ ತೆನೆಯ ತೂಕ ಹಾಗೂ ಪ್ರತಿ ಗಿಡದ ಒಣ ಹುಲ್ಲಿನ ತೂಕವು, ಪ್ರತಿ ಗಿಡದ ಇಳುವರಿಯ ಮೇಲೆ ನೇರ ಧನಾತ್ಮಕ ಪರಿಣಾಮ ಹೊಂದಿರುವುದು ಕಂಡುಬಂದಿರುತ್ತದೆ. ಸಸ್ಯ ಇಳುವರಿ ಮತ್ತು ಗುಣಮಟ್ಟದ ಅಂಶಗಳಿಗೆ ಅಂತರ ಗುಂಪುಗಳ ನಡುವಿನ ಹೆಚ್ಚಿನ ಅಂತರವು ಅನುಕ್ರಮವಾಗಿ ಗುಂಪು-೪ ಮತ್ತು ಗುಂಪು-೮ ಹಾಗೂ ಗುಂಪು-೪ ಮತ್ತು ಗುಂಪು-೧ ರ ನಡುವೆ ದಾಖಲಾಗಿರುತ್ತದೆ. ಈ ಗುಂಪುಗಳ ವಂಶವಾಹಿರೂಪಕಗಳನ್ನು ಗುಣಮಟ್ಟ ಮತ್ತು ಇಳುವರಿಯುಳ್ಳ ಅತ್ಯುತ್ತಮ ತಳಿಗಳನ್ನು ಅಭಿವೃದ್ಧಿಪಡಿಸಲು ಮುಂದಿನ ತಳಿ ಅಭಿವೃದ್ಧಿ ಕಾರ್ಯಗಳಲ್ಲಿ ಬಳಸಬಹುದು. ಪ್ರಸ್ತುತ ಅಧ್ಯಯನದಲ್ಲಿ ಎಲ್ಲಾ ಗುಣಲಕ್ಷಣಗಳ ಪೈಕಿ ಗಿಡದ ಎತ್ತರ ಮತ್ತು ಕ್ಯಾಲ್ಸಿಯಂ ಅಂಶವು ವಂಶವಾಹಿ ವೈವಿಧ್ಯತೆಯ ಕಡೆಗೆ ಹೆಚ್ಚಿನ ಕೊಡಿಗೆ ನೀಡಿವೆ. ಮಳಲಿ (ಪ್ರತಿ ಸಸ್ಯಕ್ಕೆ ೨೫.೩೦ ಗ್ರಾಂ.) ಹಾಗೂ ಐಸಿ-೪೭೩೧೫೫ (ಪ್ರತಿ ಸಸ್ಯಕ್ಕೆ ೨೫.೨೦ ಗ್ರಾಂ.) ಜಿಪಿಯು-೨೮ (ಪ್ರತಿ ಸಸ್ಯಕ್ಕೆ ೨೧.೩೫ ಗ್ರಾಂ.) ಗಿಂತ ಹೆಚ್ಚಿನ ಗಮನಾರ್ಹ ಇಳುವರಿ ಹೊಂದಿರುವುದು ಕಂಡುಬಂದಿದೆ. ಐಸಿ-೪೭೪೯೫೯ ವಂಶವಾಹಿರೂಪಕವು ಅತಿ ಹೆಚ್ಚು ಕ್ಯಾಲ್ಸಿಯಂ ಅಂಶ (ಪ್ರತಿ ೧೦೦ ಗ್ರಾಂ. ಗೆ ೩೯೮.೬೨ ಮಿ.ಗ್ರಾಂ.), ಮೆಗ್ನಿಷಿಯಂ (ಪ್ರತಿ ೧೦೦ ಗ್ರಾಂಗೆ ೧೬೭.೭೭ ಮಿ.ಗ್ರಾಂ.) ಮತ್ತು ತಾಮ್ರದಂಶ (ಪ್ರತಿ ೧೦೦ ಗ್ರಾಂ.ಗೆ ೦.೯೫ ಮಿ.ಗ್ರಾಂ.) ವನ್ನು ಹೊಂದಿರುತ್ತದೆ. ಅತಿ ಹೆಚ್ಚಿನ ಕಬ್ಬಿಣಾಂಶ ಹಾಗೂ ಸತುವಿನ ಅಂಶವು ವಂಶವಾಹಿರೂಪಕಗಳಾದ ಐಸಿ-೪೭೩೩೮೮ (ಪ್ರತಿ ೧೦೦ ಗ್ರಾಂ.ಗೆ ೧೪.೧೯, ೫.೪೫ ಮಿ.ಗ್ರಾಂ.), ಐಸಿ-೪೭೩೧೪೩ (ಪ್ರತಿ ೧೦೦ ಗ್ರಾಂ.ಗೆ ೧೩.೮೫, ೫.೬೫ ಮಿ.ಗ್ರಾಂ.) ಮತ್ತು ಜೇನುಮುಂಡಗ ರಾಗಿ (ಪ್ರತಿ ೧೦೦ ಗ್ರಾಂ.ಗೆ ೭.೦೫, ೫.೬೫ ಮಿ.ಗ್ರಾಂ.) ಗಳಲ್ಲಿ ಕಂಡುಬಂದಿರುತ್ತವೆ. ಅತಿ ಹೆಚ್ಚು ಕ್ಯಾಲ್ಸಿಯಂ, ಮೆಗ್ನೀಷಿಯಂ, ಕಬ್ಬಿಣ, ತಾಮ್ರ ಮತ್ತು ಸತುವಿನ ಅಂಶವನ್ನು ಹೊಂದಿದ ಸಂಭಾವ್ಯ ವಂಶವಾಹಿರೂಪಕಗಳನ್ನು ಮತ್ತಷ್ಟು ಹೆಚ್ಚು ಇಳುವರಿ ಹಾಗೂ ಹೆಚ್ಚಿನ ಹೊಂದಿಕೊಳ್ಳುವಿಕೆಯುಳ್ಳ ತಳಿಗಳಿಗೆ ದಾನಿ ಪೋಷಕಗಳಾಗಿ ಮುಂದಿನ ತಳಿ ಅಭಿವೃದ್ಧಿ ಕಾರ್ಯಗಳಲ್ಲಿ ಬಳಸಬಹುದು.

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ಕೃಷಿ ಮತ್ತು ತೋಟಗಾರಿಕೆ ವಿಶ್ವವಿದ್ಯಾಲಯ, ಶಿವಮೊಗ್ಗ
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INTRODUCTION

I INTRODUCTION

Finger millet (*Eleusine coracana* (L.) Gaertn) commonly known as Ragi, is one of the important cereal crop largely grown in the arid and semi-arid areas of Africa and Asia. The cultivated *E. coracana* is an allotetraploid with chromosome number 2n=4x=36, which have been evolved from *E. indica* (AA) and *E. floccifolia* or *E. tristachya* (BB). It is a self-pollinated annual herbaceous plant that belongs to the family Poaceae. Finger millet is an important source of grain and straw in dry land areas because of its ease in cultivation and drought tolerance. It is an important staple food in India for people of low income groups.

In world, finger millet ranks fourth in importance among millets after sorghum, pearl millet and foxtail millet. It is estimated that some 10 per cent of the world's 30 million tonnes of millet produced is finger millet (Chandra *et al*., 2016). In India, the crop is grown in an area of 1.01 million hectares with a production of 1.38 million tonnes and productivity of 1.36 tonnes ha^{-1}. The major finger millet growing states are Karnataka, Uttarakhand, Maharashtra, Tamil Nadu, Odisha, Andhra Pradesh and Jharkhand. Karnataka, Uttarakhand and Tamil Nadu are the major contributors accounting for more than 80 per cent of the total production. In Karnataka, it occupies an area of 0.59 million hectares with a production of 0.85 million tonnes and productivity of 1.43 tonnes ha^{-1}. Its cultivation is concentrated mostly in the districts of Bangalore, Kolar, Tumkur, Chitradurga, Hassan, Mysore and Mandya (Anonymous, 2016).

Finger millet is commonly called as "Nutritious millet" as its grains are nutritionally superior over other cereals. It stands out as the richest source of calcium (380-450 mg/100g) among all the cereals. It has three times more calcium than milk and 10-fold higher calcium than brown rice, wheat or maize. Besides calcium, finger millet is also very rich source of crude fibre (3.6 mg/100g), iron (3.39 mg/100g), zinc (1.5 mg/100g), essential amino acids, leucine (594 mg/100g of protein) and valine (413 mg/100g of protein), slowly digestible starch and phytochemicals like polyphenols. It is a gluten-free, low fat cereal which is non-allergic and easily digestible. For these characteristics, it is often termed as a "Super cereal". Apart from its nutritional attributes, finger millet has excellent environmental sustainability credentials. It can easily withstand harsh climatic conditions, low soil fertility, requires very little inputs with a short growing season. It has excellent storage quality traits and can be valuable in areas where farmers suffer losses due to dearth of post-harvest management (Kumar *et al*., 2016).

Finger millet, one of the minor cereals, is known for several health benefits and some of the health benefits are attributed to its polyphenol and dietary fibre contents.

They are also recognized for their health beneficial effects, such as anti-diabetic, anti-tumerogenic, atherosclerogenic effects, anti-oxidant and antimicrobial properties. On daily consumption of whole grain of finger millet and its products can protect against the risk of cardiovascular diseases, type II diabetes, and gastrointestinal cancers and other health issues. The dietary fibre, minerals, phenolics and vitamins concentrated in the outer layer of the seed coat form the part of the food and offer their nutritional and health benefits (Chandra *et al*., 2016).

Looking to the merits of this crop, this crop needs major attention with respect to crop improvement programme to enhance the productivity. One of the means to boost its production and productivity is by identification and development of the improved genotypes with wider adaptability over environments with knowledge of variability, inheritance, direction and magnitude of association between various traits. The progress in breeding for yield and yield contributing characters of any crop is genetically controlled, environmentally influenced and determined by the magnitude and nature of their genetic variability (Wright, 1921 and Fisher, 1936). Study of genetic variability is pre-requisites for improvement of any crop including finger millet for selection of superior genotypes and improvement of any character.

It is very difficult to judge whether observed variability is heritable or due to environment alone. Moreover, knowledge of heritability is essential for selection based improvement as it indicates the extent of transmissibility of a character in future generations. Further the information on heritability and genetic advance is more useful in predicting the expected progress to be achieved through selection, also it provides quantitative estimate of relative importance of heredity and environment in character expression which ultimately helps in planning an efficient breeding programme.

Enhancement in economic yield is the prime objective in all plant breeding programmes. But yield has low heritability and direct selection for yield is not sufficiently effective. Therefore, the knowledge of association is useful to the breeders for the improvement among the yield attributing characters considerably affect the methods of selection (Mishra *et al.*, 1980). Correlation and path coefficient analyses are better conventional biometrical methods to know the intrinsic relationship among characters and their contribution to yield. It has been extensively used for choosing suitable genotypes to know the traits of interest in high yielding background. Partitioning of total correlation into direct and indirect effect by path coefficients analysis helps in making the selection more effective.

The presence of genetic diversity and genetic relationships among genotypes is a prerequisite and paramount important for success of any crop breeding programme including finger millet. The Precise information on the nature and degree of genetic diversity helps the plant breeder in choosing the diverse parents for purposeful hybridization. The character contributing maximum to the divergence should be given greater emphasis for deciding the type of cluster for purpose of further selection and the choice of parents for hybridization (Jagadev *et al.*, 1991).The D^2 statistics is one of the powerful tools to assess the relative contribution of different component traits to the total diversity.

Micronutrients are essential for balanced nutrition in plants and animals (Welch and Graham, 1999 and Graham *et al.*, 2000). Green revolution laid emphasis on increased grain yield, which led to reduced availability of micronutrients in food (Mason and Garcia, 1993, Tontisirin and Nantel, 2002 and Welch *et al.*, 1997). Mineral deficiencies are most prevalent among human population which is not only due to insufficient availability of food but also due to the poor nutritional quality of food available for consumption. This can be neutralized by identification, characterization and mapping of genes from the genetic material for various quality traits. The availability of genetic variation for quality traits can be exploited in developing new genotypes with enhanced quality traits. The knowledge of association of quantitative and nutritional traits would further strengthen the precision of breeder in efficient planning of breeding programme for both the yield and quality traits.

Realizing the importance and need of finger millet genotypes, the present study utilized sixty finger millet genotypes for assessing the worth of genotypes for grain yield and its attributing traits and quality traits with the following objectives:

1. To assess the extent of genetic variability present in the finger millet genotypes
2. To assess the extent of micronutrient content in the finger millet genotypes
3. To study the character association and path analysis for yield and its component traits
4. To assess the extent of genetic divergence present in the finger millet genotypes

REVIEW OF LITERATURE

II REVIEW OF LITERATURE

The literature related to the objectives of the present study in finger millet is reviewed under the following headings.

2.1 Genetic variability parameters for grain yield and yield related traits

2.2 Genetic variability parameters for grain quality traits

2.3 Correlation coefficient analysis for grain yield and yield related characters

2.4 Correlation coefficient analysis for grain yield and grain quality parameters

2.5 Path coefficient analysis for grain yield and its component traits

2.6 Genetic divergence among yield and yield contributing characters

2.1 Genetic variability parameters for grain yield and yield related traits

The assessment of variability present in any crop species is the essential pre-requisite for formulating an effective breeding programme. The inherited portion of the variability is termed as heritability. Consistency in the performance of selection in finger millet depends on the magnitude of heritable variation. Johnson *et al.* (1955) reported that through, heritability estimates give useful indication of relative values of selection based on phenotypic expression, heritability values along with the genetic advancement should be considered jointly to arrive at a more reliable conclusion. Hence, the estimates of genetic variability, heritability and genetic advance as per cent of mean are having immense value in identifying the superior genotypes.

The comprehensive review of literature on phenotypic coefficient of variability, genotypic coefficient of variability, heritability and genetic advance as per cent mean of finger millet as follows.

Bendale *et al.* (2002) studied 29 phenotypically diverse genotypes of finger millet and observed that phenotypic variances were higher than genotypic variances. Phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) were high for number of tillers, number of productive tillers, grain yield per plant, straw yield per plant and weight of grains of main ear head.

Satish (2003) recorded high phenotypic and genotypic coefficient of variation for number of fingers per main ear, test weight, total dry matter production, number of productive tillers per plant, grain yield per plant. High heritability coupled with high genetic advance was recorded for days to 50 per cent flowering, number of fingers per main ear, test weight, total dry matter production, number of productive tillers per plant and grain yield per plant.

Bezaweletaw *et al*. (2006) reported high heritability for days to heading (84 %) and low heritability for grain filling duration (20 %) in 66 genotypes of finger millet. Values of expected genetic advance varied from (6.67 to 44.14 %) for grain filling duration and finger width, respectively. Finger width and length exhibited high heritability coupled with high genetic advance.

John (2006) evaluated the 20 finger millet genotypes and reported the moderate to higher estimates of GCV, PCV, heritability and genetic advance as percentage of mean for all characters except days to maturity. It was indicated that these characters were controlled by additive gene effect and days to maturity showed non-additive gene effect.

Arun *et al*. (2008) evaluated the 150 germplasm accessions of finger millet and observed the high heritability and high genetic advance for number of tillers and single plant yield, indicating the possibility of improvement for this trait by simple selection.

Sharathbabu *et al*. (2008) recorded the high estimates of PCV & GCV for straw yield per plant whereas, moderate estimates of PCV & GCV for number of productive tillers per plant. Finger length recorded the highest heritability values and grain yield per plant recorded the lowest heritability value. High genetic advance as per cent of mean for straw yield per plant followed by number of productive tillers per plant grain yield per plant, test weight, ear weight per plant and finger length.

Sonnad *et al*. (2008) reported that grain yield per plant showed moderate genotypic and phenotypic coefficients of variability with high heritability and genetic advance as per cent of mean indicates it is controlled by additive gene action and less influenced by environment. Straw yield per plant had higher variability, heritability and genetic advance as per cent of mean. While other characters under study had low variability, high heritability and moderate to high genetic advance as per cent of mean.

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

Kadam *et al*. (2010) in total of 65 different finger millet genotypes noticed the highly significant genotypic and phenotypic variability for the characters like days to 50 per cent flowering, plant height, basal number of tillers, flag leaf length, flag leaf sheath length, peduncle length, exertion length, inflorescence length, longest finger length, peduncle branch length and yield. The highest heritability and genetic advance was observed for yield and plant height.

Nandini *et al*. (2010) investigated the F_2 generation of four crosses of finger millet to quantify the variability created along with heritability and genetic advances for important yield and its attributing characters. In general moderate to high broad sense heritability was observed for days to 50 per cent flowering, finger length, 1000 seed weight, whereas high broad sense heritability was observed for plant height, total tillers per plant and number of productive tillers per plant. A very high genetic advance was observed for total tillers per plant, productive tillers per plant, finger number per main ear, finger length and weight of main ear.

Shet *et al*. (2010) observed high PCV and GCV values for grain yield per plant, finger width and plant height and days to 50 per cent flowering whereas low to moderate values were obtained for remaining characters. The characters like, plant height, finger length, test weight and grain yield per plant exhibited high broad sense heritability accompanied with high genetic advance.

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

Ganapathy *et al*. (2011) investigated 230 finger millet germplasm accessions and found that the coefficient of variation at phenotypic (PCV) and genotypic (GCV) levels were high for productive tillers per plant. Low GCV and PCV were observed for days to maturity. High heritability coupled with high genetic advance was observed for days to 50 per cent flowering, plant height, productive tillers per plant, finger numbers per ear, finger length and seed yield per plant.

Priyadharshini *et al*. (2011) evaluated the 21 hybrids along with seven parents of finger millet for genetic variability and observed the High PCV and GCV for number of productive tillers per plant. High heritability along with high genetic advance as per cent of mean was observed for plant height, number of productive tillers per plant, number of fingers per ear head, longest finger length, seed protein content, harvest index and single plant grain yield, indicating involvement of additive gene action for these traits.

Haradari *et al*. (2012) assessed the extent of genetic variability in base germplasm (1000 accessions) of finger millet for eleven quantitative characters. Close relationship was found between GCV and PCV for most of the characters. High heritability was expressed by plant height, finger length and days to 50 per cent flowering. Genetic advance as per cent of mean was observed maximum for finger length, number of productive tillers per plant, grain yield per plant, ear weight per plant and plant height.

Lule *et al*. (2012) evaluated 144 finger millet landraces to assess the extent of variability, heritability, genetic advance and association of quantitative traits. Analysis of variance indicated mean sum of squares was highly significant for all the characters under study. PCV were higher than GCV for all the traits. High heritability coupled with high genetic advance was noticed for ear weight (71.14), lodging index (53.49), finger length (41.94), test weight (28.88), grain yield per plant (26.43) indicating, the ease of phenotype based selection for improvement of these traits.

Bharathi *et al*. (2013) evaluated the global composite collection of finger millet germplasm for fifteen quantitative characters to assess the variability and association between the characters related to yield. The genotypic variances were highly significant for all characters except plot yield. Plot yield exhibited the highest range (0.02 - 2.6 t ha^{-1}). The PCV and GCV varied from (9.59 to 57.13 %) and (11.14 to 64.96 %) respectively. Heritability estimates ranged from (37.01 %) for single panicle weight to (98.34 %) for days to 50 per cent flowering.

Karad and Patil (2013) found the significant difference among the 65 genotypes for all the characters under study indicating the presence of substantial degree of variability. The days to maturity exhibited the lowest GCV (7.37 %) as well as PCV (7.36 %) whereas, the iron per cent had highest GCV and PCV (55.33 %) and (53.46 %) respectively. The genetic advance was found ranging from (0.58 to 23.38). High heritability coupled with high genetic advance was noticed for the fodder yield per plant, days to 50 per cent flowering, days to maturity and plant height advocated high genetic progress for them.

Manjunath *et al.* (2013) revealed the genetic variability existing in the 64 finger millet white seeded accession. The PCV and GCV levels were high for number of productive tillers, finger length (cm), finger width (cm), ear weight per plant (g), straw weight per plant (g) and test weight (g). Low PCV and GCV were observed for the traits like days to 50 per cent flowering, number of leaves (no.) and flag leaf length (cm). High heritability coupled with high genetic advance was observed for days to 50 per cent flowering, plant height (cm), flag leaf width (cm), finger length (cm) and test weight (g), which indicates the predominance of additive gene effects, in controlling these traits, early and simple selection could be exercised due to fixable additive gene effects.

Patil and Mane (2013) evaluated the 11 genotypes of finger millet with respect to genetic variability for the yield and contributing traits in three environments. High GCV and PCV were recorded for number of productive tillers per plant, weight of panicle and fodder kg per plot. High heritability along with high genetic advance as per cent of mean was noticed for weight of panicle, fodder yield per plot, number of productive tillers per plant and main ear length indicating the involvement of additive gene action for these traits and phenotypic selection based on these traits would likely to be more effective.

Reddy *et al*. (2013) studied 18 elite entries of finger millet to assess the magnitude of genetic variability, heritability and genetic advance for yield and yield contributing traits. A higher value of PCV and GCV was recorded for number of fingers per ear head. High heritability and high genetic advance was noticed for ear head yield, ear head length and number of fingers per ear head indicating that these characters were controlled by additive gene effects. Threshing percentage showed low heritability as well as low genetic advance.

Savitha *et al.* (2013) evaluated 21 hybrids along with their parents for genetic variability. Higher values of PCV and GCV were recorded for iron content, number of fingers per ear head. High heritability along with high genetic advance were observed for plant height, number of productive tillers per plant, number of fingers per ear head, longest finger length, grain protein content, harvest index and single plant grain yield, indicating involvement of additive gene action for these traits and phenotypic selection based on these traits in the segregating generations would likely to be more effective.

