# DIVERSITY IN MORPHO-PHYSIOLOGICAL AND BIOCHEMICAL COMPONENTS IN GENETIC RESOURCES OF FOXTAIL MILLET (*Setaria italica* (L.) Beauv.)


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**B.Sc. (Ag.)**


**MASTER OF SCIENCE IN AGRICULTURE**
**(GENETICS AND PLANT BREEDING)**

ANGRAU

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# DIVERSITY IN MORPHO-PHYSIOLOGICAL AND BIOCHEMICAL COMPONENTS IN GENETIC RESOURCES OF FOXTAIL MILLET (*Setaria italica* (L.) Beauv.)


**BY**

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**B.Sc. (Ag.)**


**THESIS SUBMITTED TO THE**
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**FOR THE AWARD OF THE DEGREE OF**

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**CHAIRPERSON: Dr. A.V.S. DURGA PRASAD**

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**2019**

# DECLARATION

I, **Mr. G.K. PAVAN KUMAR**, hereby declare that the thesis entitled **"DIVERSITY IN MOPHO-PHYSIOLOGICAL AND BIOCHEMICAL COMPONENTS IN GENETIC RESOURCES OF FOXTAIL MILLET (*Setaria italica* (L.) Beauv.)**" submitted to the **Acharya N.G. Ranga Agricultural University** for the degree of **Master of Science in Agriculture** is the result of original research work done by me. I also declare that no material contained in the thesis has been published earlier in any manner.

Place :

Date :

**(G.K. PAVAN KUMAR)**
**I.D. No. MAM / 2017-07**

# CERTIFICATE

**Mr. G.K. PAVAN KUMAR** has satisfactorily prosecuted the course of research and that thesis entitled **"DIVERSITY IN MORPHO-PHYSIOLOGICAL AND BIOCHEMICAL COMPONENTS IN GENETIC RESOURCES OF FOXTAIL MILLET (*Setaria italica* (L.) Beauv.)"** submitted is the result of original research work and is of sufficiently high standard to warrant its presentation to the examination. I also certify that neither the thesis nor its part thereof has been previously submitted by him for a degree of any University.

**Date** :

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# CERTIFICATE

This is to certify that the thesis "**DIVERSITY IN MORPHO-PHYSIOLOGICAL AND BIOCHEMICAL COMPONENTS IN GENETIC RESOURCES OF FOXTAIL MILLET (*Setaria italica* (L.) Beauv.)**" submitted in partial fulfillment of the requirements for the degree of '**Master of Science in Agriculture'** of the **Acharya N.G. Ranga Agricultural University, Guntur** is a record of the bonafide original research work carried out by **Mr. G.K. PAVAN KUMAR** under our guidance and supervision.

No part of the thesis has been submitted by the student for any other degree or diploma. The published part and all assistance received during the course of the investigations have been duly acknowledged by the author of the thesis.

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**G.K. PAVAN KUMAR ….**

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# LIST OF ABBREVIATIONS AND SYMBOLS

| | | |
|---|---|---|
| % | : | Per cent |
| < | : | Less than |
| > | : | more than |
| ANOVA | : | Analysis of Variance |
| ARCBD | : | Augmented randomized complete block design |
| CD | : | Critical Difference |
| cm | : | Centimeter |
| CV | : | Coefficient of variation |
| d.f | : | Degrees of freedom |
| *et al.* | : | and others people |
| Fig. | : | Figure |
| g | : | Gram |
| GA | : | Genetic Advance |
| GAM | : | Genetic Advance as per cent of Mean |
| GCV | : | Genotypic Co-efficient of Variation |
| *ha* | : | Hectare |
| *i.e* | : | That is |
| kg | : | Kilogram |
| kg $ha^{-1}$ | : | Kilograms per hectare |
| L t | : | Lakh tonnes |
| L ha | : | Lakh hectares |
| m | : | Meter |
| $m^2$ | : | Metre square |
| M ha | : | Million hectares |
| Mm | : | millimeters |
| MSL | : | Mean sea level |
| MSS | : | Mean sum of square |
| Mt | : | Million tonnes |
| P | : | Phenotypic path coefficient |

| | | |
|---|---|---|
| PCA | : | Principal Component Analysis |
| PCV | : | Phenotypic Co-efficient of Variation |
| *per se* | : | As such with mean |
| RARS | : | Regional Agricultural Research Station |
| $r_g$ | : | Genotypic correlation coefficient |
| $r_p$ | : | Phenotypic correlation coefficient |
| S.E. | : | Standard error |
| S.Ed | : | Standard Error of difference |
| SS | : | Sum of square |
| t $ha^{-1}$ | : | Tonnes per hectare |
| *via* | : | Through |
| *viz.*, | : | Namely |
| $\sigma$ | : | Standard deviation |
| $\sigma^2$ | : | Variance |
| 2D | : | Two dimensional |
| 3D | : | Three dimensional |

# ABSTRACT


| | | |
|---|---|---|
| Name of the Author | : | **G.K. PAVAN KUMAR** |
| Title of the thesis | : | "**DIVERSITY IN MORPHO-PHYSIOLOGICAL AND BIOCHEMICAL COMPONENTS IN GENETIC RESOURCES OF FOXTAIL MILLET (*Setaria italica* (L.) Beauv.)**" |
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The present research investigation on "Diversity in morpho-physiological and biochemical components in genetic resources of foxtail millet (*Setaria italica* (L.) Beauv.)" was conducted during *kharif*, 2018 at Regional Agricultural Research Station, Nandyal, with 100 genetic resources in augmented randomized complete block design (ARCBD).

The results of ANOVA revealed significant differences among the genetic resources indicating ample genetic variability in the germplasm for all the 18 metric traits studied *viz*., SCMR at 30 DAS, SCMR at 45 DAS, days to 50 % flowering, plant height, panicle length, number of productive tillers /plant, days to maturity, number of grains / ear head, 1000 grain weight, protein, carbohydrate, calcium, magnesium, iron, zinc, copper, manganese and grain yield/ plant.

The analysis of genetic parameters revealed the traits *viz*., number of productive tillers / plant, magnesium, iron, zinc, copper and grain yield/ plant possessed higher estimates of GCV, PCV, heritability and genetic advance as *per cent* of mean implying that these traits were predominantly under the control of additive gene action and genetic improvement can be achieved through simple selection for these traits.

Studies on genetic divergence in 100 foxtail millet genetic resources through Mahalonobis $D^2$ analysis using Tocher's method showed formation of 11 distinct non-overlapping clusters. The maximum inter-cluster distance was found between cluster V (SiA 4044) and cluster XI (SiA 3222) indicated high degree of genetic diversity and thus may be utilized under inter-varietal hybridization programme (transgressive segregation) for obtaining superior segregants. Similarily hierarchial cluster analysis, done by ward's minimum variance method also showed formation of 11 non-overlapping distinct clusters. The maximum genetic distance between SiA 3222 and SiA 3580, reflecting the wide diversity among the genotypes. The genotypes with high genetic distance can be utilized directly as potent parents in breeding programmes to achieve improved yields. Canonical root analysis accounted for 67.371 per cent of total genetic divergence and showed seven canonical roots retained based on the scree plot and threshold eigen value greater than one. The traits plant height, 1000 grain weight,

panicle length, days to maturity, grain yield/ plant, days to 50% flowering and zinc contributed maximum to the existing variability.

The correlation studies revealed positively significant association of grain yield / plant with the traits *viz.*, SCMR at 30 DAS, plant height, panicle length, number of grains / ear head and 1000 grain weight at phenotypic level implying that these traits may be chosen for selection criterion for developing high yielding cultivars.The path coefficient analysis revealed that the traits SCMR at 30 DAS, plant height, number of grains / ear head and 1000 grain weight had true relationship with grain yield per plant by establishing significant positive association and positive direct effect at phenotypic levels.

Thus as a whole, the studies conclude that the genetic resources *viz*., SiA 3222, SiA 4044 and SiA 3580 were found promising for majority of the traits and might serve as 'potential parents' in future hybridization programmes. The traits, number of productive tillers / plant, magnesium content, iron content, zinc content, copper content and grain yield / plant with higher estimates of variability parameters can be improved through simple selection strategies. Association studies through correlation and path analysis revealed that the trait SCMR at 30 DAS, plant height, number of grains / ear head and 1000 grain weight had true relationship with grain yield per plant by establishing significant positive association and positive direct effect on grain yield implying the scope of direct selection for these traits in genetic improvement of foxtail millet.


# Chapter – I

# INTRODUCTION

## Chapter I

# INTRODUCTION

Millets refers to a group of annual grasses, belonging to the family *Poaceae* with tiny edible seeds that do not shatter readily at maturity. Often termed as coarse cereals, they thrive predominantly in the arid and semi-arid tracts globally as 'rainfed crops', under marginal conditions of soil fertility and moisture owing to their hardy nature and yield stability. Ideally, these crops are amenable for climate resilent agriculture as they are tuned to adapt varying thermal-moisture regimes, scarce input conditions and serve diversified purposes as food, feed, fodder, biofuels and brewing. Thus, millets are regarded as 'smart food' as they are good for you, good for the farmer and good for the planet. Realizing the significance of millets, the Government of India (GOI) had observed the year 2018 as 'National Year of Millets' inorder to boost domestic production and achieve self-sufficiency. Besides, the GOI went a step forward and even sent a proposal to U.N. Food and Agriculture Organization which after careful examination endorsed India's view and declared **2023** as the 'International Year of Millets'.

Millets comprising of six small seeded cereal grasses *viz.*, finger millet (ragi), foxtail millet (korra), kodo millet (arikelu), little millet (samalu), proso millet (varigalu) and barnyard millet (odalu) constitute the 'Small millets'. These are often regarded as 'heritage crops' owing to their cultivation from times immemorial for their stability in yield levels. Among the small millets, *Setaria italica* (L.) P. Beauv, popularly known as foxtail millet, chinese millet, german millet, hungarian millet and italian millet resembling a fox's tail in appearance *i.e.* a long panicle with soft, long and erect hairs ranks second in economic importance, next to finger millet in terms of global production. Being an annual $C_4$ autogamous diploid (2n=2x=18) with small genome size (~ 515 Mb), short duration and prolific seed bearing ability, this millet serves as a 'model species' in functional genomic studies. The grains of this millet are enriched with quality protein (leucine and methionine), β carotene, minerals (Ca, Fe, K, Mg and Zn), antioxidants, dietary fibre, phytochemicals, vitamins ($B_1$, $B_2$ and $B_3$) and possess low glycemic index, a requisite for healthy human diet (Murugan and Nirmalakumari, 2006).

In India, foxtail millet is cultivated in an area of 80000 ha. accounting for 900 kg $ha^{-1}$ in productivity, while in Andhra Pradesh, it occupies an area of 51000 ha. with a

productivity of 945 kg $ha^{-1}$ (Annual report, 2016-17). Since the reported yield levels of this small millet is more or less stagnant and existence of huge demand in market scenario, there is an urgent need to break the yield plateau and boost the grain productivity.

For the inception of any crop improvement programme, prevalence of wide spectrum of genetic variability in the population is a requisite in selection of desired genotype(s). Yield being a complex polygenic character is influenced by its own attributes and environment. The phenotypic expression of a character is resultant of the interactions between genotype and environment. Hence, the total variation needs to be partitioned into variance due to genotype (heritable) and variance due to environment (non heritable) for assessing the true breeding behaviour of the genotype. Genetic variability estimated by various genetic parameters *viz.*, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance. Besides genetic variability, knowledge on heritability and genetic advance measures the relative degree to which a character is transmitted to progeny, thereby assists the breeder to formulate a suitable selection breeding strategy inorder to achieve the desired objective. Thus, estimation of genetic variability in conjunction with heritability and genetic advance gives an idea of the possible improvement of the character through selection.

Assessment of genetic diversity plays a vital role in crop breeding either to exploit heterosis or to generate productive recombinants. The choice of parents is of utmost priority in designing the breeding programme. Screening of a large number of genetic resources is a key aspect to facilitate selection of diverse genotypes for hybridization programme. Realising the importance of genetic resources in the development of desirable genotypes, breeders are now looking for more diverse forms from various sources to further augment the yield potential of the genotypes. Hierarchical cluster analysis, Mahalanobis' $D^2$ statistic and Principal component analysis are few powerful tools employed for quantifying genetic divergence among the available genetic resources with respect to characters considered together. Thus, the quantification of genetic divergence in the genetic resources for various morpho-physiological and biochemical traits and relating clustering pattern with the geographical origin provides ample scope for identification of 'potential parents' in hybridization programme.

Knowledge of association between yield and its attributes analyzed through correlation and path studies ascertain the intrinsic relationship among characters and their contribution to yield. Correlation measures the degree and direction of association between two or more variables and assists the breeder to identify the characters or combination of characters that might be useful in improving yield by way of evaluating relative influence of various characters on yield and among themselves as well. On the other hand, path coefficient analysis estimates the direct and indirect contribution of various traits to yield and thus ascertain cause and effect relationship between different pairs of characters.

Keeping the aforesaid points in view and to combat the challenges of higher productivity, food security and nutritional security, the present investigation in foxtail millet is attempted with the following objectives for unlocking the genetic variation and identification of elite genetic resources with desired morpho-physiological and biochemical traits suited for designing future breeding strategies in order to develop bio-fortified cultigens.

**Objectives**

1. To determine the extent of genetic variance, heritability (broad sense) and genetic advance for yield and its attributes.
2. To estimate the extent of genetic diversity in the genetic resources utilized for study.
3. To ascertain the extent of character association between yield and its component characters.
4. To assess the nature and extent of direct and indirect effects of component characters on yield.
5. To study the morpho-physiological and biochemical components in the genotypes.


# Chapter – II

# REVIEW OF LITERATURE

## Chapter II

# REVIEW OF LITERATURE

The literature available on foxtail millet [*Setaria italica* (L.) Beauv] as pertinent to the present study has been comprehensively reviewed under the following headings.

2.1 Genetic parameters

2.2 Genetic divergence

2.3 Correlation analysis

2.4 Path coefficient analysis

## 2.1 Genetic parameters

The relative estimates of variability and their heritable components for yield contributing characters in the germplasm are of immense value in any breeding programme to achieve higher yields. The phenotype of quantitative trait is a resultant of genotype, environment and their interaction. The success of any breeding activity depends on the extent of genetic variability available for utilization in crop improvement.

### 2.1.1 Genetic variability:

The information on nature and magnitude of variability for both quantitative and qualitative traits in any crop species plays a vital role in formulating an effective breeding programme. However, the phenotypic expression of complex polygenic characters like yield is a combination of genotype, environment and their interaction. This indicates the need for partition of overall variability into heritable and non-heritable components with appropriate statistical techniques. The success of any breeding programme depends on the degree of genetic variability available for exploitation.

High PCV and GCV for a character indicate high variability in that population for that character. The magnitude of heritability coupled with nature and extent of variability in the breeding material gives an idea for effective genetic improvement through selection.

Govindaraj *et al.* (2011) studied 61 exotic genotypes of pearl millet for 15 characters to find out the extent of genetic variation. The phosphorus content had expressed the highest phenotypic and genotypic variances. The magnitudes of phenotypic and genotypic variances were low for the 100 grain weight.

Reddy *et al.* (2012) studied 18 elite entries of finger millet to find out the extent of genetic variation.The phenotypic coefficient of variation was greater than genotypic coefficient of variation for all the characters studied which shows the influence of the environmental effect on the characters. High values for phenotypic coefficient and genotypic coefficient was recorded for number of fingers per ear head.

Prasanna *et al.* (2013c) studied 34 exotic genotypes of Italian millet for 13 characters to find out the extent of genetic variation. High phenotypic coefficients of variation (PCV) coupled with high genotypic coefficients of variation (GCV) were observed for grain yield per plant, ear weight, calcium content and carotene during both seasons. The trait 1000 grain weight recorded high PCV and GCV during autumn, whereas number of productive tillers per plant and straw weight during spring. Straw weight showed high GCV during autumn.

Brunda *et al.* (2014) studied 78 foxtail millet genotypes and reported high values of PCV and GCV for grain yield per plot, straw yield per plant and moderate estimates for panicle length, panicle weight, test weight and low estimates for plant height and panicle breadth. This indicates the existence of comparatively high variability for these traits, which could be exploited for improvement of the traits through selection in advanced generations.

Suryanarayana *et al.* (2014) evaluated 35 diverse genotypes of finger millet and revealed the variation at phenotypic (PCV) and genotypic (GCV) levels were high for seed yield per plant, productive tillers per plant and main ear length.

Johar (2015) studied 34 exotic Italian millet genotypes and identified that high PCV and GCV were recorded for grain yield per plant, ear weight, calcium content and

carotene during autumn and spring seasons. The trait 1000 grain weight recorded high PCV and GCV during autumn, whereas number of productive tillers per plant and straw weight during spring. It indicated presence of wider variability for these traits in the genotypes studied.

Kumari and Singh (2015) assessed 35 promising finger millet genotypes and revealed that harvest index, grain yield of main panicle, 1000-grain weight, number of tillers per plant and flag leaf area exhibited very high GCV and PCV implying the importance of these traits in evaluation and selection of the genotypes.

Yogeesh *et al.* (2015) evalvated 52 foxtail millet accessions for extent genetic variation. Days to 50% flowering, Plant height, and seed yield per plant showed grater variability. Phenotypic coefficient of variation and genotypic coefficient of variation were high for plant height, Tillers per plant and length of inflorescence. High heritability with high Genetic advance as percent mean were found for Days to 50% flowering and seed yield.

Nandini *et al.* (2016) studied 542 $F_3$ progeny lines of little millet for seven characters to find out the extent of genetic variation. High GCV and PCV were observed for number of productive tillers per plant and per plant yield.

Anuradha *et al*. (2017) assessed 30 little millet genotypes and revealed that GCV and PCV values for fodder yield, days to 50% flowering and grain yield indicating selection for these traits might be chosen for crop improvement.

Mahanthesha *et al*. (2017a) evaluated 48 finger millet germplasm lines and observed high genotypic and phenotypic coefficients of variation for grain yield per plot, grain yield per plant, number of basal tillers per plant, productive tillers per plant, main ear width and finger length indicating that simple selection can be practiced for improvement of these characters.

Ramya *et al*. (2017a) evaluated 182 restorer (R-) lines of pearl millet and reported that the characters *viz.* ear length, ear diameter, productive tillers per plant, head yield per plant, grain yield per plant, fresh stover yield per plant, dry matter yield per plant and 1000 grain weight showed high PCV and GCV values implying selection for these traits will be rewarding for genetic improvement.

Shingane *et al*. (2017) studied 44 foxtail millet genotypes and noted high estimates of genotypic and phenotypic coefficients of variation for number of productive tillers per plant, number of panicles per plant, grain yield per plant, straw yield per plant and iron content suggesting that these traits selection will boost for further improvement of the crop.

Talawar *et al*. (2017) assessed 52 germplasm lines of pearl millet for eight quantitative characters with a view to study the genetic variability. The high values of GCV and PCV were obtained for the characters like productive tillers per plant, grain yield per plant, 1000 seed weight, seed yield per ear head and panicle length traits, indicating variation for these characters contributed markedly to the total variability and also scope for genetic improvement through selection for all these traits.

Amarnath *et al.* (2018a) invetigated 50 Indian foxtail millet genetic resources to estimate the extent of genetic variance for 12 metric traits. The phenotypic coefficient of variation (PCV) was greater than genotypic coefficient of variation (GCV) for all the characters studied implying that these characters were highly influenced by the environmental effects. High PCV and GCV values (>20%) was recorded for number of productive tillers / plant and culm branches indicating that these characters contributed markedly to the total variability.

Anusha *et al.* (2018) analyzed genetic variability of 12 characters in 22 pearl millet genotypes. The traits, fat content and dry matter yield per plant exhibited higher PCV and GCV, indicating high variation for these traits among the genotypes implying that their selection would contribute to genetic improvement.

Arya *et al.* (2018) evaluated genetic variability for yield and yield contributing characters in 35 diverse genotypes including three checks of barnyard millet. Highest PCV and GCV were not observed for any of the characters. While moderate phenotypic coefficient of variation were observed for flag leaf area (18.82%) followed by number of fingers per ear (16.74%), 1000 seed weight (15.74%), biological yield per plant (15.43%) and peduncle length (15.40%) indicating that these characters are more suited for direct selection procedure.

Ashok *et al.* (2018) evaluated 13 elite entries of finger millet for seven quantitative traits to assess the magnitude of genetic variability for yield and yield attributing traits. PCV estimate was slightly higher than the GCV for all the traits,

indicating low environmental influence on the expression of all the traits.The genetic parameters revealed moderate GCV and PCV for days to 50% flowering, plant height and main ear length indicating that these traits selection will be rewarding for genetic improvement.

Devaliya *et al.* (2018) evalvated 68 diverse genotypes of finger millet for 13 quantitative traits to assess the magnitude of genetic variability for yield and yield contributing traits. High PCV and GCV were recorded for grain yield per plant, indicating that this character is more variable in the genotype hence there is a great scope for improvement of this character by direct selection among the genitypes.

Geetha *et al.* (2018) studied genetic variability of 12 quantitative traits in 64 elite genotypes of little millet. PCV was higher than the corresponding GCV for all the characters studied. High values for phenotypic and genotypic coefficients were recorded for plant height, number of tillers per plant, flag leaf length, flag leaf width, panicle length, thousand seed weight and grain yield per plant, implying that these traits may be selected for genetic improvement.

Kumar *et al.* (2018) studied genetic variability in 32 little millet genotypes for 16 traits. Estimates of PCV and GCV were high for number of productive tillers per plant, grain yield and straw yield per plant, implying that these traits selection will contribute to genetic improvement in breeding programmes.

Sharma *et al.* (2018) assessed 34 pearl millet germplasm for genetic variability of 10 traits. High etimates of PCV and GCV were recorded for number of effective tillers / plant, grain yield, seed size and ear length indicating significant role of these charecters in improvement of breeding programme.

Singh *et al.* (2018) investigated genetic variability among 50 advance inbred lines of pearl millet for 15 growth traits, yield components, grain yield and reported wide range for all the genetic variability parameters of the traits. A higher PCV for various characters than its corresponding GCV suggested the role of considerable component of environment in the expression of all these characters.

Subbulakshmi *et al.* (2018) analysed the genetic variability of 54 pearl millet hybrids for 13 traits and reported that PCV was greater than GCV for all the charecters studied indicating little influence of environment. High PCV and GCV was obtained for

plant height, single plant yield, single head grain weight, crude fibre, beta carotene content, iron and zinc, indicating that selection for these traits will lead to genetic improvement.

Ayesha *et al.* (2019a) assessed the nature and magnitude of genetic variability for yield and quality related traits in 50 genotypes of foxtail millet germplasm collections. Studies on coefficent of variation inferred that the estimates of GCV were lesser than the corresponding PCV estimates for all the traits indicating the influence of environment on expression of the traits. High PCV and GCV was noted for no. of productive tillers per plant, fat, iron, phosphorus, calcium and grain yield per plant, implying that selection for these traits will contribute to genetic improvement.

### 2.1.2 Heritability (broad sense) and Genetic advance as per cent of mean:

The broad sense heritability is the ratio of genotypic variance to the total variance in non-segregating population. Heritability ($h^2$) measures the relative amount of heritable portion of the variability, while genetic advance (GA) indicates the amount of progress that can be expected with selection for a character. The estimation of heritability along with the genetic advance was reported to be more useful instead of relying upon heritability alone. Hence, high heritability coupled with high genetic advance was reported to be very much useful in practicing selection in a population. Panse (1957) reported that, low genetic advance irrespective of high (or) low heritability is due to non-additive gene action and improvement of that trait by simple selection may not be rewarding.

Reddy *et al.* (2012) studied 18 elite entries of finger millet and identified that high heritability and high genetic advance was recorded for ear head yield, ear head length and number of fingers per head indicating that these characters were controlled by additive gene effects.