Wolie and Dessalegn (2013) investigated the 88 finger millet germplasm collections to find out heritability, variance components, variability and genetic advance for some yield and yield related agronomic characters. High heritability coupled with high expected genetic advance as per cent of mean was obtained for number of ears per plant (96.55, 90.59 %), number of finger per ear (85.48, 43.81 %), finger length (94.48, 50.95 %), and days to heading (96.01, 14.13 %), biomass yield (87.67, 154.52 %), 1000 kernel weight (93.69, 37.70 %), lodging susceptibility (98.92, 384.24 %) and blast severity (87.60, 89.47 %) indicating the presence of more additive gene effects for potential crop improvement and so these characters could be improved through selection.

Chaudhari *et al*. (2014) estimated the genetic variability for yield and yield attributing characters in 35 finger millet genotypes. The phenotypic and genotypic variability were high for days to 50 per cent flowering, days to maturity, plant height and straw yield where medium for total fingers per plant and grain yield and low for number of tillers per plant, number of productive tillers per plant, fingers per main ear, ear head length and test weight.

Shinde *et al*. (2014) in 41 genotypes of finger millet assessed the genetic variability, heritability and character association for 12 important traits. High (GCV) and (PCV) were observed for productive tillers per plant followed by grain yield per plant and iron content. A high estimate of heritability (83.40 - 99.30 %) was obtained for all the characters studied except protein content (70.40 %). Productive tillers per plant, seed yield per plant and iron content exhibited high heritability coupled with high genetic advance as per cent of mean, indicating that these characters are governed by additive gene effects. Hence, selection for these traits would be more effective.

Suryanarayana *et al*. (2014) evaluated the 35 diverse genotypes of finger millet with seven quantitative traits to know the existing genetic variability in the material. The coefficient of variation at phenotypic (PCV) and genotypic (GCV) levels were high for seed yield plant per plant, productive tillers plant per plant and main ear length. High heritability coupled with high genetic advance observed for seed yield per plant and main ear length.

Ulaganathan and Nirmalakumari (2014) a total of 105 finger millet genotypes were evaluated for 13 quantitative traits to assess the variability and association of characters. High values for PCV and GCV were recorded for grain yield per plant (29.48 and 28.93 %) and productive tillers per plant (23.96 and 22.74 %). All the characters recorded high heritability ranged from (63.95 to 96.27 %) indicated that these characters were relatively less influenced by environmental factors and phenotypic selection would be effective for the improvement of these characters.

Manjunath *et al*. (2015) revealed the importance of some quantitative traits and genetic variability existing in the 274 finger millet reference set. The (PCV) and (GCV) levels were high for number of productive tillers, finger length (cm), finger width (cm), ear weight per plant (g), straw weight per plant (g) and test weight (g). High heritability coupled with high genetic advance was exhibited by days to 50 per cent flowering, plant height (cm), flag leaf width (cm), finger length (cm) and test weight (g), which indicates the predominance of additive gene effects, in controlling these traits, early and simple selection could be exercised due to fixable additive gene effects.

Rani *et al*. (2015) investigated the genetic variability and inter-relationships for 11 quantitative characters in 40 diverse genotypes of finger millet. The magnitude of GCV ranged from (9.24 to 27.21 %), PCV ranged from (9.51 to 32.75 %), heritability (in broad sense) ranged from (64.70 % to 99.80 %) and genetic gain ranged from

(23.73 to 59.72 %). High genetic gain was observed for seed yield per plant (59.72) followed by seed protein content (53.29) and ear weight per plant (52.02) indicating the prevalence of additive gene action for inheritance of these traits.

Saundarya and Satish (2015) showed the importance of variability in 35 genotypes of finger millet by indicating the high to moderate PCV and GCV accompanied by high heritability and genetic advance as per cent of mean for traits like, grain yield per plant, harvest index, grain weight of main panicle, number of tillers per plant, flag leaf area, 1000 grain weight, number of fingers per panicle, panicle length and days to 50 per cent flowering.

Ulaganathan and Nirmalakumari (2015) assessed the contribution of qualitative traits variability in 305 finger millet accessions. Variations were absent for grain uniformity and pericarp persistence after threshing. Principal component analysis showed that first eight components with Eigen value of greater than 0.80 contributed about 85.34 per cent of total variability. Principal component analysis indicated that all traits considered in the study had contribution for the overall genetic variations observed among the genotypes.

Eric *et al.* (2016) studied 340 finger millet landraces from Kenya, Tanzania and Uganda and 80 global mini core accessions from ICRISAT Gene bank in India. High broad-sense heritability estimates noticed for fingers per panicle, flag leaf blade length, 1000 grain weight, productive tillers per plant, finger length, and peduncle length and panicle exertion indicating the potential for their improvement through selection.

Jyothsna *et al.* (2016) in 25 genotypes of finger millet found that GCV for all the characters studied were lesser than the PCV indicating the interaction of genotypes with environment. High heritability coupled with high genetic advance was observed for grain yield per plot and straw yield per plot indicating the importance of additive gene action in governing the inheritance of these traits. Hence, simple selection is effective to improve the respective trait.

Sao *et al*. (2016a) showed the importance of some quantitative traits and genetic variability existing in the 15 finger millet entries. The PCV and GCV were high for finger length whereas low for days to maturity and plant height. High heritability coupled with high genetic advance was noticed for days to 50 per cent flowering, length of finger, days to maturity, fodder weight and grain yield per plant, which indicates the predominance of additive gene effects, in controlling these traits, early and simple selection could be exercised due to fixable additive gene effects.

Sao *et al*. (2016b) evaluated 26 high yielding finger millet genotypes to determine the genetic variability for eight quantitative characters. The PCV and GCV levels were high for length of finger and number of fingers per panicle. High heritability coupled with high genetic advance was observed for days to 50 per cent flowering, length of finger, days to maturity, fodder weight and grain yield per plant, which indicates the predominance of additive gene effects in controlling these traits.

Anuradha *et al*. (2017) in 25 advanced breeding lines of finger millet studied the genetic variability, heritability and revealed the significant variation for all the traits studied. The mean grain yield was 31.50 q/ha, with a minimum of 29.22 and maximum of 39.74 q/ha. Grain yield recorded GCV of (12.86 %), while PCV was (18.06 %). Heritability ranged from 0.35 (number of finger per ear) to 0.88 (days to 50 per cent flowering), while heritability for yield was 0.51.

Auti *et al*. (2017) evaluated the 64 finger millet landraces and two cultivars for yield contributing and morpho-agronomic characters. Among all the characters highest GCV and PCV was recorded for tillers per plant (54.95 % and 71.38 %). All the characters showed higher PCV values which indicate the influence of the environment. Heritability estimates ranged from 90.03 per cent for 1000 seed weight to lowest 44.03 per cent for height. 1000 seed weight exhibited high heritability coupled with low genetic advance.

Mahanthesha *et al*. (2017) observed the high GCV and PCV values for grain yield per plot followed by grain yield per plant, number of basal tillers per plant, productive tillers per plant, main ear width and finger length. High heritability coupled with high genetic advance as per cent of mean was observed for plant height, number of basal tillers per plant, number of productive tillers per plant, main ear length, main ear width, and finger length, grain yield per plant and grain yield per plot. Thus, these traits are predominantly under the control of additive gene action and hence these characters can be improved by selection.

Devaliya *et al.* (2018) evaluated the 68 diverse genotypes of finger millet to assess the magnitude of genetic variability, heritability and genetic advance for yield and yield contributing traits. Highest PCV and GCV were recorded for grain yield per plant. High heritability along with high genetic advance as per cent of mean observed for grain yield per plant, number of productive tillers per plant, straw yield per plant and main ear head length, indicating involvement of additive gene action for these traits and phenotypic selection based on these traits in the segregating generations would likely to be more effective.

2.2 Genetic variability parameters for grain quality traits

Barbeau and Hilu (1993) studied the two wild and eight domesticated cultivars of finger millet to determine their proximate composition and calcium, iron, and amino acid content. Wide variations were observed in the calcium (376 to 515 mg/100g) and iron (3.7 to 6.8 mg/100g) content of the wild and domesticated cultivars. The calcium and iron content of the wild progenitor was also significantly greater than that of two domesticated cultivars and concluded that the nutritional value of finger millet may be significantly improved by selective crossbreeding of the cereal's wild and domesticated cultivars.

Vadivoo *et al.* (1998) investigated the 36 finger millet genotypes to assess the amount of calcium content and reported that calcium content of 36 genotypes of finger millet ranged from (162 to 487 mg %) with mean value of (320.8 mg %).

Seetharam (2001) reported that the average calcium content (329 mg %) in white varieties was considerably higher than the brown (296 mg %) varieties.

Bhatt *et al.* (2003) reported the calcium content of finger millet as (344 mg %).

Satish (2003) analysed chemical composition and protein content in 40 finger millet accessions. Protein content in the genotypes ranged from 6.80 to 11.36 per cent with a mean of 9.10 per cent. Accession IE 2235 recorded highest protein content (11.36 %) and it was lowest in IE 3135 (6.80 %), whereas IE 3135 showed highest content of calcium.

Singh and Srivastava (2006) studied the 16 finger millet varieties and reported that iron content ranged from 3.61 mg/100g to 5.42 mg/100g with a mean value of 4.40 mg/100g. Zinc content ranged from (0.92 to 2.55 mg %) with a mean value of (1.34 mg %).

Shashi *et al.* (2007) studied the micronutrient composition, antinutritional factors and bio accessibility of iron in seven finger millet varieties and concluded that calcium was found to be in the range of 264 to 365 mg/100g, magnesium 66 to 130 mg/100g, iron 3.60 to 7.31 mg/100g, sodium 0.60 to 0.95 mg/100g and potassium 294 to 1160 mg/100g.

Dhamdhere *et al.* (2011) estimated the genetic variability parameters for 17 quantitative characters and four nutritional attributes on 29 elite genotypes of finger millet. Results revealed that PCV was invariably higher than GCV for most of the characters studied. Crude fibre content showed high PCV followed by ear weight, iron content.

Upadhyaya *et al*. (2011) found that finger millet core collection for grain nutrients and agronomic traits revealed a substantial genetic variability for grain iron (Fe), zinc (Zn), calcium (Ca) and protein contents. Accessions rich in Zn content have significantly higher grain yield potential than those rich in Fe and protein content. Grain nutrient-specific accessions and those contrasting for nutrient contents were identified for use in the strategic research and cultivar development in finger millet.

Bachar *et al.* (2013) showed that calcium and magnesium were the most concentrated nutrients in all studied accessions (189.93-1272.36 mg/100g and 84.71-567.45 mg/100g) respectively, followed by potassium (11.24-284.7 mg/100g), sodium (13.73-42.47 mg/100g) and phosphorus (2.208-11.033 mg/100g).

Shibairo *et al.* (2014) analysed that calcium, Fe and Zn mineral contents were not significantly different ($p>0.05$) among genotypes. Calcium content had a mean content of 2944 mg/kg while Fe and Zn contents averaged 98 mg/kg and 16.9 mg/kg, respectively.

Solmon *et al.* (2014) found the wide variation for iron and zinc content in six finger millet genotypes with an average of 9.8 and 1.69 mg/100 g.

Rani *et al*. (2015) investigated the genetic variability and inter-relationships for 11 quantitative characters in 40 diverse genotypes of finger millet. The magnitude of GCV and PCV was moderate for seed calcium content. High heritability coupled with high genetic advance of mean was obtained for seed calcium content indicating the prevalence of additive gene action for inheritance of this trait.

Badigannavar *et al*. (2016) studied the concentrations of micronutrients and protein and yield parameters in 112 local landraces and varieties of sorghum. Univariate analysis revealed wide variation for iron (1.10–9.54 mg 100 g^{-1}), zinc (1.12–7.58 mg 100 g^{-1}), protein (3.50–12.60 %), and grain yield (2.50–76.50 g) among the landraces. High estimates of genetic, phenotypic coefficient of variation and genetic advances over the mean were identified for landraces and varieties. High heritability was also obtained for yield and mineral content.

Kazi and Auti (2017) analysed 64 landraces of finger millet collected from Maharashtra for 8 mineral elements Cu, Zn, Fe, Mn, K, Ca, Mg and Na by tri-acid digestion method. Obtained results showed substantial genetic variability for grain minerals among the landraces. Calcium (159.7-364.6mg/100gm) and iron (10.2-424.16 mg/100gm) were the most concentrated nutrients, followed by potassium (26-184 mg/100gm) and sodium (107-268.23 mg/kg).

Netravati *et al.* (2018) studied the 20 finger millet germplasm including RAU-8 variety to find the variation in minerals, phytic acid and molar ratios of phytic acid to minerals. Mean values for minerals such as iron, zinc, calcium, magnesium, manganese and phosphorous showed 3.00±0.08, 2.79±0.05, 281.98±3.18, 166.35±2.66, 24.04±0.69 and 228.09±9.90 mg/100 g respectively and with the mean of 654.34 mg/100 g phytic acid.

2.3 Correlation coefficient analysis for grain yield and yield related characters

The yield and component characters among themselves may show different degree of associations. Hence, knowledge of the character association among such characters is essential while aiming at a rational improvement in yield through selection. The unfavourable associations between the desirable component traits under selection may result in genetic slippage (Dickerson, 1955) and limits the genetic advancement so that the antagonistic correlations do not nullify the expected progress during selection programmes.

The comprehensive review of literature on correlation studies as follows.

Bezaweletaw *et al*. (2006) observed strongest positive association between culm thickness and leaf blade width while the strongest negative association was found between 1000 grain weight and finger number. Grain yield per plant associated positively with productive tillers, 1000 grain weight, the number of grains per spikelet and finger number and negatively associated with days to heading and maturity. The genotypic correlation and path coefficient analysis showed 1000 grain weight, finger number and productive tillers as a major contributor to grain yield per plant.

John (2006) in 20 finger millet genotypes revealed that total dry matter production showed a positive and highly significant association with test weight (0.458). Grain yield showed a positive and highly significantly correlated with test weight (0.458), total dry matter production (0.585) and harvest index (0.597), hence grain yield could be improved through these characters. Significant positive regression coefficient was observed between grain yield and dry matter production (r^2=0.3747).

Sharathbabu *et al*. (2008) observed that grain yield per plant had strong positive association with finger number per ear and ear weight per plant. Number of tillers per plant had positive association with number of productive tillers per plant whereas florets number per spikelet had significant positive association with test weight.

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

Nandini *et al*. (2010) indicated that grain yield had strong positive correlation with weight of main ear, 1000 seed weight and total tillers per plant whereas the Productive tillers and plant height exhibited moderate positive correlation in the F_2 population of seven crosses of finger millet.

Shet *et al*. (2010) showed that grain yield per plant exhibited highly significant positive association with finger width and test weight in the F_2 populations of three different popular varieties *viz.,* HR 911 and PR 202 with *E. Africana.*

Ganapathy *et al*. (2011) studied 240 finger millet germplasm accessions and observed that productive tillers per plant and finger length are the important yield contributing traits and due critical emphasis needs be given to productive tillers per plant and finger length while selecting for grain yield improvement in finger millet. Since these traits had significant positive correlation with grain yield and positive inter-correlation also themselves.

Priyadharshini *et al*. (2011) studied the 21 hybrids along with seven parents of finger millet to know the nature and magnitude of association among the yield traits and observed that Grain yield had positive correlation with number of productive tillers, finger length and harvest index.

Haradari *et al*. (2012) studied the character association in base germplasm (1000 accessions) of finger millet and found that grain yield per plant had highly positive significant association with plant height, days to 50 per cent flowering, days to maturity and ear weight per plant.

Lule *et al*. (2012) reported that finger length, finger number, 1000 grain weight and tiller number had positive significant correlation with grain yield per plant. Days to heading days to maturity had negative correlation with grain yield per plant.

Anuradha *et al*. (2013) studied the association and effect of yield attributing traits on seed yield in 20 finger millet genotypes having late maturity period to identify a set of characters for effective selection during breeding programme. Days to maturity, number of fingers per ear showed positive significance at genotypic level.

Bharathi *et al*. (2013) investigated the global composite collection of finger millet germplasm for 15 quantitative characters to assess the association between the characters related to yield. Results showed that plot yield was strongly associated positively with productive tillers, number of fingers and days to 50 per cent flowering.

Das *et al*. (2013) from correlation studies observed that grain yield per plant had exhibited significant positive association with total number of basal tillers per plant, productive tillers per plant, total fingers on the main ear, finger length and finger width in 48 genotypes of finger millet.

Dhamdhere *et al*. (2013) in 29 elite finger millet genotypes revealed that finger length, straw weight and total biomass showed highly significant positive correlation with yield. Grain yield was found positively associated with days to

50 per cent flowering, days to maturity, thousand grain weight, ear weight and harvest index. All the nutritional characters were found negatively correlated with yield.

Shinde *et al*. (2014) reported that grain yield per plant was positively and significantly correlated with productive tillers per plant, plant height, finger length and number of fingers per main ear head at both genotypic and phenotypic levels, indicating that grain yield would be improved through these characters.

Suryanarayana *et al*. (2014) from Inter-relationship analysis in the 35 genotypes of finger millet observed that seed yield per plant showed positive and significant genotypic inter relationship with days to maturity, plant height and days to 50 per cent flowering suggesting that these are the major yield contributing traits.

Ulaganathan and Nirmalakumari (2014) a total of 105 finger millet genotypes were investigated to assess the association of characters and reported that days to 50 per cent flowering (0.93), productive tillers per plant (0.92), plant height (0.89), days to maturity (0.88), 1000 grain weight (0.85), flag leaf sheath length (0.77) and flag leaf blade length (0.52) and finger width (0.17) are significant and positively correlated with grain yield per plant.

Rani *et al*. (2015) showed that traits like, 1000-seed weight (0.9021 and 0.7640), number of fingers per ear (0.8534 and 0.6838), ear weight per plant (0.7850 and 0.6450), finger length (0.7573 and 0.5103), days to maturity (0.6245 and 0.5137), productive tillers per plant (0.5669 and 0.4148), days to 50 per cent flowering (0.5079 and 0.4249) and plant height (0.2665 and 0.2006) were found to possess significant positive association with seed yield per plant at both genotypic and phenotypic levels respectively.

Eric *et al.* (2016) showed the inherent strong genetic relationships among most traits as evidenced by the higher genotypic than phenotypic correlations. Grain yield had high, positive correlations with finger width (rg =0.876), grains per spikelet (rg =0.623), threshing percent (rg =0.677), peduncle length (rg =0.517) and panicle exertion (rg =0.571). These traits could be considered for grain yield selection.

Sao *et al*. (2016a) in 15 entries of finger millet concluded that productive tillers per plant and finger length are the important yield contributing traits and due critical emphasis needs to be given to productive tillers per plant and finger length while selecting for grain yield improvement in finger millet. Since these traits had significant positive correlation with grain yield and positive inter-correlation among themselves.

Sao *et al*. (2016b) studied the character association in 26 high yielding finger millet genotypes and revealed that productive tillers per plant and finger length traits had significant positive correlation with grain yield and positive inter-correlation among themselves. Days to maturity, fodder weight, days to 50 per cent flowering and length of finger showed positive significant correlation at genotypic level.

Saundarya and Satish (2016) studied the character association in 35 finger millet genotypes and observed that grain yield per plant exhibited significant positive association with harvest index, number of tillers per plant, grain weight of main panicle, 1000-grain weight and fingers per panicle. This indicated that harvest index; number of tillers per plant, grain weight of main panicle, 1000 grain weight and fingers per panicle may be important traits for predicting grain yield.

Anuradha *et al.* (2017) in 25 advanced breeding lines of finger millet studied the correlation of grain yield and yield related traits and reported that number of tillers per plant and number of fingers per ear were observed to be highly associated with yield.

Auti *et al.* (2017) investigated the 64 finger millet landraces and two cultivars for yield contributing and morpho-agronomic characters and observed that all the characters except height and tillers exhibited higher level of correlation.

Negi *et al.* (2017) found that grain yield per plant exhibited very strong positive association with biological yield per plant (0.6196, 0.6805), harvest index (0.4370, 0.3624), number of productive tillers per plant (0.3950, 0.4477), 1000 seed weight (0.3697, 0.3972) and peduncle length (0.2473, 0.2694) at phenotypic and genotypic level.

Suman *et al.* (2018) studied the associations among grain yield and yield components in 55 genotypes of finger millet. The correlation study revealed that flag leaf area, effective tiller per plant, ear per plant, days to maturity, biomass yield per plant, harvest index and 1000 seed weight recorded significant positive correlation with grain yield per plant.

2.4 Correlation coefficient analysis for grain yield and grain quality parameters

Padmaja (2006) revealed that the association of calcium content with grain yield is negative in 80 genotypes and simultaneous improvement of the yield with this trait is not possible so we have to seek an adjustment among the attributes to find out an acceptable level of the characters under improvement.

Gupta *et al.* (2009) evaluated the selfed progenies ($S_{1,,}$s) derived from two diverse population (PVGGP-6 and IAC-ISC-TCP1) in order to examine the association of grain iron (Fe) and zinc (Zn) content with grain yield and component traits in pearl millet. Significant positive correlation found between iron and zinc content (r=0.81 to 0.82; p <0.01) in both the populations suggesting the possibility of simultaneous effective genetic improvement of both micronutrients.

Kumar *et al.* (2012) Observed the highly significant positive correlation between the grain Fe and Zn content (r = 0.853; P < 0.01) in 29 sorghum accessions indicating that either the genetic factors for Fe and Zn contents are linked, or the physiological mechanisms were interconnected for Fe and Zn uptake and translocation in the grain. These results indicate the potential of simultaneous genetic improvement for both micronutrients.

Nagesh *et al.* (2012) studied 48 hybrids of rice to estimate phenotypic and genotypic association among grain iron, zinc, yield attributes and grain yield. A positive correlation between iron and zinc content was observed while there is no correlation between grain iron and zinc content with grain yield.

Savitha *et al.* (2013) evaluated 21 hybrids along with their parents to know the nature and the extent of association that exists between the grain yield and iron and zinc content. At genotypic level, iron content recorded significant positive correlations with grain yield. Whereas zinc content recorded the negative non-significant correlations with grain yield. Regarding the indirect effect of component traits on grain yield, iron content and zinc content was found to be low and negligible.

Srilakshmi (2013) studied 43 genotypes of finger millet and revealed that at phenotypic level, calcium content had non-significant negative association (-0.008) and negative direct effect (-0.2089) on seed yield per plant.

Rani *et al.* (2015) evaluated 40 genotypes of finger millet for character association and path co efficient analysis among grain yield and quality traits like seed calcium content. Results revealed that the trait calcium content showed negative non-significant association with seed yield per plant at both genotypic and phenotypic levels.

Badigannavar *et al.* (2016) studied the concentrations of micronutrients and protein and yield parameters in 112 local landraces and varieties of sorghum. Correlation estimates among the genotypes indicated that grain yield was positively correlated with copper and protein with copper and zinc.

Sarjansinh (2016) studied 68 genotypes of finger millet for character association revealed that Iron content had highly significant positive correlation with calcium content at both the genotypic and phenotypic levels. Calcium content had highly significant positive correlation with grain yield per plant but, direct effect was negative.

Kazi and Auti (2017) studied 64 landraces from Maharashtra and Correlation studies showed significant correlation among K and Mn (0.648), Zn and Mg (0.551), Ca and Mg (0.476) and Fe and Ca (0.414).

2.5 Path coefficient analysis for grain yield and its component traits

Path analysis permits the understanding of the cause and effect of related characters (Wright, 1921). The path analysis reveals whether the association of characters with yield is due to their direct effect on yield or is a consequence of their indirect effects via other component characters. Hence, the estimate of path coefficient effects of different yield components on grain yield is essential.

The comprehensive review of literature on path coefficient analysis as follows.

Sharathbabu *et al*. (2008) observed that ear weight per plant and straw yield per plant had highest direct contribution on grain yield per plant in 19 white seeded finger millet genotypes.

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

Nandini *et al*. (2010) in F_2 population of seven crosses of finger millet indicated that weight of main ear, 1000 seed weight showed positive direct effect on grain yield of main ear.

Shet *et al*. (2010) in F_2 populations of three different popular varieties *viz.,* HR 911 and PR 202 with *E. Africana* indicated that productive tillers per plant had the highest positive direct effect followed by finger width and test weight on grain yield in these two crosses while finger number exerted low positive direct effect on grain yield.

Ganapathy *et al*. (2011) in 230 finger millet germplasm accessions reported that number of productive tillers per plant had very high direct effect on yield whereas finger number per ear, finger length had low indirect effect on yield.

Priyadharshini *et al*. (2011) studied the 21 hybrids along with seven parents of finger millet to know the nature and magnitude of association among the yield traits and their direct and indirect effects on grain yield. Harvest index had high positive direct effect on grain yield and number of productive tillers and finger length had moderate direct effect and revealed true relationship of these traits with grain yield and hence direct selection for these traits would be rewarding for yield improvement.

Wolie and Dessalegn (2011) observed that phenotypic path analysis of the traits like, biomass yield (0.835), finger length (0.159), number of fingers per ear (0.016), and number of ears per plant (0.038) had direct effects on grain yield, while plant height, days to heading and days to maturity exhibited negative direct effects.

Haradari *et al*. (2012) On the basis of path analysis revealed that number of productive tillers per plant, days to maturity and ear weight per plant had direct positive effect on grain yield in base germplasm (1000 accessions) of finger millet.

Lule *et al*. (2012) studied the path coefficient analysis and showed the higher and positive direct effect of productive tillers per plant (0.356) and 1000 grain weight (0.285) and positive indirect effect of finger length, finger number, ear weight, number of grains per spikelet and culm diameter on grain yield indicating that any genetic improvement on those traits had positive contribution to improve productivity of finger millet.

Anuradha *et al*. (2013) in 20 finger millet genotypes having late maturity period revealed that days to maturity and number of fingers per ear exhibited positive direct association towards seed yield.

Dhamdhere *et al*. (2013) studied the 29 elite finger millet genotypes to estimate direct and indirect effect of various component characters on grain yield. The results revealed that total biomass, harvest index, number of tillers per plant, flag leaf area and days to 50 per cent flowering showed positive direct effect on yield while 1000 grain weight showed positive indirect effect on yield through ear weight.

Das *et al*. (2013) from path analysis revealed that maximum positive direct effect on grain yield per plant was exhibited by productive tillers per plant followed by finger length and finger width in the 48 genotypes of finger millet.

Savitha *et al.* (2013) evaluated the 21 hybrids along with their parents for direct and indirect effects yield and yield contributing traits. Path analysis on grain yield showed that the harvest index and dry fodder yield had high positive direct effects and this revealed the true relationship of these traits with grain yield. Hence, direct selection for these traits would be rewarding for yield improvement.

Kumar *et al*. (2014) indicated that positive genotypic and phenotypic direct effects were observed for productive tillers per plant, biological yield, harvest index and number of fingers per ear had higher positive direct effect on grain yield. These traits having a positive direct effect on grain yield can be considered as a suitable selection criterion for evolving high yielding finger millet genotype.

Suryanarayana *et al*. (2014) in 35 genotypes of finger millet based on path coefficient analysis found that days to maturity, plant height and days to 50 per cent flowering had high positive direct effect followed by main ear length, fingers per ear and concluded that these traits deserve special emphasis in selection while selecting for improvement of seed yield in finger millet.

Rani *et al*. (2015) revealed that 1000 seed weight, number of fingers per ear, days to maturity, ear weight per plant, finger length and days to 50 per cent flowering showed true relationship with seed yield per plant by establishing significant positive association and high positive direct effect.

Eric *et al.* (2016) revealed that productive tillers per plant (0.473), 1000 grain weight (0.136), grains per spikelet (0.131) and threshing per cent (0.118) had positive, direct effects on grain yield. Due consideration should be placed on these traits when selecting for grain yield improvement in finger millet whereas strong, positive indirect effects contributed to grain yield by finger width, peduncle length, panicle exertion and leaf sheath width.

Jyothsna *et al*. (2016) concluded that plant height and main ear length showed true relationship by establishing positive association and direct effect on grain yield per plant both at genotypic and phenotypic levels and number of productive tiller per plant, days to 50 per cent flowering and number of fingers per ear at genotypic level and days to maturity at phenotypic level.

Sao *et al*. (2016a) in 15 entries of finger millet revealed that days to maturity and fodder weight per ear exhibited positive direct effect association and positive direct towards seed yield.

Sao *et al*. (2016b) revealed that days to maturity and fodder weight exhibited positive direct association and positive direct effect towards seed yield in 26 high yielding finger millet genotypes.

Saundarya and Satish (2016) showed that highest positive direct effect was exhibited by harvest index, number of tillers per plant, grain weight of main panicle, 1000 grain weight and number of fingers per panicle. Thus, these traits may be used as selection criteria for screening of promising finger millet genotypes.

Negi *et al*. (2017) through path analysis revealed that biological yield per plant (0.8983, 1.1590) and harvest index (0.7390, 0.9162) are major direct contributors towards grain yield per plant at phenotypic and genotypic level.

Suman *et al.* (2018) studied the associations among grain yield and yield components and their direct and indirect influence on the grain yield in 55 genotypes of finger millet. Phenotypic path analysis revealed that harvest index, biomass yield per plant, ears per plant, days to 50 per cent flowering, plant height, 1000 seed weight, fingers/plant, and flag leaf area to exert positive direct effects on grain yield.

2.6 Genetic divergence among yield and yield contributing characters

Knowledge of genetic diversity among genotypes on the basis of divergence analysis usually helps a breeder in choosing diverse parents for breeding programme. In breeding programme, progenies derived from diverse parents selected on the basis of genetic divergence analysis are expected to show a broad spectrum of genetic variability, providing a greater scope for isolating transgressive segregants in advanced generations (Singh and Mishra, 1996) and promising heterotic effect may be observed in early generation. Hence, a study on genetic divergence is essential to identify suitable finger millet parents having diverse characters through genetic divergence analysis.

Arun *et al*. (2008) studied genetic diversity among 150 finger millet accessions using Mahalanobis D^2 statistics and grouped them into 18 clusters based on genetic distance. Fourteen solitary clusters were superior viz., II, III, V, VI, VIII, X, XI, XII, XIII, XIV, XV, XVI, XVII and XVIII. Inter crossing between genotypes of these diverse clusters would generate a broad spectrum of variability for effective selection in the segregating generations for the development of high yielding cultivars.

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

Das *et al.* (2013) assessed the genetic divergence in 48 germplasm lines of finger millet using D^2 statistics for 11 quantitative characters and grouped into eight clusters. The most important character contributing to the diversity was main ear length followed by total number of fingers on the main ear, grain yield per plot, grain yield per plant, main ear width, total number of basal tillers per plant, number of leaves on the main tiller, total number of productive tiller per plant, finger width, and finger length. Higher yielder clusters are VII, I and II.

Karad and Patil (2013) studied the genetic diversity in 65 genotypes using D^2 statistics and grouped into five clusters based on the genetic distance. Cluster I contains highest 50 genotypes, followed by cluster II (11 genotypes) and cluster III (2 genotypes). The cluster IV and V were mono genotypic. In overall, D^2 analysis suggested KOPN 161, KOPN 370, VL 149, KOPN 387, PR 202, PES 110, KOPN 495, KOPN 892 and KOPN 926 were the most diverse parents could be utilized to improve, widen the genetic base and would be used as parents in breeding programme to enhance the productivity of finger millet.

Shinde *et al*. (2013) grouped 41 genotypes of finger millet collected from different geographical areas into seven clusters using D^2 statistics. They reported that the characters such as Iron content (70.12 %) contributed maximum towards divergence followed by plant height (11.72 %), days to 50 per cent flowering (5.49 %) and days to physiological maturity (7.07 %).

Rani *et al*. (2014) grouped the 40 genotypes of finger millet into seven distinct classes based on their genetic diversity using D^2 statistics. The maximum inter-cluster distance was between cluster V and VII, followed by cluster IV and VII and cluster V and VI, suggesting there by that there is wide genetic diversity between these clusters.

Suryanarayana *et al*. (2014) on the basis of non-hierarchical Euclidean cluster analysis 35 genotypes of the finger millet grouped into six non-overlapping clusters. The clustering pattern revealed that the genotypes originating from different geographical regions got themselves grouped into different clusters, indicated that the geographic biodiversity is not the responsible factor in determining genetic biodiversity. Among all the characters, plant height followed by seed yield plant per plant, main ear length contributed maximum towards the total divergence.

Bendi *et al*. (2015) evaluated the 55 genotypes of finger millet to study genetic divergence by using principal component analysis (PCA) and cluster analysis. The total genotypes were grouped into eight clusters. Principal component analysis identified five principal components with Eigen values more than one which contributed 83.69 per cent of cumulative variance. The genotypes selected from the above analysis were IE 501, IE 196, IE 2093, IE 3543, IE 2293, IE 2323 and IE 2790 appear to be desirable for inclusion in crossing programme aimed for improvement of finger millet.

Saundarya and Satish (2015) studied the nature and magnitude of divergence using Mahalanobis D^2 statistics. The 35 genotypes of finger millet were grouped into six clusters using Tocher’s method. Genotypes present in cluster IV and cluster VI, exhibited high degree of genetic diversity. Cluster III was suitable for grain yield per plant, 1000 grain weight, grain yield of main panicle and harvest index. Days to 50 per cent flowering and grain yield per plant contributed maximum towards genetic divergence.

Ulaganathan and Nirmalakumari (2015) grouped 305 genotypes into 28 different clusters through multivariate hierarchical clustering. Cluster III was the largest cluster having 62 genotypes and cluster XXIII and XXVIII formed solitary clusters. The genotypes TNEc 0386 and TNEc 1914 were selected for hybrid program and utilizing these genotypes has the chance to obtain higher heterosis with high performing crosses.

Sao *et al*. (2016a) partitioned 15 finger millet entries into 4 different clusters through Euclidian clustering. Cluster I and II formed solitary clusters which revealed the presence of wide diversity for various characters among these entries.

Sao *et al*. (2016b) grouped 21 finger millet entries into 6 different clusters through Euclidian clustering. Cluster I formed solitary clusters with 13 genotypes which revealed the presence of wide diversity for various characters among genotypes. Cluster II and IV composed two genotypes each and Cluster III, IV and VI composed one genotypes in each.

Mahanthesha *et al*. (2017) partitioned the 48 genetically diverse genotypes of finger millet into eight clusters. Maximum number of germplasm lines (24) were included in cluster I followed by twelve germplasm lines in cluster II, five germplasm lines in cluster IV, cluster VI with three genotypes and one each in cluster III, V, VII and VIII. The maximum intra-cluster distance was shown by cluster VI. Maximum divergence was observed between cluster VI and VIII, while minimum was between cluster I and V suggesting, more variability in genetic makeup of germplasm lines included in these clusters.

Negi *et al*. (2017) investigated the genetic divergence among 35 finger millet genotypes for fourteen morphological characters using Mahalanobis D^2 statistics and grouped them into 6 clusters irrespective of geographical diversity, indicating no parallelism between geographic and genetic diversity. Clusters I and VI had maximum number of 8 genotypes, followed by cluster II and V with seven genotypes and cluster III with 4 genotypes. Cluster IV was mono genotypic. The highest inter-cluster distances was observed between cluster IV and V followed by cluster IV and VI, cluster II and IV, cluster I and IV, cluster III and V and cluster III and IV suggesting the use of genotypes from these clusters to serve as potential parents for hybridization.

Patel *et al*. (2017) on basis of Euclidean distance studied the 65 germplasm accessions of finger millet to assess the genetic diversity for yield and yield contributing traits. In cluster analysis, sixty five genotypes were grouped into five distinct clusters and concluded that obtained results can be exploited in planning and execution of future breeding strategy in finger millet.

Sarjansinh *et al*. (2017) grouped the 68 diverse finger millet genotypes into eight clusters on the basic of genetic distances. Cluster I contains maximum number of 60 genotypes, followed by cluster VII (2 genotypes) and cluster III (2 genotypes) while the remaining six clusters were solitary. The maximum inter-cluster distance was observed between cluster-VIII and III. In overall, D^2 analysis suggested genotypes belonging to the distinct cluster (VIII and III) could be used in hybridization programme for enhance the productivity of finger millet.

MATERIAL AND METHODS

III MATERIAL AND METHODS

An experiment was conducted to assess the extent of micronutrient content, genetic variability, diversity, character association, direct and indirect effects of grain yield and its component traits in the finger millet genotypes. The details of the material utilized, methods followed, and sampling of plants, collection, analysis, and interpretation of data are described in this chapter.

3.1 Experimental Material

The material for present investigation comprised of sixty finger millet genotypes along with four varietal checks (GPU-28, KMR-301, MR-1 and MR-6) was collected from Project Coordinating Unit (Small Millets), GKVK, Bangalore under All India Coordinated Research Project on Small Millets, Zonal Agricultural Research Station, VC Farm, Mandya and Organic Farming Research Centre, UAHS, Shivamogga. The list of genotypes utilized under study is presented in (Table 1).

3.2. Experimental site and layout

All the collected sixty finger millet genotypes along with four varietal checks were grown in an Augmented RBD (Federer, 1956) at Research Farm of Zonal Agricultural and Horticultural Research Station, College of Agriculture, UAHS, Shivamogga during *Kharif* (2017) with recommended agronomical package of practices. Each genotype was sown in one row of 4.5 m length by adopting a spacing of 25 cm between rows and 10 cm between the plants.

3.3 Observations and measurements

Observations on grain yield and its related traits were recorded at different stages of crop growth on five randomly selected plants excluding those at the border and mean values were computed.

3.3.1 Days to 50 per cent flowering

The number of daystaken by main tiller, from sowing to opening of first flower in 50 per cent of the plants in a row was recorded.

3.3.2 Days to maturity

The number of days taken to show more than 90 per cent of earhead browning before drying up, confirmed by grain hardness to bite, was taken as days to physiological maturity.

Table 1: Name and source of finger millet genotypes utilized in the present study

Sl. No.	Genotypes	Source	Sl. No.	Genotypes	Source
1	IC-473142	AICRPSM, Bangalore	18	IC-474959	AICRPSM, Bangalore
2	IC-473143	AICRPSM, Bangalore	19	IC-475224	AICRPSM, Bangalore
3	IC-473146	AICRPSM, Bangalore	20	Hamsa	AICRPSM, Bangalore
4	IC-473155	AICRPSM, Bangalore	21	ML-365	AICRPSM, Bangalore
5	IC-473157	AICRPSM, Bangalore	22	OUAT-2	AICRPSM, Bangalore
6	IC-473160	AICRPSM, Bangalore	23	Udara malligae	AICRPSM, Bangalore
7	IC-473165	AICRPSM, Bangalore	24	KMR-204	ZARS, Mandya
8	IC-473168	AICRPSM, Bangalore	25	KMR-340	ZARS, Mandya
9	IC-473172	AICRPSM, Bangalore	26	GPU-26	ZARS, Mandya
10	IC-473178	AICRPSM, Bangalore	27	GPU-45	ZARS, Mandya
11	IC-473181	AICRPSM, Bangalore	28	GPU-48	ZARS, Mandya
12	IC-473183	AICRPSM, Bangalore	29	L-5	ZARS, Mandya
13	IC-473377	AICRPSM, Bangalore	30	Indaf-5	ZARS, Mandya
14	IC-473379	AICRPSM, Bangalore	31	Indaf-7	ZARS, Mandya
15	IC-473381	AICRPSM, Bangalore	32	Indaf-8	ZARS, Mandya
16	IC-473382	AICRPSM, Bangalore	33	Indaf-9	ZARS, Mandya
17	IC-473385	AICRPSM, Bangalore	34	GPU-67	ZARS, Mandya

Contd.

35	IC-473388	AICRPSM, Bangalore	48	KMR-316	ZARS, Mandya
36	IC-474138	AICRPSM, Bangalore	49	KMR-632	ZARS, Mandya
37	IC-474525	AICRPSM, Bangalore	50	KMR-634	ZARS, Mandya
38	IC-474574	AICRPSM, Bangalore	51	SMRC-1	OFRC, Shivamogga
39	IC-474603	AICRPSM, Bangalore	52	SMRC-2	OFRC, Shivamogga
40	IC-474616	AICRPSM, Bangalore	53	SMRC-3	OFRC, Shivamogga
41	IC-474640	AICRPSM, Bangalore	54	Koolimotee Ragi	OFRC, Shivamogga
42	IC-474649	AICRPSM, Bangalore	55	Jagaluru Ragi	OFRC, Shivamogga
43	IC-474651	AICRPSM, Bangalore	56	Boonda Ragi	OFRC, Shivamogga
44	IC-474652	AICRPSM, Bangalore	57	Karikatti Ragi	OFRC, Shivamogga
45	IC-474662	AICRPSM, Bangalore	58	Jeenumundaga Ragi	OFRC, Shivamogga
46	IC-474792	AICRPSM, Bangalore	59	Karimundaga Ragi	OFRC, Shivamogga
47	IC-474925	AICRPSM, Bangalore	60	Malali	OFRC, Shivamogga
CHECKS					
1	GPU-28	AICRPSM, Bangalore	3	MR-1	AICRPSM, *Bangalore*
2	KMR-301	ZARS, Mandya	4	MR-6	ZARS, Mandya

AICRPSM- All India Coordinated Research Project on Small Millets, Bangalore

ZARS- Zonal Agricultural Research Station, Mandya

OFRC- Organic Farming Research Centre, Shivamogga

3.3.3 Plant height (cm)

The height of the main tiller from ground level to the tip of the earhead was recorded in centimeters and mean was computed.

3.3.4 Number of tillers per plant

The number of basal tillers was counted from each of the tagged plants and averaged per plant.

3.3.5 Number of productive tillers per plant

The number of basal tillers bearing inflorescence/ ears werecounted from each of the tagged plants and averaged per plant.

3.3.6 Number of fingers per ear

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

3.3.7 Finger length (cm)

Length of the longest finger on the main tiller was measured in centimeters and mean was computed.

3.3.8 Finger width (cm)

It is measured at the center of any one of the fingers on the main tiller and expressed in centimeters.

3.3.9 Earhead length per plant (cm)

It was measured in centimeters from the base to the tip of the main ear of tagged plants.

3.3.10 Earhead weight per plant (g)

Total earhead weight of five plants was recorded and the mean value is computed as earhead weight per plant in gram.

3.3.11 Grain yield per plant (g)

Total grain yield of five plants was recorded and the mean value is computed as grain yield per plant in gram.

Plate 1: General view of the field experiment

3.3.12 Straw yield per plant (g)

Straw from the tagged plants was harvested, properly dried and weighed and the mean value is computed as straw yield per plant in gram.

3.3.13 Harvest index (%)

It is calculated as the ratio of grain yield to the biologicalyieldmultiplied by 100 and expressed in percentage (%).

$$\text{Harvest index (\%)} = \frac{\text{Grain yield (g)}}{\text{Biological yield (g)}} \times 100$$

3.3.14 Test weight (g)

The weight of 1000 randomly selected grains from tagged plants was recorded in grams and mean was worked out.