Prasanna *et al.* (2013c) studied 34 exotic genotypes of italian millet for 13 characters to find out the extent of heritability and genetic advance as percent of mean. High heritability coupled with high genetic advance as percent of mean recorded for all characters except days to 50% flowering, days to maturity and plant height during both seasons reveals operation of additive gene action in the inheritance of these traits and improvement in these characters is possible through simple selection.

Brunda *et al.* (2014) evaluated 78 foxtail millet germplasm and observed that high genetic advance as per cent of mean was reported for traits like days to flowering, number of productive tillers, panicle length, test weight, grain yield and straw yield per plant indicating that, the variations are attributable to high level of heritable variation and selection would be effective for improvement of these traits.

Shinde *et al.* (2014) studied 41 finger millet genotypes and found that high heritability accompanied by high genetic advance as per cent of mean recorded for productive tillers per plant, seed yield per plant and iron content indicating that these characters were governed by additive gene effects. Hence, selection for these traits would be more effective.

Johar (2015) studied in 34 exotic foxtail millet genotypes and estimated that high heritability and genetic advance, an indicator of additive gene action was noted in all the characters except for days to 50% flowering, days to maturity and plant height reveals the operation of additive gene action in the inheritance of these traits and improvement in these characters is possible through simple selection.

Das *et al*. (2016) evaluated 48 finger millet germplasm lines and noticed that high heritability along with high genetic advance as percent (%) of mean was registered for main ear length, grain yield per plant, finger length, total number of finger on the main ear, number of productive tillers per plant, number of basal tillers per plant indicating that these traits were controlled by additive gene effects and selection for them would be rewarding.

Jyothsna *et al*. (2016 b) investigated 24 barnyard millet genotypes in which high heritability accompanied with genetic advance was noticed for grain yield per plot indicating the importance of additive gene action in governing the inheritance of these traits and improvement in these characters is possible through simple selection.

Jyothsna *et al*. (2016c) assessed 23 foxtail millet genotypes and observed that high heritability coupled with high genetic advance for number of productive tillers and grain yield per plot indicating the importance of additive gene action in governing the inheritance of these traits and improvement in these characters is possible through simple selection.

Nandini *et al.* (2016) studied 542 $F_3$ progeny lines of little millet for seven characters to find out the extent of heritability (broad sense) and genetic advance. High heritability was observed for plant height and 1000 seed weight. Number of productive tillers per plant showed maximum genetic advance as per cent of mean followed by grain yield per plant, panicle length and plant height. High heritability coupled with moderate genetic advance as per cent of mean were observed for plant height and 1000 seed weight.

Banu *et al*. (2017) studied 223 foxtail millet germplasm accessions and noticed that high heritability coupled with high genetic advance for number of basal tillers and flag leaf blade width, whereas grain yield per plant exhibited moderate heritability with genetic advance indicating the possibility of improvement for these trait by simple selection.

Kavya *et al*. (2017a) assessed 40 genotypes of foxtail millet and revealed that high heritability coupled with high genetic advance as percent of mean was observed for number of basal tillers, number of culm branches, panicle exertion, ear length, ear width, 1000 seed weight, seed yield / plant, straw yield / plant and protein content indicating that these traits were predominantly under the control of additive gene action and hence these characters can be improved by selection.

Mahanthesha *et al*. (2017a) investigated 48 finger millet germplasm lines and noticed that 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, finger length, grain yield per plant and grain yield per plot indicating that these traits predominantly under the control of additive gene action can be improved by selection.

Nirubana *et al.* (2017) assessed 103 kodo millet germplasm accessions and observed high heritability coupled with high genetic advance as per cent of mean was observed for plant height, number of basal tillers, number of productive tillers, flag leaf width, inflorescence length, thumb length, Zn content, Fe content and grain yield per plant indicating that these traits were under the influence of additive gene effects and selection may be effective for these characters.

Ramya *et al*. (2017a) studied 182 restorer (R-) lines of pearl millet and noticed high estimates of heritability along with genetic advance (% mean) were observed for

plant height, ear length, ear diameter, productive tillers per plant and 1000 grain weight indicating that the selection for these traits would be more effective.

Talawar *et al.* (2017) evaluated 52 germplasm lines of pearl millet for eight quantitative characters to asess the heritability and genetic advance. High Heritability estimates coupled with maximum genetic advance over mean were obtained for the characters like productive tillers per plant, grain yield per plant, seed weight, seed yield per ear head and panicle length indicating that selection for those traits will be rewarding due to additive gene effects.

Amarnath *et al.* **(**2018a) studied on 50 Indian foxtail millet genetic resources to estimate the extent of heritability (broad sense) and genetic advance as per cent of mean for 12 metric traits. High heritability (>60%) coupled with high genetic advance as per cent of mean was registered for culm branches, number of productive tillers / plant and grain yield / plant indicating that these characters were governed by additive gene effects and may be chosen as selection criteria for formulating breeding strategies in foxtail millet.

Anusha *et al.* (2018) estimated genetic heritability and genetic advance in 22 pearl millet genotypes for 12 characters. High heritability coupled with high genetic advance as per cent of mean recorded by the traits, green fodder yield/plant and dry matter yield/plant indicating the preponderance of additive gene action and hence phenotypic selection would be more effective for these traits.

Arya *et al.* (2018) evaluated 35 diverse genotypes including three checks of barnyard millet to estimate heritability and genetic advance as per cent of mean for 14 characters. High estimates of heritability and genetic advance as per cent of mean was recorded by finger length while moderate estimates was noted for flag leaf area and biological yield per plant. Therefore, direct selection for different characters would be effective as heritability and genetic advance might be due to additive gene interaction.

Ashok *et al.* (2018) analysed 13 elite genotypes of finger millet for seven traits to assess the magnitude of heritability and genetic advance for yield and its components. High broad sense heritability coupled with high genetic advance as percent of mean were observed for days to 50% flowering, plant height and main ear length implying the inheritance of these traits is under additive gene action and therefore, simple selection facilitates improvement of these characters.

Devaliya *et al.* (2018) assessed the magnitude of heritability and genetic advance in 68 diverse finger millet genotypes for 13 quantitative traits. High heritability along with high genetic advance (% of mean) was recorded for 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 be more effective.

Geetha *et al.* (2018) estimated heritability and genetic advance for nine quantitative traits in 64 diverse germplasm accessions of little millet. High heritability coupled with high genetic advance were recorded for all the characters indicating that these characters were governed by additive genes and selection would be effective for improvement of such characters.

Kumar *et al.* (2018) evaluated 32 genotypes of little millet to estimate heritability and genetic advance for 16 characters. High heritability coupled with high genetic advance was observed for number of productive tillers per plant, grain yield per plant, straw yield per plant, 1000 seed weight, protein content, ash content, fat content, calcium content, iron content and fiber content indicating that these characters were predominantly governed by additive genes and selection for improvement of such characters could be rewarding.

Sharma *et al.* (2018) assessed 34 germplasm of pearl millet for heritability and genetic advance in 10 characters. High heritability with high genetic advance as per cent of mean for ear girth, protein content and seed density suggested the prevalence of additive gene action in their inheritance specifying that selection for these traits will be effective.

Singh *et al.* (2018) investigated heritabaility and genetic advance in 50 advanced inbred lines of pearl millet for 15 growth traits, yield components and grain yield. It was noted that all the characters *i.e.* number of tillers per plant, plant height, panicle length, panicle diameter, number of leaves per plant, test weight, days to 50% flowering, and grain yield showed high heritability with high genetic advance that indicated the predominance of additive type of gene action for these characters.

Subbulakshmi *et al.* (2018) studied heritability and genetic advance in 54 pearl millet hybrids for 13 yield and nutritional traits. High estimate of heritability wa noted for all the characters except for number of productive tillers per plant and ear head girth,

where it is moderate. High heritability in conjunction with genetic advance was observed for most of the characters indicating that these are operative under additive gene action and selection for these characters will be rewarding.

Ayesha *et al.* (2019a) investigated heritability and genetic advance for 13 grain yield and quality components in 50 genotypes of foxtail millet germplasm collections. The traits *viz.* days to 50% flowering, plant height, panicle length, protein, fat, iron, phosphorus and calcium exhibited high genetic advance as per cent of mean coupled with high estimates of heritability indicating preponderance of additive gene action in governing the inheritance of these traits and hence, direct phenotypic selection may be deployed for improvement of these traits.

## 2.2 Genetic divergence:

Genetic diversity is the variation of heritable characteristics in a population. It results from one or more of the following; evolution, mutation, migration, domestication, plant breeding and selection. Knowledge about genetic diversity and relationships among plants may be an invaluable aid in plant breeding and classification.

The plant breeder's choice of source germplasm determines the potential improvement for traits under selection in a breeding programme as it will provide greater chances of obtaining the desirable gene combinations. The success of any breeding method depends on the availability of genetic diversity in the base population. Utilisation of diverse parents in hybridisation programmes has been observed to yield better hybrids.

Three important points are to be considered while selecting genotypes for hybridization purpose.

1. Choice of the particular cluster from which genotypes are to be used as parents.

2. Selection of particular genotypes from selected cluster.

3. Relative contribution of characters towards total divergence.

To identify the parents that nick better, several methods of divergence analysis based on quantitative characters have been proposed to suit various objectives.

## 2.2.1 Mahalanobis $D^2$ Analysis:

Anantharaju and Meenakshiganesan (2008) categorised the 50 genotypes of finger millet into 14 clusters through $D^2$ analysis for 10 quantitative traits. Higher intra cluster distance was recorded for cluster I (17.01) followed by III (16.52). The inter cluster distance ranged from 12.62 (between cluster VII and X) to 79.21 (between XI and XIII). Among the characters, days to 50% flowering followed by number of leaves contributed more towards the total divergence.

Karad and Patil (2013) analysed 65 finger millet accessions for 12 morphological characteristics using Mahalanobis $D^2$ statistic and grouped them into five clusters. Genotypes falling between cluster III and IV exhibited maximum inter-cluster distances followed by cluster I and cluster IV and cluster III and cluster V suggesting wider diversity between genotypes based on clustering pattern. The minimum inter-cluster distance was found in cluster III, followed by cluster I. The maximum intra cluster distance was observed for the genotype falling in cluster II. This implies that these clusters have the genotypes with varied genetic architecture. The clusters IV and cluster V showed zero intra cluster distance due to monogenotypic nature.

Shinde *et al.* (2013) estimated genetic distance using $D^2$ statistic in 41 finger millet genotypes for 12 characters and grouped the genotypes into seven clusters. The highest inter-cluster distance was observed between clusters II and VII followed by IV and VII suggesting the use of genotypes from these clusters to serve as potential parents for hybridization programme. The characters iron content contributed maximum towards divergence followed by plant height, days to physiological maturity and days to 50% flowering.

Anuradha *et al*. (2014) assessed 21 barnyard millet germplasm lines for genetic divergence through Mahalanobis $D^2$ statistic and grouped them into four clusters. The inter cluster $D^2$ values were maximum between cluster I and IV followed by cluster IV and III while for intra cluster $D^2$ values, cluster II registered maximum followed by cluster I. The widest inter cluster distance between cluster I and IV gives scope for hybridization programme with improvement of genotypes.

Suryanarayana *et al.* (2014) reported six clusters for 35 finger millet genotypes through Mahalanobis $D^2$ statistic. The maximum $D^2$ values registered for inter-cluster

was between cluster II and V while it was in cluster III for intra cluster. The trait plant height contributed maximum towards total diversity followed by seed yield per plant, main ear length, number of fingers per ear, productive tillers per plant and days to 50% flowering.

Brunda *et al.* (2015b) investigated genetic diversity in 78 foxtail millet genotypes through Mahalonobis $D^2$ statistic and classified them into seven clusters. The inter-cluster $D^2$ value was maximum between cluster IV and VII suggesting the presence of wider diversity between these clusters and genotypes from them may be selected for hybridization programme to obtain desired recombinants. The highest intra-cluster distance was recorded for cluster III. The traits days to 50% flowering contributed maximum towards genetic divergence followed by test weight and grain weight.

Kumari and Singh (2015) grouped 35 finger millet genotypes into six clusters using Tocher's method. The highest intra-cluster distance was observed in cluster IV followed by cluster II and cluster I indicating differences in genotypes within cluster. The genotypes in cluster IV and cluster VI due to maximum inter-cluster distance between them, exhibited high degree of genetic diversity and thus may be utilized under inter-varietal hybridization programme for getting high yield recombinants. The maximum contribution in the manifestation of genetic divergence was exhibited by days to 50% flowering followed by days to maturity and grain yield per plant suggesting scope for improvement in these characters.

Yogeesh *et al.* (2015) grouped 52 germplasm accessions of foxtail millet into three clusters based on Ward's analysis. Cluster III was the largest one comprising of 20 genotypes followed by cluster I with 17 genotypes and cluster II with 15 genotypes. Among the five characters studied, the seed yield showed greater diversity as compared to days to 50% flowering, plant height and length of inflorescence.

Gangurde *et al.* (2016) conducted divergence studies in 66 foxtail millet genotypes through $D^2$ statistics and grouped them into five distinct non-overlapping clusters. Inter- cluster distance was observed to be maximum between cluster III and IV followed by cluster IV and V. The highest intra-cluster distance was found in cluster II followed by clusters II and I. The traits grain iron content (ppm) followed by flag leaf length (cm), grain zinc content (ppm), straw weight, flag leaf area, plant height(cm),

flag leaf width, panicle weight (g) and grain yield contributed highest in the manifestation of genetic divergence.

Sao *et al.* (2016) carried out genetic divergence analysis through Mahalonobis $D^2$ statistic in 27 kodo millet advanced breeding lines and grouped them into four clusters. The inter cluster distance was maximum between cluster II and IV while for intra cluster distance, cluster II recorded the highest. The traits days to maturity followed by days to 50% flowering showed maximum contribution towards genetic divergence.

Singh *et al*. (2016) evaluated 34 foxtail millet genotypes to assess morphological diversity for 12 quantitative traits using Mahalonobis $D^2$ statistic and grouped the genotypes into six clusters. The genotypes in cluster IV and cluster VI due to maximum inter cluster distance between them, exhibited high degree of genetic diversity and thus may be utilized under inter varietal hybridization programme. The maximum contribution in the manifestation of genetic divergence was exhibited by inflorescence length followed by flag leaf blade length, basal tillers number and panicle exertion suggesting scope for improvement in these characters.

Bheemesh (2017) studied the genetic divergence of 60 foxtail millet genotypes for 19 characters. Based on the genetic distance ($D^2$ value), the 60 accessions were grouped into 13 clusters. Of them, cluster I with 36 genotypes forms the largest followed by cluster IV and II with eight and five in each. The character relative injury at 30 DAS contributed the maximum to the divergence. Based on the average inter-cluster distance (D), the clusters XII and XII followed by clusters VIII and XIII were found to be highly divergent from the other clusters. Selection of parents from these clusters and using them in a breeding programme is advocated to develop divergence lines.

Devaliya *et al.* (2017) studied genetic divergence in 68 finger millet genotypes for 13 quantitative traits using Mahalanobis $D^2$ statistic and classified them into eight clusters. The maximum inter-cluster distance was observed between cluster VIII and cluster III followed by cluster VII and IV indicating that the genotypes belonging to the distinct cluster (VIII and III) could be used in hybridization programme for obtaining a wide spectrum of variation among the segregants. At the intra cluster level cluster VIII had the highest value. The character iron content contributed maximum towards genetic divergence followed by main earhead length, harvest index, test weight and number of

productive tillers per plant while calcium content , days to maturity, grain yield per plant and straw yield per plant contributed very low towards divergence.

Kavya *et al.* (2017b) investigated on 40 genotypes of Italian millet for 15 characters to find out divergence analysis using Mahalanobis $D^2$ statistic. The diversity was noticed in 40 germplasm accessions which diverged into five clusters. The maximum inter-cluster distance occurred between cluster II and III. Among the characters studied protein content, carbohydrate content, days to 50% flowering, seed yield/plant contributed maximum towards divergence.

Mahanthesha *et al.* (2017b) studied 48 genotypes of finger millet for 11 characters to find out genetic divergence. The 48 germplasm lines grouped into eight clusters. The most important trait contributing to the divergence was grain yield per plant followed by main ear width, total no. of basal tillers per plant, total no. of fingers on the main ear and finger width. Usefulness of parents has been identified based on genetic divergence for improving finger millet. Higher yielding clusters were VI, II and IV.

Suryanarayana and Sekhar (2018) carried out Mahalanobis $D^2$ statistics to estimate the genetic divergence of 23 little millet genotypes for five quantitative traits. All the genotypes were grouped into six clusters. Maximum number of genotypes (8) were included in cluster VI followed by cluster-I (7), cluster-II, III, IV and V with two genotype in each cluster. Considering the inter cluster distances, it was highest between cluster IV and V (163.09) followed by V and VI (145.69). Among the five characters studied, grain yield (q/ha), days to 50% flowering and plant height (cm) contributed maximum towards the total divergence and were found to be responsible for primary differentiation.

Thippeswamy *et al.* (2018) analysed the genetic diversity for yield and its components in 149 germplasm accessions of foxtail millet for 19 characters. Based on $D^2$ values, the genotypes were grouped into 15 clusters. Maximum intra cluster distance among the genotypes was recorded by cluster I having 134 genotypes followed by cluster VIII with two genotypes. The maximum inter cluster distance was found between clusters IX and XIV followed by cluster VI and XIV. The maximum contribution towards divergence was recorded by number of tillers per meter row length and 1000 seed weight.

Amarnath *et al.* (2019) assessed the magnitude of genetic diversity through Mahalanobis $D^2$ Statistic in 50 indian italian millet genetic resources for 12 quantitative traits. Based on Tocher's method, the entire genetic resources were partitioned into nine distinct non-overlapping clusters. Cluster I was the largest comprising of large number of accessions (36) followed by cluster II with (7) accessions. Clusters II and IX showed maximum inter-cluster distance between them implying these genetic resources with high degree of genetic diversity may be utilized in inter-varietal hybridization programme. The traits, culm branches followed by 1000 grain weight contributed maximum towards total divergence indicating feasibility of improvement through those characters.

Ayesha and Babu (2019b) performed genetic divergence studies in 50 genotypes of foxtail millet through Mahalanobis' $D^2$ statistics (Tocher's method) and Wards' minimum variance method. Both $D^2$ analysis and Ward's method grouped the 50 foxtail millet genotypes into eight clusters each. In $D^2$ analysis, cluster III is the largest with 13 genotypes followed by cluster II, IV, I, VI, V, VII and VIII. Whereas in Ward's method, the cluster VI is the largest with 14 genotypes followed by, cluster VII, I, II, IV, V, III and VIII. There was no solitary cluster in Ward's minimum variance method, where as in Tocher's method, three clusters *viz.* cluster V, VII and VIII are solitary clusters. Further, it was reported that in both the methods studied, there was a wider genetic diversity.

### 2.2.2 Canonical root analysis:

Canonical (vector) root analysis or Principal component analysis (PCA) is a sort of multivariate analysis where canonical vectors or roots representing different axes of differentiation and amount of variation accounted for by each of such axes, respectively, are derived (Rao, 1952). It provides information on the independent impact of a particular trait to the total variance, wherein each coefficient of eigen vectors indicates the degree of contribution of every original variable, with which each principal component is associated. Principal component scores for genotypes were used as an input for clustering using Ward's minimum variance method. The tree like structure called dendrogram, constructed based on Euclidean$^2$ distance computed from PCA scores of genotypes gives the information about the clusters. Thus, PCA analysis is used to confirm the diversity pattern brought about by cluster analysis.

Reddy *et al.* (2009) carried out principal component analysis for 1993 East African finger millet germplasm accessions for 14 quantitative traits. The first three Principal components scored 95.1% (PC 1 - 52.8%, PC 2 28.9% and the PC 3 - 13.45 %) variation. The traits viz. basal tillers per plant, flag leaf sheath length, inflorescence length and width, longest finger length and width and panicles per plant reflects the maximum variation in PC1.

Salini *et al.* (2010) evaluated 364 proso millet germplasm entries through PCA for seven quantitative traits and noticed that first five eigen vectors contributed about 93.2 per cent of total variance. The analysis revealed that the traits panicle length, days to 50 % flowering, grain yield per plant, plant height, total number of tillers and hundred grain weight might be used to distinguish the germplasm entries.

Lule *et al.* (2012) performed principal component analysis in 144 finger millet landraces for 17 quantitative traits. Based on the mean of the first two principal components of the three eigen vectors (population level, country/regional and altitudinal level), grain yield per plant, thousand grain weight, days to heading, days to maturity, lodging index and biomass weight per plant were the most important traits contributing for the overall variability - observed among landraces, geographical locations and agro-ecologies. This is an important backup for breeder to investigate for high yielding (both in food and feed aspect), agro-ecology and climate condition (rainfall) based maturity groups and lodging resistant varieties through conventional breeding.

Jadhav *et al.* (2014) carried out principal component analysis in 40 finger millet genotypes for 11 characters and revealed that, the first three principal components with eigen values more than one contributed 76.41 per cent towards the total variability. The significant factors loaded in PC1 *viz.* number of productive tillers per plant, ear weight per plant, days to maturity, days to 50% flowering, number of fingers per ear, plant height, 1000-seed weight, seed yield per plant and finger length contributed maximum towards divergence.

Bendi *et al.* (2015) assessed 55 finger millet genotypes for 14 quantitative characters through principal component analysis and identified five principal components with eigen values more than one contributing to 83.69 per cent of cumulative variance. The PC1, PC2 and PC3 accounted for 46.19%, 13.38% and 10.22% respectively towards the total variability.

Kumar *et al.* (2015) studied principal component analysis of 24 genotypes of rice for nine characters. The analysis revealed that first three principal components explained 83 % of variability existing in the rice genotypes for yield contributing characters and importance of all the reproductive traits in selections for developing new rice cultures.

Reddy *et al.* (2015) studied 24 foxtail millet genotypes for seven quantitative traits through principal component analysis. Among the seven principal components obtained for total variability, PC1 and PC2 contributed 61.90% and 16.15% variation respectively. Characters with largest absolute value closer to unity *viz.* days to maturity, plant height, panicle length, number of tillers/plant, and fodder yield within the PC1 component and grain yield in PC2 influences more clustering.

Selvi *et al.* (2015) evaluated 110 little millet genotypes for 12 quantitative traits through principal component analysis. Among the 12 PCs, first four PCs *viz.* PC1, PC2, PC3 and PC4 had eigen values more than one accounting for 31.84, 50.66, 60.74 and 69.30 per cent of cumulative variation. These PCs contributed the maximum variability by more number of characters to aid selection and which in turn be effectively used for further breeding programmes.

Ulaganathan and Nirmalakumari (2015) carried out principal component analysis in 305 finger millet genotypes for 13 quantitative traits. The results revealed that the first four components with eigen value of greater than 0.65 contributed about 87.8% of total variability. The proportions of the total variance attributable to the first 4 principal components were 66.7, 10.7, 5.5 and 5.0 % respectively. The traits *viz.* grain yield per plant, 1000-grain weight, productive tillers per plant, days to flowering, days to maturity, finger number per panicle, finger length and finger width contributed for overall variability.

Dasanayaka (2016) performed principal component analysis in 24 finger millet germplasm accessions for 13 quantitative characters. Thirteen principal components were obtained. Among them, four PCs *viz.* PC1 (42.9%), PC2 (17.0%), PC3 (10.6%) and PC4 (8.3%) with eigen values greater than unity contributed about 78.8 % of total variability.

Geethanjali and Jegadeeswaran (2016) evaluated 51 foxtail millet accessions for nine morphometric traits through principal component analysis. The results revealed

that the first four PCA components contributed to a maximum of 69.55 per cent of the variability, the contributions from PC1, PC2, PC3 and PC4 being 30.15, 14.25, 13.85 and 11.4% respectively. The first two components were a measure of vegetative and inflorescence characters, while the third component was a measure of thousand seed weight.

Sapkota *et al.* (2016) conducted principal component analysis in ten foxtail millet accessions for 10 agro-morphological traits. The results revealed that the first two principal components with ≥ 1 eigen value accounted for 81.6% of the total variance. Individually, PC 1, PC 2 and PC 3 contributed 61.9, 19.7 and 9.4 % of total variation, respectively.

Patel *et al.* (2017) carried out principal component analysis in 65 finger millet germplasm accessions for eight quantitative traits. Among the eight principal components obtained, first five PCs *viz.* PC1 (42.81%), PC2 (18.43%), PC3 (11.80%), PC4 (9.36%) and PC5 (7.68%) accounted for 90.09 % of the entire variability. Further it can be inferred that the traits days to 50% flowering, days to maturity, plant height, grain yield and straw yield are important from breeding perspective to distinguish between accessions.

Ramya *et al*. (2017b) performed principal component analysis in 60 inbred lines of pearl millet for 11 quantitative traits. The PCA identified four principal component components (PCs) with Eigen value greater than unity which accounted for 70.97 per cent of total variation. The percentages of total variability accounted by each of the first four PCs were 26.85, 18.06, 15.61 and 10.45 per cent respectively. The highest loading displayable variables on four PCs were grain yield per plant, grain harvest index, 1000 grain weight and productive tillers per plant.

Through principal component analysis of 50 foxtail millet genetic resources for 12 metric traits, Amarnath *et al.* (2018c) reported that about 69.15 per cent of total variation accrued, exhibited four Principal components (PC1-29.65%, PC2-16.94%, PC3-12.27% and PC4- 10.27%) that is retained based on the scree plot and threshold Eigen value greater than one (>1). The PC1 with prime economical traits *viz.* days to 50% flowering, days to maturity, culm branches, thousand grain weight, number of productive tillers / plant and flag leaf blade length accounted for maximum variance (29.65%) connoting that these traits be given priority in future foxtail millet breeding programmes.

Ayesha and Babu (2018) analysed 50 foxtail millet genotypes through principal component analysis on were evaluated for understanding genetic diversity of 13 metric traits. The study revealed that first six principal components with eigen values more than one contributed 85.578 percent towards the total variability. PC1 contributed maximum towards the total variability, where characters *viz.* iron, phosphorus, fat and days to 50% flowering explained the maximum variance in this component.

Nandini *et al.* (2018) carried out principal component analysis in 1312 foxtail millet germplasm for 10 quantitative traits. It was noted that the first five principal components contributed about 72.87% of the total variability. The proportions of the total variance attributed to the first five principal components were 26.40, 17.47, 10.64, 9.91 and 8.44%, respectively. The characters days to 50% flowering, plant height, peduncle length, flag leaf length and flag leaf width were the most important traits contributing to the overall variability implying that these traits should be emphasized in foxtail millet improvement programme.

Singh *et al.* (2018) conducted principal component analysis in 40 pearl millet germplasm for 13 morphological traits. The analysis revealed that the first six components were with Eigen values more than one and contributed to a maximum of 78.29 per cent of the variability. In all the six components traits like number of productive tillers per plant, spike girth and single plant yield and in few cases traits like plant height, spike length and test weight contributed positively to the total variation. Hence these traits can be used for selection in pearl millet breeding programmes.

### 2.2.3 Heirarchical cluster analysis

Hierarchical analysis highlights the nature of relationship between and among type samples as outlined by standard descriptors. It produces an output called dendrogram, which depicts the hierarchical structure of genetic interaction in clusters/groups. It could serve as a basis for selection of parental types that could result to superior hybrids.

Li *et al.* (1996) analysed phenotypic diversity of 23381 foxtail millet landraces of Chinese origin for seven qualitative traits and four quantitative traits. Hierachical analysis of variance indicated that most of the variation was due to differences among characteristics. Only the diversity indices for leaf colour of seedlings, starch composition and 1000 grain weight showed significant differences among regions.

Subramanian and Subbaraman (2010) conducted sequential agglomerative hierarchical non-overlapping (SAHN) clustering analysis of genetic diversity analysis in 38 maize germplasm accessions based on 25 morphological traits The genotypes were classified into four clusters at a truncation level of 1.0 in the coefficient scale. Widely divergent clusters and genotypes were identified which could be further evaluated for their breeding value as parents that could be exploited in maize crop improvement.

Upadhyaya *et al.* (2011) evaluated 155 foxtail millet germplasm accessions together for 21 descriptors at five agro ecologically diverse locations. The hierarchical cluster analysis of data using phenotypic distances resulted in 25 clusters, from each cluster, nearly 10% or a minimum of one accession was selected to form a mini core, which comprised of 35 accessions.

Sathya *et al.* (2013) assessed the extent of genetic diversity in nine morpho-physiological traits of 47 pearl millet accessions through multivariate hierarchial cluster analysis resulting into eight clusters. The dissimilarity was highest between the inbreds TNBI 30 and TNBI 39 for yield and yield component traits implying that these are highly divergent and serve as potential parents in pearl millet hybridization programme for evolving superior varieties/hybrids.

Kiprotich *et al.* (2015) carried out multivariate cluster analysis using JMP statististical software in 60 pearl millet genotypes for seven biochemical parameters (starch, amylose, amylopectin, protein, K, Zn and P). Cluster analysis grouped the data into 6 clusters and a singleton with a genetic distance 0.37 – 8.73 showing enormous variability. Thus, these biochemical traits serve as handy tool for deternining nutritional diversity and greatly contributes in breeding programs, thereby enhancing food security.

Iqbal *et al.* (2018) studied genetic diversity of 205 sesame genotypes for eight agro-morphological characters through hierarchical cluster analysis. The results revealed that the inter cluster distance in most cases was larger indicating wider diversity among the germplasm of different groups. The maximum inter cluster distance was found between clusters V and III, followed by clusters V and II, clusters VI and II.

## 2.3 Correlation Analysis:

The knowledge on the extent of association between yield and its components is of paramount importance for a plant breeder to determine effective selection criteria. Studies on correlation explain the nature and degree of relationship between any two measurable characters. They also reveal the intrinsic relationship between yield and other component traits thereby assist the breeder in improving the selection efficiency to obtain improved yields. Phenotypic correlation reflects the observed relationship, while genotypic correlation underlines the true relationship among characters.

Ganapathy *et al.* (2011) analyzed seven characters in 230 finger millet germplasm accessions through correlation analysis. The results revealed that, Grain yield was positive and significant correlated with days to 50 per cent flowering, plant height, productive tillers per plant and finger numbers per ear.

Prasanna *et al.* (2013a) analyzed 13 characters in 18 Indian genotypes of Italian millet through correlation analysis. The study revealed that positive significant correlation of days to 50% flowering, plant height, number of productive tillers per plant, flag leaf area, ear length, ear weight, straw weight and protein content with grain yield per plant and improvement of seed yield may be possible if the above traits are considered in the selection programme.

Prasanna *et al.* (2013b) analyzed 13 characters in 34 exotic genotypes of Italian millet through correlation analysis. The analysis revealed that positive significant correlation of days to 50% flowering, plant height, days to maturity, number of productive tillers per plant, ear length, ear weight and straw weight with yield per plant where as during rabi besides these characters flag leaf area and 1000 grain weight were also observed to influence yield.

Shinde *et al*. (2014) carried out correlation analysis in 41 finger millet genotypes for 12 characters and observed that grain yield per plant was positively and significantly correlated with productive tillers per plant, plant height, finger length and number of fingers/main ear head both at genotypic and phenotypic levels. These traits could be considered for grain yield selection.

Ulaganathan and Nirmalakumari (2014) studied on correlation analysis in 305 finger millet genotypes for 13 quantitative traits and noticed that phenotypic correlation

between grain yield per plant was highly significant and positively associated with days to flowering, productive tillers per plant, plant height, 1000-grain weight, flag leaf sheath length, days to maturity, flag leaf blade length and finger width. These traits could be considered for grain yield selection.

Bastola *et al.* (2015) analyzed 50 finger millet landraces by correlation analysis. It was noted that grain yield per plant was positive and highly significant correlated with grain yield per ear followed by plant height, productive tillers number, days to maturity, days to heading, days to flowering, straw yield per plant, finger number per ear, thousand kernel weight, flag leaf sheath width and finger length. These traits could be considered for grain yield selection.

Brunda *et al.* (2015a) studied correlation analysis in 78 foxtail millet genotypes for 10 characters during rainy season and summer season in 2013 and 2014. The study indicated that direct selection based on the traits, days to maturity, plant height, number of tillers, panicle length, panicle weight, test weight and straw weight during rainy season where as in post-rainy season days to maturity, panicle length, panicle breadth, panicle weight and straw weight are effective as the association and direct effects were positive for these traits with grain yield.

Jadhav *et al*. (2015) performed correlation analysis in 40 finger millet genotypes for 11 quantitative characters and noted that the 1000-seed weight, number of fingers per ear, ear weight per plant, finger length, days to maturity, productive tillers per plant, days to 50% flowering and plant height possessed significant positive association with seed yield plant both at genotypic and phenotypic levels. These characters could be considered for grain yield selection.

Sasamala *et al*. (2015) conducted correlation analysis in 22 genotypes of little millet for 14 metric traits over 12 environments and inferred that grain yield exhibited high positive correlation with all the characters except panicle exertion and panicle number. These traits could be considered for grain yield selection.

Ashok *et al.* (2016) analyzed five characters in 13 foxtail millet genotypes through correlation analysis. The analysis revealed that plant height and number of tillers per plant showed significant positive correlation grain yield per plot at both phenotypic and genotypic levels.

Jyothsna *et al*. (2016b) worked on correlation studies in 24 barnyard millet genotypes for five quantitative characters and reported that the traits number of productive tillers per plant, days to 50% flowering, days to maturity were found to possess significant association in desirable direction with grain yield per plot at both genotypic and phenotypic levels. Hence, selecting these characters with high positive correlation would improve the grain yield.

Jyothsna *et al*. (2016c) carried out character association analysis in 23 foxtail millet genotypes for five quantitative characters. The traits plant height, number of productive tillers per plant, days to 50% flowering and days to maturity were found to possess significant association in desirable direction with grain yield per plant at both at phenotypic and genotypic levels. This suggests selecting for the characters with high positive correlation would improve the grain yield.

Nandini *et al*. (2016) carried out correlation analysis for seven quantitative traits in 542 $F_3$ progeny lines developed from cross JK 8 x Peddasame (Purple late) of little millet and noted that grain yield per plant possessed significant positive correlation with plant height, panicle length, number of productive tillers per plant and 1000 seed weight indicating that improvement in these characters will lead to improvement in yield.

Negi *et al*. (2016) carried out character association studies in 34 finger millet genotypes including three local checks for 18 characters and found that the characters like plant height, culm thickness, number of productive tillers per plants, number of leaves per plant, flag leaf area, seed diameter, number of grains per panicle, thousand grain weight showed highly significant positive correlation with grain yield per hectare at genotypic level. A positive and highly significantly value of genotypic correlation coefficient ensures the effectiveness of characters for selection procedure in order to maximize yield.

Sapkota *et al.* (2016) performed correlation analysis in 10 foxtail millet accessions for 15 characters. The results revealed that grain yield was positively influenced by the traits like peduncle exertion, panicle length, peduncle length, flag leaf length, stay green period, five panicle weight and number of panicle per square meter. Hence, selecting these characters with high positive correlation would improve the grain yield.

Shingane *et al.* (2017) analyzed 44 foxtail millet genotypes through correlation analysis. The analysis revealed that grain yield plant was highly significant and positively correlated with number of productive tillers plant, panicle length, number of panicles plant, 1000-grain weight, straw yield plant and protein content. The selection in positive direction for these traits with grain yield plant can be practiced for genetic enhancement of grain yield.

Arya *et al.* (2017) performed correlation analysis in 35 diverse barnyard millet genotypes including three checks for 13 quantitative traits and found that biological yield per plant, number of fingers per ear, number of leaves on main tiller and 1000 seed weight exerted a very strong positive association towards grain yield per plant at phenotypic and genotypic levels. This suggests selecting for the characters with high positive correlation would improve the grain yield.

Kavya *et al.* (2017c) investigated on 40 elite genotypes of Italian millet for 15 characters to measure correlation. Among the yield attributing traits, seed yield/plant recorded a significant positive correlation with number of basal tillers, ear length, 1000 seed weight and straw yield/plant.

Kumari *et al.* (2017) conducted character association studies in 139 finger millet accessions for 14 quantitative characters and reported that the grain yield was positive and significantly correlated with number of productive tillers, weight of 20 mature ears, threshing ratio and panicle exertion. Hence, selecting these characters with high positive correlation would improve the grain yield.

Talawar *et al*. (2017) performed correlation analysis in 52 germplasm lines of pearl millet for eight quantitative characters and noted that the trait panicle length alone exhibited positive significant correlation with grain yield per ear head at genotypic and phenotypic levels thereby, indicating its contribution towards expression of grain yield. Therefore, selection for the trait panicle length would be more desirable for improvement of grain yield in pearl millet.

Amarnath *et al.* (2018b) studied character association in 50 foxtail millet genetic resources for 12 quantitative characters. The study revealed positively significant association of grain yield / plant with majority of traits *viz.* plant height, peduncle length, panicle length, flag leaf blade length, flag leaf blade width and 1000 grain weight at both phenotypic and genotypic levels implying that these traits are

predominantly governed by additive gene action and hence direct selection for these traits will lead to simultaneous improvement in grain yield.

Anusha *et al.* (2018) carried out correlation analysis in 22 pearl millet genotypes for 12 charecters. The traits *viz.* plant height, leaf breadth and dry matter yield per plant showed positively significant correlation with green fodder yield/plant. Therefore, selection for these traits may aid in the enhancement of the green fodder yield.

Anuradha *et al.* (2018) analyzed 13 characters in 130 pearl millet lines through correlation analysis. The analysis indicates that grain yield showed significant positive correlation (phenotypic) with Fe, Zn, Cu and Mn content but, genotypically the grain yield was correlated with Fe content only indicating the role of environment for association of Zn, Cu and Mn content with grain yield.

Dhami *et al.* (2018) analysed correlation in 16 finger millet genotypes for nine metric traits. The grain yield had positive significant correlation with plant height followed by plant stand per square meter, bearing head per square meter, number of finger per head and straw yield with minimum lodging percentage were most yield determinative traits. Therefore simultaneous selection for these traits might bring an improvement in finger millet grain yield.

Gohel and Chaudhari (2018) carried out correlation studies for 15 traits in 30 finger millet genotypes. A very strong positive association of grain yield per plant at phenotypic and genotypic level was observed with number of productive tillers per plant, grain weight per main ear, biological yield per plant and harvest index with grain yield. Therefore preference may be given for these traits to improve grain yield.

Mahanthesha *et al.* (2018) carried out correlation analysis for 11 traits in 48 finger millet genotypes and reported that grain yield per plant 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. These characters can be considered as criteria toward selection for higher yield, as these are mutually and directly associated with grain yield.

Singh *et al.* (2018) analyzed 50 advanced inbred lines of pearl millet for 15 growth traits, yield components, and grain yield through correlation analysis. It was noted that the traits *viz.* stem thickness, plant height, panicle length, grain yield per

panicle and panicles per plant were positively associated with grain yield and dry fodder yield. Hence selection for these traits would result into grain yield improvement.

Sharma *et al.* (2018) performed correlation analysis in 34 germplasm of pearl millet for 10 component traits. The traits, number of effective tillers per plant, ear length, ear girth and seed density showed high positive association with grain yield per plant for which indirect selection can be made in future breeding programme to enhance grain yield.

Suman *et al.* (2018) studied the correlation for 15 quantitative traits in 55 finger millet genotypes. The results of the study revealed that the traits 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. Hence selection for these important yield components can be used to improve the yield potential of the genotypes.

Vishnuprabha and Vanniarajan (2018) carried out correlation analysis for five traits in 25 genotypes of barnyard millet comprising five parents and their 20 $F_1$ crosses. The result revealed that single plant yield exhibited significant positive correlation with total phenol content and iron content. Hence, selection for improvement of yield will lead to simultaneous improvement of these traits.

Ayesha *et al.* (2019c) analyzed correlation analysis in 50 genotypes of foxtail millet for 13 characters. The analysis revealed positive significant correlation of plant height, panicle length, number of productive tillers per plant, test weight and carbohydrate with grain yield per plant at phenotypic level.

Sapkal *et al.* (2019) performed correlation Analysis for 11 characters in 40 finger millet germplasm and reported that grain yield per plant was positively and significantly correlated with number of tillers per plant, number of productive tillers per plant, main earhead length, number of fingers per plant. Therefore, direct selection for these traits will lead to simultaneous improvement in grain yield.

## 2.4 Path coefficient analysis

Path analysis, advocated by Wright (1921) is a standardized partial regression coefficient that takes into account the cause and effect relationship between the

variables by partitioning the correlation coefficient into direct and indirect effects of independent variables on the dependent variable. It may also help to minimize the number of attributes for which simultaneous selection must be exercised. Though the direct effect of a character on yield may be found through the study of genetic correlation, the magnitude of direct effects of various characters on yield as well as their indirect effects via other component traits can be studied only through path coefficient analysis. Thus, it enables the breeders to assess the cause-effect relationship as well as assists in effective selection.

Ganapathy *et al.* (2011) analyzed seven characters in 230 finger millet germplasm accessions through path analysis. The analysis revealed that number of productive tillers per plant has direct effect and also important yield contributing character and need to be considered while framing selection criteria in finger millet breeding program.

Tyagi *et al*. (2011) performed path analysis in 57 foxtail millet accessions for nine characters and inferred that biological yield and harvest index had high positive 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 genotypes.

Prasanna *et al.* (2013a) analyzed 13 characters in 18 Indian genotypes of Italian millet through path analysis. The path analysis study in Indian genotypes indicated that direct selection based on the characters, number of productive tillers per plant and ear weight during kharif where as in rabi days to maturity and ear weight are effective as their association and direct effects were positive.

Prasanna *et al.* (2013b) analyzed 13 characters in 34 exotic genotypes of Italian millet through path analysis. The study of exotic genotypes indicated that direct selection based on the characters, number productive tillers per plant during kharif where as in rabi ear weight and straw weight are effective as the association and direct effects were positive for these traits.

Kumar *et al*. (2014) conducted path coefficient analysis in 140 genetically diverse genotypes of finger millet for 10 quantitative characters and inferred that positive genotypic and phenotypic direct effects for productive tillers/plant, biological yield, harvest index and number of fingers/ ear had higher positive direct effects on

grain yield. Hence, these traits possessing positive direct effect on grain yield may be used as a suitable selection criterion for evolving high yielding genotypes.

Brunda *et al.* (2015a) studied path analysis in 78 foxtail genotypes for 10 characters during rainy season and summer season in 2013 and 2014. The analysis revealed that direct selection based on the characters, panicle weight, test weight and straw weight showed high and positive effect on grain yield per plant in both rainy and summer season indicating the true relationship between these characters with grain yield per plant, which helps in direct selection for these traits thus in improving the grain yield per plant.

Jadhav *et al*. (2015) performed path analysis in 40 finger millet genotypes for 11 quantitative characters and showed that 1000-seed weight, number of fingers per ear, days to maturity, ear weight per plant, finger length and days to 50% flowering exhibited true relationship with seed yield per plant through positive and high direct effect.

Ashok *et al.* (2016) analyzed five characters in 13 foxtail millet genotypes through path analysis. The studies revealed that plant height, number of tillers per plant and days to 50% flowering showed true relationship by establishing positive association and positive direct effect on grain yield per plant both at genotypic and phenotypic levels.

Jyothsna *et al*. (2016a) carried out path analysis in 25 finger millet genotypes for eight quantitative characters. The results revealed 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 tillers per plant, days to 50% flowering and number of fingers per ear at genotypic level and days to maturity at phenotypic level.

Prakash and Vanniarajan (2015) studied path analysis in 65 genotypes of barnyard millet for 13 quantitative traits showed that single ear head weight had maximum direct effects on grain yield/plant followed by straw yield/plant, ear head length and plant height, may be used as a suitable selection criterion for evolving high yielding genotypes.

Eric *et al*. (2016) conducted path co-efficient analysis for 19 quantitative traits in 340 finger millet landraces collected from various places and 80 global minicore accessions from ICRISAT Gene bank in India. The results inferred that productive tillers per plant, 1000 grain mass, grains per spikelet and threshing per cent had positive, direct effects on grain yield. Hence, these traits could be used as a suitable selection criterion for evolving high yielding genotypes.

Jyothsna *et al*. (2016c) carried out path analysis in 23 foxtail millet genotypes for five characters and reported that the plant height, number of productive tillers per plant showed significant positive direct effect on grain yield per plant both at phenotypic and genotypic levels and days to maturity at phenotypic levels. These traits used as a suitable selection criterion for evolving high yielding genotypes.

Nandini *et al*. (2016) performed path analysis for nine characters in 542 $F_3$ progeny lines developed from cross JK 8 x Peddasame (purple late) of little millet. The findings showed that number of productive tillers per plant imparted direct effect on grain yield followed by panicle length, 1000 seed weight and plant height. Hence, these charecters used as a suitable selection criterion for evolving high yielding genotypes.

Negi *et al*. (2016) carried out path analysis in 34 finger millet genotypes for 17 quantitative characters and inferred that the characters like flag leaf area, number of productive tillers per plant, number of leaves per plant, thousand grain weight and number of grains per panicle showed high positive direct effect on yield. These traits used as a suitable selection criterion for evolving high yielding genotypes.

Shingane *et al.* (2017) analyzed 44 foxtail millet genotypes through path analysis. The analysis revealed that 1000-grain weight had the highest positive direct effects on grain yield plant. The indirect effect of number of panicles, panicle length, number of productive tillers and straw yield through 1000-grain weight was positive and moderate to high indicating the direct selection for 1000-grain weight in foxtail millet will lead to simultaneous indirect selection of these traits for increased grain yield plant.

Arya *et al.* (2017) carried out path analysis in 35 diverse genotypes of barnyard millet for 14 quantitative traits. The results revealed that maximum positive direct effect on grain yield per plant was imposed by biological yield per plant and harvest index at genotypic and phenotypic level. Hence, direct selection of these traits would be effective in enhancing the grain yield.

Kavya *et al.* (2017c) investigated on 40 genotypes of foxtail millet for 15 characters to measure path coefficients. The path analysis revealed that number of basal tillers, number of culm branches, ear length, ear width and straw yield/plant are the most important characters which could be used as selection criteria for effective improvement of grain yield. these characters can be used as most important traits which should be used as selection criteria to develop high yielding cultivars in Italian millet.

Renganathan *et al.* (2017) performed path analysis in 40 barnyard millet germplasm lines for 15 quantitative traits. The findings showed that plant height, flag leaf breadth, ear head breadth, number of raceme, single ear head weight, number of productive tillers, thousand grain weight, number of leaves/tiller, stem girth and zinc content had direct positive effect on grain yield. Hence, direct selection of these traits would be effective in enhancing the grain yield levels.

Talawar *et al*. (2017) conducted path analysis in 52 germplasm lines of pearl millet for eight quantitative characters. The results revealed that panicle girth contributed the highest positive direct effect on grain yield followed by plant height and panicle length. Therefore, these characters could be considered as main components for selection in a breeding programme for higher grain yield.

Amarnath *et al.* (2018b) performed path coefficient analysis in 50 foxtail millet genetic resources for 12 quantitative characters. The results showed that the traits, plant height and flag leaf blade length exhibited high positive direct effect on grain yield / plant suggesting the importance of direct selection for these traits in attaining higher grain yields.

Anusha *et al.* (2018) carried out path analysis of 22 diverse pearl millet genotypes for 12 metric traits. The trait dry matter yield per plant has registered high direct positive effect on green fodder yield, followed by number of tillers per plant. Therefore, these traits may be indicated to have a true correlation and could be taken as component trait for the improvement of fodder yield.