3.4 Estimation of micronutrient content using ICP-OES instrument

Micronutrient content in seeds of finger millet genotypes were analysed in laboratories of Department of Soil Science and Agricultural Chemistry and Crop Physiology, UAHS, Shivamogga. The nutrient contents like calcium, magnesium, iron, copper and zinc were estimated by using Inductively Coupled Plasma-Optical Emission Spectrometry (ICP-OES) method by following diacid mixture procedure as suggested by Lindsay and Norvell (1978). ICP-OES is an analytical technique with plasma and spectrometer used for the detection of the composition of elements in (mostly water-dissolved) samples.

3.4.1 Principle of ICP-OES

The solution to analyze is conducted by a peristaltic pump through a nebulizer into a spray chamber. The produced aerosol is lead into argon plasma. Plasma is the fourth state of matter, next to the solid, liquid and gaseous state. In the ICP-OES the plasma is generated at the end of a quartz torch by a cooled induction coil through which a high-frequency alternate current flows. As a consequence, an alternative magnetic field is induced which accelerated electrons into a circular trajectory. Due to a collision between the argon atom and the electrons ionization occurs, giving rise to stable plasma. The plasma is extremely hot, 6000-7000 K. In the induction zone, it can even reach 10000 K. In the torch desolvation, atomization and ionization of the sample take place. Due to the thermic energy is taken up by the electrons, they reach a higher "excited" state. When the particles drop back to ground level energy is liberated as light (photons). Each element has characteristic emission spectrum which is measured with a spectrometer. The light intensity on the wavelength is measured and with the calibration calculated into a concentration.

3.4.2 Procedure followed for micronutrients content estimation

1. The seeds were ground using mixer grinder and made fine powdered.
2. One gram of fine powdered sample was taken and was added with 10 ml of 0.1N Nitric acid and kept it overnight for pre-digestion process.
3. The mixture was added with 10 ml of diacid mixture (9:4, Nitric acid to Perchloric acid), after adding, light brown colour was noticed.
4. Then the mixture was kept on sand bath for 3 to 4 hours till the brown colour turns clear white colour.
5. The mixture was diluted by adding 10 ml of double distilled water and that mixture was filtered using vacuum filter.
6. The volume of filtered solution is increased to 100ml by addition of double distilled water.
7. Then the samples were fed into ICP-OES instrument and the values were recorded.
8. The concentration in terms of mg/100g was calculated by dividing the parts per million (ppm) values obtained in ICP-OES by 10.

3.5 Statistical analysis

The statistical analysis of the data collected in the experiment on the individual character was carried out on the mean values of five randomly selected plants on each genotype. Different statistical methods employed for analysis are as follows. The following descriptive statistics were calculated as per Sunderaraj *et al.* (1972).

3.5.1 Mean

Sum of all observations in a sample divided by the number of observations (n).

$$\text{Mean} = \frac{\sum \text{Xi}}{\text{n}}$$

Where,

Xi = ith observation of a population

n = Total number of observations

3.5.2 Range

Minimum and maximum value by individual plant observations was used to indicate the limits of range for a given character.

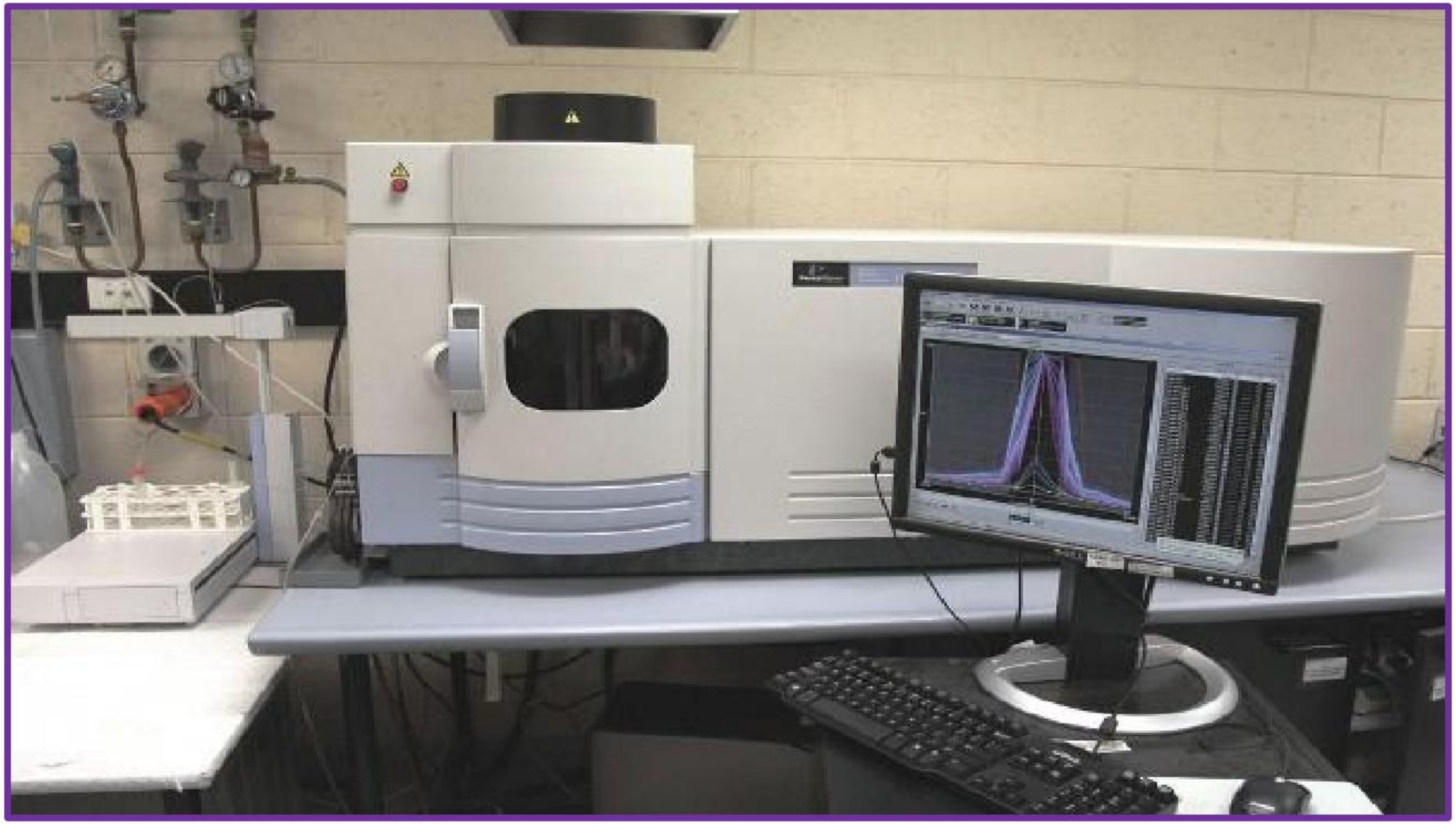

Plate 2: ICP-OES instrument used in the present investigation for estimation of quality traits

3.5.3 Variance

Variance is defined as the square of the standard deviation, or it is the average of the squared deviations of individual observation from the mean. It is expressed as the sum of squares of the deviations of all observations of a sample from its mean and divided by (n-1), where n is the number of observations. It is estimated by the following formula,

$$\mathrm{Variance} = \frac{\sum \mathrm{x}^2 - \sum(\mathrm{x})^2}{\mathrm{n}}$$

Where,

Xi = i^{th} observation of a population

n = number of observations

3.5.4 Standard deviation

$$\mathrm{Standard\ deviation\ (SD)} = \sqrt{\mathrm{Variance}} = \frac{\sum \mathrm{d}^2}{\mathrm{n}}$$

Where,

d = Deviation of individual values from mean

n = Number of observations

3.5.5 Standard error

It is the measure of uncontrolled variation present in a sample which is estimated by dividing the standard deviation by the square root ofa number of observations in the sample and is denoted by SE.

$$\mathrm{SE} = \frac{\mathrm{SD}}{\sqrt{\mathrm{n}}}$$

Where,

SD = Standard deviation

n = Number of observations

3.5.6 Analysis of variance (ANOVA)

The mean values of the quantitative traits for all the sixty finger millet genotypes as well as check entries were computed and used for statistical analysis. Analysis of variance was performed to partition the total variation following an Augmented design (Federer, 1956). The analysis was done using "Windostat" version 9.2 software.

Source of variation	**Df**	**MSS**	**'F' ratio**
Blocks (b)	(b-1)	MSS(b)	MSS(b)/ EMSS
Entries(e) [varieties + check entries]	(e-1)	MSS(e)	MSS(e)/ EMSS
Checks (c)	(c-1)	MSS(c)	MSS(c)/ EMSS
Varieties (v)	(v-1)	MSS(v)	MSS(v)/ EMSS
Checks vs. (varieties)	(c-1) (v-1)	MSS(vc)	MSS(vc)/ EMSS
Error	(c-1) (b-1)	EMSS	

(Federer, 1956)

Where,

v = Number of varieties

c= Number of check varieties

b= Number of blocks

e= Number of entries

The significance was tested by referring to the table by Fisher and Yates (1936).

3.6 Estimation of genetic variability parameters for grain yield and yield attributing traits and quality traits

3.6.1 Coefficient of variation

The components *viz.*, phenotypic, genotypic and environmental variances were utilized for estimation of the coefficient of variation at both phenotypic and genotypic levels for all the characters were computed as suggested by Burton and De Vane (1953).

3.6.2 Genotypic and phenotypic co-efficient of variation

The coefficient of variation both at genotypic and phenotypic levels for all the characters were computed by applying the formula as suggested by Burton and De vane (1953).

$$\text{Genotypic Coefficient of Variation (GCV)} = \left(\frac{\sigma g}{\overline{X}}\right) x\ 100$$

$$\text{Phenotypic Coefficient of Variation (PCV)} = \left(\frac{\sigma p}{\overline{X}}\right) x\ 100$$

Where,

$\overline{X}$ = Grand mean of the character

σp = Phenotypic standard deviation

σg = Genotypic standard deviation

PCV and GCV were classified into low, moderate and high as suggested by Subramanian and Menon (1973).

0 – 10 %	:	Low
10.1 – 20 %	:	Moderate
20.1 % and above	:	High

3.6.3 Heritability (h^2) in broad sense

Heritability in broad sense for all the characters was computed by the formula suggested by Hanson *et al.* (1956) and expressed as percentage.

Heritability (h^2_{bs}) = ($\sigma g^2 / \sigma p^2$) × 100

Where,

h^2_{bs} = Heritability (broad sense)

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

Heritability was classified into low, moderate and high as suggested by Robinson *et al.*, (1949).

0 – 30 %	:	Low
30.1 – 60 %	:	Moderate
60.1 % and above	:	High

3.6.4 Genetic Advance (GA)

The predicted genetic advance was estimated according to the formula given by Johnson *et al.*, (1955).

$GA = h^2bs \times K \times \sigma P$

Where,

h^2bs = Heritability in broad sense

K= Selection differential, a constant (z/p) the valve of which is 2.06 at 5 per cent selection intensities.

σP= Phenotypic standard deviation

3.6.5 Genetic Advance as per cent Mean (GAM)

This was calculated using the formula given below.

$GAM\ (\%) = (GA/\overline{X} \times 100)$

Where,

GA = Genetic advance

$\overline{X}$ = General mean

The genetic advance as per cent of mean was categorized into low, moderate and high as suggested by Johnson *et al.* (1955).

0 – 10 % : Low

10.1 – 20 % : Moderate

> 20.1 and above : High

3.7 Estimation of correlation coefficients for grain yield and yield attributing traits and grain quality traits

In all the genotypes, the simple correlation coefficients were calculated to determine the direction and magnitude of associations among different characters and tested against table ‘r’ values (Fisher., 1932) for (n-2) degrees of freedom both at 0.05 and 0.01 probability levels for their significance. Simple correlations were calculated by using the formula as given Weber and Moorthy (1952).

$$r_{xy} = \frac{\mathrm{Covxy}}{\sqrt{\mathrm{Vx} \times \mathrm{Vy}}}$$

Where,

r_{xy}= Correlation coefficient between x and y

$Cov_{(xy)}$ = Covariance between x and y

V_x= Variance of character x

V_y= Variance of character y

The significance of correlation coefficients was tested at (n-2) degrees of freedom using‘t’ table from Fisher and Yates at (5 % and 1%) probability level.

3.8 Path coefficient analysis for grain yield and yield attributing traits

The path coefficient analysis is partitioning of the correlation coefficients into the measures of direct and indirect effects of yield components on yield as suggested by Wright (1921) and illustrated by Dewey and Lu (1959). Standard path coefficients which are the standardized partial regression coefficients were obtained using statistical software “Windostat version 9.2”. These values were obtained by solving the following set of ‘P’ simultaneous equations by using the above package.

$P_{01} + P_{02}\, r_{12} + \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ P_{0p}\, r_{1p} = r_{01}$

$P_{01}\, r_{21} + P_{02}\, r_{22} + \ldots\ldots\ldots\ldots\ldots\ P_{0p}\, r_{2p} = r_{02}$

$P_{0p}\, r_{1p} + P_{0p}\, r_{2p} + \ldots\ldots\ldots\ldots\ldots\ldots P_{0p} = r_{0p}$

Where,

P_{01}, P_{02}... P_{0p} is the direct path effect of variables 1, 2, 3…. p on the dependent variable 0.

r_{12}, r_{13}…. r_{1p}…….$r_{p\ (p-1)}$ are the possible correlation coefficients between various independent variables and r_{01}, r_{02} …. r_{0p} are the correlations of the independent variable with dependent and independent variables.

The indirect effect of the i^{th} variable *via* j^{th} variable obtained as

$$P_{0j} \times r_{ij}$$

(From the simultaneous equation, it is clear that the correlation coefficient is the sum of the direct and indirect path coefficients).

The contribution of the remaining unknown factors was measured as the residual factor and calculated as below:

$P^2_{0x} = (1 - (P^2_{01} + 2^2_{01} + 2P^2_{03} + \ldots\ldots\ldots + P^2_{0n} + 2P_{01}P_{02}r_{12} + 2P_{01}P_{09}r_1 + \ldots\ldots\ldots\ldots + P^2_{02} + P_{02}r_{29} + \ldots\ldots P^2p_0).$

$$\text{Residual factor} = \sqrt{p^2_{0x}}$$

3.9 Genetic divergence analysis for grain yield and yield attributing traits and quality traits

The genetic divergence between genotypes was estimated using Mahalanobis D^2 statistic (Mahalanobis, 1936). The distance D from the sample was computed using the formula.

$D^2p = d^1 S^{-1}d$

Where,

D^2p = Square of distance considering ‘p’ variables

D =Vector observed differences of the mean values of all the characters (x_{i1}- x_{i2})

S^{-1}= inverse of variance and covariance matrix

3.9.1 Clustering of the D^2 values

All the genotypes used were clustered into different groups following Tocher’s method (Rao, 1952). The intra and inter-distance were also computed the criterion used in clustering to the same cluster should at least on the average, show a smaller D^2 values than those belonging to different clusters.

The device suggested by Tocher (Rao, 1952) was started with two closely associated populations and find a third population which had the smallest average of D^2 from the first two. Similarly, the fourth was chosen to have a smallest average D^2 value from the first three and so on. If at any stage increase in average D^2 value exceeded the average of already included, because of the addition of a new genotypes, than that genotypes was deleted. The genotypes that are included already in that group were considered as the first cluster. This procedure was repeated till D^2 values of the other genotypes were exhausted omitting those that were already included in the former cluster and grouping them into different cluster.

3.9.2 Intra-cluster distance

The average intra-cluster distances were calculated by the formula given by Singh and Chaudhary (1977).

Square of intra-cluster distance = $\Sigma Di^2/n$

Where,

ΣDi^2 = sum of distance between all possible combinations.

n= number of all possible combinations

3.9.3 Inter-cluster distance

The average inter-cluster distance was calculated by the formula described by Singh and Chaudhary (1977).

Square of inter-cluster distance = $\Sigma Di^2/n_i n_j$

Where,

ΣDi^2 = Sum of distances between all possible combinations ($n_i n_j$) of the entries included in the cluster study.

n_i = Number of entries in cluster i

n_j = Number of entries in cluster j

3.9.4 Contribution of individual characters towards genetic divergence

The character contribution towards genetic divergence was computed using method given by Singh and Chaudhary (1977). In all the combination, each character is ranked on the basis of $di = y_i^j - y_i^k$ values.

Where,

di = mean deviation

y_i^j = mean value of the jth genotype for the ith character and

y_i^k = mean value of the kth genotype for the ith character.

EXPERIMENTAL RESULTS

IV EXPERIMENTAL RESULTS

The data obtained on sixty finger millet genotypes for grain yield and quality traits was subjected to standard statistical analysis for drawing valid conclusions. The details of results obtained from the present investigation are discussed character-wise and presented under the following headings.

4.1 Genetic variability parameters for grain yield and yield attributing characters

4.2 Genetic variability parameters for grain quality traits

4.3 Correlation coefficient analysis for grain yield and yield related characters

4.4 Correlation coefficient analysis for grain yield and grain quality parameters

4.5 Path coefficient analysis for grain yield and its component traits

4.6 Genetic divergence among grain yield and yield contributing traits

4.7 Genetic divergence of grain quality traits

4.8 Superior finger millet genotypes identified for grain yield and grain quality traits

4.9 Finger millet genotypes identified for both grain yield and grain quality traits

4.1 Genetic variability parameters for grain yield and yield attributing characters

The success of any breeding programme depends upon the quantum of genetic variability present in the population. Wider range of genetic variability helps in selecting desired genotypes. In addition to the genetic variability, knowledge on heritability and expected genetic advance helps the breeder to employ the suitable breeding strategy. Therefore, it is necessary to have knowledge of genetic variability, heritability and genetic advance present in the available genetic material.

The analysis of variance revealed significant differences among the genotypes for all characters, indicating a high degree of variability in the material studied. The details are presented in (Table 2).

The genetic variability parameters *viz.,* mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (broad sense) and genetic advance as per cent mean (GAM) for all the fourteen characters are presented in the (Table 3). All the fourteen traits under study showed wide range of variation indicating an enormous opportunity for bringing about improvement in essential direction.

Table 2: Analysis of variance for grain yield and yield related traits in sixty genotypes of finger millet

S V	DF	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	X_{12}	X_{13}	X_{14}
		MEAN SUM OF SQUARES													
Block	3	40.504	42.456	23.899	0.459	0.391	0.901	2..599	0.009	2.828	26.530	3.290	48.131	0.002	0.088
Entries	63	52.919**	53.200**	378.154**	0.609**	0.525**	1.255**	4.539**	0.011**	5.094**	37.205**	27.984**	142.147*	0.003*	0.098*
Checks	3	44.917**	47.167**	316.032**	0.504*	0.417*	1.205**	13.548**	0.007**	11.478**	0.969	7.286	185.656*	0.003	0.099*
Varieties	59	47.529**	46.956**	297.205**	0.613**	0.535**	1.000**	2.724**	0.010**	3.324**	20.812*	11.516*	84.662*	0.003*	0.092*
Checks vs Varieties	1	394.948**	439.705**	5340.51**	0.666*	0.254	16.440**	84.619**	0.063**	90.336**	1113.14**	1061.66**	3403.26**	0.004*	0.454**
Error	9	0.861	1.000	13.155	0.097	0.083	0.049	0.117	0.001	0.215	6.391	5.716	48.783	0.001	0.022
Ci-Cj (CD @ 5%)	1	1.484	1.600	5.802	0.498	0.460	0.354	0.546	0.042	0.741	4.044	3.824	11.172	0.047	0.237
Ci-VI (CD @ 1%)	1	2.624	2.828	10.256	0.879	0.814	0.625	0.965	0.075	1.310	7.149	6.761	19.750	0.084	0.420

Where,

** - Significant @1%, * - Significant @ 5%
SV: Source of variation,
DF: Degrees of freedom
X_1: Days to 50 per cent flowering
X_2: Days to maturity
X_3: Plant height (cm)
X_4: Number of tillers/plant
X_5: Number of productive tillers/plant
X_6: Number of fingers/ear
X_7: Finger length (cm)
X_8: Finger width (cm)
X_8: Finger width (cm)
X_9: Earhead length (cm)
X_{10}: Ear weight/plant (g)
X_{11}: Grain yield/plant (g)
X_{12}: Straw yield/plant (g)
X_{13}: Harvest index (%)
X_{14}: Test weight (g)

Table 3: Estimation of genetic variability parameters for grain yield and yield attributing traits in sixty genotypes of finger millet

Sl. No.	Characters	Mean	Range		Coefficient of variation		$h^2_{(bs)}$ (%)	GAM (%)
			Minimum	Maximum	PCV (%)	GCV (%)		
01	Days to 50 % flowering	75.96	60.00	85.00	8.36	8.26	97.80	16.84
02	Days to maturity	115.84	100.00	125.00	5.42	5.35	97.41	10.88
03	Plant height (cm)	94.91	58.10	129.60	17.31	16.84	94.65	33.75
04	Number of tillers plant^{-1}	3.40	2.40	6.10	20.90	18.86	81.39	35.05
05	Productive tillers plant^{-1}	3.19	2.20	5.70	20.93	18.92	81.74	35.24
06	Number of fingers ear^{-1}	7.65	4.80	9.50	12.28	11.91	94.10	23.80
07	Finger length (cm)	7.65	4.66	12.33	22.15	21.57	94.83	43.27
08	Finger width (cm)	1.00	0.56	1.28	9.20	8.80	91.51	17.35
09	Ear head length plant^{-1} (cm)	8.10	4.66	13.76	22.04	21.17	92.24	41.88
10	Ear weight plant^{-1} (g)	25.18	13.50	33.28	18.38	14.81	64.90	24.58
11	Seed yield plant^{-1} (g)	14.24	8.00	25.30	25.39	22.92	81.50	42.63
12	Straw weight plant^{-1} (g)	31.53	11.60	52.38	31.49	20.31	37.60	24.39
13	Harvest index (%)	31.00	19.00	40.00	17.10	14.19	68.90	24.27
14	Test weight (g)	2.93	2.42	3.63	9.74	8.28	72.27	14.50

Where,

PCV- Phenotypic coefficient of variation
GCV- Genotypic coefficient of variation
h^2 - Heritability (broad sense)
GAM- Genetic advance as per cent of mean

4.1.1 Days to 50 per cent flowering

The variation for number of days taken to 50 per cent flowering ranged from 60.00 (IC-474649, IC-474651and KMR-204) to 85.00 days (GPU-48 and Indaf-7) with a mean of 75.96 days. Out of sixty genotypes, thirty genotypes were early in flowering when compared to general mean (75.96). The PCV (8.36 %) and GCV (8.26 %) estimates were low and difference between them is narrow. High heritability (97.80 %) combined with moderate genetic advance as per cent of mean (16.84) was observed.