Gohel and Chaudhari (2018) investigated path coefficient analysis on 30 diverse genotypes of finger millet for 14 characters. The trait grain weight per main ear had highest direct positive effect towards the grain yield followed by number of productive tillers per plant, panicle length, days to flowering, harvest index, biological yield per plant and leaf blade length. The characters identified above merit due consideration in

formulating effective selection strategy in finger millet for developing high yielding varieties.

Mahanthesha *et al.* (2018) studied path analysis in 48 genotypes of finger millet for 11 metric traits. It was observed that maximum positive direct effect on grain yield per plant was exhibited by productive tillers per plant followed by finger length and finger width. Therefore, it is emphasized to lay attention on these traits while selecting for improvement in grain yield of finger millet.

Suman *et al.* (2018) performed path analysis in 55 elite finger millet germplasm for 14 charecters. The results revealed that harvest index had maximum positive direct contribution towards grain yield per plant followed by biomass yield per plant, ears per plant, days to 50% flowering, plant height, 1000-seed weight, fingers/plant, and flag leaf area at phenotypic level. Thus, selection for these traits may lead to an overall increase in grain yield per plant.

Vishnuprabha and Vanniarajan (2018) carried out path analysis in 25 genotypes comprising of five parents and their 20 $F_1$ crosses of barnyard millet for five characters. Total phenols and iron content recorded moderate positive direct effects on single plant yield while total anti-oxidant and zinc content showed negative direct effects on single plant yield. Hence, improvement of yield will simultaneously bring improvement on total phenols and iron content directly and on total anti-oxidant activity and zinc content indirectly.

Ayesha *et al.* (2019c) analyzed path analysis in 50 genotypes of foxtail millet for 13 characters. The analysis studies revealed that panicle length, number of productive tillers per plant, test weight and carbohydrate had true relationship with grain yield per plant by establishing significant positive association and positive direct effect at phenotypic level.

Sapkal *et al.* (2019) performed path Analysis for 11 characters in 40 germplasm of finger millet. At genotypic level, the characters days to 50% flowering followed by number of tillers per plant, main earhead length and number of fingers per earhead had highest direct effects on grain yield per plant while the trait number of productive tillers per plant alone registered maximum direct effect on grain yield per plant at phenotypic level. Therefore, direct selection of these characters would help in selecting the high yielding genotypes in finger millet.


# Chapter – III

# MATERIAL AND METHODS

## Chapter III

# MATERIAL AND METHODS

The experimental material, method of recording observations on various traits and the statistical methods employed in the conduct of study are presented in this chapter.

## 3.1 LOCATION

The present investigation on "Diversity in morpho-physiological and biochemical components in genetic resources of foxtail millet (*Setaria italica* (L.) Beauv.)" was carried out in black cotton soils during *Kharif*, 2018 at Regional Agricultural Research Station (RARS), ANGRAU, Nandyal, Andhra Pradesh located at 15°29' N latitude and 78°29' E longitude from an altitude of 211.76 m above mean sea level .

### 3.1.1 MATERIAL

The experimental material utilized for the present study comprised of 100 foxtail millet germplasm accessions obtained from various collections maintained at RARS, Nandyal. The details of the germplasm accessions are presented in Table 3.1.

## 3.2 METHODS

### 3.2.1 FIELD LAYOUT

The experimental techniques of the present investigation are detailed hereunder. The layout of the experiment is presented in the Fig. 3.1

Location : RARS, Nandyal

Season : *Kharif*, 2018

Design : Augmented Randomized Complete Block Design (ARCBD)

Entries : 100 (96 germplasm lines + 4 checks replicated eight times)

Spacing : 22.5 cm × 10 cm

Number of rows : 1 row / genotype

Row length : 3 m

Plot size : 40 x 3 $m^2$

Fertilizers : 40kgN: 30kg$P_2O_5$: 10kg $K_2O$/ ha

**Table 3.1 Details of 100 foxtail millet germplasm accessions utilized for study**

| S. No | Germplasm accession | Parentage |
|---|---|---|
| 1 | SiA 805 | Selection from Devarakonda village |
| 2 | SiA 1244 | Selection from Peddapadu village |
| 3 | SiA 1266 | Selection from Salkapuram village |
| 4 | SiA 2579 | Re-selection from SiA 1062/27 |
| 5 | SiA 2662 | Selection from Prasad x SiA 805 |
| 6 | SiA 2663 | Selection from Prasad x SiA 805 |
| 7 | SiA 2667 | Selection from 2566 x ISC 93 |
| 8 | SiA 2671 | Selection from Nandyal local |
| 9 | SiA 2674 | Selection from SiA 2579 |
| 10 | SiA 2681 | Selection from Prasad x ISC 131 |
| 11 | SiA 2697 | Selection from SiA 326 x ISC 163 |
| 12 | SiA 2713 | Selection from Gopavaram village |
| 13 | SiA 2737 | Selection from SiA 2566 x ISC 163 |
| 14 | SiA 2745 | Selection from TNAU 46 x ISC 163 |
| 15 | SiA 2757 | Selection from Chilakaladona village |
| 16 | SiA 2844 | Selection from Giddalur mandal |
| 17 | SiA 2849 | Selection from Giddalur mandal |
| 18 | SiA 2850 | Selection from Giddalur mandal |
| 19 | SiA 2856 | Selection from Giddalur mandal |
| 20 | SiA 2864 | Selection from Giddalur mandal |
| 21 | SiA 3038 | Selection from ISC 33AK |
| 22 | SiA 3281 | Selection from RFM 84A |
| 23 | SiA 3282 | Selection from RFM 84B |
| 24 | SiA 3291 | Selection from RFM 61 |
| 25 | SiA 3323 | Selection from ISC 1059 |
| 26 | SiA 3409 | Selection from ISC 1338 |
| 27 | SiA 3413 | Selection from ISC 1460 |
| 28 | SiA 3419 | Selection from ISC 1406 |
| 29 | SiA 3420 | Selection from ISC 1320 |
| 30 | SiA 3422 | Selection from ISC 1541 |
| 31 | SiA 3423 | Selection from ISC 1888 |
| 32 | SiA 3429 | Selection from ISC 1302 |
| 33 | SiA 3430 | Selection from ISC 1762 |
| 34 | SiA 3435 | Selection from ISC 1458 |
| 35 | SiA 3436 | Selection from ISC 1251 |
| 36 | SiA 3462 | Selection from ISC 1305 |
| 37 | SiA 3465 | Selection from Arjuna |
| 38 | SiA 3469 | Selection from RAU - 12 |
| 39 | SiA 3492 | Selection from 233-S-2 |
| 40 | SiA 3496 | Selection from PSRJ 13132-S-1 |
| 41 | SiA 3498 | Selection from Se 13698 |
| 42 | SiA 3499 | Selection from Se 13685 |
| 43 | SiA 3511 | Selection from GS 40 |
| 44 | SiA 3513 | Selection from GS 415 |
| 45 | SiA 3516 | Selection from GS 164 |
| 46 | SiA 3554 | Selection from GS 890 |
| 47 | SiA 3559 | Selection from GS 1043 |
| 48 | SiA 3560 | Selection from GS 1297 |
| 49 | SiA 3577 | Selection from GS 1570 |
| 50 | SiA 3580 | Selection from GS 1016 |

**Table 3.1 Contd…**

| S. No | Germplasm accession | Parentage |
|---|---|---|
| 51 | SiA 3588 | Selection from GS 764 |
| 52 | SiA 3611 | Selection from GS 1012 |
| 53 | SiA 3627 | Selection from GS 602 |
| 54 | SiA 3639 | Selection from GS 71 |
| 55 | SiA 3643 | Selection from ISC 38AK |
| 56 | SiA 3657 | Selection from ISC 1230 |
| 57 | SiA 3674 | Selection from ISC 410 |
| 58 | SiA 3697 | Selection from IC 436885 |
| 59 | SiA 3701 | Selection from IC 345123 |
| 60 | SiA 3737 | Selection from ISC 315 |
| 61 | SiA 3749 | Selection from GS 40 |
| 62 | SiA 3753 | Selection from GS 104 |
| 63 | SiA 3754 | Selection from GS 105 |
| 64 | SiA 3756 | Selection from GS 107 |
| 65 | SiA 3793 | Selection from GS 678 |
| 66 | SiA 3827 | Selection from GS 2184 |
| 67 | SiA 3851 | Selection from GS 35 |
| 68 | SiA 3855 | Selection from GS 56 |
| 69 | SiA 3894 | Selection from GS 403 |
| 70 | SiA 3908 | Selection from GS 576 |
| 71 | SiA 3965 | Selection from GS 1489 |
| 72 | SiA 3969 | Selection from GS 34 |
| 73 | SiA 3971 | Selection from GS 345 |
| 74 | SiA 3972 | Selection from GS 359 |
| 75 | SiA 4005 | Selection from GS 695 |
| 76 | SiA 4009 | Selection from GS 317 |
| 77 | SiA 4013 | Selection from GS 617 |
| 78 | SiA 4016 | Selection from GS 788 |
| 79 | SiA 4020 | Selection from GS 887 |
| 80 | SiA 4027 | Selection from GS 1460 |
| 81 | SiA 4044 | Selection from GS 2210 |
| 82 | SiA 4045 | Selection from GS 2248 |
| 83 | SiA 4061 | Selection from IC 426712 |
| 84 | SiA 4063 | Selection from NDL 1 |
| 85 | SiA 4068 | Selection from IC 308976 |
| 86 | SiA 4107 | Selection from PCGS 12 |
| 87 | SiA 4114 | Selection from PCGS 19 |
| 88 | SiA 4141 | Selection from PCGS 46 |
| 89 | SiA 4155 | Selection from SiA 3088 x Ic 308967 |
| 90 | SiA 4036 | Selection from GS 1956 |
| 91 | SiA 4167 | Selection from GS 1897 |
| 92 | SiA 4179 | Selection from TNAU 20 |
| 93 | SiA 4180 | Selection from TNAU 32 |
| 94 | SiA 4181 | Selection from TNAU 59 |
| 95 | SiA 4182 | Selection from TNAU 135 |
| 96 | SiA 3222 | Selection from SiA 3075 x SiA 326 |
| | **Checks** | |
| 97 | Prasad | Selection from Dronachalam village |
| 98 | Suryanandi | Pureline selection from SiA 1244 |
| 99 | SiA 3156 | Pureline selection from SiA 2871 |
| 100 | SiA 3085 | Selection from SiA 2644 from farmers field |


| Block:1 | Block:2 | Block:3 | Block:4 | Block:5 | Block:6 | Block:7 | Block:8 |
|---|---|---|---|---|---|---|---|
| SiA 3222 | Suryanandi (C) | SiA 3496 | SiA 805 | Prasad (C) | SiA 4013 | SiA 3156 (C) | SiA 3554 |
| SiA 3156 (C) | SiA 2849 | SiA 3580 | SiA 3156 (C) | Suryanandi (C) | Suryanandi (C) | SiA 3749 | SiA 3753 |
| SiA 3323 | SiA 3577 | SiA 3971 | SiA 3855 | SiA 2713 | Prasad (C) | SiA 4141 | SiA 2844 |
| Prasad (C) | SiA 3701 | SiA 3038 | SiA 3420 | SiA 3085 (C) | SiA 3754 | SiA 2667 | SiA 4180 |
| SiA 3657 | SiA 3559 | Prasad (C) | SiA 4167 | SiA 2757 | SiA 3413 | SiA 3422 | SiA 4005 |
| SiA 3085 (C) | SiA 3851 | SiA 3588 | SiA 2864 | SiA 2681 | SiA 3435 | SiA 3894 | SiA 2850 |
| SiA 2745 | SiA 4016 | SiA 3737 | Prasad (C) | SiA 3511 | SiA 4045 | Suryanandi (C) | SiA 3513 |
| SiA 2579 | SiA 4179 | SiA 3462 | SiA 3409 | SiA 3674 | SiA 3156 (C) | SiA 3282 | SiA 3469 |
| SiA 3627 | SiA 3498 | SiA 2671 | SiA 3085 (C) | SiA 3827 | SiA 3499 | SiA 3639 | Suryanandi (C) |
| SiA 4061 | SiA 4107 | SiA 3492 | SiA 4027 | SiA 3908 | SiA 3436 | SiA 3085 (C) | SiA 3281 |
| SiA 4036 | SiA 3156 (C) | SiA 3085 (C) | SiA 3423 | SiA 3697 | SiA 3560 | SiA 2856 | SiA 1266 |
| Suryanandi (C) | SiA 2674 | SiA 3429 | Suryanandi (C) | SiA 4009 | SiA 4114 | SiA 3291 | Prasad (C) |
| SiA 2662 | SiA 2697 | SiA 4063 | SiA 4181 | SiA 3965 | SiA 3085 (C) | SiA 3430 | SiA 3156 (C) |
| SiA 2737 | Prasad (C) | Suryanandi (C) | SiA 1244 | SiA 3156 (C) | SiA 3419 | Prasad (C) | SiA 4182 |
| SiA 3611 | SiA 3085 (C) | SiA 3793 | SiA 4044 | SiA 3972 | SiA 3465 | SiA 4020 | SiA 3085 (C) |
| SiA 4155 | SiA 3516 | SiA 3156 (C) | SiA 3643 | SiA 3756 | SiA 4068 | SiA 2663 | SiA 3969 |

**Fig. 3.1 Experimental field layout in Augmented Randomised Complete Block Design (ARCBD)**

## P 3.1 Experimental field view


## P 3.2 Seed colour variation

Red

Black

Black and White

Yellow

**P 3.3 Panicle length variation**


**Long**


**Medium**


**Short**

**P 3.4 Bristle length variation**

**Long**

**Medium**

**Short**

## 3.2.2 RECORD OF OBSERVATIONS

Observations were recorded on five randomly selected plants per germplasm and were used for statistical analysis. However, days to 50% flowering and days to maturity were recorded on plot basis. The data on the following morpho-physiological and nutritional traits were recorded.

### 3.2.2.1 Morpho-Physiogical traits

Observations on the following yield characters were recorded at appropriate stages of plant growth.

#### 3.2.2.1.1 SCMR at 30 DAS

Data was recorded at 30 DAS to estimate leaf chlorophyll content by SCMR Chlorophyll meter.

#### 3.2.2.1.2 SCMR at 45 DAS

Data was recorded at 45 DAS to estimate leaf chlorophyll content by SCMR Chlorophyll meter.

#### 3.2.2.1.3 Days to 50% flowering

The number of days taken by each genotype, from sowing to the day when 50 % of the plants were seen flowering in the population.

#### 3.2.2.1.4 Plant height (cm)

It is the height of the main tiller from ground level to the tip of the panicle and is measured at the time of maturity.

#### 3.2.2.1.5 Panicle length (cm)

It is measurement of the length from base to tip of the ear, at the time of maturity.

#### 3.2.2.1.6 Number of productive tillers/plant

It refers to counting of basal ear bearing tillers at harvest stage

#### 3.2.2.1.7 Days to maturity

The number of days taken by each genotype, from sowing to the day when it reaches physiological maturity

**3.2.2.1.8 Number of grains / ear head**

Grains harvested from the plants of each treatment were dried and counted.

**3.2.2.1.9 1000 grain weight (g)**

It is the absolute weight of 1000 selected healthy grains from the total seed yield of each genotype. Thousand grain of each genotype per replication is counted and weighed with a seed counter and digital weighing machine, respectively.

**3.2.2.1.10 Grain yield/plant (g)**

Weight of the total grain yield of tagged plants was recorded and the mean yield per plant was calculated after harvest.

**3.2.2.2 Estimation of Nutritional parameters**

Estimation of nutritional parameters (protein, carbohydates, Ca, Mg, Fe, Zn, Cu and Mn) collection of sample harvested seed samples from varieties were used for estimation. Care was taken to avoid the contamination of grains with dust and metal particles during their cleaning. All samples were dehulled and oven dried at 60˚C for 10 hrs and later powdered using Willey stainless steel mill and stored for nutrient analysis. The grain samples from each trait were collected in clean brown covers and analyzed at RARS, Nandyal.

**3.2.2.2.1 Protein analysis**

Protein content was estimated by Micro – Kjeldhal method by the AOAC (1984) procedure.

**Procedure:**

Digestion:

500mg of sample, 1g of digestion mixture and 10ml of concentrated $H_2SO_4$ were carefully added and the samples were digested in a digestion block for 1 h at $375^0$C. The tubes were removed and cooled; distilled water (50ml) was added carefully from sides.

**Distillation:**

In a 100ml conical flask, 40ml of boric acid was added with a few drops of mixed indicator. Distillation was done in the Gerhardt instrument with the following settings.

- Step 1 (NaoH) : 50ml
- Step 2 (steam digestion time) : 10s
- Step 3 (distillation time) : 180 min

Titration:

The contents of conical flask turned green during distillation. Titration was done with standard HCl till the content of the flask turned to original colour (pink). A blank was all run simultaneously.

**Calculations:**

$$\text{Protein (\%)} = \frac{\text{Titre value (X) x 14.007x 0.5(N of HCl) x 6.25}}{\text{Weight of sample (mg)}} \text{ X } 100$$

**3.2.2.2.2 Carbohydrate analysis**

The seeds were ground into flour and carbohydrate content was estimated as per procedure given by Sadasivam and Manickam (1996)

**Procedure**

- Weigh 100mg of the sample into a boiling tube.
- Hydrolyse by keeping it in boiling water bath for 3 hours with 5ml of 2.5 N-HCl and cool to room temperature.
- Neutralise it with solid sodium carbonate until the effervescence ceases.
- Make up the volume to 100ml and centrifuge.
- Collect the supernatant and take 0.5 and 1ml aliquots for analysis.
- Prepare the standards by taking 0, 0.2, 0.4, 0.6, 0.8 and 1ml of the working standard. '0' serves as blank.
- Make up the volume to 1ml in all the tubes including the sample tubes by adding distilled water
- Then add 4ml of anthrone reagent.

- Heat for eight minutes in a boiling water bath.
- Cool rapidly and read the green to dark green color at 630nm.
- Draw a standard graph by plotting concentration of thestandard on the X-axis versus absorbance on the Y-axis.
- From the graph calculate the amount of carbohydrate present in the sample tube.

**Calculation:**

Amount of carbohydrate present in 100 mg of the sample can be obtained using the following formula.

$$\text{Carbohydrate (mg/100g)} = \frac{\text{mg of glucose}}{\text{Volume of test sample}} \times 100$$

**3.2.2.3 Minerals estimation:**

The trace elements (iron, zinc, copper and manganese) were estimated by wet digestion using triacid mixture. A known aliquot of test sample was suitably diluted and micronutrients in the test sample (Cu, Mn, Zn and Fe) were determined using Atomic Absorption Spectrophotometer.

**3.2.2.3.1 Estimation of mineral nutrients (Calcium, Magnesium, Iron, Zinc, Cu and Mn) in mg/100) by Di-acid mixture method**

**Procedure:**

- Ground and oven dried plant samples of 0.5 g were transferred to 75ml digestion flasks.
- Add 10 ml of Di-acid mixture (Nitric acid, Perchloric acid in 4:1 v/v) and mixed with magnetic stirrer.
- Left overnight for cold digestion in digestion chamber (Pre-digestion).
- Digested the sample initially at $120^0$C for 1 hour, followed by $230^0$C for 2 hours on a hot plate in a digestion chamber.
- Then, heat the flask at higher temperature until the production of red $NO_2$ fumes ceases, continue digestion until the volume is reduced to about 3-5 ml but not to dryness. The completion of digestion is confirmed by the snow white residue or when the liquid becomes colourless.

- The flasks were allowed to cool and the contents were diluted to an appropriate volume and seal the flask with parafilm paper.
- Shake gently for 10 times manually.
- Finally standards were feeded to atomic absorption spectrometer (AAS) having appropriate hallow cathode lamps and readings had been recorded.

**Calculations**:

$$\text{Nutrient Conc. (ppm)} = \frac{\text{Graph ppm x Vol. of digested sample}}{\text{Weight of sample}}$$

**Standard Preparation**

Iron, zinc, copper and manganese require 0.4 ppm, 0.8 ppm, 1.2 ppm, 1.6 ppm and 2.0 ppm standards (Reference: Sahrawat *et al.,* 2002)

### 3.2.2.3.2 Estimation of Calcium by titration method

**Principle:**

A known volume of the solution containing Ca is titrated against 0.01 N EDTA in the presence muroxide indicator in alkaline medium ($P^H$ 12.0). When the Ca forms a complex with EDTA the orange red colour changes to lavender purple at the end point.

**Procedure:**

- Pipette out 5 ml of aliquat of Sample extracted in clean china dish and add a few ml of distilled water, 16.NaOH (1 to 2ml), pinch (0.1g) muroxide indicator and 10 g of calcon solution. Contents turn red. Stirr the contents with a glass rod.
- Titrate against 0.01 N EDTA till colour changed to reddish violet (Lavender colour). Note down the reading and repeat till to concorrent values are obtained.

### 3.2.2.3.3 Estimation of Calcium and Magnesium by titration method

**Procedure:**

- Pipette out 5 ml of aliquat of Sample extracted in clean china dish and add a few ml of distilled water, 1ml of $NH_4Cl$ + $NH_4OH$ buffer and 3-5 drops of EBT indicator stirr the contents with a glass rod. The content turn to wine red colour.
- Titrate against 0.01 N EDTA till colour changed to wine red col to bright blue or sky blue colour. Note down the reading and repeat till two concurrent values are obtained.

$$\text{Ca (m.eq. /l)} = \frac{\text{T.V} \times \text{Normality of EDTA} \times 1000}{\text{Volume of Sample extract}}$$

$$\text{Mg (m.eq. /l)} = \frac{\text{T.V} \times \text{Normality of EDTA} \times 1000}{\text{Volume of Sample extract}}$$

# 3.3 STATISTICAL ANALYSIS

The data recorded on various characters were subjected to the following statistical analysis.

## 3.3.1 Analysis of Variance

Analysis of variance of the characters was done as per standard statistical procedure for Augmented Randomized Complete Block Design (Augmented Design II) as given by Federer (1956).

**ANOVA Table for Augmented Randomized Complete Block Design**

| **Source of variation** | **Degrees of freedom** | **Sum of squares** | **Mean sum of squares** | **"F" calculated value** |
|---|---|---|---|---|
| Blocks (b) | b-1 | bSS | bMSS | bMSS/EMSS |
| Entries (e) | e-1 | eSS | eMSS | eMSS/ EMSS |
| Checks (c) | c-1 | cSS | cMSS | cMSS/EMSS |
| Varieties (v) | v-1 | vSS | vMSS | vMSS/EMSS |
| Checks *vs* Varieties | 1 | cvSS | cvMSS | cvMSS/ EMSS |
| Error | (c-1)(b-1) | ESS | EMSS | |
| Total | N-1 | TSS | | |

Where,

b = number of blocks

e = number of entries

c = number of checks

v = number of genotypes

N = (v+bc)

The significance test was carried out by referring to "F" table value given by Fisher and Yates (1967).

## 3.3.2 Estimation of genetic parameters

### 3.3.2.1 Estimation of variance components

Phenotypic and genotypic variances were estimated using the following formula,

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

$$\text{Phenotypic variance } (\sigma^2_p) = \sigma^2_g + M_e \quad \frac{M_t - M_e}{r} + M_e$$

The test of significance was carried out using 'F' table value of Fisher and Yates (1963).

### 3.3.2.2 Coefficient of variation

The genotypic and phenotypic coefficients of variation were calculated using the formula by Burton (1952).

a) Genotypic coefficient of variation (GCV)

$$GCV = \frac{\text{Genotypic standard deviation } (\sigma_g)}{\text{General mean } (\bar{X})} \times 100$$

b) Phenotypic coefficient of variation (PCV)

$$PCV = \frac{\text{Phenotypic standard deviation } (\sigma_p)}{\text{General mean } (\bar{X})} \times 100$$

The GCV and PCV values were classified as described by Sivasubramanian and Menon (1973).

| Classification | GCV/ PCV |
|---|---|
| Low | Less than 10% |
| Moderate | 10 – 20% |
| High | More than 20% |

### 3.3.2.3 Heritability

Heritability in broad sense was computed as the ratio of genetic variance to the total phenotypic variance and narrow sense heritability was the ratio of additive genetic variance to the total phenotypic variance as suggested by Hanson *et al.* (1956) and expressed as percentage.

$$\text{Heritability in broad sense } (h^2_{bs}) = \frac{\text{Genotypic variance } (\sigma^2_g)}{\text{Phenotypic variance } (\sigma^2_p)} \times 100$$

Heritability in broad sense was categorized as per the classification given by Johnson *et al.* (1955).

| Classification | Heritability |
|---|---|
| Low | Less than 30% |
| Moderate | 30 – 60% |
| High | More than 60% |

### 3.3.2.4 Expected genetic advance

Genetic advance was calculated based on formula given by Johnson *et al.* (1955).

$$\text{Expected genetic advance (GA)} = K \times \sigma_p \times h^2$$

Where,

K = Selection differential at 5% selection intensity (2.06)

$\sigma_p$ = Phenotypic standard deviation

$h^2$ = Heritability in broad sense

**3.3.2.5 Genetic advance as per cent of mean (GAM)**

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

Where,

GA = Genetic advance

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

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

| **Classification** | **GAM** |
|---|---|
| Low | Less than 10% |
| Moderate | 10 – 20% |
| High | More than 20% |

## 3.3.3 Genetic divergence

### 3.3.3.1 Mahalanobis' $D^2$ analysis

The data collected on different yield contributing characters was analysed using Mahalanobis $D^2$ analysis to determine the genetic divergence among the genotypes in terms of 'generalised group distance' (Mahalanobis, 1928).

#### 3.3.3.1.1 Test of significance

Variances were calculated for all the characters studied and test of significance was done. For the character pairs analysis of covariance was estimated on the basis of mean values (Panse & Sukhatme, 1978). After testing the difference between genotypes for each of the characters, a simultaneous test of significance for differences in the mean values of a number of correlated variables with regard to the pooled effect of characters was carried out using 'V' statistic, which in turn utilizes Wilk's criterion.

The sum of squares and sum of products of error and error + variety, variance-covariance matrix were used for this purpose. The estimation of Wilk's criterion was done using the following relationship.

$$\wedge = \frac{|E|}{|E+V|}$$

Where,

$\wedge$ = Wilk's criterion

$|E|$ = Determinant of error matrix and

$|E+V|$ = Determinant of error + variety matrix

$$V_{(stat.)} = - m \log_e \wedge \qquad \text{(at pq degrees of freedom)}$$

Where,

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

n = degree of freedom for error + varieties

p = number of variables /characters

q = number of varieties –1 (or degrees of freedom)

$V_{(stat.)}$ is distributed as $\chi^2$ with pq degrees of freedom.

**Transformation of correlated variables**

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

**3.3.3.1.2 Computation of $D^2$ values**

For the given combination of i and j genotypes, the mean deviation *i.e.*, $Y_{it} - Y_{jt}$ for t=1, 2…p variables are computed and the $D^2$ values were calculated as,

$$D^2_{ij} = \sum_{t=1} (y_i^t - y_j^t)^2$$

Where,

$y_i^t$ is uncorrelated mean value of $i^{th}$ genotype for character 't'

$y_j^t$ is uncorrelated mean value of $j^{th}$ genotype for character 't'

$D^2_{ij}$ is $D^2$ between $i^{th}$ and $j^{th}$ genotypes.

**3.3.3.1.3 Testing the significance of $D^2$ values**

The $D^2$ value obtained for a pair of population is taken as calculated value of $\chi^2$ and is tested against the tabulated value of $\chi^2$ for p degrees of freedom, where p is the number of characters considered *i.e.* 18 in the present study.

**3.3.3.1.4 Contribution of individual characters towards divergence**

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

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

Where,

N = Number of genotype combinations where the character was ranked first.

M = All possible combinations of number of genotypes considered.

**3.3.3.1.5 Grouping of genotypes into various clusters**

The grouping of genotypes into different clusters was done using the Tocher's method as described by Rao (1952). The criterion was that the two varieties belonging to the same cluster at least on an average show a smaller $D^2$ value than those belonging to different clusters. For this purpose, $D^2$ values of all combinations of each genotype were arranged in ascending order of magnitude in a tabular form as described by Singh and Chaudhary (2010).

To start with, two populations having the closest distance from each other were considered, to which the third population having the smallest $D^2$ value from the first two populations was added. Similarly, the next nearest fourth population was considered and this procedure was continued. At certain stage when it was felt that after adding a

particular population there was an abrupt increase in the average $D^2$, that population was not considered for including in that cluster.

The genotypes of the first cluster were then eliminated and the rest were treated in a similar way. This procedure was continued till all the genotypes were included into one or other cluster.

**3.3.3.1.6 Average intra-cluster distance**

For the measurement of intra-cluster distances, the formula used was $\Sigma D^2_i/n$ where, $\Sigma D^2_i$ was the sum of distances between all possible combinations (n) of the populations included in a cluster.

**3.3.3.1.7 Average inter-cluster distance**

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

$$\text{Average inter-cluster distance} = \frac{D^2}{(n_1 \times n_2)}$$

Where,

$D^2$ = difference in the mean values between two populations when all the character are considered simultaneously.

$n_1$ & $n_2$ = number of genotypes of two clusters.

**3.3.3.2 Principal component analysis and cluster analysis**

Principal component analysis was carried according to procedure described by Banfield (1978). PCA can be performed on two types of data matrices *viz.*, variance-covariance matrix and correlation matrix. With characters of different scale, a correlation matrix standardizing the original data set is preferred. If the characters are of same scale, a variance-covariance matrix can be used. In the present study, PCA was performed on the correlation matrix of traits, thereby removing the effects of scale (Jackson, 1991).

**3.3.3.2.1 Eigen values and eigen vectors**

The eigen values and eigen vectors were computed from data matrix. Eigen values define the amount of total variation that is displayed on principal components. The proportion of variation accounted for each principal component (PC) is expressed as the eigen value divided by the sum of the eigen values.

$$\text{Per cent variance explained for } PC_1 = \frac{\text{eigen value } (PC_1)}{\text{Sum of eigen values}}$$

The eigen vector (loading) defines the correlation of each variable with the principal components. The principal components were identified by following procedure. The $j^{th}$ principal component ($Y_j$) of the observations X is the linear combination given as follows:

$$Y_j = A_{1j}X_1 + \ldots\ldots\ldots + A_{pj}X_p$$

Where,

Aij are found such that $Y_j$ is uncorrelated $Y_1$, $Y_2$,……..$Y_{j-1}$ the $j^{th}$ largest variance. The Aij are the elements of the normalized eigen vector associated with largest $j^{th}$ eigen value. The variance of the $j^{th}$ principal component of the $\lambda j$ and the total system variance trace (S) = $\lambda_1+\lambda_2+\ldots+\lambda p$.

The importance of the $j^{th}$ principal component is given by,

$$\frac{\lambda_j}{\text{Trace (S)}}$$

This is informative about the proportion of total variation that can be accounted for the $i^{th}$ principal component. The correlation between the $i^{th}$ original variable $X_i$ and the $j^{th}$ principal component $Y_j$ is given by,

$$\rho(X_i, Y_j) = \frac{A_{ij}.\sqrt{\lambda_j}}{\sqrt{S_i}}$$

Where, $S_i$ is the standard deviation of $X_i$.

Thus, a principal component is linear function of the test variables given as follows,

$$\text{Principal component} = ax_1 + bx_2 + \ldots\ldots\ldots + hx_8$$

Where, a, b,…. are coefficients and $x_1$, $x_2$ ….. etc., are the variables in such a way that the principal component has a unit variance as reported by Ehrenberg (1985).

PCA scores for each genotype under concerned PCs were computed and utilized to derive a 2D or 3D (dimensional) scatter plot of individuals.

### 3.3.3.2.2 Hierarchical cluster analysis

Agglomerative hierarchical clustering technique was done as per Anderberg (1993).

#### 3.3.3.2.2.1 Obtaining data matrix

PCA scores for 100 genotypes were used as input for clustering because principal component analysis provides variable independence and balanced weighting of traits, which leads to an effective contribution of different characters on the basis of respective variation.

#### 3.3.3.2.2.2 Standardizing the data matrix

To compare the similarities among the genotypes, the data matrix was standardized with a column standardizing function *i.e.*, Q analysis. The data matrix is standardize in cluster analysis to make the characters contribute more equally to the similarities among genotypes and to nullify the arbitrarily affect the units chosen for measuring the attributes among the genotypes.

Column standardizing function CA-Q analysis was carried by the following formula.

$$Z_{ij} = \overline{X}_{ij} - X_j / S_{ij}$$

Where, $\overline{X}_j = \sum_{i=1}^{n} X_{ij} / n$

Where, $S_{ij} = \dfrac{\sum_{i=1}^{n} X_{ij}^{-} - X_j / n}{n-1}$

For, i = genotypes

j = total variables

The resulting data after standardization is unit less and have mean zero and variance one.

#### 3.3.3.2.2.3 Computing the resemblance matrix

A resemblance coefficient, which measures the overall resemblance (the degree of similarity or distance) between a pair of genotypes, was computed. Here 100 genotypes were taken in data matrix therefore resemblance coefficient was computed.

The data matrix was transformed to distance matrix (resemblance matrix) based on the dissimilarity coefficients using squared Euclidean distance method.

Squared Euclidean distance [ $d_{ij}$] = $\sum_{K=1}^{P}(X_{ik} - X_{jk})^2$

Where,

P = Number of genotypes

$X_{ik}$ = Value of $i^{th}$ genotype for k PCA scores

$X_{jk}$ = Value of $j^{th}$ genotype for k PCA scores

#### 3.3.3.2.2.4 Execution of the clustering method

Distance matrix was converted into dendrogram by using Ward's method where the distance between two clusters is the sum of squares between two clusters summed over all variables. At each stage in the clustering procedure within cluster sum of squares is minimized over all partitions obtained by combining two clusters from previous stage.

## 3.3.4 Correlation studies

The phenotypic and genotypic correlation coefficients were worked out to determine the degree of association of a character with yield and also among the yield components by using covariance technique as per Falconer (1964).

$$\text{Phenotypic coefficients of correlation } (r_p) = r(x_i x_j)_p = \frac{Cov(x_i x_j)_p}{\left[V(x_i)_p \,.\, V(x_j)_p\right]^{½}}$$

Where,

$r(x_i x_j)_p$ = Phenotypic correlation between $i^{th}$ and $j^{th}$ characters

$Cov(x_i x_j)_p$ = Phenotypic covariance between $i^{th}$ and $j^{th}$ characters

$V(x_i)_p$ and $V(x_j)_p$ = Phenotypic variance of $i^{th}$ and $j^{th}$ characters respectively

$$\text{Genotypic coefficients of correlation } (r_g) = r(x_i x_j)_g = \frac{Cov(x_i x_j)_g}{\left[V(x_i)_g \cdot V(x_j)_g\right]^{½}}$$

Where,

$r(x_i x_j)_g$ = Genotypic correlation between $i^{th}$ and $j^{th}$ characters

$Cov(x_i x_j)_g$ = Genotypic covariance between $i^{th}$ and $j^{th}$ characters

$V(x_i)_g$ and $V(x_j)_g$ = Genotypic variance of $i^{th}$ and $j^{th}$ characters respectively

**3.3.4.1 Test of significance**

Significance of correlation coefficients was tested by comparing phenotypic correlation coefficients with the table values (Fisher and Yates, 1963) at (n-2) degrees of freedom at 5% and 1% level where 'n' denotes the number of paired observations used in the calculation.

## 3.3.5 Path coefficient analysis

Path coefficient analysis was carried out by using the correlation coefficients to know the direct and indirect effects of the component characters on yield as suggested by Wright (1921) and illustrated by Dewey and Lu (1959).

Path coefficients were obtained by solving the simultaneous equations which express the basic relationship between correlations and path coefficients.

The equations are as follows:

$$r_{1,y} = P_{1,y} + r_{1,2} P_{2,y} + r_{1,3} P_{3,y} + \ldots + r_{1,k} P_{k,y}$$

$$r_{2,y} = r_{2,1} P_{1,y} + P_{2,y} + r_{2,3} P_{3,y} + \ldots + r_{2,k} P_{k,y}$$

. . . . .

. . . . .

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$$r_{k,y} = r_{k,1} P_{1,y} + r_{k,2} P_{2,y} + r_{k,3} P_{3,y} + \ldots + r_{k,k} P_{k,y}$$

Where,

$r_{1,y}$ to $r_{k,y}$ = Correlation coefficients between independent characters

$r_{1,2}$ to $r_{k-1,k}$ = Correlation coefficients between all possible combinations of independent characters

$P_{1,y}$ to $P_{k,y}$ = Direct effects of characters 1 to k on character y

The residual effect was computed by using the formula

$$R = \left[ 1 - (P_{1,y} r_{1,y} + P_{2,y} r_{2,y} + P_{3,y} r_{3,y} + \ldots\ldots\ldots\ldots\ldots) \right]^{½}$$

Where,

R = Residual effect

$P_{1,y}$ = Direct effect of independent character '1' on dependent character 'y'

$r_{1,y}$ = Correlation coefficient of independent character '1' on dependent character 'y'


# Chapter – IV

# RESULTS AND DISCUSSION

## Chapter IV

# RESULTS AND DISCUSSION

The present investigation entitled “Diversity in morpho-physiological and biochemical components in genetic resources of foxtail millet (*Setaria italica* (L.) Beauv.)” was conducted utilizing 100 (96 entries + 4 checks) foxtail millet germplasm accessions in *kharif*, 2018 at Regional Agricultural Research Station, ANGRAU, Nandyal, Andhra Pradesh. The data recorded on 18 metric traits was computed for genetic parameters, genetic divergence, character association and path coefficient analysis in order to identify divergent genetic resources that can be readily exploited in hybridization programmes to evolve superior crosses with improved yields.

The details of results obtained from the above investigation are discussed character wise and presented under the following headings.

4.1 Mean, Genetic Variability, Heritability and Genetic Advance

4.2 Character association

4.3 Path coefficient analysis

4.4 Genetic divergence

## 4.1 MEAN, GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE

The success of any breeding activity depends upon the extent of genetic variability prevalent in the population. Wider spectrum of genetic variability assists in choosing the desired genotypes. Besides genetic variability, knowledge on heritability and genetic advance is of immense help to a breeder to design a suitable breeding programme. Hence, it is imperative to have a thorough knowledge of genetic variability, heritability and genetic advance available in the germplasm.

Genetic variability together with the heritability estimates would give a better idea on the amount of genetic gain expected out of selection (Burton, 1952; Swarup and Chaugle, 1962). Further, the magnitude of heritable variability is the most important aspect (Panse, 1957), which is directly proportional to response to selection. Heritability estimates coupled with genetic advance are more beneficial 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).

The *per se* performance of 100 foxtail millet genetic resources for the 18 characters studied was presented in Table 4.1. The analysis of variance revealed significant differences among the genetic resources for all the characters studied (Table 4.2) indicating existence of ample genetic variation in the test genotypes studied. The estimates of variability, heritability and genetic advance were shown in Table 4.3.

### 4.1.1 SCMR at 30 DAS

The variation for SCMR at 30 DAS ranged from 34.70 (SiA 3323) to 55.20 (SiA 4180) with a mean of 46.34. The PCV (8.56) and GCV (7.00) estimates for this trait were low indicating less variation among the genotypes studied. Similar result was reported by Bheemesh (2017) for this character.

High heritability (66.80%) coupled with moderate genetic advance as per cent of mean (11.78%) was noted for this trait which may be accounted for both additive and non-additive gene actions implying that simple selection may not be rewarding for this trait. These results were in agreement with the findings of Bheemesh (2017) in foxtail millet.

### 4.1.2 SCMR at 45 DAS

This trait varied from 42.90 (SiA 3323) to 65.50 (SiA 3222) with a mean of 53.63. The estimates of PCV (7.13) and GCV (6.01) were also low implying existence of low variation for this trait in the genotypes studied. This result was in conformity with the findings of Bheemesh (2017) in foxtail millet.

High heritability (71.02%) and moderate genetic advance as per cent of mean (10.44%) indicated that this trait was controlled by both additive gene and non-additive gene actions and therefore, selection has no role in improving this character. Similar result was noted by Bheemesh (2017) for this trait.

**Table 4.1. *Per se* performance of 100 foxtail millet [*Setaria italica* (L.) Beauv.] genetic resources for the characters studied**

| S.No. | Genotype | SCMR at 30 DAS | SCMR at 45 DAS | Days to 50% flowering | Plant height (cm) | Panicle length (cm) | No. of productive tillers /plant | Days to maturity | No. of Grains / ear head | 1000 grain wt (g) | Protein (g/ 100g) | Carbo hydrate (g/ 100g) | Calcium (mg/ 100g) | Magnesium (mg/ 100g) | Iron (mg/ 100g) | Zinc (mg/ 100g) | Copper (mg/ 100g) | Manganese (mg/ 100g) | Grain yield/ plant (g) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | (1) | (2) | (3) | (4) | (5) | (6) | (7) | (8) | (9) | (10) | (11) | (12) | (13) | (14) | (15) | (16) | (17) | (18) |
| 1 | SiA 3222 | 46.20 | 65.50 | 32.00 | 110.50 | 14.90 | 1.00 | 60.00 | 1816.66 | 2.54 | 12.69 | 63.15 | 32.00 | 12.00 | 4.65 | 1.62 | 0.96 | 1.68 | 9.77 |
| 2 | SiA 3323 | 34.70 | 42.90 | 47.00 | 152.80 | 12.00 | 2.93 | 85.00 | 1820.12 | 2.51 | 16.63 | 58.94 | 28.00 | 12.00 | 12.45 | 2.84 | 1.04 | 2.13 | 5.29 |
| 3 | SiA 3657 | 51.40 | 56.00 | 45.00 | 152.50 | 21.00 | 3.36 | 87.00 | 1818.30 | 3.24 | 14.44 | 61.14 | 24.00 | 12.00 | 17.08 | 3.05 | 1.12 | 2.43 | 17.67 |
| 4 | SiA 2745 | 53.00 | 55.10 | 44.00 | 157.00 | 17.20 | 3.36 | 92.00 | 1817.39 | 3.19 | 12.25 | 63.51 | 24.00 | 12.00 | 13.08 | 3.24 | 1.05 | 2.33 | 18.66 |
| 5 | SiA 2579 | 49.40 | 50.50 | 45.00 | 167.80 | 21.00 | 3.00 | 79.00 | 1819.03 | 3.26 | 10.50 | 62.84 | 28.00 | 16.80 | 13.82 | 3.45 | 1.01 | 2.30 | 18.22 |
| 6 | SiA 3627 | 46.20 | 48.90 | 45.00 | 155.80 | 16.50 | 3.36 | 86.00 | 1610.90 | 3.15 | 14.44 | 61.21 | 24.00 | 21.60 | 13.96 | 3.50 | 0.98 | 2.63 | 9.47 |
| 7 | SiA 4061 | 47.50 | 51.00 | 37.00 | 131.00 | 13.50 | 2.93 | 80.00 | 1818.12 | 3.27 | 14.00 | 56.81 | 20.00 | 14.40 | 12.49 | 2.99 | 1.04 | 2.53 | 15.33 |
| 8 | SiA 4036 | 49.50 | 54.70 | 44.00 | 154.80 | 16.50 | 5.71 | 82.00 | 1562.01 | 3.03 | 14.00 | 62.96 | 32.00 | 16.80 | 16.63 | 2.92 | 0.90 | 2.35 | 13.10 |
| 9 | SiA 2662 | 48.70 | 56.60 | 40.00 | 152.80 | 17.40 | 4.00 | 82.00 | 1816.84 | 3.22 | 17.50 | 56.14 | 24.00 | 14.40 | 19.47 | 2.89 | 1.09 | 2.28 | 17.17 |
| 10 | SiA 2737 | 46.60 | 53.00 | 45.00 | 162.50 | 19.50 | 2.36 | 85.00 | 1815.39 | 3.12 | 13.56 | 50.93 | 16.00 | 19.20 | 9.38 | 3.50 | 0.89 | 2.06 | 13.35 |
| 11 | SiA 3611 | 46.50 | 54.20 | 41.00 | 168.50 | 17.20 | 4.22 | 82.00 | 1816.12 | 2.87 | 13.13 | 56.75 | 20.00 | 24.00 | 22.50 | 3.01 | 2.76 | 2.50 | 14.70 |
| 12 | SiA 4155 | 51.40 | 56.80 | 44.00 | 166.00 | 19.00 | 3.58 | 84.00 | 1815.57 | 3.53 | 15.31 | 53.34 | 24.00 | 19.20 | 11.72 | 2.93 | 1.23 | 2.30 | 13.06 |
| 13 | SiA 2849 | 49.20 | 55.80 | 44.00 | 163.20 | 21.70 | 2.36 | 90.00 | 1560.29 | 3.16 | 14.00 | 51.46 | 24.00 | 19.20 | 12.53 | 2.97 | 1.15 | 2.44 | 9.44 |
| 14 | SiA 3577 | 49.70 | 50.80 | 45.00 | 166.90 | 19.50 | 4.64 | 87.00 | 1703.00 | 2.97 | 14.88 | 61.29 | 24.00 | 21.60 | 14.79 | 3.02 | 1.23 | 2.49 | 12.09 |
| 15 | SiA 3701 | 47.20 | 48.60 | 44.00 | 140.80 | 18.10 | 2.36 | 80.00 | 1814.84 | 2.97 | 12.69 | 62.00 | 20.00 | 21.60 | 23.62 | 3.11 | 1.16 | 2.70 | 10.57 |
| 16 | SiA 3559 | 46.60 | 55.00 | 44.00 | 155.70 | 18.10 | 4.07 | 84.00 | 1814.11 | 2.88 | 13.13 | 57.96 | 24.00 | 7.20 | 6.55 | 2.71 | 1.13 | 4.12 | 10.66 |
| 17 | SiA 3851 | 45.40 | 46.30 | 44.00 | 168.20 | 18.40 | 2.71 | 86.00 | 1815.75 | 3.00 | 11.38 | 64.11 | 28.00 | 7.20 | 21.12 | 3.63 | 1.85 | 3.07 | 13.64 |
| 18 | SiA 4016 | 45.00 | 48.00 | 54.00 | 155.50 | 15.40 | 4.00 | 80.00 | 1604.70 | 3.08 | 12.69 | 76.42 | 24.00 | 9.60 | 13.72 | 3.28 | 2.76 | 2.20 | 11.44 |
| 19 | SiA 4179 | 52.10 | 58.80 | 45.00 | 154.40 | 15.30 | 2.13 | 80.00 | 1817.21 | 2.93 | 14.44 | 50.11 | 20.00 | 14.40 | 7.06 | 2.36 | 1.07 | 2.04 | 15.36 |
| 20 | SiA 3498 | 43.80 | 47.10 | 44.00 | 156.80 | 19.40 | 2.58 | 82.00 | 1813.75 | 2.47 | 14.88 | 58.57 | 20.00 | 21.60 | 13.70 | 2.43 | 2.75 | 2.05 | 9.98 |
| 21 | SiA 4107 | 50.30 | 52.20 | 50.00 | 171.60 | 19.00 | 4.29 | 85.00 | 1818.30 | 2.81 | 14.88 | 52.99 | 20.00 | 19.20 | 14.54 | 2.36 | 1.06 | 2.01 | 14.95 |
| 22 | SiA 2674 | 51.70 | 57.70 | 45.00 | 148.70 | 17.40 | 3.93 | 83.00 | 1815.02 | 3.39 | 14.00 | 74.16 | 24.00 | 14.40 | 12.65 | 2.35 | 1.11 | 1.99 | 9.66 |
| 23 | SiA 2697 | 51.70 | 52.70 | 44.00 | 152.80 | 19.40 | 3.93 | 80.00 | 1792.90 | 2.84 | 16.63 | 73.40 | 28.00 | 9.60 | 14.94 | 2.41 | 2.75 | 1.75 | 11.76 |
| 24 | SiA 3516 | 52.10 | 54.50 | 40.00 | 144.50 | 16.40 | 3.71 | 81.00 | 1563.10 | 3.02 | 12.69 | 57.18 | 36.00 | 19.20 | 16.69 | 3.08 | 2.74 | 1.94 | 10.95 |
| 25 | SiA 3496 | 49.00 | 49.10 | 45.00 | 153.50 | 12.50 | 3.29 | 83.00 | 1818.66 | 1.70 | 11.38 | 54.18 | 16.00 | 19.20 | 9.72 | 3.65 | 1.12 | 1.82 | 8.98 |
| 26 | SiA 3580 | 47.00 | 49.00 | 47.00 | 147.40 | 16.60 | 4.00 | 87.00 | 1574.80 | 2.82 | 15.31 | 52.30 | 24.00 | 21.60 | 29.00 | 4.04 | 2.74 | 2.61 | 7.93 |
| 27 | SiA 3971 | 52.60 | 54.00 | 45.00 | 142.20 | 15.00 | 4.36 | 81.00 | 1558.10 | 2.62 | 16.19 | 53.61 | 24.00 | 19.20 | 13.38 | 3.81 | 1.01 | 2.12 | 8.68 |
| 28 | SiA 3038 | 49.10 | 52.30 | 39.00 | 139.50 | 14.80 | 3.00 | 88.00 | 1560.13 | 2.92 | 13.56 | 66.25 | 40.00 | 4.80 | 9.21 | 3.03 | 2.40 | 2.16 | 12.76 |