4.1.2 Days to maturity

The number of days to maturity ranged from 100 (IC-474649, IC-474651and KMR-204) to 125 days (GPU-48 and Indaf-7) with a mean of 115.84 days. Among sixty genotypes, thirty three genotypes were early in maturity when compared to general mean (115.84). The estimates of PCV (5.42 %) and GCV (5.35 %) were very low. High heritability (97.41%) accompanied with moderate genetic advance as per cent of mean (10.88) was observed.

4.1.3 Plant height (cm)

The variation for plant height ranged from 58.10 (IC-474649) to 129.60 cm (Boonda Ragi) with a mean of 94.91 cm. The estimates of PCV (17.31 %) and GCV (16.84 %) were moderate. High heritability (94.65 %) accompanied with high genetic advance as per cent of mean (33.75) was observed.

4.1.4 Number of tillers per plant

This character exhibited variability ranged from 2.40 (GPU-26 and Indaf-9) to 6.10 (OUAT-2) with a general mean of 3.40. Out of sixty genotypes, twenty five genotypes exhibited higher values than the general mean (3.40). The PCV (20.90 %) and GCV (18.86 %) were high and moderate respectively. High heritability (81.39 %) in conjunction with high genetic advance as per cent of mean (35.05) was recorded.

4.1.5 Number of productive tillers per plant

This character possessed variability ranging from 2.20 (IC-474525) to 5.70 (OUAT-2) with a mean of 3.19. Among sixty genotypes, twenty three genotypes obtained higher the values of general mean (3.19). The estimates of PCV (20.93 %) and GCV (18.92 %) were high and moderate respectively. High heritability (81.74 %) combined with high genetic advance as per cent of mean (35.24) was recorded.

4.1.6 Number of fingers per ear

This character ranged from 4.80 (IC-474649) to 9.50 (Indaf-9) with a mean of 7.65. The PCV (12.28 %) and GCV (11.91 %) of this trait were moderate. High heritability (94.10 %) in conjunction with high genetic advance as per cent of mean (23.80) was recorded.

4.1.7 Finger length (cm)

The variation for length of finger varied from 4.66 (IC-474649) to 12.33 cm (IC-473143) with a mean of 7.65 cm. Among sixty genotypes, fourteen genotypes possessed the greater values than the general mean (7.65). The PCV (22.15 %) and GCV (21.57 %) estimate were high. High heritability (94.83 %) in conjunction with high genetic advance as per cent of mean (43.27) was obtained.

4.1.8 Finger width (cm)

This character exhibited the variation which ranges from 0.56 (IC-473143) to 1.28 cm (KMR-340) with a general mean of 1.00 cm. Out of sixty genotypes, twenty three genotypes noticed higher values than the general mean (1.00). This character obtained the lower PCV (9.20 %) and GCV (8.80 %) values. High heritability (91.51 %) coupled with moderate genetic advance as per cent of mean (17.35) was recorded.

4.1.9 Earhead length per plant (cm)

The variation for length of earhead varied from 4.66 (IC-474649) to 13.76 cm (IC-473143) with a mean of 8.10 cm. Among sixty genotypes, eighteen genotypes possessed greater values than the general mean (8.10). The PCV (22.04 %) and GCV (21.17 %) estimate were high. High heritability (92.24 %) in conjunction with high genetic advance as per cent of mean (41.88) was recorded.

4.1.10 Earhead weight per plant (g)

Earhead weight per plant showed variation from 13.50 (IC-473142) to 33.28 g/plant (Malali) with a mean of 25.18 g plant. Among the sixty genotypes, nineteen genotypes exhibited higher values than general mean (25.18). The PCV (18.38 %) and GCV (14.81 %) estimate were moderate. High heritability (64.90 %) in conjunction with high genetic advance as per cent of mean (24.58) was obtained.

4.1.11 Seed yield per plant (g)

The range of variation noted for this trait varied from 8.00 (IC-474603) to 25.30 g/plant (Malali) with a mean of 14.24 g/plant. Out of sixty genotypes, eleven genotypes were obtained the values above the general mean 14.24 g/plant. The PCV (25.39 %) and GCV (22.92 %) estimate were high for this trait. High heritability (81.50 %) combined with high genetic advance as per cent of mean (42.63) was noted for this trait.

4.1.12 Straw yield per plant (g)

This character exhibited variability ranged from 11.60 (IC-473165, IC-474603 and IC-IC-474525) to 52.38 g/plant (MR-1) with a general mean of 31.53 g/plant. Out of sixty genotypes, twenty genotypes exhibited higher values than the general mean (31.53). The PCV (31.49 %) and GCV (20.31 %) were high. Moderate heritability (37.60 %) in conjunction with high genetic advance as per cent of mean (24.39) was recorded.

4.1.13 Harvest index (%)

The variation for harvest index ranged from 19 per cent (Karikatti Ragi) to 40 per cent (IC-474640) with a mean of 31 per cent. The estimates of PCV (17.10 %) and GCV (14.19 %) were moderate. High heritability (68.90 %) coupled with high genetic advance as per cent of mean (24.27) was observed.

4.1.14 Test weight (g)

The variation for test weight ranged from 2.42 (IC-473181) to 3.63 g (Indaf-9) with a mean of 2.93 g. Among sixty genotypes, twenty nine genotypes possessed the higher values than the general mean (2.93). This character possessed low PCV (9.74 %) and GCV (8.28 %) values. High heritability (72.27 %) combined with moderate genetic advance as per cent of mean (14.50) was noted for this trait.

4.2 Genetic variability parameters for grain quality traits

The analysis of variance revealed significant differences among the genotypes for all characters, indicating a high degree of variability in the material studied. The details are presented in (Table 4).

The genetic variability parameters for five quality characters are presented in the (Table 5). All the five traits under study showed wide range of variation indicating an enormous opportunity for bringing about improvement in essential direction.

Table 4: Analysis of variance for grain quality traits in sixty genotypes of finger millet

SV	DF	Calcium (mg/100g)	Magnesium (mg/100g)	Iron (mg/100g)	Copper (mg/100g)	Zinc (mg/100g)
		MEAN SUM OF SQUARES				
Block	3	3811.01	305.76	0.30	0.05	1.27
Entries	63	5360.66**	1495.58**	17.62**	0.06**	2.43**
Checks	3	4925.84**	576.93**	48.83**	0.17**	8.70**
Varieties	59	5100.11**	1489.27**	16.33**	0.06**	1.47**
Checks vs Varieties	1	22037.98**	4623.74**	0.33*	0.009*	40.11**
Error	9	42.47	2.84	0.04	0.001	0.009
Ci-Cj (CD @ 5%)	1	10.42	2.69	0.32	0.04	0.15
Ci-VI (CD @ 1%)	1	18.42	4.77	0.57	0.08	0.26

Where,

** - Significant @1%
* - Significant @ 5%
SV- Source of variation
DF- Degrees of freedom

Table 5: Estimation of genetic variability parameters for grain quality traits in sixty genotypes of finger millet

Sl. No.	Quality traits	Mean	Range		Coefficient of variation		$h^2_{(bs)}$ (%)	GAM (%)
			Minimum	Maximum	PCV (%)	GCV (%)		
1	Calcium (mg/100g)	263.27	147.68	398.62	24.57	24.45	98.99	50.11
2	Magnesium (mg/100g)	120.49	62.35	176.70	28.99	28.96	99.77	59.59
3	Iron (mg/100g)	7.22	2.38	14.19	50.66	50.58	99.69	104.03
4	Copper (mg/100g)	0.55	0.20	1.05	40.53	40.18	98.28	82.06
5	Zinc (mg/100g)	3.18	2.01	5.65	34.45	34.33	99.26	70.45

Where,

PCV- Phenotypic coefficient of variation

GCV- Genotypic coefficient of variation

$h^2_{(bs)}$ - Heritability (broad sense)

GAM- Genetic advance as per cent of mean

4.2.1 Calcium content (mg/100g)

The variation for calcium content ranged from 147.68 (IC474792) to 398.62 mg/100g (IC-474959) with a mean of 263.27 mg/100g. Among sixty genotypes, twenty six genotypes possessed the higher values than the general mean (263.27). This character possessed high PCV (24.57 %) and GCV (24.45 %) values. High heritability (98.99 %) combined with high genetic advance as per cent of mean (50.11) was noted for this trait.

4.2.2 Magnesium content (mg/100g)

The variation for magnesium content ranged from 62.35 (IC-473168) to 176.70 mg/100g (L-5) with a mean of 120.49 mg/100g. Among sixty genotypes, thirty two genotypes possessed the higher values than the general mean (120.49). This character possessed high PCV (28.99 %) and GCV (28.96 %) values. High heritability (99.77 %) combined with high genetic advance as per cent of mean (59.59) was noted for this trait.

4.2.3 Iron content (mg/100g)

The variation for iron content ranged from 2.38 (IC-473181and IC-474574) to 14.19 mg/100g (IC-473388) with a mean of 7.22 mg/100g. Among sixty genotypes, twenty nine genotypes possessed the higher values than the general mean (7.22). This character possessed high PCV (50.66 %) and GCV (50.58 %) values. High heritability (99.69 %) combined with high genetic advance as per cent of mean (104.03) was noted for this trait.

4.2.4 Copper content (mg/100g)

The variation for copper content ranged from 0.20 (IC-473379, IC-473381 and IC-474792) to 1.05 mg/100g (KMR-340) with a mean of 0.55 mg/100g. Among sixty genotypes, thirty three genotypes possessed the higher values than the general mean (0.55). This character possessed high PCV (40.53 %) and GCV (40.18 %) values. High heritability (98.28 %) combined with high genetic advance as per cent of mean (82.06) was noted for this trait.

4.2.5 Zinc content (mg/100g)

The variation for zinc content ranged from 2.01 (IC-473160, IC-473165, IC-473381 and Jagaluru Ragi) to 5.65 mg/100g (IC-473143 and Jeenumundaga Ragi) with a mean of 3.18 mg/100g. Among sixty genotypes, twenty three genotypes possessed the higher values than the general mean (3.18). This character possessed high PCV (34.45 %) and GCV (34.33 %) values. High heritability (99.26 %) combined with high genetic advance as per cent of mean (70.45) was noted for this trait.

4.3 Correlation coefficient analysis for grain yield and yield related characters

Correlation studies provide information on the nature and magnitude of the association of different component characters with grain yield. It also helps us to understand the nature of interrelationship among the component traits themselves. Ultimately this could help the breeder to design selection strategies to improve grain yield.

Phenotypic correlations were assessed among fourteen characters in order to find the direction and magnitude of association, existing between grain yield with other component characters and also among themselves. The result with respect to correlation at phenotypic levels between grain yield and other related characters are presented in (Table 6).

4.3.1 Correlation between grain yield and its component traits

Grain yield exhibited positive and significant association with days to 50 per cent flowering (0.354), days to maturity (0.348), earhead weight per plant (0.881) and straw yield per plant (0.477), While the traits like *viz.*, plant height (0.194), number of tillers per plant (0.122), number of productive tillers per plant (0.149), number of fingers per ear (0.215), finger length (0.250), finger width (0.102), earhead length (0.181), harvest index (0.197) and test weight (0.173) had positive non-significant association with grain yield.

4.3.2 Inter correlation among yield components

4.3.2.1 Days to 50 per cent flowering

This trait showed significant and positive association with days to maturity (0.994), plant height (0.675), number of fingers per ear (0.638), finger length (0.549), earhead length (0.482), earhead weight per plant (0.476), straw yield per plant (0.630) and test weight (0.316). It also had non-significant positive correlation with finger width (0.169). However this trait exhibited the significant and negative association with the number of tillers per plant (-0.325), number of productive tillers per plant (-0.274) and harvest index (-0.399).

Table 6: Estimation of phenotypic correlation coefficients for grain yield and its related traits in sixty genotypes of finger millet

	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	X_{12}	X_{13}
X_1	1.000												
X_2	0.994**	1.000											
X_3	0.675**	0.663**	1.000										
X_4	-0.325*	-0.332**	-0.423**	1.000									
X_5	-0.274*	-0.286*	-0.353**	0.968**	1.000								
X_6	0.638**	0.648**	0.502**	0.393**	-0.334**	1.000							
X_7	0.549**	0.514**	0.527**	0.394**	-0.53**	0.439**	1.000						
X_8	0.169	0.216	0.403**	-0.219	-0.200	0.311*	0.184	1.000					
X_9	0.482**	0.446**	0.508**	-0.389**	-0.355**	0.385**	0.941**	0.135	1.000				
X_{10}	0.476**	0.480**	0.319*	0.082	0.133	0.396**	0.213	0.285*	0.115	1.000			
X_{11}	0.630**	0.630**	0.758**	-0.026	0.036	0.384**	0.326*	0.416**	0.266*	0.601**	1.000		
X_{12}	-0.399**	-0.405**	-0.678**	0.116	0.069	-0.215	-0.199	-0.379**	-0.194	0.012	-0.705**	1.000	
X_{13}	0.316*	0.322*	0.352**	0.027	0.086	0.297*	0.214	0.417**	0.139	0.408**	0.401**	-0.290*	1.000
Yield plant^{-1}	**0.354****	**0.348****	**0.194**	**0.122**	**0.149**	**0.215**	**0.250**	**0.102**	**0.181**	**0.881****	**0.477****	**0.197**	**0.173**

Where,

** - Significant @1%

X_1: Days to 50 per cent flowering

X_2: Days to maturity

X_3: Plant height (cm)

X_4: Number of tillers/plant

X_5: Number of productive tillers/plant

X_6: Number of fingers/ear

X_7: Finger length (cm)

* - Significant @ 5%

X_8: Finger width (cm)

X_9: Earhead length (cm)

X_{10}: Ear weight/plant (g)

X_{11}: Straw yield/plant (g)

X_{12}: Harvest index (%)

X_{13}: Test weight (g)

4.3.2.2 Days to maturity

Days to maturity displayed significant and positive phenotypic association with plant height (0.663), the number of fingers per ear (0.648), straw yield per plant (0.630), finger length (0.514), earhead weight per plant (0.480), earhead length (0.446) and test weight (0.322). It also had positive correlation but non-significant with finger width (0.216). Whereas, this character recorded significant and negative association with the number of tillers per plant (-0.332), the number of productive tillers per plant (-0.286) and harvest index (-0.405).

4.3.2.3 Plant height (cm)

Plant height showed the significant and positive phenotypic association with the number of fingers per ear (0.502), finger length (0.527), finger width (0.403), earhead length (0.508), earhead weight per plant (0.319), straw yield per plant (0.758) and test weight (0.352). However this trait recorded significant negative association with the number of tillers per plant (-0.423), the number of productive tillers per plant (-0.353) and harvest index (-0.678).

4.3.2.4 Number of tillers per plant

The number of tillers per plant had significant and positive phenotypic association with the number of productive tillers per plant (0.968), number of fingers per ear (0.393) and finger length (0.394). It had non-significant positive correlation with earhead weight per plant (0.082), harvest index (0.116), test weight (0.027) at lower magnitude. It exhibited significant and negative association with earhead length (-0.389). On contrary this trait exhibited non-significant negative association with finger width (-0.219) and straw yield per plant (-0.026) at lower magnitude.

4.3.2.5 Number of productive tillers per plant

The number of productive tillers per plant had positive non-significant correlation with earhead weight per plant (0.133), straw yield per plant (0.036), harvest index (0.069) and test weight (0.086) at lower magnitude. On contrary, it had shown significant negative phenotypic association with the number of fingers per ear (-0.334), finger length (-0.353) and earhead length (-0.355). It also showed the non-significant and negative association with finger width (-0.200).

4.3.2.6 Number of fingers per ear

The number of fingers per ear displayed significant positive phenotypic association with finger length (0.439), finger width (0.311), earhead length (0.385), earhead weight per plant (0.396), straw yield per plant (0.384) and test weight (0.297).

On contrary, its association with harvest index (-0.215) was negative and non-significant.

4.3.2.7 Finger length (cm)

Finger length exhibited significant positive association with earhead length (0.941) and straw yield per plant (0.326), whereas it had a positive and non-significant association with finger width (0.184), earhead weight per plant (0.213) and test weight (0.214). Meanwhile, its association with harvest index (-0.199) was negative and non-significant.

4.3.2.8 Finger width (cm)

Finger width showed significant and positive phenotypic association with earhead weight per plant (0.285), straw yield per plant (0.416) and test weight (0.417) whereas it had a positive and non-significant association with earhead length (0.135) and negative and significant association with harvest index (-0.379).

4.3.2.9 Earhead length (cm)

Significant positive phenotypic association of earhead length with straw yield per plant (0.266) was observed. Its association with ear weight (0.115) and test weight (0.139) was positive but non-significant. Whereas its association with harvest index (-0.194) was negative and non-significant.

4.3.2.10 Earhead weight per plant (g)

Earhead weight per plant had significant and positive phenotypic association with straw yield per plant (0.601) and test weight (0.408), while its association with harvest index (0.012) was positive and non-significant.

4.3.2.11 Straw yield per plant (g)

Straw yield per plant had significant and positive phenotypic association with test weight (0.401) and it had negative significant association with harvest index (-0.705).

4.3.2.12 Harvest index (%)

Harvest index had a significant and negative phenotypic association with test weight (-0.290).

4.4 Correlation coefficient analysis for grain yield and grain quality parameters

Correlation coefficient analysis helps to determine the nature and degree of relationship between characters. Correlations between important characters are of immense help in the selection of suitable plant type. Phenotypic correlations were assessed among five quality characters in order to find the direction and magnitude of association, existing between grain yield and quality traits and also among themselves. The result with respect to correlation at phenotypic levels between grain yield and quality characters are presented in (Table 7).

4.4.1 Correlation between grain yield and quality parameters

Grain yield exhibited positive and non-significant association with magnesium content (0.013), copper content (0.147) and zinc content (0.170). While the traits *viz.,* calcium content (-0.008) and iron content (-0.081) had negative non-significant association with grain yield.

4.4.2 Inter correlation among quality parameters

4.4.2.1Calcium content (mg/100g)

Calcium content showed the significant and positive association with magnesium content (0.401), iron content (0.326), copper content (0.542) and zinc content (0.364).

4.4.2.2 Magnesium content (mg/100g)

Magnesium content exhibited the significant and positive association with iron content (0.682), copper content (0.739) and zinc content (0.406).

4.4.2.3 Iron content (mg/100g)

Iron content had the significant and positive association with copper content (0.654) and zinc content (0.460).

4.4.2.4 Copper content (mg/100g)

Copper content displayed the significant and positive association with zinc content (0.369).

Table 7: Estimation of phenotypic correlation coefficients for grain yield and grain quality traits in sixty genotypes of finger millet

	Calcium (mg/100g)	**Magnesium (mg/100g)**	**Iron (mg/100g)**	**Copper (mg/100g)**	**Zinc (mg/100g)**
Calcium (mg/100g)	1.000				
Magnesium (mg/100g)	0.401**	1.000			
Iron (mg/100g)	0.326**	0.682**	1.000		
Copper (mg/100g)	0.542**	0.739**	0.654**	1.000	
Zinc (mg/100g)	0.364**	0.406**	0.460**	0.369**	1.000
Grain yield/plant (g)	-0.008	0.013	-0.081	0.147	0.170

Where,

* = Significant @ 5%

**= Significant @1%

4.5 Path coefficient analysis for grain yield and its component traits

Path coefficient analysis was carried out at phenotypic level taking the grain yield as a dependent character. Path coefficient analysis was used to partition the observed correlation coefficients between grain yield per plant as dependent variable and its component traits into direct and indirect effects because the genetic architecture of economic yield must be resolved with the genetic contribution of all other characters influencing it directly or indirectly.

The outcomes of results obtained from present study for direct and indirect effects of yield components on grain yield at phenotypic level in sixty finger millet genotypes are presented in (Table 8).

4.5.1 Direct effect of yield contributing characters on grain yield

Out of thirteen characters studied, eight characters exhibited positive and direct effect on grain yield at phenotypic level *viz.*, days to maturity (0.4489), plant height (0.0107), number of tillers per plant (0.0947), finger length (0.0661), earhead length (0.1248), earhead weight per plant (0.6949), straw yield per plant (0.4959), and harvest index (0.4650).

While the characters *viz.*, days to 50 per cent flowering (-0.5099), number of productive tillers (-0.0722), number of fingers per ear (-0.1271), finger width (-0.0737) and test weight (-0.1213) had negative direct effects on grain yield. Earhead weight per plant (0.6949) had highest positive direct effect, whereas days to 50 per cent flowering (-0.5099) had the highest negative direct effect on grain yield.

4.5.2 Indirect effects of yield components on grain yield

4.5.2.1 Days to 50 per cent flowering

Days to 50 per cent flowering displayed positive indirect effects on grain yield through days to maturity (0.4464), plant height (0.0073), productive tillers per plant (0.0198), finger length (0.0363), earhead length (0.0602), earhead weight per plant (0.3308) and straw yield per plant (0.3127). On the other hand, it registered negative indirect effects on grain yield through number of tillers per plant (-0.0308), number of fingers per ear (-0.0812), finger width (-0.0.125), harvest index (-0.1859) and test weight (-0.0384).

4.5.2.2 Days to maturity

The character days to maturity recorded positive indirect effects on grain yield through plant height (0.0071), productive tillers per plant (0.0207), finger length (0.0340), earhead length (0.0557), earhead weight per plant (0.3339), straw yield per

Table 8: Estimation of direct and indirect effects of yield components on grain yield at phenotypic level in sixty genotypes of finger millet

	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	X_{12}	X_{13}
X_1	**-0.5099**	-0.5070	-0.3443	0.1658	0.1400	-0.3257	-0.2800	-0.0865	-0.2457	-0.2427	-0.3215	0.2039	-0.1613
X_2	0.4464	**0.4489**	0.2979	-0.1492	-0.1284	0.2909	0.2311	0.0971	0.2003	0.2157	0.2829	-0.1820	0.1446
X_3	0.0073	0.0071	**0.0107**	-0.0046	-0.0038	0.0054	0.0057	0.0043	0.0055	0.0034	0.0081	-0.0073	0.0038
X_4	-0.0308	-0.0315	-0.0401	**0.0947**	0.0918	-0.0373	-0.0374	-0.0207	-0.0369	0.0078	-0.0025	0.0110	0.0026
X_5	0.0198	0.0207	0.0255	-0.0699	**-0.0722**	0.0241	0.0255	0.0145	0.0257	-0.0096	-0.0026	-0.0050	-0.0062
X_6	-0.0812	-0.0824	-0.0638	0.0500	0.0425	**-0.1271**	-0.0559	-0.0396	-0.0490	-0.0504	-0.0489	0.0273	-0.0378
X_7	0.0363	0.0340	0.0348	-0.0261	-0.0234	0.0291	**0.0661**	0.0122	0.0622	0.0141	0.0216	-0.0132	0.0141
X_8	-0.0125	-0.0159	-0.0297	0.0161	0.0148	-0.0229	-0.0136	**-0.0737**	-0.0100	-0.0210	-0.0307	0.0280	-0.0308
X_9	0.0602	0.0557	0.0635	-0.0486	-0.0444	0.0481	0.1175	0.0169	**0.1248**	0.0144	0.0333	-0.0242	0.0174
X_{10}	0.3308	0.3339	0.2219	0.0570	0.0926	0.2756	0.1482	0.1982	0.0800	**0.6949**	0.4182	0.0088	0.2836
X_{11}	0.3127	0.3126	0.3759	-0.0132	0.0178	0.1909	0.1620	0.2064	0.1321	0.2985	**0.4959**	-0.3499	0.1993
X_{12}	-0.1859	-0.1885	-0.3156	0.0540	0.0323	-0.1000	-0.0929	-0.1765	-0.0903	0.0059	-0.3281	**0.4650**	-0.1349
X_{13}	-0.0384	-0.0391	-0.0428	-0.0033	-0.0104	-0.0361	-0.0260	-0.0506	-0.0169	-0.0495	-0.0487	0.0352	**-0.1213**
r value	0.3548**	0.3485**	0.1940	0.1228	0.1491	0.2151	0.2503	0.1021	0.1819	0.8814**	0.4771**	0.1975	0.1731

Where,

Residual effect= 0.311

** - Significant @1%,

* - Significant @ 5%,

X_1: Days to 50 per cent flowering
X_2: Days to maturity
X_3: Plant height (cm)
X_4: Number of tillers/plant
X_5: Number of productive tillers/plant
X_6: Number of fingers/ear
X_7: Finger length (cm)
X_8: Finger width (cm)
X_9: Earhead length (cm)
X_{10}: Ear weight/plant (g)
X_{11}: Straw yield/plant (g)
X_{12}: Harvest index (%)
X_{13}: Test weight (g)

plant (0.3126) and negative indirect effects on grain yield through days to 50 per cent flowering (-0.5070), number of tillers per plant (-0.0315), number of fingers per ear (-0.0824), finger width (-0.0159), harvest index (-0.1885) and test weight (-0.0391).

4.5.2.3 Plant height (cm)

The highest positive indirect effect of plant height on grain yield was expressed through straw yield per plant (0.3759) followed by days to maturity (0.2979), earhead weight per plant (0.2219), earhead length (0.0635), finger length (0.0348) and productive tillers per plant (0.0255). On contrary, its negative indirect effect on grain yield was observed through days to 50 per cent flowering (-0.3443), number of tillers per plant (-0.0401), number of fingers per ear (-0.0638), finger width (-0.0297), harvest index (-0.3156) and test weight (-0.0428).

4.5.2.4 Number of tillers per plant

Number of tillers per plant exerted its positive indirect effect on grain yield through days to 50 per cent flowering (0.1658), number of fingers per ear (0.0500), finger width (0.0161), earhead weight per plant (0.0570) and harvest index (0.0540). Conversely number of tillers per plant displayed negative indirect effects on grain yield through days to maturity (-0.1492), plant height (-0.0046), productive tillers per plant (-0.0699), finger length (-0.0261), earhead length (-0.0486), straw yield per plant (-0.0132) and test weight (-0.0033).

4.5.2.5 Number of productive tillers per plant

The number of productive tillers per plant exhibited its positive indirect effect on grain yield through days to 50 per cent flowering (0.1400), number of tillers per plant (0.0918), number of fingers per ear (0.0425), finger width (0.0148), earhead weight per plant (0.0926), straw yield per plant (0.0178) and harvest index (0.0323), while the traits like *viz.*, days to maturity (-0.1284), plant height (-0.0038), finger length (-0.0234), earhead length (-0.0444) and test weight (-0.0104) displayed negative indirect effects on grain yield.

4.5.2.6 Number of fingers per ear

The character number of fingers per ear showed positive indirect effect on grain yield through days to maturity (0.2909), plant height (0.0054), number of productive tillers per plant (0.0241), finger length (0.0291), earhead length (0.0481), earhead weight per plant (0.2756) and straw yield per plant (0.1909). However, it has registered negative indirect effects on grain yield through days to 50 per cent flowering (-0.3257), number of tillers per plant (-0.0373), finger width (-0.0229), harvest index (-0.1000) and test weight (-0.0361).

4.5.2.7 Finger length (cm)

Finger length exerted positive indirect effects on grain yield through days to maturity (0.2311), plant height (0.0057), number of productive tillers per plant (0.0255), earhead length (0.1175), earhead weight per plant (0.1482) and straw yield per plant (0.1620). Conversely, its indirect effects on grain yield were negative through days to 50 per cent flowering (-0.2800), number of tillers per plant (-0.0374), number of fingers per ear (-0.0559), finger width (-0.0136), harvest index (-0.1000) and test weight (-0.0361).

4.5.2.8 Finger width (cm)

The character finger width recorded positive indirect effects on grain yield through days to maturity (0.0971), plant height (0.0043), productive tillers per plant (0.0145), finger length (0.0122), earhead length (0.0169), earhead weight per plant (0.1982), straw yield per plant (0.2064) and it had negative indirect effects on grain yield through days to 50 per cent flowering (-0.0865), number of tillers per plant (-0.0207), number of fingers per ear (-0.0396), harvest index (-0.1765) and test weight (-0.0506).

4.5.2.9 Earhead length (cm)

Earhead length exhibited positive indirect effects on grain yield through days to maturity (0.2003), plant height (0.0055), number of productive tillers per plant (0.0257), finger length (0.0622), earhead weight per plant (0.0800) and straw yield per plant (0.1321), whereas earhead length had negative indirect effect on grain yield through days to 50 per cent flowering (-0.2457), number of tillers per plant (-0.0369), number of fingers per ear (-0.0490), finger width (-0.0100), harvest index (-0.0903) and test weight (-0.0169).

4.5.2.10 Earhead weight per plant (g)

Earhead weight per plant exhibited the highest positive indirect effects on grain yield through straw yield per plant (0.2985) followed by days to maturity (0.2157), earhead length (0.0144) finger length (0.0141), number of tillers per plant (0.0078), harvest index (0.0059) and plant height (0.0034). On the other hand earhead weight per plant exhibited negative indirect effects on grain yield through days to 50 per cent flowering (-0.2427), number of productive tillers per plant (-0.0096), number of fingers per ear (-0.0504), finger width (-0.0210) and test weight (-0.0495).

4.5.2.11 Straw yield per plant (g)

Straw yield per plant exhibited positive indirect effects on grain yield through days to maturity (0.2829), plant height (0.0081), finger length (0.0216), earhead length (0.0333) and earhead weight per plant (0.4182), whereas straw yield per plant had negative indirect effect on grain yield through days to 50 per cent flowering (-0.3215), number of tillers per plant (-0.0025), number of productive tillers per plant (-0.0026), number of fingers per ear (-0.0489), finger width (-0.0307), harvest index (-0.3281) and test weight (-0.0487).

4.5.2.12 Harvest index (%)

Harvest index exerted positive indirect effects on grain yield through days to 50 percent flowering (0.2039), number of tillers per plant (0.0110), number of fingers per ear (0.0273), finger width (0.0280), earhead weight per plant (0.0088) and test weight (0.0352). Conversely, its indirect effects on grain yield were negative through days to maturity (-0.1820), plant height (-0.0073), number of productive tillers per plant (-0.0050), finger length (-0.0132), earhead length (-0.0242) and straw yield per plant (-0.3499).

4.5.2.13 Test weight (g)

The indirect effects of test weight on grain yield were positive through days to maturity (0.1446), plant height (0.0038), number of tillers per plant (0.0026), fingers length (0.0141), earhead length (0.0174), earhead weight per plant (0.2836) and straw yield per plant (0.1993), whereas it showed negative indirect effect on grain yield through days to 50 per cent flowering (-0.1613), number of productive tillers per plant (-0.0062), number of fingers per ear (-0.0378), finger width (-0.0308), harvest index (-0.1349) and test weight (-0.1213).

4.6 Genetic divergence among grain yield and yield contributing traits

Mahalanobis D^2 statistics was used for quantitative assessment of genetic divergence for yield and its contributing characters among sixty finger millet genotypes were presented in (Table 9–12).

4.6.1 Group constellation

All the sixty genotypes of finger millet were grouped into eight different non-overlapping clusters by following the Tocher’s method. The basic idea behind formation of clusters is to get the intra and inter-cluster distances. This serves as index for selection of parents with diverse origin. The distributions of genotypes into eight clusters are presented in (Table 9). Cluster I, Cluster II, Cluster IV included maximum

Table 9: Grouping of sixty genotypes of finger millet into different clusters based on D^2 values for grain yield and its related traits

Clusters	Number of genotypes per cluster	Finger millet genotypes
I	14	IC-473160, IC-473181, GPU-45, IC-473146, IC-473381, IC-473168, IC-473155, IC-473178, OUAT-2, IC-473382, IC-474925, IC-473385, IC-473388 and KMR-632
II	14	Karikatti ragi, Jeenumundaga ragi, SMRC-1, Indaf-7, Koolimotte ragi, KMR-316, KMR-340, KMR-634, IC-473183, Indaf-5, Jagaluru ragi, Indaf-9, Indaf-8 and ML-365
III	4	IC-474662, IC-474792, GPU-67 and IC-473157
IV	14	IC-474574, IC-474616, IC-474640, IC-473172, Uddara malligae, IC-473377, IC-473142, KMR-204, IC-473165, IC-474651, IC-474525, IC-474603, IC-474652 and IC-474649
V	1	SMRC-3
VI	11	IC-474959, Karimundaga ragi, IC-475224, IC-473379, IC-474138, IC-473143, L-5, GPU-48, GPU-26, Hamsa and Malali
VII	1	SMRC-2
VIII	1	Boonda ragi

number of genotypes fourteen followed by cluster VI with eleven genotypes and cluster III with four genotypes and remaining three clusters *viz.*, V, VII and VIII are solitary clusters.

4.6.2 Intra and inter-cluster distances

Intra and inter relation of clusters were judged based on the average D^2 values. The average D^2 values of intra and inter clusters distances are presented in (Table 10). The Intra cluster average D^2 values ranged from 0.00 to 365.57. Among the clusters, cluster VI had the maximum intra cluster distance (365.57), while the minimum was recorded in clusters V, VII and VIII as they included only single genotype in each cluster. The maximum inter cluster D^2 value was recorded between cluster IV and cluster VIII (4653.03), while the minimum D^2 value was found between cluster V and cluster VIII (207.49).

4.6.3 Cluster means analysis for different characters

The cluster means regarding fourteen characters across the eight clusters are mentioned in (Table 11). Considerable differences between clusters were observed for most of the characters studied.

4.6.3.1 Days to 50 per cent flowering

The genotypes belong to cluster V showed highest mean value of (83.00 days) for days to 50 per cent flowering, while cluster IV showed the least mean value for days to 50 percent flowering (66.29 days).

4.6.3.2 Days to maturity

The genotypes belong to cluster V showed the highest mean value for days to maturity (123.00 days), while cluster IV showed the least mean value for days to days to maturity (106.29 days).

4.6.3.3 Plant height (cm)

For plant height, genotypes belong to cluster VIII showed highest mean value of (129.60 cm), while cluster IV showed the least mean value of plant height (71.17 cm).

4.6.3.4 Number of tillers per plant

Cluster III genotypes showed the highest mean number of tillers per plant (4.10). Whereas cluster V and VII consists of genotypes with lowest mean number of tillers per plant (2.80).

Table 10: Average intra and inter cluster distance values of sixty genotypes of finger millet for grain yield and its related traits

	Cluster I	**Cluster II**	**Cluster III**	**Cluster IV**	**Cluster V**	**Cluster VI**	**Cluster VII**	**Cluster VIII**
Cluster I	**172.28**	1255.15	368.97	486.18	2175.87	562.97	1541.90	2855.49
Cluster II		**189.42**	1368.60	2607.28	309.33	491.65	314.23	610.85
Cluster III			**192.33**	854.73	2491.82	701.55	2007.89	3171.11
Cluster IV				**288.44**	3827.44	1452.90	2860.45	4653.03
Cluster V					**0.00**	998.97	288.76	207.49
Cluster VI						**365.57**	734.67	1511.71
Cluster VII							**0.00**	274.38
Cluster VIII								**0.00**

Table 11: Cluster means for grain yield and its related traits of sixty genotypes of finger millet

	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	X_{12}	X_{13}	X_{14}
Cluster I	72.43	112.36	82.76	3.51	3.19	7.34	6.32	0.97	6.91	23.04	12.56	23.58	34.00	2.82
Cluster II	81.29	121.21	109.69	2.97	2.82	8.06	8.05	1.06	8.80	25.32	12.98	37.45	26.00	3.04
Cluster III	77.50	117.50	76.75	4.10	3.93	7.48	5.66	0.92	5.90	30.00	17.08	31.15	35.00	2.91
Cluster IV	66.29	106.29	71.17	3.61	3.34	6.51	5.61	0.94	6.46	18.61	9.36	17.93	35.00	2.74
Cluster V	83.00	123.00	122.90	2.80	2.70	7.80	8.96	1.04	8.13	20.00	10.00	38.90	20.00	2.88
Cluster VI	78.45	117.73	96.89	3.67	3.45	7.70	7.48	0.96	5.50	24.28	13.51	30.33	31.00	2.97
Cluster VII	74.00	113.00	119.05	2.80	2.70	7.60	6.09	1.02	8.99	23.00	11.11	35.20	24.00	2.90
Cluster VIII	77.000	117.00	129.60	3.10	3.10	7.80	6.88	1.00	7.70	24.70	11.70	46.70	20.00	2.99

Where,

X_1: Days to 50 per cent flowering
X_2: Days to maturity
X_3: Plant height (cm)
X_4: Number of tillers/plant
X_5: Number of productive tillers/plant
X_6: Number of fingers/ear
X_7: Finger length (cm)

X_8: Finger width (cm)
X_9: Earhead length (cm)
X_{10}: Ear weight/plant (g)
X_{11}: Grain yield/plant (g)
X_{12}: Straw yield/plant (g)
X_{13}: Harvest index (%)
X_{14}: Test weight (g)

4.6.3.5 Number of productive tillers per plant

Cluster III consists of genotypes with highest mean number of productive tillers per plant (3.93), whereas cluster V and VII genotypes exhibited the lowest mean number of productive tillers per plant (2.70).

4.6.3.6 Number of fingers per ear

For number of fingers per ear, genotypes in cluster II showed the highest number (8.06) and those in clusters IV had lowest number of number of fingers per ear (6.51).

4.6.3.7 Finger length (cm)

For to finger length, genotypes in cluster V showed the highest mean value (8.96 cm) and those in clusters IV had lowest mean value for finger length (5.61 cm).

4.6.3.8 Finger width (cm)

Regarding finger width, genotypes in cluster II showed the highest (1.06 cm) and those in clusters III had lowest mean value for finger width (9.02 cm).

4.6.3.9 Earhead length (cm)

Cluster III consists of genotypes with lowest mean value for earhead length (5.90 cm) whereas cluster VII genotypes exhibited the highest mean value for earhead length (8.99 cm).

4.6.3.10 Earhead weight per plant

Cluster III genotypes showed the highest mean value for earhead weight per plant (30.00 g/plant). Whereas Cluster IV genotypes showed the lowest mean value for earhead weight per plant (18.61 g/plant).

4.6.3.11 Grain yield per plant

The genotypes in cluster III showed the highest grain yield (17.08 g/plant) and those in cluster IV had lowest mean grain yield (9.36 g/plant).

4.6.3.12 Straw yield per plant

The genotypes in cluster VIII showed the highest straw yield (46.70 g/plant) and those in cluster IV had lowest mean straw yield of (17.93 g/plant).

4.6.3.13 Harvest Index (%)

Cluster V and VIII consists of genotypes with lowest harvest index (20.00 %) whereas cluster III and IV genotypes exhibited the highest harvest index (35.00 %).

4.6.3.14 Test weight (g)

The lowest mean test weight was observed in the genotypes of cluster IV (2.74 g) and the genotypes in cluster II was recorded the highest test weight (3.04 g).

4.6.4 Relative contribution of different characters towards divergence

Proportion of contribution of each character to total divergence presented in (Table 12).The character, plant height contributed maximum of (66.67 %) to the total divergence among the sixty finger millet genotypes studied, followed by straw yield per plant (16.16 %), days to 50 per cent flowering (9.15 %), earhead weight per plant (3.79 %), days to maturity (2.54 %), grain yield per plant (1.41 %) and earhead length (0.28 %). On contrary, total number of tillers per plant, number of productive tillers per plant, number of fingers per ear, finger length, finger width, harvest index and test weight had negligible contribution towards genetic divergence.

4.7 Genetic divergence of grain quality traits

Mahalanobis D^2 statistics was used for quantitative assessment of genetic divergence for grain quality characters among sixty finger millet genotypes were presented in (Table 13–16).

4.7.1 Group constellation

Totally sixty finger millet genotypes were grouped into eight different clusters (Table 13). Cluster II, included maximum number of genotypes sixteen followed by cluster I with twelve genotypes, cluster III with ten genotypes, cluster VI with seven genotypes, cluster IV with six genotypes, cluster V with five genotypes, cluster VII with three genotypes whereas, cluster VIII was solitary cluster.

4.7.2 Intra and inter-cluster distances

Intra and inter relation of clusters were judged based on the average D^2 values. The average D^2 values of intra and inter clusters distances are presented in (Table 14). The Intra cluster average D^2 values ranged from 0.00 to 2184.19. Among the clusters, cluster VI had the maximum intra cluster distance (2184.19), while the minimum was recorded in clusters VIII as it included only single genotype. The maximum inter

Table 12: Per cent contribution of characters towards divergence in sixty genotypes of finger millet

Sl. No.	**Characters**	**Contribution (%) towards divergence**
1	Plant height (cm)	66.67
2	Straw yield per plant (g)	16.16
3	Days to 50 per cent flowering	9.15
4	Earhead weight per plant (g)	3.79
5	Days to maturity	2.54
6	Grain yield per plant (g)	1.41
7	Earhead length (cm)	0.28

Table 13: Grouping of sixty genotypes of finger millet into different clusters based on D^2 values for grain quality traits

Clusters	Number of genotypes	Finger millet genotypes
I	12	IC-473165, IC-473168, IC-473157, IC-473155, IC-473181, IC-474651, IC-474574, IC-474662, Indaf-7, IC-473385, IC-474138 and IC-474792
II	16	IC-473160, IC-473377, IC-473382, IC-473388, IC-474525, IC-473142, IC-473178, IC-474616, IC-474640, IC-474649, IC-474603, IC-473172, IC-473183, Indaf-8, Indaf-9 and KMR-634
III	10	ML-365, GPU-45, Udara malligae, IC-473143, SMRC-1, KMR-340, IC-473155, IC-473146, IC-474652 and KMR-204
IV	6	KMR-316, KMR-632, IC-474959, Jeenumundaga ragi, L-5 and SMRC-3
V	5	IC-473381, Hamsa, GPU-48, IC-473379 and SMRC-2
VI	7	Koolimotte ragi, Jagaluru ragi, GPU-26, Krimundaga ragi, Karikatti ragi, IC-474925 and Boonda ragi
VII	3	OUAT-2, Indaf-5 and IC-475224
VIII	1	Malali

Table14: Average intra and inter cluster distance values of sixty genotypes of finger millet for grain quality traits

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Cluster I	**941.41**	9515.31	25377.71	55708.84	4155.59	29634.84	12143.84	35419.39
Cluster II		**1007.96**	5901.57	25713.15	4404.69	16140.76	5941.22	12965.76
Cluster III			**868.44**	8576.86	12389.51	8587.61	6871.14	2522.91
Cluster IV				**1007.57**	33258.04	9410.92	18728.40	2676.58
Cluster V					**1605.84**	14527.58	3720.69	18203.05
Cluster VI						**2184.19**	5308.69	4602.12
Cluster VII							**1352.87**	8346.63
Cluster VIII								**0.00**

cluster D^2 value was recorded between clusters I and IV (55708.44), while the minimum D^2 value was found between clusters III and VIII (2522.91).