**Table 4.1 Contd…**

| S.No. | Genotype | SCMR at 30 DAS | SCMR at 45 DAS | Days to 50% flowering | Plant height (cm) | Panicle length (cm) | No. of productive tillers /plant | Days to maturity | No. of Grains / ear head | 1000 grain wt (g) | Protein (g/ 100g) | Carbohydrate (g/ 100g) | Calcium (mg/ 100g) | Magnesium (mg/ 100g) | Iron (mg/ 100g) | Zinc (mg/ 100g) | Copper (mg/ 100g) | Manganese (mg/ 100g) | Grain yield/ plant (g) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | (1) | (2) | (3) | (4) | (5) | (6) | (7) | (8) | (9) | (10) | (11) | (12) | (13) | (14) | (15) | (16) | (17) | (18) |
| 29 | SiA 3588 | 52.50 | 55.30 | 45.00 | 158.00 | 19.10 | 4.78 | 83.00 | 1558.72 | 3.28 | 14.88 | 66.99 | 20.00 | 21.60 | 8.54 | 3.54 | 1.67 | 2.31 | 10.18 |
| 30 | SiA 3737 | 53.90 | 56.60 | 46.00 | 153.10 | 17.20 | 3.71 | 85.00 | 1803.30 | 3.19 | 14.88 | 59.55 | 24.00 | 14.40 | 14.74 | 3.14 | 0.90 | 2.04 | 9.12 |
| 31 | SiA 3462 | 51.30 | 58.90 | 42.00 | 152.80 | 18.00 | 3.42 | 82.00 | 1561.07 | 3.14 | 15.75 | 61.94 | 20.00 | 16.80 | 9.61 | 3.47 | 1.30 | 2.32 | 8.86 |
| 32 | SiA 2671 | 47.20 | 53.90 | 46.00 | 151.30 | 21.00 | 4.58 | 85.00 | 1814.48 | 2.93 | 14.00 | 72.83 | 24.00 | 14.40 | 7.85 | 3.00 | 1.05 | 1.91 | 12.03 |
| 33 | SiA 3492 | 43.00 | 53.80 | 45.00 | 162.00 | 18.80 | 3.87 | 80.00 | 1815.21 | 3.00 | 14.00 | 55.57 | 24.00 | 21.60 | 8.18 | 3.53 | 0.91 | 2.22 | 15.81 |
| 34 | SiA 3429 | 44.30 | 47.70 | 46.00 | 142.60 | 16.40 | 3.64 | 82.00 | 1587.20 | 2.87 | 12.25 | 54.14 | 28.00 | 14.40 | 23.60 | 3.35 | 0.90 | 2.05 | 11.80 |
| 35 | SiA 4063 | 47.30 | 57.70 | 46.00 | 143.80 | 17.80 | 4.36 | 84.00 | 1813.93 | 2.81 | 14.88 | 57.36 | 24.00 | 9.60 | 5.74 | 2.39 | 1.63 | 2.10 | 10.44 |
| 36 | SiA 3793 | 42.30 | 53.20 | 52.00 | 152.10 | 16.20 | 4.36 | 87.00 | 1562.79 | 3.11 | 17.06 | 65.82 | 24.00 | 9.60 | 7.19 | 2.65 | 0.91 | 2.23 | 11.34 |
| 37 | SiA 805 | 47.60 | 50.60 | 44.00 | 146.10 | 17.60 | 4.78 | 81.00 | 1817.57 | 2.68 | 13.13 | 51.34 | 16.00 | 24.00 | 6.59 | 2.40 | 0.89 | 2.20 | 8.60 |
| 38 | SiA 3855 | 46.40 | 52.10 | 46.00 | 152.10 | 19.20 | 3.29 | 85.00 | 1817.03 | 3.20 | 16.19 | 64.86 | 20.00 | 9.60 | 10.05 | 2.53 | 2.70 | 2.26 | 7.60 |
| 39 | SiA 3420 | 46.70 | 60.00 | 45.00 | 130.20 | 15.50 | 6.22 | 80.00 | 1556.85 | 2.68 | 14.00 | 57.36 | 24.00 | 9.60 | 6.52 | 2.31 | 0.91 | 2.26 | 6.42 |
| 40 | SiA 4167 | 43.30 | 50.10 | 47.00 | 139.80 | 15.70 | 4.36 | 81.00 | 1557.79 | 2.75 | 15.31 | 51.20 | 24.00 | 7.20 | 5.99 | 2.39 | 2.72 | 2.29 | 8.79 |
| 41 | SiA 2864 | 42.30 | 49.80 | 46.00 | 134.60 | 16.80 | 5.36 | 85.00 | 1559.97 | 2.80 | 14.44 | 75.67 | 24.00 | 12.00 | 7.88 | 2.32 | 0.90 | 2.08 | 9.78 |
| 42 | SiA 3409 | 43.20 | 46.60 | 50.00 | 123.70 | 11.00 | 2.00 | 70.00 | 1556.22 | 1.57 | 12.25 | 56.26 | 24.00 | 7.20 | 6.19 | 2.47 | 0.89 | 2.30 | 1.37 |
| 43 | SiA 4027 | 44.20 | 52.40 | 47.00 | 151.80 | 15.80 | 5.29 | 85.00 | 1562.47 | 2.78 | 12.25 | 52.03 | 20.00 | 31.20 | 11.03 | 2.40 | 2.73 | 2.36 | 12.10 |
| 44 | SiA 3423 | 42.90 | 49.40 | 42.00 | 131.80 | 12.80 | 4.36 | 80.00 | 1556.69 | 2.76 | 14.88 | 57.51 | 24.00 | 14.40 | 10.47 | 2.55 | 0.90 | 2.16 | 6.66 |
| 45 | SiA 4181 | 47.30 | 58.80 | 46.00 | 160.30 | 20.00 | 3.29 | 83.00 | 1799.70 | 3.29 | 15.75 | 63.39 | 24.00 | 16.80 | 8.28 | 3.12 | 2.75 | 2.11 | 10.64 |
| 46 | SiA 1244 | 46.70 | 54.00 | 47.00 | 143.80 | 17.30 | 3.64 | 81.00 | 1674.90 | 2.68 | 11.81 | 57.96 | 20.00 | 9.60 | 6.33 | 2.72 | 2.73 | 2.19 | 9.22 |
| 47 | SiA 4044 | 40.40 | 51.20 | 50.00 | 151.90 | 18.80 | 5.36 | 85.00 | 1559.82 | 2.61 | 13.56 | 51.20 | 40.00 | 21.60 | 23.36 | 2.68 | 0.89 | 2.70 | 5.46 |
| 48 | SiA 3643 | 48.10 | 62.50 | 42.00 | 148.40 | 21.20 | 3.36 | 79.00 | 1560.44 | 3.17 | 16.19 | 52.97 | 20.00 | 12.00 | 8.68 | 2.68 | 2.73 | 2.19 | 16.95 |
| 49 | SiA 2713 | 46.40 | 47.90 | 45.00 | 147.00 | 18.30 | 4.47 | 78.00 | 1562.94 | 3.00 | 11.81 | 68.19 | 20.00 | 14.40 | 7.70 | 2.57 | 0.91 | 2.19 | 11.93 |
| 50 | SiA 2757 | 45.80 | 52.50 | 44.00 | 156.70 | 18.40 | 4.47 | 90.00 | 1813.57 | 3.00 | 12.69 | 76.38 | 20.00 | 14.40 | 9.54 | 2.53 | 2.74 | 2.14 | 17.59 |
| 51 | SiA 2681 | 49.80 | 56.10 | 42.00 | 149.80 | 19.10 | 4.80 | 85.00 | 1621.10 | 3.05 | 14.00 | 55.26 | 20.00 | 12.00 | 9.40 | 2.61 | 2.74 | 1.99 | 10.22 |
| 52 | SiA 3511 | 40.90 | 54.10 | 45.00 | 159.60 | 18.80 | 2.53 | 83.00 | 1817.94 | 2.97 | 14.44 | 55.65 | 20.00 | 9.60 | 32.50 | 2.24 | 1.76 | 2.47 | 19.33 |
| 53 | SiA 3674 | 51.50 | 52.10 | 52.00 | 148.70 | 20.00 | 4.73 | 80.00 | 1557.16 | 2.67 | 13.13 | 59.45 | 32.00 | 21.60 | 18.40 | 3.94 | 0.89 | 2.40 | 6.12 |
| 54 | SiA 3827 | 54.00 | 55.90 | 47.00 | 154.30 | 19.00 | 4.20 | 79.00 | 1562.16 | 2.74 | 11.38 | 66.72 | 24.00 | 9.60 | 5.37 | 2.24 | 0.86 | 1.58 | 13.07 |
| 55 | SiA 3908 | 47.10 | 50.20 | 46.00 | 138.80 | 21.20 | 4.80 | 84.00 | 1557.32 | 3.07 | 14.00 | 64.27 | 16.00 | 14.40 | 4.45 | 1.97 | 0.86 | 1.31 | 14.03 |
| 56 | SiA 3697 | 51.30 | 53.50 | 46.00 | 145.90 | 20.40 | 6.40 | 82.00 | 1560.91 | 2.85 | 12.25 | 68.07 | 24.00 | 21.60 | 7.96 | 3.49 | 0.89 | 2.31 | 14.50 |

**Table 4.1 Contd…**

| S. No. | Genotype | SCMR at 30 DAS | SCMR at 45 DAS | Days to 50% flowering | Plant height (cm) | Panicle length (cm) | No. of productive tillers /plant | Days to maturity | No of Grains / ear head | 1000 grain wt (g) | Protein (g/ 100g) | Carbohydrate (g/ 100g) | Calcium (mg/ 100g) | Magnesium (mg/ 100g) | Iron (mg/ 100g) | Zinc (mg/ 100g) | Copper (mg/ 100g) | Manganese (mg/ 100g) | Grain yield/ plant (g) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | (1) | (2) | (3) | (4) | (5) | (6) | (7) | (8) | (9) | (10) | (11) | (12) | (13) | (14) | (15) | (16) | (17) | (18) |
| 57 | SiA 4009 | 42.60 | 56.50 | 42.00 | 138.80 | 19.20 | 3.73 | 85.00 | 1557.63 | 2.92 | 14.44 | 67.82 | 20.00 | 16.80 | 6.83 | 3.00 | 0.87 | 1.78 | 7.24 |
| 58 | SiA 3965 | 43.70 | 54.20 | 42.00 | 143.80 | 16.80 | 3.93 | 80.00 | 1557.47 | 2.91 | 13.56 | 61.39 | 28.00 | 19.20 | 5.40 | 3.81 | 0.89 | 2.64 | 5.85 |
| 59 | SiA 3972 | 47.20 | 53.00 | 46.00 | 133.00 | 13.50 | 3.73 | 80.00 | 1559.19 | 2.89 | 15.75 | 61.21 | 32.00 | 14.40 | 5.41 | 4.03 | 0.91 | 2.55 | 10.96 |
| 60 | SiA 3756 | 41.60 | 53.80 | 51.00 | 147.70 | 16.00 | 4.93 | 81.00 | 1556.53 | 2.68 | 14.00 | 50.07 | 24.00 | 14.40 | 12.44 | 2.50 | 0.88 | 2.35 | 6.24 |
| 61 | SiA 4013 | 38.00 | 56.10 | 45.00 | 145.20 | 16.40 | 5.67 | 88.00 | 1559.50 | 2.86 | 16.19 | 64.62 | 24.00 | 26.40 | 24.00 | 4.26 | 0.90 | 2.44 | 13.83 |
| 62 | SiA 3754 | 49.20 | 58.00 | 45.00 | 146.60 | 18.30 | 5.53 | 80.00 | 1815.93 | 3.28 | 17.94 | 53.97 | 36.00 | 14.40 | 7.48 | 3.80 | 0.88 | 2.34 | 15.13 |
| 63 | SiA 3413 | 39.40 | 53.50 | 47.00 | 145.00 | 16.90 | 5.00 | 81.00 | 1818.85 | 2.92 | 14.00 | 55.10 | 24.00 | 21.60 | 10.36 | 3.75 | 0.88 | 2.18 | 6.20 |
| 64 | SiA 3435 | 45.70 | 55.60 | 47.00 | 155.60 | 17.20 | 5.53 | 83.00 | 1690.80 | 2.76 | 14.00 | 56.59 | 24.00 | 21.60 | 8.31 | 3.81 | 0.88 | 2.40 | 10.21 |
| 65 | SiA 4045 | 43.50 | 56.60 | 40.00 | 140.70 | 18.50 | 6.40 | 80.00 | 1556.38 | 3.12 | 15.75 | 51.66 | 20.00 | 12.00 | 8.43 | 2.44 | 0.89 | 2.48 | 4.98 |
| 66 | SiA 3499 | 35.80 | 50.60 | 45.00 | 152.60 | 20.30 | 4.67 | 81.00 | 1750.80 | 2.59 | 15.31 | 56.28 | 20.00 | 12.00 | 7.61 | 2.56 | 0.88 | 2.05 | 10.49 |
| 67 | SiA 3436 | 41.80 | 54.90 | 47.00 | 149.10 | 15.60 | 4.47 | 85.00 | 1558.57 | 3.15 | 14.88 | 73.34 | 28.00 | 14.40 | 8.17 | 2.75 | 0.88 | 2.31 | 7.31 |
| 68 | SiA 3560 | 44.20 | 50.60 | 45.00 | 157.20 | 20.50 | 3.53 | 80.00 | 1558.41 | 3.11 | 16.19 | 69.46 | 24.00 | 26.40 | 7.40 | 4.21 | 0.90 | 2.44 | 10.41 |
| 69 | SiA 4114 | 52.60 | 55.60 | 47.00 | 145.60 | 20.00 | 2.53 | 78.00 | 1562.32 | 3.10 | 15.31 | 75.20 | 24.00 | 9.60 | 6.14 | 2.80 | 0.87 | 2.26 | 6.56 |
| 70 | SiA 3419 | 45.10 | 59.30 | 47.00 | 166.10 | 18.60 | 2.73 | 80.00 | 1561.54 | 2.80 | 14.44 | 50.05 | 16.00 | 9.60 | 5.90 | 2.59 | 0.87 | 2.09 | 8.40 |
| 71 | SiA 3465 | 39.50 | 45.10 | 42.00 | 136.00 | 16.00 | 2.73 | 82.00 | 1558.88 | 2.93 | 13.13 | 74.10 | 20.00 | 12.00 | 5.97 | 2.17 | 0.87 | 2.19 | 8.71 |
| 72 | SiA 4068 | 45.20 | 56.40 | 45.00 | 144.80 | 19.00 | 3.27 | 80.00 | 1561.38 | 2.81 | 15.31 | 67.27 | 24.00 | 12.00 | 6.06 | 2.39 | 0.87 | 2.38 | 11.49 |
| 73 | SiA 3749 | 46.30 | 57.10 | 47.00 | 146.20 | 17.60 | 4.80 | 88.00 | 1557.94 | 2.96 | 15.75 | 71.38 | 32.00 | 4.80 | 6.12 | 2.62 | 0.88 | 2.09 | 8.24 |
| 74 | SiA 4141 | 48.20 | 59.40 | 45.00 | 146.40 | 17.80 | 4.80 | 80.00 | 1560.76 | 2.71 | 15.75 | 63.58 | 28.00 | 9.60 | 5.63 | 2.38 | 0.87 | 2.21 | 8.03 |
| 75 | SiA 2667 | 52.00 | 54.30 | 46.00 | 154.80 | 17.80 | 4.47 | 80.00 | 1560.60 | 3.09 | 13.13 | 70.50 | 32.00 | 9.60 | 5.10 | 2.48 | 0.87 | 1.79 | 16.06 |
| 76 | SiA 3422 | 46.40 | 62.40 | 53.00 | 153.70 | 16.90 | 4.93 | 84.00 | 1605.30 | 2.76 | 15.31 | 57.12 | 28.00 | 7.20 | 5.61 | 3.06 | 0.88 | 2.03 | 9.59 |
| 77 | SiA 3894 | 50.30 | 59.00 | 45.00 | 151.80 | 17.90 | 3.33 | 84.00 | 1558.25 | 3.07 | 14.88 | 51.56 | 20.00 | 14.40 | 7.29 | 2.76 | 0.87 | 1.66 | 11.16 |
| 78 | SiA 3282 | 43.00 | 49.10 | 36.00 | 128.00 | 14.00 | 1.47 | 82.00 | 1818.48 | 2.14 | 11.38 | 72.13 | 20.00 | 12.00 | 6.41 | 2.26 | 0.88 | 1.77 | 6.96 |
| 79 | SiA 3639 | 50.00 | 52.60 | 45.00 | 166.00 | 18.40 | 2.73 | 86.00 | 1817.75 | 3.02 | 10.94 | 68.36 | 20.00 | 12.00 | 11.27 | 1.76 | 0.86 | 1.84 | 13.56 |
| 80 | SiA 2856 | 49.00 | 53.80 | 46.00 | 127.40 | 16.70 | 4.00 | 83.00 | 1814.66 | 2.90 | 14.44 | 62.33 | 20.00 | 16.80 | 5.76 | 2.62 | 0.87 | 1.92 | 15.06 |
| 81 | SiA 3291 | 36.60 | 50.40 | 35.00 | 117.10 | 13.00 | 2.27 | 70.00 | 1816.48 | 2.15 | 16.19 | 53.05 | 20.00 | 9.60 | 6.81 | 2.58 | 0.88 | 2.23 | 6.60 |
| 82 | SiA 3430 | 39.50 | 45.00 | 45.00 | 155.20 | 16.90 | 2.73 | 80.00 | 1819.76 | 3.25 | 12.69 | 61.08 | 24.00 | 7.20 | 4.42 | 2.68 | 0.86 | 2.02 | 17.77 |
| 83 | SiA 4020 | 45.80 | 53.20 | 47.00 | 154.20 | 17.80 | 3.73 | 78.00 | 1816.30 | 2.73 | 10.94 | 75.04 | 24.00 | 12.00 | 5.77 | 2.76 | 0.87 | 2.15 | 15.20 |
| 84 | SiA 2663 | 46.70 | 49.70 | 45.00 | 147.60 | 17.60 | 3.73 | 84.00 | 1561.22 | 3.18 | 10.94 | 73.40 | 24.00 | 14.40 | 6.17 | 1.53 | 0.87 | 2.13 | 12.14 |

**Table 4.1 Contd…**

| S. No. | Genotype | SCMR at 30 DAS | SCMR at 45 DAS | Days to 50% flowering | Plant height (cm) | Panicle length (cm) | No. of productive tillers /plant | Days to maturity | No.of Grains / ear head | 1000 grain wt (g) | Protein (g/ 100g) | Carbo hydrate (g/ 100g) | Calcium (mg/ 100g) | Magnesium (mg/ 100g) | Iron (mg/ 100g) | Zinc (mg/ 100g) | Copper (mg/ 100g) | Manganese (mg/ 100g) | Grain yield/ plant (g) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | (1) | (2) | (3) | (4) | (5) | (6) | (7) | (8) | (9) | (10) | (11) | (12) | (13) | (14) | (15) | (16) | (17) | (18) |
| 85 | SiA 3554 | 41.20 | 57.20 | 46.00 | 160.40 | 19.00 | 3.93 | 88.00 | 1766.20 | 3.22 | 15.31 | 66.88 | 28.00 | 14.40 | 11.90 | 7.07 | 1.12 | 2.94 | 10.60 |
| 86 | SiA 3753 | 43.80 | 53.40 | 42.00 | 157.50 | 17.40 | 3.73 | 79.00 | 1559.35 | 2.98 | 14.88 | 67.35 | 20.00 | 12.00 | 12.08 | 7.05 | 1.19 | 3.30 | 6.75 |
| 87 | SiA 2844 | 43.10 | 51.60 | 46.00 | 163.20 | 22.80 | 2.80 | 80.00 | 1562.63 | 3.04 | 12.69 | 53.81 | 24.00 | 14.40 | 9.69 | 6.42 | 1.04 | 2.93 | 9.84 |
| 88 | SiA 4180 | 55.20 | 57.70 | 47.00 | 154.10 | 18.60 | 4.27 | 85.00 | 1559.04 | 2.79 | 18.38 | 68.87 | 20.00 | 12.00 | 11.67 | 4.22 | 0.91 | 3.40 | 14.02 |
| 89 | SiA 4005 | 39.80 | 59.00 | 42.00 | 147.40 | 16.30 | 4.20 | 75.00 | 1719.40 | 3.27 | 15.75 | 52.97 | 20.00 | 28.80 | 8.73 | 5.26 | 0.89 | 2.79 | 18.26 |
| 90 | SiA 2850 | 46.90 | 52.00 | 46.00 | 155.80 | 16.80 | 3.20 | 92.00 | 1813.39 | 3.13 | 14.88 | 74.53 | 24.00 | 26.40 | 6.19 | 5.84 | 0.88 | 2.65 | 15.68 |
| 91 | SiA 3513 | 42.00 | 55.50 | 42.00 | 149.00 | 16.80 | 3.53 | 83.00 | 1557.00 | 3.07 | 13.56 | 68.42 | 20.00 | 14.40 | 7.86 | 5.74 | 0.90 | 3.07 | 13.76 |
| 92 | SiA 3469 | 41.60 | 59.60 | 43.00 | 147.00 | 18.20 | 2.53 | 78.00 | 1814.30 | 3.06 | 13.56 | 62.04 | 28.00 | 24.00 | 11.22 | 5.22 | 0.90 | 3.11 | 8.87 |
| 93 | SiA 3281 | 46.90 | 52.70 | 54.00 | 158.40 | 16.80 | 2.53 | 78.00 | 1799.20 | 2.81 | 14.44 | 67.42 | 20.00 | 14.40 | 10.35 | 6.64 | 0.90 | 3.52 | 14.83 |
| 94 | SiA 1266 | 51.10 | 55.60 | 47.00 | 152.40 | 17.20 | 3.53 | 80.00 | 1559.66 | 2.84 | 13.56 | 73.40 | 36.00 | 24.00 | 8.53 | 6.14 | 0.90 | 3.16 | 16.29 |
| 95 | SiA 4182 | 41.80 | 50.10 | 47.00 | 149.80 | 15.70 | 4.00 | 79.00 | 1561.85 | 2.71 | 10.50 | 72.99 | 20.00 | 12.00 | 10.55 | 6.27 | 0.89 | 3.46 | 13.12 |
| 96 | SiA 3969 | 48.70 | 57.50 | 47.00 | 142.60 | 17.50 | 6.20 | 81.00 | 1756.20 | 3.14 | 11.38 | 67.17 | 24.00 | 12.00 | 12.84 | 6.21 | 0.89 | 3.68 | 18.82 |
| 97 | Prasad (C) | 43.76 | 51.03 | 44.25 | 130.25 | 15.75 | 2.97 | 74.50 | 1811.38 | 2.64 | 15.29 | 62.52 | 23.88 | 12.02 | 11.95 | 2.81 | 1.86 | 2.35 | 11.29 |
| 98 | SiA 3085 (C) | 48.90 | 57.44 | 44.50 | 155.89 | 19.70 | 3.40 | 82.50 | 1762.45 | 3.05 | 14.14 | 63.34 | 20.64 | 16.79 | 21.64 | 3.11 | 1.14 | 2.41 | 14.83 |
| 99 | SiA 3156 (C) | 46.06 | 57.36 | 44.38 | 146.65 | 18.08 | 3.03 | 84.63 | 1572.10 | 2.92 | 13.32 | 61.46 | 23.63 | 14.37 | 9.54 | 2.82 | 1.26 | 1.78 | 11.65 |
| 100 | Suryanandi (C) | 42.98 | 45.60 | 38.25 | 135.96 | 15.08 | 3.67 | 71.00 | 1561.69 | 2.90 | 14.02 | 62.40 | 35.35 | 12.54 | 18.37 | 3.45 | 0.97 | 2.44 | 11.39 |
| | **Minimm** | **34.70** | **42.90** | **32.00** | **110.50** | **11.00** | **1.00** | **60.00** | **1556.22** | **1.57** | **10.50** | **50.05** | **16.00** | **4.80** | **4.42** | **1.53** | **0.86** | **1.31** | **1.37** |
| | **Maximum** | **55.20** | **65.50** | **54.00** | **171.60** | **22.80** | **6.40** | **92.00** | **1820.12** | **3.53** | **18.38** | **76.42** | **40.00** | **31.20** | **32.50** | **7.07** | **2.76** | **4.12** | **19.33** |
| | **Mean** | **46.34** | **53.63** | **44.93** | **149.27** | **17.51** | **3.84** | **81.99** | **1677.68** | **2.91** | **14.10** | **61.87** | **24.03** | **15.10** | **10.88** | **3.26** | **1.26** | **2.33** | **11.39** |
| | **Std. Error** | **0.42** | **0.41** | **0.35** | **1.11** | **0.22** | **0.11** | **0.45** | **12.12** | **0.03** | **0.17** | **0.75** | **0.50** | **0.55** | **0.56** | **0.12** | **0.06** | **0.05** | **0.37** |
| | **Std. Deviation** | **4.25** | **4.13** | **3.50** | **11.08** | **2.18** | **1.07** | **4.49** | **121.24** | **0.30** | **1.67** | **7.55** | **4.98** | **5.52** | **5.62** | **1.19** | **0.65** | **0.46** | **3.70** |