4.7.3 Cluster means analysis for quality characters

The cluster means regarding five quality characters across the eight clusters are presented in (Table 15). Considerable differences between clusters were observed for all the characters studied.

4.7.3.1 Calcium content (mg/100g)

The genotypes belong to cluster IV showed highest mean value of (390.84 mg/100g) for calcium content, while the genotypes in cluster I showed the least mean value (169.40 mg/100g) for calcium content.

4.7.3.2 Magnesium content (mg/100g)

The genotypes belong to cluster III showed highest mean value of (160.40 mg/100g) for magnesium content, while the genotypes in cluster I showed the least mean value (78.61 mg/100g) for magnesium content.

4.7.3.3 Iron content (mg/100g)

The genotypes belong to cluster II showed highest mean value (10.44 mg/100g) for iron content, while the genotypes in cluster V showed the least mean value (2.98 mg/100g) for iron content.

4.7.3.4 Copper content (mg/100g)

The genotypes belong to cluster III showed highest mean value (0.78 mg/100g) for copper content, while the genotypes in cluster I showed the least mean value (0.25 mg/100g) for copper content.

4.7.3.5 Zinc content (mg/100g)

The genotypes belong to cluster VIII showed highest mean value (4.82 mg/100g) for zinc content, while the genotypes in cluster I showed the least mean value (2.31 mg/100g) for zinc content.

4.7.4 Relative contribution of quality characters towards divergence

Proportion of contribution of each character to total divergence showed significant differences and they are mentioned in (Table 16). The trait, calcium content contributed maximum (69.83 %) to the total divergence among the sixty finger millet genotypes studied. This was followed by magnesium content (30.00 %) and iron content (0.17 %). On contrary, copper and zinc content had negligible contribution towards the total divergence.

Table 15: Cluster means for grain quality traits in sixty genotypes of finger millet

	Calcium (mg/100g)	**Magnesium (mg/100g)**	**Iron**	**Copper**	**Zinc**
Cluster I	169.40	78.61	3.05	0.25	2.31
Cluster II	233.58	145.22	10.44	0.65	3.78
Cluster III	302.91	160.40	9.57	0.78	3.04
Cluster IV	390.84	154.66	9.19	0.72	4.34
Cluster V	223.90	89.19	2.98	0.32	2.37
Cluster VI	337.46	82.58	6.12	0.51	3.17
Cluster VII	275.07	88.02	5.65	0.63	2.60
Cluster VIII	345.15	142.59	4.33	0.76	4.82

Table 16: Per cent contribution of grain quality traits towards divergence in sixty genotypes of finger millet

Sl. No.	**Quality traits**	**% Contribution towards divergence**
1	**Calcium**	**69.83**
2	**Magnesium**	**30.00**
3	**Iron**	**0.17**

4.8 Superior finger millet genotypes identified for grain yield and grain quality traits

Superior finger millet genotypes identified for grain yield and its related traits are presented in (Table 17). The genotypes, Malali (25.30 g/plant) and IC-473155 (25.20 g/plant) were recorded high yield compared to check GPU-28 (21.35 g/plant). Superior finger millet genotypes identified for quality traits are presented in (Table 18). Genotype IC-474959 was superior for three quality traits namely calcium (398.62 mg/100g), magnesium (167.77 mg/100g) and copper content (0.95 mg/100g) followed by genotypes superior for two quality traits namely, IC-473388, IC-473143 and Jeenumundaga Ragi for iron (14.19, 13.85, 7.05 mg/100g) and zinc content (5.45, 5.65, 5.65 mg/100g) respectively.

4.9 Finger millet genotypes identified for both grain yield and grain quality traits

Finger millet genotypes identified for both grain yield and grain quality traits are presented in (Table 19). The genotypes, IC-473178 (165.48, 10.01 mg/100g), IC-473143 (166.78, 13.85 mg/100g), IC-473183 (146.28, 9.65 mg/100g) and SMRC-3 (166.86, 11.70 mg/100g) are superior to the varietal check GPU-28 (139.54, 6.42 mg/100g) for magnesium and iron content. IC-473183 (0.98 mg/100g) genotype is superior to the varietal check GPU-28 (0.78 mg/100g) for copper content. The genotypes, IC-473143 (5.23 mg/100g), IC-473183 (5.17 mg/100g) and SMRC-3 (5.21 mg/100g) is superior to the varietal check GPU-28 (2.80 mg/100g) for zinc content. All the identified genotypes are superior over the mean value for grain yield per plant.

Table 17: Superior finger millet genotypes identified for grain yield and its related traits

Sl. No:	Genotypes	Days to 50% flowering	Days to maturity	Plant height	Productive tillers/plant	Finger length	No. of fingers/ear	Ear weight/plant (g)	Grain yield/plant (g)
1	**Malali**	77.00	117.00	98.50	3.90	6.50	7.00	33.28	25.30
2	**IC-473155**	72.00	112.00	84.60	3.10	7.52	6.77	32.50	25.20
Mean		75.96	115.84	94.91	3.19	7.65	7.65	25.18	14.24
GPU-28 (check)		83.00	124.00	97.70	3.20	8.13	8.70	32.48	21.35
CD @5%		1.48	1.60	5.80	0.46	0.54	0.35	4.04	3.82

Table 18: Superior finger millet genotypes identified for grain quality traits

Sl. No.	Genotypes	Calcium (mg/100g)	Magnesium (mg/100g)	Iron (mg/100g)	Copper (mg/100g)	Zinc (mg/100g)	Grain yield/plant (g)
1	**IC-474959**	398.62	167.77	13.57	0.95	4.22	10.89
2	**IC-473143**	305.03	166.78	13.85	0.66	5.65	14.90
3	**IC-473388**	225.54	130.66	14.19	0.58	5.45	12.77
4	**Jeenumundaga Ragi**	379.65	145.74	7.05	0.70	5.65	11.25
Mean		263.27	120.49	7.22	0.55	3.18	14.24
GPU-28 (check)		299.82	139.54	6.42	0.78	2.80	21.35
CD @5%		10.42	2.69	0.32	0.04	0.15	3.82

Table 19: Finger millet genotypes identified for both grain yield and grain quality traits

Sl. No.	Genotypes	Calcium (mg/100g)	Magnesium (mg/100g)	Iron (mg/100g)	Copper (mg/100g)	Zinc (mg/100g)	Grain yield/plant (g)
1	**IC-473178**	222.34	165.48	10.01	0.75	2.72	16.88
2	**IC-473143**	305.03	166.78	13.85	0.66	5.23	14.90
3	**IC-473183**	272.68	146.28	9.65	0.98	5.17	14.50
4	**SMRC-3**	212.48	166.86	11.70	0.68	5.21	16.80
Mean		263.27	120.49	7.22	0.55	3.18	14.24
GPU-28 (check)		299.82	139.54	6.42	0.78	2.80	21.35
CD @5%		10.42	2.69	0.32	0.04	0.15	3.82

DISCUSSION

V DISCUSSION

Finger millet (*Eleusine coracana* (L.) Gaertn) is cultivated under varied ecological conditions for both grain and fodder purposes in Africa and South Asia. Finger millet is the staple food of rural and working people in many states of India. In India, among millets finger millet stands third only to sorghum and pearl millet. Finger millet has also a high yielding potential though yields are variable compared to other cereals but are generally good and needs improvement.

Improvement of seed yield is one of the primary objectives in finger millet breeding programmes. Seed yield is a complex character and is considered as the ultimate product of its components. Selection of superior genotypes based on yield as such is difficult due to the integrated structure of plant in which most of the characters are inter-related and being governed by more number of genes. This necessitates a thorough knowledge on the nature of relationship prevalent between contributory characters and grain yield and the extent of genetic variability.

Exploitation of genetic variability existing in the working germplasm is the first principle in the improvement of finger millet. Genetic variability together with the heritability estimates would give a better idea on the amount of genetic gain expected out of selection (Burton, 1952 and Swarup and Chaugle, 1962). Further, the magnitude of heritable variability is the most important aspect (Panse, 1957), which has close relationship with response to selection. Heritability estimates along with genetic advance are more helpful in predicting the gain under selection than heritability estimates alone. However, it is not necessary that a character showing high heritability will always exhibit high genetic advance (Johnson *et al*., 1955).

A thorough understanding of the association of quantitative characters with yield and among themselves is essential for successful crop improvement programme. It enables the breeder to manipulate the expression of these traits in crop improvement. The efficiency of selection for grain yield mainly depends on the direction and magnitude of association between yield and its components and among themselves. Unlike the correlation coefficient values which measure the extent of relationship, path coefficient analyses help in partitioning of the correlation coefficient into direct and indirect effects through other components (Wright, 1921).

Finger millet has accumulated considerable diversity over the years for vegetative, reproductive and physiological traits. The availability of diverse genetic resources is a prerequisite for genetic improvement of any crop including finger millet. Besides the availability of genetic resources, their characterization is essential for effective utilization in crop improvement programs. The D^2 statistics is one of the powerful tools to assess the relative contribution of different component traits to the total diversity. Knowledge of genetic diversity among genotypes on the basis of divergence analysis usually helps a breeder in choosing diverse parents for breeding program.

Being rich in protein, carbohydrate, calcium and magnesium, finger millet plays an important role in removing the serious problems of the malnutrition in the underdeveloped countries. Along with yield, some nutritional characters such as mineral content are very important in the selection of elite genotypes. The knowledge of association of quantitative and nutritional traits would further strengthen precision of breeder in efficient planning of breeding programme for both the yield and quality traits.

The knowledge about the amount of genetic variability present in a crop species with respect to yield and its attributes and their association, which reflects the nature and degree of relationship between any two measurable characters is of great importance in achieving genetic improvement in that crop. Therefore, in the present investigation, variability parameters *viz.*, range, PCV, GCV, broad sense heritability and genetic advance as per cent of mean as well as character association, direct and indirect effects among yield and its attributing characters, genetic divergence and micro nutrients content were estimated and the results are discussed below.

5.1 Analysis of variance and genetic variability parameters for grain yield and yield contributing characters

The analysis of variance among sixty genotypes indicated highly significant differences among the genotypes studied with respect to all the characters. All the genotypes displayed considerable amount of differences in their mean performance with respect to all the characters studied. This had been exemplified by highly significant mean sum of squares for these traits, which indicated that, the genotypes under study were genetically diverse.

5.1.1 Mean performance of genotypes

The mean performance of sixty genotypes used in the present study revealed that genotype, IC-474649 was superior for three out of 14 characters *viz.*, days to 50 per cent flowering, days to maturity and reduced plant height. The genotype, OUAT-2 was superior for number of tillers per plant and productive tillers per plant. IC-473143 genotype recorded the highest finger length and earhead length, whereas genotype, Malali exhibited the higher earhead weight per plant and seed yield per plant.

5.1.2 Genetic variability studies for grain yield and its attributing characters

The range in mean values does not reflect the total variance in the material studied. Hence, actual variance has to be estimated for the characters to know the extent of existing variability. So, the coefficient of variation (PCV and GCV) which is calculated by considering the respective means has been used for the comparisons. High values of these parameters indicate wider variability and vice versa. In the same context, narrow differences between the phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) implies lesser influence of environment on these traits.

High phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) recorded for characters like, finger length, earhead length, seed yield per plant and straw yield per plant. Similar results of high PCV and GCV for finger length and seed yield per plant were also recorded by Mahanthesha *et al.* (2017). Similarly, high PCV and GCV recorded for earhead length and straw yield per plant were in conformity with the observations of Chaudhari *et al.* (2014). Higher magnitude of PCV and GCV for these characters indicates presence of high degree of variability and better scope for further crop improvement programme.

The moderate phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (PCV) was observed for characters like plant height, number of fingers per ear, earhead weight per plant and harvest index. This indicates the existence of comparatively moderate variability for these traits, which could be exploited for improvement of these traits through selection in advanced generations. These results are in consonance with earlier reports of Bezaweletaw *et al*. (2006), Ganapathy *et al*. (2011) and Priyadharshini *et al.* (2011) for moderate PCV and GCV of plant height and number of fingers per ear. The moderate GCV and PCV for earhead weight per plant results are in accordance with reports of Reddy *et al*. (2013). The moderate GCV and PCV for harvest index were reported by John (2006).

The low phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (PCV) was observed for characters like days to 50 per cent flowering, days to maturity, finger width and test weight, indicating narrow genetic base for this trait. Similar results were reported by Priyadharshini *et al.* (2011) and Manjunath *et al.* (2013) for days to 50 per cent flowering, finger width and test weight. Bezaweletaw *et al*. (2006), John (2006), Ganapathy *et al*. (2011), Karad and Patil (2013) and Soa *et al*. (2016a) observed narrow variability for days to maturity.

In general, coefficient of variation indicated moderate to high amount of variability for most of the traits with exception for few traits. The close correspondence between the estimates of GCV and PCV for most of the traits indicated lesser environmental influence on the expression of these traits, which is also reflected by their high heritability values.

5.1.3 Heritability and genetic advance

Broad sense heritability gives an idea about portion of observed variability attributable to genetic differences. According to Johnson *et al.* (1955), heritability estimates along with genetic gain would be more useful than the former alone in predicting the effectiveness of selecting the best individual. Therefore, it is essential to consider the predicted genetic advance along with heritability estimate as a tool in selection programme for better efficiency.

In the current study, high heritability coupled with high genetic advance as per cent of mean were recorded for plant height, number of tillers per plant, number of productive tillers per plant, finger length, number of fingers per ear, earhead length, earhead weight per plant, seed yield per plant and harvest index. This indicates there was low environmental influence on the expression of these characters and one can practice selection for improvement of these traits. High heritability coupled with high genetic advance as per cent of mean was recorded by Mahanthesha *et al.* (2017) for plant height, number of tillers per plant, number of productive tillers per plant, finger length, earhead length, and seed yield per plant. Nandini *et al*. (2010) reported similar results for earhead weight per plant and for number of fingers per ear and harvest index by John (2006) and Saundarya and Satish (2016).

High heritability coupled with moderate genetic advance as per cent of mean observed for days to 50 per cent flowering, days to maturity, finger width and test weight. Similar results of high heritability coupled with moderate genetic advance for days to 50 per cent flowering and days to maturity was recorded by Sharathbabu *et al*. (2008), while for finger width and test weight similar results reported by Dhamdhere *et al*. (2011).

The present investigation revealed high heritability coupled with high genetic advance as per cent of mean for most of the characters indicating the presence of considerable genetic variation and additive gene effects. Hence, improvement for these characters could be effective through phenotypic selection.

5.2 Analysis of variance and genetic variability parameters for grain quality traits

The analysis of variance for five quality traits among sixty genotypes indicated highly significant differences among the studied genotypes. All the genotypes displayed considerable amount of differences in their mean performance with respect to all the characters studied. This had been exemplified by highly significant mean sum of squares for these traits, which indicated that, the genotypes under study were genetically diverse.

5.2.1Mean performance of genotypes

For grain quality, the genotypes like, IC-474959, L-5, IC-473388 and KMR-340 exhibited higher calcium, magnesium, iron and copper content respectively. IC-473143 and Jeenumundaga Ragi genotypes exhibited higher zinc content.

5.2.2 Genetic variability studies for grain quality characters

High phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) recorded for all quality characters like, calcium, magnesium, iron, copper and zinc content. Higher magnitude of PCV and GCV for these characters indicates presence of high degree of variability and better scope for further crop improvement. Similar results were reported by Dhamdhere *et al.* (2011) in their study.

High heritability coupled with high genetic advance as per cent of mean were recorded for all the characters like, calcium, magnesium, iron, copper and zinc content. This indicates that there was low environmental influence on the expression of these characters and hence one can practice selection. Similar results of high heritability coupled with high genetic advance as per cent of mean was reported by Sarala *et al.* (2007).

5.3 Correlation studies for grain yield and yield related traits

Grain yield being a complex polygenic character, direct selection based on these traits would not yield fruitful results without giving due importance to their genetic background. The association of yield and its component traits reflects the nature and degree of relationship between them. The correlation analysis helps in examining the possibility of improving yield through indirect selection of its component traits which are highly correlated.

5.3.1 Correlation of grain yield with its component traits

In the present study, grain yield had significant and positive phenotypic association with days to 50 per cent flowering, days to maturity, earhead weight per plant and straw yield per plant. This suggests that these characters should be considered while selecting plants for grain yield improvement. These results are in accordance with reports of Rani *et al.* (2014) and Haradari *et al*. (2012) for 50 per cent flowering, days to maturity, earhead weight per plant and Bendale *et al.* (2002) for straw yield per plant.

While the traits like, plant height, number of tillers per plant, number of productive tillers per plant, number of fingers per ear, finger length, finger width, earhead length, harvest index and test weight had positive non-significant association with grain yield. These results were also reports of Sarala *et al.* (2008), Das *et al.* (2011) and Lule *et al.* (2012) for plant height, number of productive tillers per plant, number of fingers per ear, finger length and test weight and Dhamdhere *et al.* (2013) for harvest index, Wolie and Dessalegn (2011) for number of number of tillers per plant, Bendale *et al.* (2002), Lule *et al.* (2012) and Haradari *et al.* (2012) for finger width.

5.3.2 Inter correlation among yield components

Days to 50 per cent flowering had significant positive correlations with days to maturity, plant height, the number of fingers per ear, finger length, earhead length, earhead weight per plant, straw yield per plant and test weight. The similar results were also reported by Ganapathy *et al*. (2011) for days to maturity, plant height and finger length, Bendale *et al*. (2002) for earhead weight per plant and straw yield per plant, Kadam *et al.* (2009) for number of fingers per ear and earhead length, John (2007) for test weight. This trait also exhibited the significant and negative association with the number of tillers per plant, number of productive tillers per plant and harvest index. The results are in accordance with the reports of Bedis *et al*. (2006).

Days to maturity displayed significant and positive phenotypic association with plant height, the number of fingers per ear, straw yield per plant, finger length, earhead weight per plant, earhead length and test weight. Similar results were reported by Ganapathy *et al.* (2011) for finger length, plant height and earhead weight per plant, Bedis *et al*. (2006) for number of fingers per ear and earhead length, Lal *et al.* (1996) for test weight. This character also recorded the significant and negative association with the number of tillers per plant, the number of productive tillers per plant and harvest index. The results are in accordance with the reports of Bedis *et al*. (2006).

Plant height showed the significant and positive phenotypic association with the number of fingers per ear, finger length, finger width, earhead length, earhead weight per plant, straw yield per plant and test weight. These findings are in accordance with that of Sonnad *et al.* (2008) for earhead length and straw yield per plant, Ganapathy *et al*. (2011) and Haradari *et al.* (2012) for earhead weight per plant, Lal *et al.* (1996), Wolie and Dessalegn (2011), Lule *et al.* (2012) and Ulaganathan and Nirmalakumari (2014) for number of fingers per ear, finger length and test weight. This indicates that increase in plant height resulted in more the number of fingers per ear, finger length, finger width, earhead length, earhead weight per plant, straw yield per plant and test weight.

The number of tillers per plant had significant and positive phenotypic association with the number of productive tillers per plant. Similar results were reported by Ravikumar and Seetharam (1993). This trait also recorded the significant and negative association with the number of fingers per ear, finger length and earhead length. Similar results reported by John *et al.* (2006), Das *et al.* (2013), Anuradha *et al.* (2013) for number of fingers per ear, Ulaganathan and Nirmalakumari (2014) for finger length It also showed the non-significant and negative association with finger width and straw yield per plant. These findings are same as that of Haradari *et al.* (2012), Dhamdhere *et al.* (2013).

The number of productive tillers per plant had a non-significant positive correlation with earhead weight per plant, straw yield per plant, harvest index and test weight. The results are similar to the reports of Sarala *et al.* (2008) and Sharathbabu *et al.* (2008). On the contrary, it had shown significant negative phenotypic association with the number of fingers per ear, finger length and earhead length. Results were in agreement with that of John (2006).

The number of fingers per ear displayed significant positive phenotypic association with finger length, finger width, earhead length, earhead weight per plant, straw yield per plant and test weight indicates that these traits can be improved simultaneously through selection. The above findings are in agreement with reports of Lal *et al*. (1996), Bendale *et al.* (2002), Sarala *et al.* (2008), Sharathbabu *et al.* (2008) and Rani *et al.* (2015). On the contrary, it had a significant negative association with the number of tillers per plant and the number of productive tillers per plant.

Finger length exhibited the significant positive association with earhead length and straw yield per plant, indicating that increase in these traits leads to increase in finger length and mean while increase in grain yield because of positive association of finger length with grain yield per plant. Whereas it had a positive and non-significant association with finger width, earhead weight per plant and test weight. These results were in conformity with the observations of Sharathbabu *et al.* (2008).

Finger width had significant and positive phenotypic association with earhead weight per plant, straw yield per plant and test weight. The results were similar to the reports of Lule *et al.* (2012). It also had a positive and non-significant association with earhead length and negative and significant association with harvest index.

Significant positive phenotypic association of earhead length with straw yield per plant was observed. It had lower magnitude of association with ear weight and test weight.

Earhead weight per plant had significant and positive association with straw yield per plant and test weight. The results were similar to the reports of Sarala *et al.* (2008) and Lule *et al.* (2012) and Rani *et al.* (2015).

It is evident from the study that the grain yield per plant could be improved with an increase days to 50 percent flowering, days to maturity, earhead weight per plant and straw yield per plant as these traits showed positive and significant association with grain yield per plant. Hence, direct selection based on these characters would be rewarding for further improvement in grain yield of finger millet.