**Table 4.2 Analysis of variance for 18 morpho-physiological and biochemical characters studied in foxtail millet [*Setaria italica* (L.) Beauv.]**

| Source of variation | d.f | SCMR at 30 DAS | SCMR at 45 DAS | Days to 50% flowering | Plant height | Panicle length | No. of productive tillers /plant | Days to maturity | No.of Grains / ear head | 1000 grain weight |
|---|---|---|---|---|---|---|---|---|---|---|
| | | Mean sum of squares | | | | | | | | |
| Block | 7 | 6.964 | 4.797 | 0.210 | 1.403 | 0.479 | 0.016 | 0.139 | 2523.687 | 0.008 |
| Entries | 99 | 19.742 ** | 19.519 ** | 15.182 ** | 161.298 ** | 5.727 ** | 1.231 ** | 32.266 ** | 18210.650 ** | 0.097 ** |
| Checks | 3 | 56.620 ** | 85.518 ** | 75.115 ** | 1036.958 ** | 36.288 ** | 0.859 ** | 334.115 ** | 132431.700 ** | 0.229 ** |
| Varieties | 95 | 18.556 ** | 17.366 ** | 12.252 ** | 121.583 ** | 4.787 ** | 1.165 ** | 19.052 ** | 14795.200 ** | 0.093 ** |
| Checks vs. Varieties | 1 | 21.788 | 26.042 * | 113.753 ** | 1307.220 ** | 3.358 ** | 8.610 ** | 382.003 ** | 15.610 | 0.031 |
| Error | 21 | 5.239 | 4.240 | 0.257 | 1.087 | 0.288 | 0.007 | 0.234 | 1484.970 | 0.012 |

| Source of variation | d.f | Protein (g/100g) | Carbo hydrate (g/100g) | Calcium (mg/100g) | Magnesium (mg/100g) | Iron (mg/100g) | Zinc (mg/100) | Copper (mg/100g) | Manganese (mg/100g) | Grain yield/ plant (g) |
|---|---|---|---|---|---|---|---|---|---|---|
| | | Mean sum of squares | | | | | | | | |
| Block | 7 | 0.588 | 0.546 | 0.122 | 0.160 | 0.104 | 0.000 | 0.001 | 0.027 | 0.747 |
| Entries | 99 | 2.922 ** | 57.173 ** | 34.524 ** | 43.080 ** | 42.754 ** | 1.437 ** | 0.452 ** | 0.233 ** | 14.513 ** |
| Checks | 3 | 5.320 ** | 4.716 ** | 336.718 ** | 311.224 ** | 250.694 ** | 0.726 ** | 1.195 ** | 0.784 ** | 23.160 ** |
| Varieties | 95 | 2.875 ** | 59.345 ** | 24.419 ** | 31.566 ** | 31.096 ** | 1.463 ** | 0.433 ** | 0.215 ** | 14.170 ** |
| Checks vs. Varieties | 1 | 0.202 | 8.184 ** | 87.879 ** | 332.457 ** | 526.524 ** | 1.184 ** | 0.062 ** | 0.214 ** | 21.188 ** |
| Error | 21 | 0.388 | 0.330 | 0.446 | 0.111 | 0.093 | 0.000 | 0.002 | 0.012 | 0.430 |

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

**Table 4.3 Estimates of genetic parameters for the 18 characters studied in foxtail millet [*Setaria italica* (L.) Beauv.]**

| S. No. | Character | Mean | Range | | Coefficient of variation | | Heritability (broad sense) (%) | Genetic advance as % of mean |
|---|---|---|---|---|---|---|---|---|
| | | | Minimum | Maximum | PCV (%) | GCV (%) | | |
| 1 | SCMR at 30 DAS | 46.34 | 34.70 | 55.20 | 8.56 | 7.00 | 66.80 | 11.78 |
| 2 | SCMR at 45 DAS | 53.63 | 42.90 | 65.50 | 7.13 | 6.01 | 71.02 | 10.44 |
| 3 | Days to 50% flowering | 44.93 | 32.00 | 54.00 | 6.93 | 6.84 | 97.36 | 13.91 |
| 4 | Plant height (cm) | 149.27 | 110.50 | 171.60 | 6.56 | 6.53 | 98.87 | 13.37 |
| 5 | Panicle length (cm) | 17.51 | 11.00 | 22.80 | 11.19 | 10.76 | 92.52 | 21.34 |
| 6 | No. of productive tillers /plant | 3.84 | 1.00 | 6.40 | 24.85 | 24.75 | 99.20 | 50.77 |
| 7 | Days to maturity | 81.99 | 60.00 | 92.00 | 4.73 | 4.70 | 98.46 | 9.60 |
| 8 | No of Grains / ear head | 1677.68 | 1556.22 | 1820.12 | 6.54 | 6.12 | 87.65 | 11.80 |
| 9 | 1000 grain wt (g) | 2.91 | 1.57 | 3.53 | 9.47 | 8.68 | 84.00 | 16.40 |
| 10 | Protein (g/100g) | 14.10 | 10.50 | 18.38 | 10.88 | 9.94 | 83.52 | 18.73 |
| 11 | Carbohydrate (g/100g) | 61.87 | 50.05 | 76.42 | 11.09 | 11.05 | 99.30 | 22.68 |
| 12 | Calcium (mg/100g) | 24.03 | 16.00 | 40.00 | 18.39 | 18.18 | 97.70 | 37.03 |
| 13 | Magnesium (mg/100g) | 15.10 | 4.80 | 31.20 | 33.01 | 32.93 | 99.56 | 67.70 |
| 14 | Iron (mg/100g) | 10.88 | 4.42 | 32.50 | 46.42 | 46.33 | 99.62 | 95.26 |
| 15 | Zinc (mg/100g) | 3.26 | 1.53 | 7.07 | 32.92 | 32.91 | 99.96 | 67.80 |
| 16 | Copper (mg/100g) | 1.26 | 0.86 | 2.76 | 46.57 | 46.47 | 99.54 | 95.50 |
| 17 | Manganese (mg/100g) | 2.33 | 1.31 | 4.12 | 17.80 | 17.15 | 92.81 | 34.03 |
| 18 | Grain yield/ plant (g) | 11.39 | 1.37 | 19.33 | 29.62 | 29.05 | 96.20 | 58.70 |

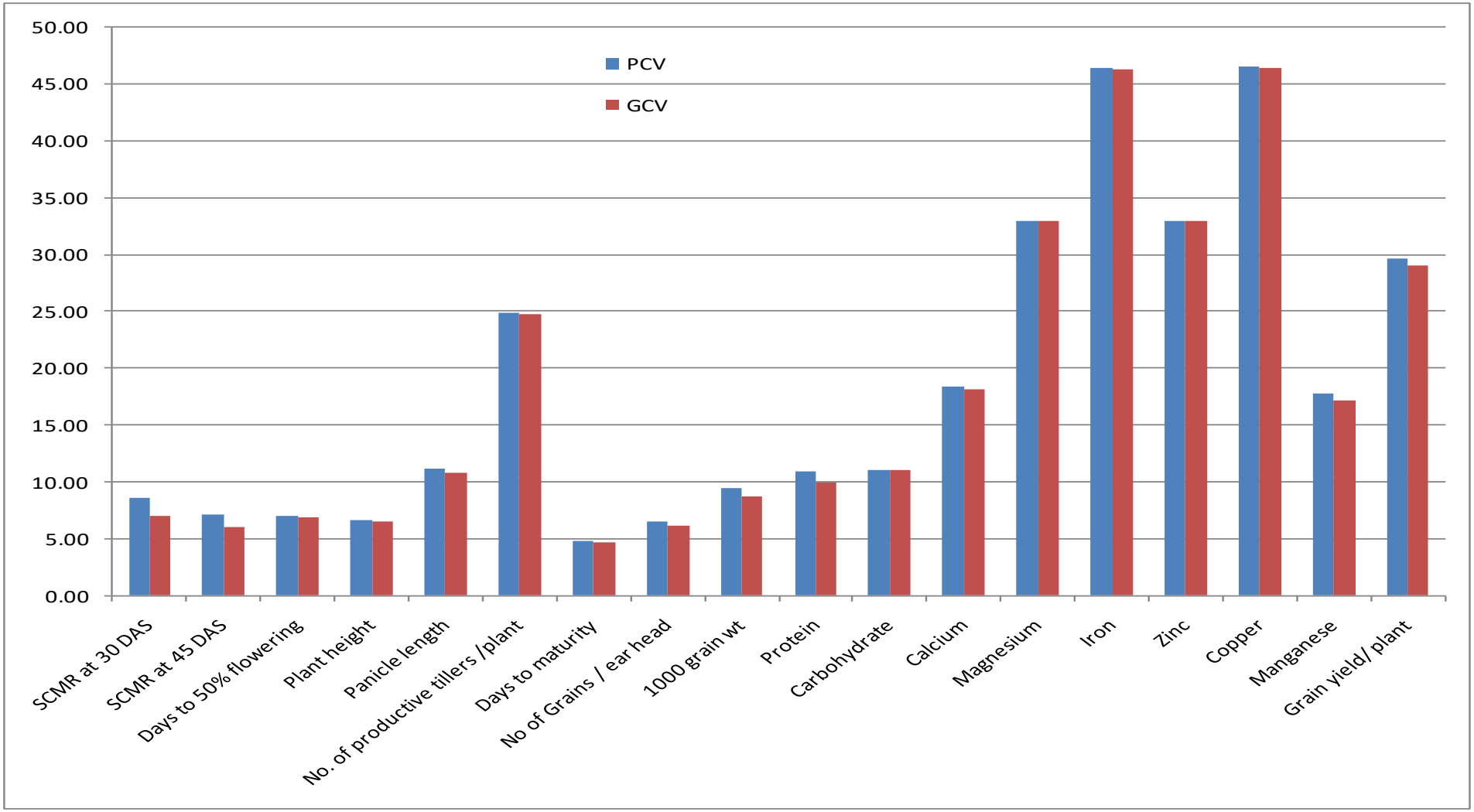



**Fig. 4.1 Phenotypic and Genotypic coefficients of variation for the 18 traits studied**

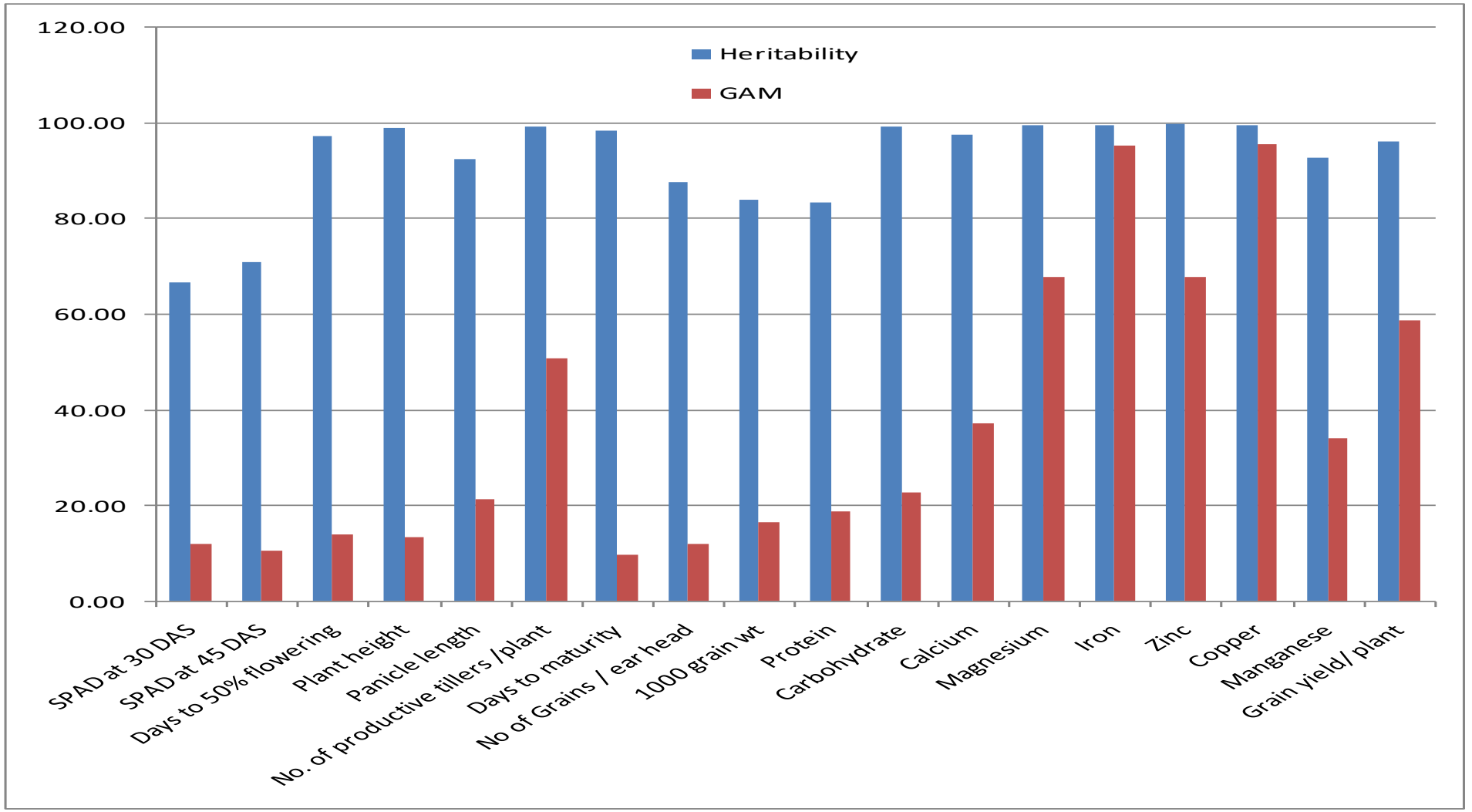



**Fig. 4.2 Pattern of Heritability and Genetic advance as *per cent* of mean for various traits in foxtail millet genetic resources**

### 4.1.3 Days to 50% flowering

The variation for number of days taken to 50% flowering ranged from 32 days (SiA 3222) to 54 days (SiA 4016 and SiA 3281) with a mean of 44.93 days. The difference between PCV (6.93) and GCV (6.84) values were very low indicating lesser impact of environmental component in the observed variation. Similar results were reported by Nirmalakumari and Vetriventhan (2010), Velzaco and Rimeri (2012), Yogeesh *et al.* (2015), Jyothsna *et al.* (2016a) and Amarnath *et al.* (2018a).

High heritability (97.36%) coupled with moderate genetic advance as per cent of mean (13.91%) noted for this trait indicated the presence of both additive and non-additive gene effects and hence, genetic improvement is possible both through varietal and hybrid development. Similar reports were published by Bheemesh (2017), Kavya *et al.* (2017a), Nirubana *et al.* (2017) and Amarnath *et al.* (2018a) for this character.

### 4.1.4 Plant height (cm)

The range of variation for plant height varied from 110.50 cm (SiA 3222) to 171.60 cm (SiA 4107) with a mean of 149.27 cm. The values of PCV (6.56) and GCV (6.53) were low indicating the variation among the genotypes was meager. Similar results were reported by Prasanna *et al.* (2013c), Brunda *et al.* (2014), Jyothsna *et al.* (2016c), Amarnath *et al.* (2018a) and Ayesha *et al.* (2019a).

High heritability (98.87%) accompanied with moderate genetic advance as per cent of mean (13.37%) observed for this trait indicated operation of both additive and non-additive gene actions and hence, simple selection may not be fruitful in improving this trait. These results were in agreement with the findings of Prasanna *et al.* (2013c), Brunda *et al.* (2014), Anuradha *et al.* (2017) and Kavya *et al.* (2017a).

### 4.1.5 Panicle length (cm)

This trait ranged from 11.00 cm (SiA 3409) to 22.80 cm (SiA 2844) amongst the 100 test genotypes with a mean of 17.51 cm. Moderate estimates of PCV (11.19) and GCV (10.76) indicated existence of comparatively moderate variability for this trait and provides scope for improvement through selection in advanced generations. These observations are in agreement with the earlier reports of Reddy *et al.* (2012), Brunda *et al.* (2014), Nandini *et al.* (2016) Anuradha *et al.* (2017), Talawar *et al.* (2017) and Amarnath *et al.* (2018a)

High heritability (92.52%) coupled with high genetic advance as per cent of mean (21.34%) was observed indicating the preponderance of additive gene action in the inheritance of this trait and simple selection would contribute to genetic improvement. Similar works were reported by Brunda *et al.* (2014), Shingane (2017), Anuradha *et al.* (2017), Talawar *et al.* (2017) and Ayesha *et al.* (2019a).

### 4.1.6 Number of productive tillers per plant

The variation for this character ranged from 1.00 (SiA 3222) to 6.40 (SiA 3697 and SiA 4045) with a mean of 3.84. The estimates of PCV (24.85) and GCV (24.75) were high. The difference between PCV and GCV value is more which indicates that there is high influence of environment in the observed variation. Similar results of were reported by Yogeesh *et al.* (2015), Mahanthesha *et al.* (2017a), Shingane *et al.* (2017), Talawar *et al.* (2017), Amarnath *et al.* (2018a) and Ayesha *et al.* (2019a).

High heritability (99.20%) accompanied with high genetic advance as per cent of mean (50.77%) observed for this trait indicated the role of additive gene action and hence, simple selection may be advocated for genetic improvement. These findings were in accordance with results of Anuradha *et al.* (2017), Mahanthesha *et al.* (2017a), Nirubana *et al.* (2017), Shingane *et al.* (2017), and Amarnath *et al.* (2018a).

### 4.1.7 Days to maturity

The range of variation for this character ranged from 60.00 days (SiA 3222) to 92.00 days (SiA 2745 and SiA 2850) with a mean of 81.99 days. The estimates of PCV (4.73) and GCV (4.70) were low. The difference between PCV and GCV value is less which indicates that there is little role of environmental component in the observed variation. These results are in agreement with Reddy *et al.* (2012), Jyothsna *et al.* (2016c), Shingane *et al.* (2017), Amarnath *et al.* (2018a) and Ayesha *et al.* (2019a)

High heritability (98.46%) coupled with low genetic advance as per cent of mean (9.60%) registered for this trait indicated the existence of non-additive gene action and therefore, simple selection will not contribute to genetic improvement. Similar results were reported by Jyothsna *et al.* (2016c) and Amarnath *et al.* (2018a).

### 4.1.8 Number of grains / ear head

This trait varied from 1556.22 (SiA 3409) to 1820.12 (SiA 3323) with a mean of 1677.68. The estimates of PCV (6.54) and GCV (6.12) were low and also the difference

between them is also less an indication, there is meagre role of environmental factor in the observed variation. Similar result was reported by Bheemesh (2017) for this character.

High heritability (87.65%) coupled with moderate genetic advance as per cent of mean (11.80%) observed for this trait revealed the existence of both additive and non-additive gene actions and indicated that genetic improvement is possible both through varietal and hybrid development. However, results of Bheemesh (2017) contradicted the findings and cited high heritability and genetic advance as per cent of mean for this trait.

### 4.1.9 1000 grain weight (g)

Thousand grain weight of the test genotypes ranged from 1.57 g (SiA 3409) to 3.53 g (SiA 4155) with a mean of 2.91 g. The values of PCV (9.47) and GCV (8.68) were low along with their differences between them indicated meagre scope of environmental factor in the observed variation. Similar results were reported by Nandini *et al.* (2016) and Amarnath *et al.* (2018a).

High heritability (84.00%) accompanied with moderate genetic advance as per cent of mean (16.40%) noted for this trait indicated the role of both additive and non-additive gene actions that paves the exploitation through heterosis breeding. Similar reports were published by Nandini *et al.* (2016) and Amarnath *et al.* (2018a) for this character.

### 4.1.10 Protein (g/100g)

The protein content ranged from 10.50 g (SiA 2579 and SiA 4182) to 18.38 g (SiA 4180) with a mean of 14.10 g. Moderate PCV (10.88) and low GCV (9.94) recorded for this trait indicated less variation among the test genotypes studied. The magnitude of PCV and GCV values is almost same implying that lesser environmental influence in the observed variation. Similar result of moderate PCV were reported by Shinde *et al.* (2014), Shingane *et al.* (2017), Kavya *et al.* (2017a) and Sharma *et al.* (2018).

High heritability (83.52%) and moderate genetic advance as per cent of mean (18.73%) was observed for this trait revealing the existence of both additive and non-additive gene actions that provides scope for exploitation through heterosis breeding. These findings were in agreement with the results of Shinde *et al.* (2014) and Subbulakshmi *et al.* (2018).