5.4 Correlation coefficient analysis for grain yield and grain quality parameters

Selection for specific character is known to result in correlated response in certain other characters. Generally, plant breeders make selection for one or two attributes at a time. Then it becomes important to know the effect on other characters. Improvement on grain yield per plant, the most important target character in many cereal crops, it can be achieved by direct selection through other easily observable characters. But, this needs a good understanding of association of different traits with grain yield per plant and their possible associations among themselves. The knowledge of association of quantitative and nutritional traits would further strengthen precision of breeder in efficient planning of breeding programme. Hence, an attempt has been made to derive some fruitful information related to the production and quality in finger millet.

5.4.1 Correlation between grain yield and quality parameters

Grain yield exhibited positive and non-significant association with magnesium content, copper content and zinc content. A positive correlation between desirable characters is favourable to the plant breeder because it helps in simultaneous improvement of both the characters. While the traits *viz.*, calcium content and iron content had negative non-significant association with grain yield. Negative correlation will hinder simultaneous expression of both the characters with high values. In such situations, some economic compromise has to be made. The results are in accordance with reports of Rani *et al.* (2015) and Srilakshmi (2013) for negative and non-significant association of calcium content with grain yield per plant.

5.4.2 Inter correlation among quality parameters

Calcium content showed the significant and positive association with magnesium content, iron content, copper content and zinc content indicating direction selection based on these characters would be rewarding for further improvement of calcium content in finger millet genotypes. Similar results were reported by Kazi and

Auti (2017) for significant and positive association of calcium content with magnesium content and calcium content with iron content.

Magnesium content exhibited the significant and positive association with iron content, copper content and zinc content indicating magnesium content can be improved simultaneous by selecting these traits. The results are in accordance with the reports of Kazi and Auti (2017) for significant and positive association of Magnesium content with zinc content.

Iron content had the significant and positive association with copper content and zinc content. By selecting the copper and zinc rich finger millet genotypes we may simultaneously improve the iron content also. Similar results were reported by Gupta *et al*. (2009) in pearl millet for significant positive association between iron and zinc content.

Copper content displayed the significant and positive association with zinc content indicating that when there is an improvement in zinc content in particular genotypes automatically indicates the breeder for direct selection for copper content also as it is positively correlated with zinc content.

5.5 Path coefficient analysis for grain yield and its component traits

Correlation coefficient values which measure the extent of relationship, path coefficient measure the magnitude of direct and indirect effects of characters on complex dependent character like yield and thus enable the breeders to judge the best about the important component characters during selection (Dewey and Lu, 1959). According to Lenka and Mishra (1973), if the direct or indirect effects were < 0.1, they were considered to be negligible. Hence, the indirect effects which have < 0.1 for other component traits were not considered for discussion in this chapter in view of their negligible influence on grain yield.

5.5.1 Direct effect of yield contributing characters on grain yield

The path analysis revealed that out of thirteen characters, eight were showed positive and direct effect on grain yield at phenotypic level *viz.*, days to maturity, plant height, number of tillers per plant, finger length, earhead length, earhead weight per plant, straw yield per plant and harvest index. This indicates that selection for these traits in yield improvement programme will reflect to overall improvement of the grain yield. Similar results of high direct effect of grain yield with days to maturity, finger length and earhead weight per plant were reported by Sharathbabu *et al.* (2008) and Ganapathy *et al.* (2011) for plant height and number of tillers per plant.

While the characters like days to 50 per cent flowering, number of productive tillers, number of fingers per ear, finger width and test weight had negative direct effects on grain yield. These findings are in accordance with the reports of Bendale *et al.* (2002) and Sharathbabu *et al.* (2008). Even though the direct effect of these traits on grain yield was negative, these traits seems to be the potential traits in improving the grain yield as these exerts indirect effect via other component traits.

5.5.2 Indirect effects of yield components on grain yield

Days to 50 per cent flowering displayed high positive indirect effect on grain yield through days to maturity (0.4464), earhead weight per plant (0.3308) and straw yield per plant (0.3127) indicating selection of these traits leads to increase in grain yield. Whereas its indirect effects on grain yield through other component traits were negligible (Lenka and Mishra, 1973). Similar results were reported by Ganapathy *et al.* (2011), Sharathbabu *et al.* (2008) and Lule *et al.* (2012).

The character days to maturity recorded high positive indirect effect on grain yield through earhead weight per plant (0.3339) and straw yield per plant (0.3126). While its indirect effects on grain yield through other component traits were negligible. The findings are in agreement with Lule *et al.* (2012).

The highest positive indirect effect of plant height on grain yield was expressed through straw yield per plant (0.3759) followed by days to maturity (0.2979) and earhead weight per plant (0.2219). While its indirect effects on grain yield through other component traits were negligible. The results are in accordance of Sharathbabu *et al.* (2008) and Lule *et al.* (2012).

Number of tillers per plant exerted low positive indirect effect on grain yield through days to 50 per cent flowering (0.1658). Whereas its indirect effects on grain yield through other component traits were negligible. The results are in agreement with of Ganapathy *et al.* (2011).

The number of productive tillers per plant exhibited low positive indirect effect on grain yield through days to 50 per cent flowering (0.1400). While its indirect effects on grain yield through other component traits were negligible. The findings are in agreement with Ganapathy *et al.* (2011).

The character number of fingers per ear showed moderate positive indirect effect on grain yield through days to maturity (0.2909), earhead weight per plant (0.2756) and straw yield per plant (0.1909). Whereas its indirect effects on grain yield through other component traits were negligible. Similar results were obtained by Sharathbabu *et al.* (2008) and Lule *et al.* (2012).

Finger length exerted moderate positive indirect effects on grain yield through days to maturity (0.2311), earhead length (0.1175), earhead weight per plant (0.1482) and straw yield per plant (0.1620). While its indirect effects on grain yield through other component traits were negligible. The findings are in agreement with of Sharathbabu *et al.* (2008), Bedis *et al*. (2006) and Lal *et al.* (1996).

The character finger width recorded positive indirect effects on grain yield through days to earhead weight per plant (0.1982), straw yield per plant (0.2064). Whereas its indirect effects on grain yield through other component traits were negligible.

Earhead length exhibited positive indirect effects on grain yield through days to maturity (0.2003), and straw yield per plant (0.1321). While its indirect effects on grain yield through other component traits were negligible.

Earhead weight per plant exhibited the highest positive indirect effects on grain yield through straw yield per plant (0.2985) followed by days to maturity (0.2157). Whereas its indirect effects on grain yield through other component traits were negligible. The findings are in agreement with of Sharathbabu *et al.* (2008) and Lule *et al.* (2012).

Straw yield per plant exhibited positive indirect effects on grain yield through days to maturity (0.2829) and earhead weight per plant (0.4182). Harvest index exerted positive indirect effects on grain yield through days to 50 per cent flowering (0.2039). The indirect effects of test weight on grain yield were positive through days to maturity (0.1446), earhead weight per plant (0.2836) and straw yield per plant (0.1993). Similar results were obtained by Wolie and Dessalegn (2011) for test weight.

Based on the path analysis studies it was evident that, the characters like days to maturity, earhead weight per plant and straw yield per plant had high direct effect on grain yield per plant, thereby indicating a true relationship between them. These traits also showed positive and significant correlation with grain yield per plant. Thus these characters could be considered as an important component for the improvement of grain yield in finger millet. Similar findings were reported by Sharathbabu *et al.* (2008) and Satish (2003).

5.6 Genetic divergence studies for grain yield and yield contributing traits

The amount of diversity available in the crop decides the success of any crop improvement programme with manifold objectives. Assemblage and assessment of divergence in the germplasm is essential to know the spectrum of diversity. Improvement in grain yield is normally attained through involvement of the genetically diverse parents in breeding programmes. For identifying such diverse parents for crossing, Mahalanobis D^2 statistics has been used in several crops. It is a powerful tool used to quantify the genetic divergence between the genotypes and to relate clustering pattern with the geographical origin.

5.6.1 Genetic diversity in different groups

Based on D^2 value, sixty finger millet genotypes were grouped into eight non-overlapping clusters. Cluster I, Cluster II, Cluster IV had maximum number of genotypes fourteen followed by cluster VI with eleven genotypes and cluster III with four genotypes and remaining three clusters, cluster V, VII and VIII are solitary. These results are in conformity with the observations made by Das *et al.* (2013) in 48 germplasm lines of finger millet.

Genotypes grouped in the same cluster presumably less diverse each another since they may be having common ancestors. Theoretically, crossing of genotypes belonging to the same cluster is not expected to yield superior hybrids or desirable recombinants. However, genotypes in different clusters may have high heterosis since all they are distributing differently from each other.

Among eight clusters, cluster VI exhibited the maximum intra cluster distance, so genotypes grouped under these cluster are somewhat diverse. While the minimum was recorded in clusters V, VII and VIII as they included only single genotype in each cluster. This reveals the presence of moderate diverse genotypes within different clusters. The minimum inter cluster distance observed between cluster V and VIII indicating less diversity between the genotypes belongs to these clusters. Whereas the maximum inter cluster distance was observed between cluster IV and VIII, indicating high diversity between the genotypes belongs to these clusters. It is desirable to select genotypes from these clusters with high inter cluster distance as one of the parent in recombination breeding programme for obtaining wide variability and desirable segregants for grain yield and its attributing characters.

5.6.2 Contribution of character towards genetic divergence

Contribution of each character towards genetic divergence has been estimated from the number of times that each character appeared in the first rank. It has been noticed that, plant height contributed the maximum towards the genetic divergence followed by straw yield per plant, days to 50 per cent flowering, earhead weight per plant, days to maturity, grain yield per plant and earhead length so selection of parents with these traits leads to production of superior segregants upon hybridization. Similar results were reported by Suryanarayana *et al.* (2014) for maximum per cent contribution of plant height towards total divergence in 48 finger millet genotypes. On contrary total number of tillers per plant, number of productive tillers per plant, number of fingers per ear, finger length, finger width, harvest index and test weight had negligible contribution towards genetic divergence.

The above results imply that, in order to select genetically diverse genotypes for hybridization, the material should be screened for the important traits like, plant height, straw yield per plant, days to 50 per cent flowering, earhead weight per plant, days to maturity, grain yield per plant and earhead length.

5.6.3 Analysis of cluster means

All the genotypes were spread over eight clusters and means were presented for fourteen character. Genotypes with minimum days to 50 per cent flowering, days to maturity, plant height with higher harvest index were observed in the cluster IV. Genotypes with high number of tillers per plant, number of productive tillers per plant, earhead weight per plant, grain yield per plant and harvest index observed in cluster III. Cluster II had high number of fingers per ear, finger width and test weight.

Hence, it is worthy to note that in calculating cluster means, the superiority of particular genotype in respect to a given character get diluted by other genotype that are related and grouped in the same cluster but which are inferior or intermediary for that character in question. Hence, apart from selecting genotypes from the clusters which have high inter-cluster distance for hybridization, one can also think of selecting genotypes based on extent of genetic divergence in respect to a particular character of interest. This is to mean that, if breeder's intention is to improve grain yield, he can select genotypes which are highly divergent with respect to these characters.

5.7 Genetic divergence studies for grain quality traits

5.7.1 Genetic diversity in different groups

Based on D^2 value, sixty finger millet genotypes were grouped into eight non-overlapping clusters. Cluster II, had maximum number of genotypes sixteen followed by cluster I with twelve genotypes, cluster III with ten genotypes, cluster VI with seven genotypes, cluster IV with six genotypes, cluster V with five genotypes, cluster VII with three genotypes whereas cluster VIII was solitary as it contained only one genotype. This suggested that genotypes occupying the same cluster have low level of diversity and selection of parents within the cluster may not be considered promising.

Among eight clusters, cluster VI exhibited the maximum intra cluster distance, so genotypes grouped under these cluster are somewhat diverse. While the minimum was recorded in clusters VIII as it included only single genotype. The minimum inter cluster distance observed between cluster III and VIII indicating less diversity between the genotypes belongs to these clusters. Whereas the maximum inter cluster distance was observed between cluster IV and I, indicating high diversity between the genotypes belongs to these clusters. It is desirable to select genotypes from these clusters with high inter cluster distance as one of the parent in recombination breeding programme for obtaining wide variability and desirable segregants for grain yield and its attributing characters.

5.7.2 Contribution of character towards genetic divergence

Contribution of each character towards genetic divergence has been estimated from the number of times that each character appeared in the first rank. It has been observed that calcium content contributed the maximum towards the genetic divergence followed by magnesium and iron content so selection of parents with these traits leads to production of superior segregants upon hybridization. On contrary copper and zinc content had negligible contribution towards the total divergence.

The above results imply that, in order to select genetically diverse genotypes for hybridization, the material should be screened for the important traits like, calcium, magnesium and iron content.

5.7.3 Analysis of cluster means

All the genotypes were spread over eight clusters and means were presented for five characters. Genotypes with higher magnesium and copper content were observed in cluster III. Whereas genotypes in cluster IV, cluster II and cluster VIII had maximum mean values for calcium, iron and zinc respectively.

The desirable genotypes within the divergent clusters can now be identified on the basis of mean performance of individual genotypes within the clusters. The following points need to be considered while selecting desirable genotypes: (1) choice of clusters that were separated by maximum inter-cluster distances, and (2) selection of particular genotypes that showed good performance in the selected clusters.

The findings of the present study suggested that the material involved in this investigation had sufficient amount of diversity for important quality characters. Diversity between clusters may the exploited in two ways, either by resorting to hybridization which subsequently would result into the development of superior lines, or by selection of traits related to divergence and using as such. However, the first approach would be more beneficial. Divergence analysis is usually performed to identify the diverse genotypes for hybridization purpose.

5.8 Superior finger millet genotypes identified for grain yield and grain quality traits

The genotypes, Malali (25.30 g/plant) and IC-473155 (25.20 g/plant) were recorded high yield compared to varietal check GPU-28 (21.35 g/plant). Genotype IC-474959 was superior for three quality traits namely calcium (398.62 mg/100g), magnesium (167.77 mg/100g) and copper content (0.95 mg/100g) followed by genotypes superior for two quality traits namely, IC-473388, IC-473143 and Jeenumundaga Ragi for iron (14.19, 13.85,7.05 mg/100g) and zinc content (5.45, 5.65, 5.65 mg/100g) respectively. Hence, these identified genotypes which are superior for respective traits can be directly used as parent in hybridization programme to get desirable transgressive segregants for particular trait.

5.9 Finger millet genotypes identified for both grain yield and grain quality traits

The genotypes, IC-473178 (165.48, 10.01 mg/100g), IC-473143 (166.78, 13.85 mg/100g), IC-473183 (146.28, 9.65 mg/100g) and SMRC-3 (166.86, 11.70 mg/100g) are superior to the varietal check GPU-28 (139.54, 6.42 mg/ 100g) for magnesium and iron content. IC-473183 (0.98 mg/100g) genotype is superior to the varietal check GPU-28 (0.78 mg / 100g) for copper content. The genotypes, IC-473143 (5.23 mg/100g), IC-473183 (5.17 mg/100g) and SMRC-3 (5.21 mg/100g) is superior to the varietal check GPU-28 (2.80 mg/100g) for zinc content. All the identified genotypes are superior over the mean value for grain yield per plant. Hence, these identified genotypes which are superior for respective traits can be directly used as parent in hybridization programme to get desirable transgressive segregants for particular nutrient.

All the identified genotypes for both grain yield and quality traits are not superior to the varietal check (GPU-28) with respect to grain yield per plant. Hence, these identified genotypes can be further improved through population improvement approaches like recurrent selection and/ or diallel selective mating. Both the approaches are very much useful in broadening the genetic base of the population by incorporation of multiple parents in the breeding programme. Finally both the approaches will creates the vast genetic diversity with respect to both grain yield and grain quality traits by fastening the genetic recombination. The end product of both the approaches can be used as pure line variety, mass selected variety or as parental lines for further breeding programme.

Conclusion

The analysis of variance revealed highly significant differences among the sixty finger millet genotypes for both grain yield and quality traits indicating the presence of sufficient variability for all the traits under the study. The maximum inter-cluster distances for grain yield and quality traits were recorded between cluster IV & cluster VIII and cluster IV and I respectively, indicates the presence of wide diversity between these clusters. Therefore, genotypes from these clusters can be selected for hybridization programme to get desirable recombinants. Plant height and calcium content contributed the maximum per cent towards genetic divergence in sixty genotypes of finger millet, indicates the presence of wide variability for these traits among the studied genotypes. The genotypes, Malali (25.30 g/plant) and IC-473155 (25.20 g/plant) were recorded high yield compared to check GPU-28 (21.35 g/plant). Genotype IC-474959 was superior for three quality traits namely calcium (398.62 mg/100g), magnesium (167.77 mg/100g) and copper content (0.95 mg/100g) followed by genotypes superior for two quality traits namely, IC-473388, IC-473143 and Jeenumundaga Ragi for iron (14.19, 13.85,7.05 mg/100g) and zinc content (5.45, 5.65, 5.65 mg/100g) respectively. These identified potential genotypes with high calcium, magnesium, iron, copper and zinc content can be further utilized as donor parents to transfer these traits to genotypes which are well adapted to local ecological niches.

Future line of work

1. The genotypes grouped in diverse clusters (between cluster IV and cluster VIII and cluster IV and cluster I) can further utilized in the hybridization programme to obtain transgressive segregants for yield and quality parameters.

2. The genotypes, Malali and IC-473155 possessed higher yield can be further tested in multi locations to assess their performance and further release as varieties.

3. The genotypes, IC-474959, IC-473143, IC-473388 and Jeenumundaga Ragi, possessed high micronutrients content can be further tested in multi locations to assess their performance.

4. The identified potential genotypes with high micronutrient content can be utilized as donor parents to transfer desired traits to superior high yielding genotypes which are well adapted to local regions.

5. The worth of potential genotypes can be assessed through molecular markers which can the improve efficiency of selection in marker assisted plant breeding.

SUMMARY

VI SUMMARY

The present investigation was carried out to assess the extent of genetic variability, divergence, nature of association, direct and indirect effects of yield contributing characters and micronutrients content of grain yield in sixty genotypes of finger millet at the Zonal Agricultural and Horticultural Research Station, Shivamogga during *kharif* 2017.

The analysis of variance revealed highly significant differences among the sixty finger millet genotypes for both grain yield and quality traits indicating the presence of sufficient variability for all the traits under the study. The mean performance of sixty genotypes used in the present study revealed that genotype, IC-474649 was superior for three out of 14 characters *viz.*, days to 50 per cent flowering, days to maturity and reduced plant height. The genotype, OUAT-2 was superior for number of tillers per plant and productive tillers per plant. IC-473143 genotype recorded the highest finger length and earhead length, whereas genotype, Malali exhibited the higher earhead weight per plant and seed yield per plant. For grain quality, the genotypes like, IC-474959, L-5, IC-473388 and KMR-340 exhibited higher calcium, magnesium, iron and copper content respectively. IC-473143 and Jeenumundaga Ragi genotypes exhibited higher zinc content.

High phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) recorded for characters like, finger length, earhead length, seed yield per plant, straw yield per plant and all the quality traits indicating the presence of high degree of variability and better scope for further crop improvement. The moderate PCV and GCV were observed for plant height, number of fingers per ear, earhead weight per plant and harvest index. This indicates the existence of comparatively moderate variability for these traits, which could be exploited for improvement of these traits through selection in advanced generations.

High heritability coupled with high genetic advance as per cent of mean was recorded for plant height, number of tillers per plant, number of productive tillers per plant, finger length, number of fingers per ear, earhead length, earhead weight per plant, seed yield per plant, harvest index and for all the quality traits indicating less influence of environment on the expression of these characters and they may be governed by additive gene action so simple selection can be practiced for improvement of these traits along with grain yield.

The high significant and positive association of grain yield with days to 50 per cent flowering, days to maturity, earhead weight per plant and straw yield per plant indicates these characters should be given emphasis while selecting plants for improvement of grain yield. The traits like plant height, number of tillers per plant, number of productive tillers per plant, number of fingers per ear, finger length, finger width, earhead length, harvest index and test weight displayed the positive association with grain yield at lower magnitude.

Path analysis revealed that, the characters like days to maturity, earhead weight per plant and straw yield per plant had direct effect on grain yield per plant, indicating a true relationship between them. These traits also showed positive and significant correlation with grain yield per plant. Thus, these characters could be considered as an important component for the improvement of grain yield in finger millet.

Genotypes grouped into the same cluster presumably diverge little from one another as the aggregates of characters measured. The maximum inter-cluster distances for grain yield and quality traits were recorded between cluster IV & cluster VIII and cluster IV and cluster I respectively, indicates the presence of wide diversity between these clusters. Therefore, genotypes from these clusters can be selected for hybridization programme to get desirable recombinants. Plant height and calcium content contributed the maximum per cent towards genetic divergence in sixty genotypes of finger millet, indicates the presence of wide variability for these traits among the studied genotypes.

The genotypes, Malali (25.30 g/plant) and IC-473155 (25.20 g/plant) were recorded high yield compared to check GPU-28 (21.35 g/plant). Genotype,IC-474959 was superior for three quality traits namely calcium (398.62 mg/100g), magnesium (167.77 mg/100g) and copper content (0.95 mg/100g) followed by genotypes superior for two quality traits namely, IC-473388, IC-473143 and Jeenumundaga Ragi for iron (14.19, 13.85,7.05 mg/100g) and zinc content (5.45, 5.65, 5.65 mg/100g) respectively. These identified potential genotypes with high calcium, magnesium, iron, copper and zinc content can be further utilized as donor parents to transfer these traits to genotypes which are well adapted to local ecological niches.

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