### 4.1.11 Carbohydrate (g/100g)

The carbohydrate in 100 g of seed ranged from 50.05 g (SiA 3419) to 76.42 g (SiA 4016) with a mean of 61.87 g. and The estimates of PCV (11.09) and GCV (11.05) were moderate indicating existence of comparatively moderate variability for this trait and its improvement is achieved through selection in later generations. However, contrary results of low PCV and GCV for this trait were registered by Kavya *et al.* (2017a) and Ayesha *et al.* (2019a) in foxtail millet.

High heritability (99.30%) coupled with high genetic advance as per cent of mean (22.68%) recorded for this character indicated the preponderance of additive gene effects and therefore, simple selection would be effective in genetic improvement. However different results of high heritability and moderate genetic advance as per cent of mean were reported by Kavya *et al.* (2017a) and Ayesha *et al.* (2019a).

### 4.1.12 Calcium (mg/100g)

The calcium content in 100 g of seed ranged from 16.00 mg (SiA 2737, SiA 3496, SiA 805, SiA 3908 and SiA 3419) to 40.00 mg (SiA 3038 and SiA 4044) with a mean of 24.03 mg. Moderate PCV (18.39) and GCV (18.18) were recorded for this trait indicating moderarte variation among genotypes studied. The magnitude of PCV and GCV were almost same indicating moderate influence of environment in inheritance of this trait. These findings are in conformity with the results of Govindaraj *et al*. (2011) and Rani (2014).

High estimates of heritability (97.70%) and genetic advance as per cent of mean (37.03%) for this trait indicated the predominance of additive gene action in the inheritance of this trait and hence, simple selection would lead to genetic improvement. These results were in tune with the findings of Prasanna *et al.* (2013c) and Ayesha *et al.* (2019a).

### 4.1.13 Magnesium (mg/100g)

The magnesium content in 100 g of seed varied from 4.80 mg (SiA 3038 and SiA 3749) to 31.20 mg (SiA 4027) with a mean of 15.10 mg. High estimates of PCV (33.01) and GCV (32.93) indicated large amount of variation among the test genotypes. The magnitude of PCV and GCV were almost the same implying lesser environmental influence in inheritance of this trait.

High heritability (99.56%) coupled with high genetic advance as per cent of mean (67.70%) indicated the role of additive gene action in governing the inheritance of this character thereby providing greater scope for improvement of this trait through simple selection procedures.

### 4.1.14 Iron (mg/100g)

The iron content in 100 g of seed ranged from 4.42 mg (SiA 3430) to 32.50 mg (SiA 3511) with a mean of 10.88 mg. The estimates of PCV (46.42) and GCV (46.33) were high indicating large variation among the genotypes studied. The magnitude of PCV and GCV were almost same indicating lesser influence of environment in inheritance of this trait. These findings are in conformity with the results of Shinde *et al.* (2014), Shingane *et al.* (2017), Nirubana *et al.* (2017), and Ayesha *et al.* (2019a).

High heritability (99.62%) coupled with high genetic advance as per cent of mean (95.26%) indicated the role of additive gene action in governing the inheritance of this character thereby indicating greater scope for improvement of this trait through simple selection. Similar results of high heritability and high genetic advance as per cent of mean were reported by Shinde *et al.* (2014), Shingane *et al.* (2017), Nirubana *et al.* (2017) and Ayesha *et al.* (2019a).

### 4.1.15 Zinc (mg/100g)

The zinc content in 100 g of seed varied from 1.53 mg (SiA 2663) to 7.07 mg (SiA 3554) with a mean of 3.26 mg. The estimates of PCV (32.92) and GCV (32.91) were high indicating large variation among the test genotypes. The magnitude of PCV and GCV were almost same indicating less influence of environment in inheritance of this trait. These findings are in conformity with the results of Nirubana *et al.* (2017) and Subbulakshmi *et al.* (2018).

High heritability (99.96%) coupled with high genetic advance as per cent of mean (67.80%) indicated the role of additive gene action in governing the inheritance of this character thereby indicating greater scope for improvement of this trait through simple selection. Similar results were reported by Nirubana *et al.* (2017) and Subbulakshmi *et al.* (2018) for this character.

### 4.1.16 Copper (mg/100g)

The copper content in 100 g of seed ranged from 0.86 mg (SiA 3827, SiA 3908, SiA 3639 and SiA 3430) to 2.76 mg (SiA 3611 and SiA 4016) with a mean of 1.26 mg. The estimates of PCV (46.57) and GCV (46.47) were high indicating large variation among the genotypes studied. The magnitude of PCV and GCV were almost the same indicating less influence of environment in inheritance of this trait. These findings are in conformity with the results of Anuradha *et al.* (2017) in pearl millet.

High heritability (99.54%) coupled with high genetic advance as per cent of mean (95.50%) indicated the role of additive gene action in governing the inheritance of this character thereby indicating greater scope for improvement of this trait through simple selection. Similar results of high heritability and high genetic advance as per cent of mean were reported by Anuradha *et al.* (2017) in pearl millet.

### 4.1.17 Manganese (mg/100g)

The manganese content in 100g of seed ranged from 1.31 mg (SiA 3908) to 4.12 mg (SiA 3559) with a mean of 2.33 mg. Moderate estimates of PCV (17.80) and GCV (17.15) indicated existence of comparatively moderate variability for this trait and thereby is amenable for improvement through selection in advanced generations. However, contrary results of high PCV and moderate GCV were reported by Anuradha *et al.* (2017) in pearl millet.

High heritability (92.81%) coupled with high genetic advance as per cent of mean (34.03%) was observed indicating the preponderance of additive gene action in the inheritance of this trait and hence, simple selection would contribute to genetic improvement. Similar results of high heritability and high genetic advance as per cent of mean were reported by Anuradha *et al.* (2017) in pearl millet.

### 4.1.18 Grain yield/plant (g)

The grain yield per plant ranged from 1.37g (SiA 3409) to 19.33g (SiA 3511) with a mean of 11.39g. High PCV (29.62) and GCV (29.05) were recorded for this trait indicating large magnitude of variation among the test genotypes. The difference between the magnitude of PCV and GCV is very less indicating little role of environment in inheritance of this trait. These findings are in accordance with the results of Brunda *et al.* (2014), Shinde *et al.* (2014), Jyothsna *et al.* (2016c), Anuradha *et al.* (2017), Kavya *et al.* (2017a), Mahanthesha *et al.* (2017a), Nirubana *et al.* (2017),

Talawar *et al.* (2017), Sharma *et al.* (2018) Subbulakshmi *et al.* (2018) and Ayesha *et al.* (2019a).

This character registered high heritability (96.20%) coupled with high genetic advance as per cent of mean (58.70%) indicating the role of additive gene effects in the inheritance of this character. Therefore breeding procedures involving simple selection will be effective for genetic improvement of this trait. Similar results of high heritability and high genetic advance as per cent of mean were reported by Brunda *et al.* (2014), Shinde *et al.* (2014), Jyothsna *et al.* (2016c), Anuradha *et al.* (2017), Kavya *et al.* (2017a), Mahanthesha *et al.* (2017a), Nirubana *et al.* (2017), Talawar *et al.* (2017), Sharma *et al.* (2018), Subbulakshmi *et al.* (2018) and Ayesha *et al.* (2019a).

An overall analysis of genetic parameters *viz*., GCV, PCV, heritability (bs) and genetic advance as *per cent* of mean revealed the following aspects.

- Estimates of PCV were slightly higher than the corresponding GCV values for all the characters studied indicating that the characters were less influenced by the environment and thereby offering ample scope for improvement of the traits through simple phenotypic selection.
- High heritability coupled with high genetic advance as *per cent* of mean was observed for the traits panicle length, number of productive tillers /plant, carbohydrate, calcium, magnesium, iron, zinc, copper, manganese and grain yield/ plant indicating the role of additive gene action in governing these traits and direct selection would be rewarding for crop improvement.
- High heritability accompanied with moderate genetic advance as *per cent* of mean recorded for the traits *viz*., SPAD at 30 DAS, SPAD at 45 DAS, days to 50% flowering, plant height, number of grains / ear head, 1000 grain weight and protein indicated the existence of both additive and non-additive genetic effects and therefore, suggested to adopt heterosis breeding for improvement of those characters.
- The traits number of productive tillers / plant, magnesium, iron, zinc, copper and grain yield/ plant possessed higher estimates of GCV, PCV, heritability and genetic advance as *per cent* of mean implying that these traits were predominantly under the control of additive gene action and genetic improvement can be achieved through simple selection for these traits.

## 4.2 GENETIC DIVERGENCE

The data collected on 18 grain yield and its attributes from 100 genetic resources of foxtail millet were computed for genetic divergence analysis employing Mahalanobis $D^2$ statistic and hierarchical cluster analysis. The groups or clusters formed using Tocher's method in $D^2$ statistic are further confirmed by principal component analysis (PCA) while grouping alone is done using Ward's method in hierarchical cluster analysis. The values obtained, indicated the existence of considerable magnitude of variability in the genetic resources studied that led to genetic diversity.

### 4.2.1 Mahalanobis' $D^2$ analysis

#### 4.2.1.1 Mahalanobis' $D^2$ values

For estimation of the $D^2$ values, correlated unstandardized means of 18 characters were transformed into standardized uncorrelated set of variables using pivotal condensation method. The $D^2$ values between a pair of genetic resources was obtained as the sum of squares of differences between pairs of corresponding uncorrelated values of any two genetic resources. Thus $D^2$ values were obtained for all the possible 4950 pairs of genetic resources.

The per cent contribution of the 18 metric characters studied in 100 genetic resources towards genetic divergence is presented in Table 4.4. Among the characters studied number of grains / ear head contributed maximum (64.85) towards genetic divergence by ranking 3210 times followed by plant height (13.35% by ranking 661 times), carbohydrate (8.14% by ranking 403 times), calcium (3.58% by ranking 177 times), iron (3.17% by ranking 157 times), magnesium (3.01% by ranking 149 times), SCMR at 30 DAS (1.43% by ranking 71 times), SCMR at 45 DAS (1.07% by ranking 53 times) contributed towards total genetic divergence in descending order.

It was noted that the traits days to maturity (0.71% by ranking 35 times), days to 50% flowering (0.36% by ranking 18times) and grain yield/ plant (0.28% by ranking 14 times) while panicle length (0.02% by ranking 1 time), protein (0.02 by ranking 1 time), number of productive tillers /plant, 1000 grain weight, zinc,copper and manganese contributed fewer (0.01% by ranking 0 times) towards the genetic divergence inferring more homogeneity for the traits in nthe genetic resources evaluated.

Similar reports were published by Kavya *et al.* (2017b) for plant height; Amarnath *et al.* (2019) for panicle length and number of productive tillers / plant; Ayesha *et al.* (2019b) for panicle length, number of productive tillers / plant, 1000 grain weight and protein content

#### 4.2.1.2 Grouping of genetic resources into various clusters

Hundred genetic resources were grouped into 11 distinct non overlapping clusters using the Tocher's method (Table 4.5, Fig 4.4.) suggesting presence of substantial genetic diversity in the experimental material screened. Of the 11 clusters obtained, cluster I was the largest comprising of largest number of genetic resources (43) followed by clusters II with 37 genetic resources, cluster VI with six genetic resources, cluster IV, IX with four genetic resources each and the remaining were monogenotypic clusters III, V, VII, VIII, X and XI containing only single genetic resource each with no intra-cluster distances ($D^2$ values) indicating high degree of heterogenity among the genetic resources. The formation of distinct monogenotypic clusters may be due to the fact that geographic barriers preventing gene flow or intensive natural and human selection for diverse and adaptable gene complexes must be responsible for this genetic diversity (Arunachalam and Ram, 1967).

#### 4.2.1.3 Average intra and inter-cluster $D^2$ value

The average intra and inter-cluster $D^2$ values of 11 clusters were presented in Table 4.6 and Fig 4.5. The inter-cluster distances were higher than the intra-cluster distances indicating presence of wider genetic diversity between the clusters rather than with in the clusters. Intra-cluster $D^2$ values ranged from 0.00 (cluster III, V, VII, VIII, X and XI) to 1256.89 (cluster IX). Least intra cluster distance (0.00) indicated the close resemblance between the genetic resources present in that cluster. Contrarily maximum intra-cluster distance represented diversity among the genetic resources within cluster. Therefore, genetic resources occupying the same cluster have low levels of diversity and selection of parents with in the cluster may not be considered promising.

Inter-cluster distance values varied from 705.65 (cluster VII and cluster X) to 69608.88 (cluster V and cluster XI). Hence the germplasm accessions between cluster V (SiA 4044) and cluster XI (SiA 3222) possessing maximum inter cluster distance between them had high degree of genetic diversity and thus may be utilized under inter-varietal hybridization programme (transgressive segregation) for obtaining

superior segregants. Similar results were reported by Mahanthesha *et al* (2017b) and Amarnath *et al.* (2019).

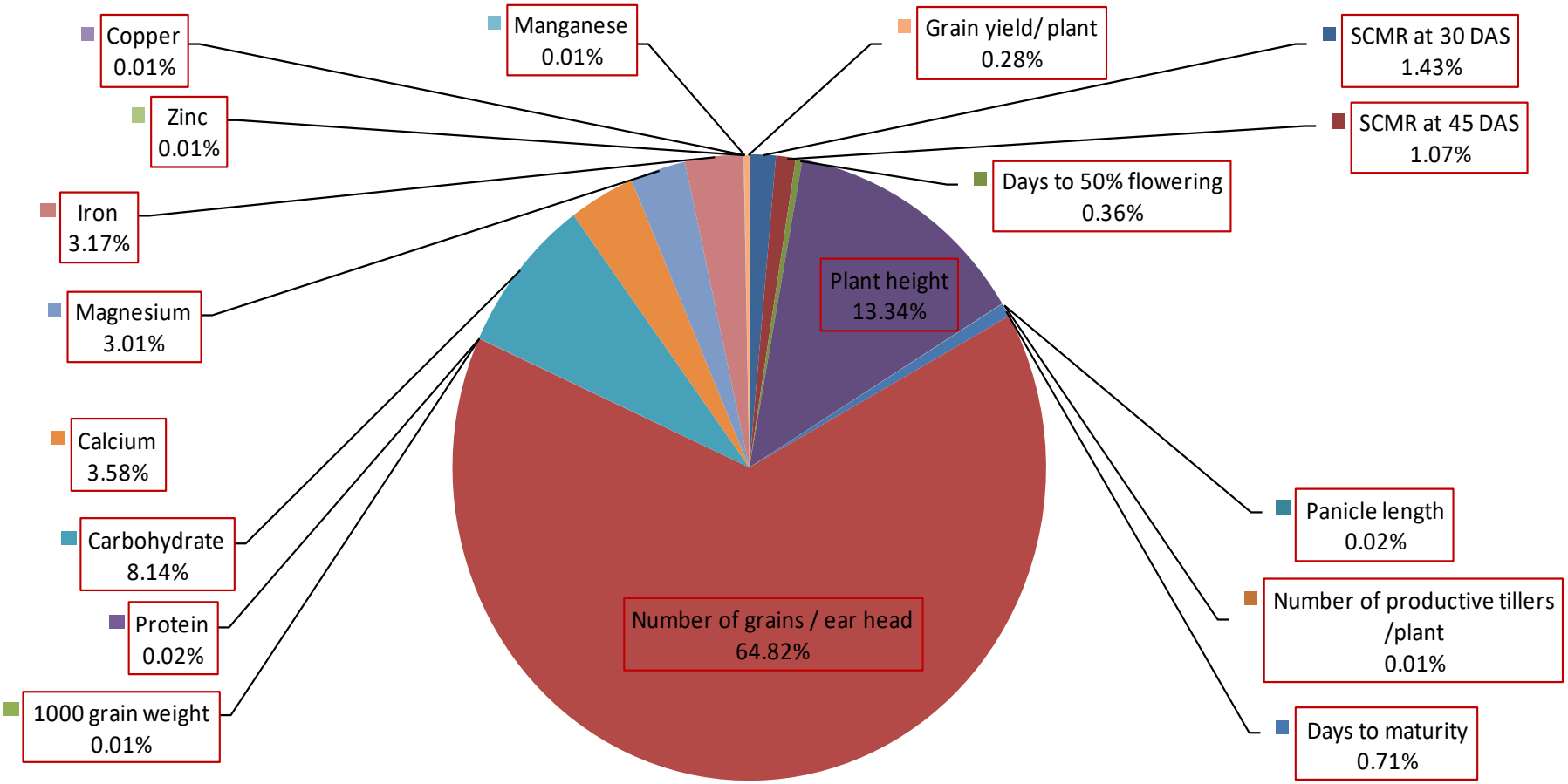



**Fig 4.3 Relative contribution of 18 characters to total genetic diversity in 100 foxtail millet genetic resources**

**Table 4.4 Contribution of different characters towards genetic divergence in 100 foxtail millet [*Setaria italica* (L.) Beauv.] genotypes**

| S.N0. | Characters | No.of times ranked first | Contribution (%) |
|---|---|---|---|
| 1 | SCMR at 30 DAS | 71 | 1.43 |
| 2 | SCMR at 45 DAS | 53 | 1.07 |
| 3 | Days to 50% flowering | 18 | 0.36 |
| 4 | Plant height | 661 | 13.35 |
| 5 | Panicle length | 1 | 0.02 |
| 6 | Number of productive tillers | 0 | 0.01 |
| 7 | Days to maturity | 35 | 0.71 |
| 8 | Number of grains / ear head | 3210 | 64.85 |
| 9 | 1000 grain weight | 0 | 0.01 |
| 10 | Protein | 1 | 0.02 |
| 11 | Carbohydrate | 403 | 8.14 |
| 12 | Calcium | 177 | 3.58 |
| 13 | Magnesium | 149 | 3.01 |
| 14 | Iron | 157 | 3.17 |
| 15 | Zinc | 0 | 0.01 |
| 16 | Copper | 0 | 0.01 |
| 17 | Manganese | 0 | 0.01 |
| 18 | Grain yield/ plant | 14 | 0.28 |

**Table 4.5 Clustering pattern of 100 foxtail millet [*Setaria italica* (L.) Beauv.] genotypes by Tocher's method**

| Cluster No. | No. of genotypes | Genotype(s) |
|---|---|---|
| I | 43 | SiA 2713, SiA 4182, SiA 2663, SiA 3513, SiA 4068, SiA 3697, SiA 3436, SiA 4009, SiA 4114, SiA 3965, SiA 3462, SiA 4141, SiA 3827, SiA 3793, SiA 3753, SiA 3156 (C), SiA 3588, SiA 2667, SiA 4036, SiA 4180, SiA 3749, SiA 3908, SiA 3560, SiA 1266, SiA 3971, SiA 3894, SiA 3643, SiA 3674, SiA 3972, SiA 3756, SiA 3516, SiA 4045, SiA 4167, SiA 2864, SiA 3423, SiA 3465, SiA 3420, SiA 3038, SiA 2844, Suryanandi (C), SiA 2849, SiA 4027, SiA 4013. |
| II | 37 | SiA 2671, SiA 4020, SiA 2674, SiA 2757, SiA 3855, SiA 3639, SiA 3559, SiA 3657, SiA 2745, SiA 3430, SiA 4063, SiA 3737, SiA 2662, SiA 4179, SiA 3496, SiA 3498, SiA 3492, SiA 2737, SiA 4155, SiA 2579, SiA 4181, SiA 3469, SiA 3851, SiA 3323, SiA 3413, SiA 3754,SiA 805, SiA 2850, SiA 4107, SiA 3611, SiA 3281, SiA 3701, SiA 3511, Prasad (C), SiA 4061, SiA 2697, SiA 2856 |
| III | 1 | SiA 3419 |
| IV | 4 | SiA 3554, SiA 3085 (C), SiA 3969, SiA 3499 |
| V | 1 | SiA 4044 |
| VI | 6 | SiA 3580, SiA 3429, SiA 3627, SiA 3422, SiA 4016, SiA 2681 |
| VII | 1 | SiA 3282 |
| VIII | 1 | SiA 3409 |
| IX | 4 | SiA 3577, SiA 3435, SiA 1244, SiA 4005 |
| X | 1 | SiA 3291 |
| XI | 1 | SiA 3222 |

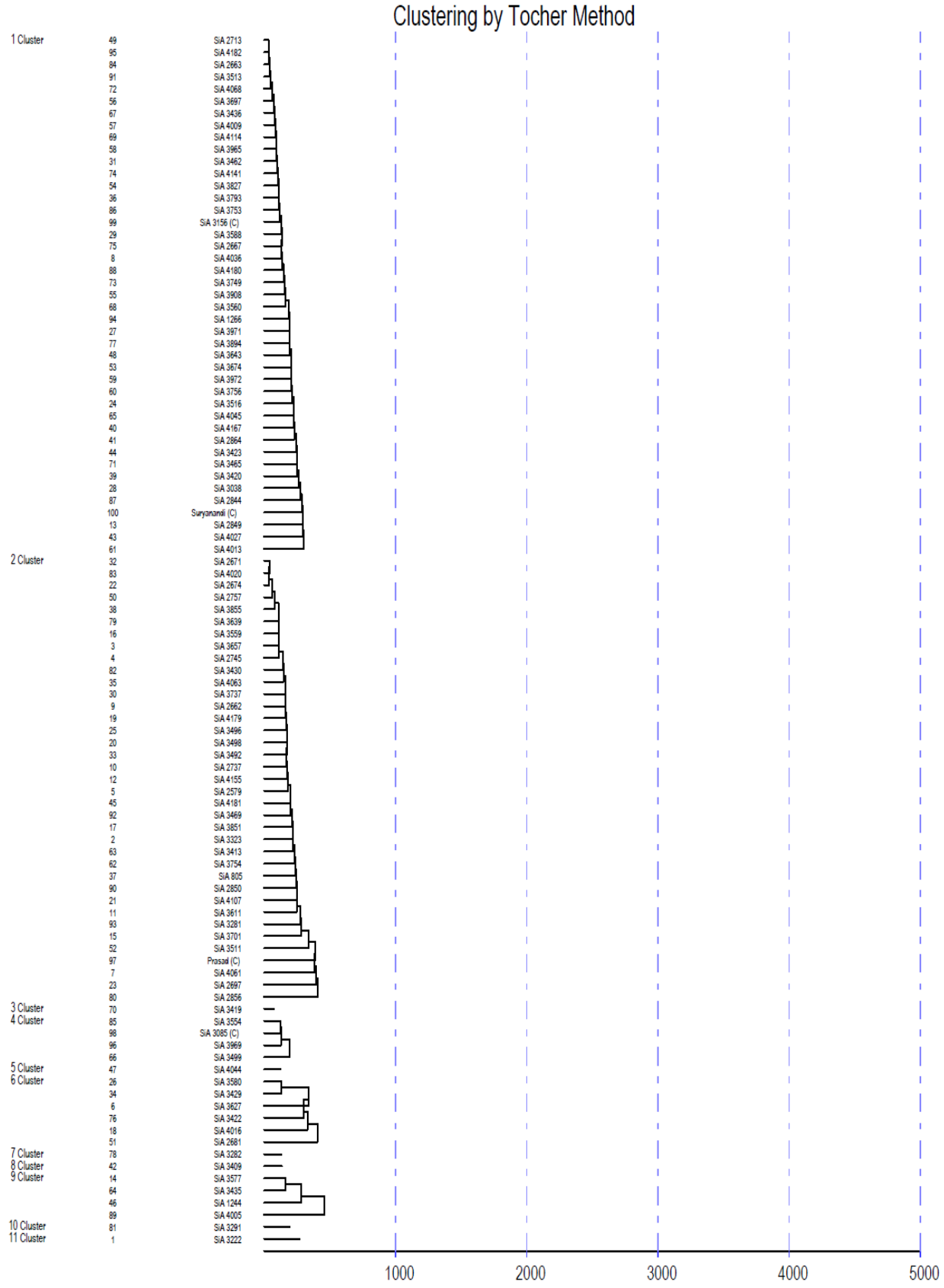
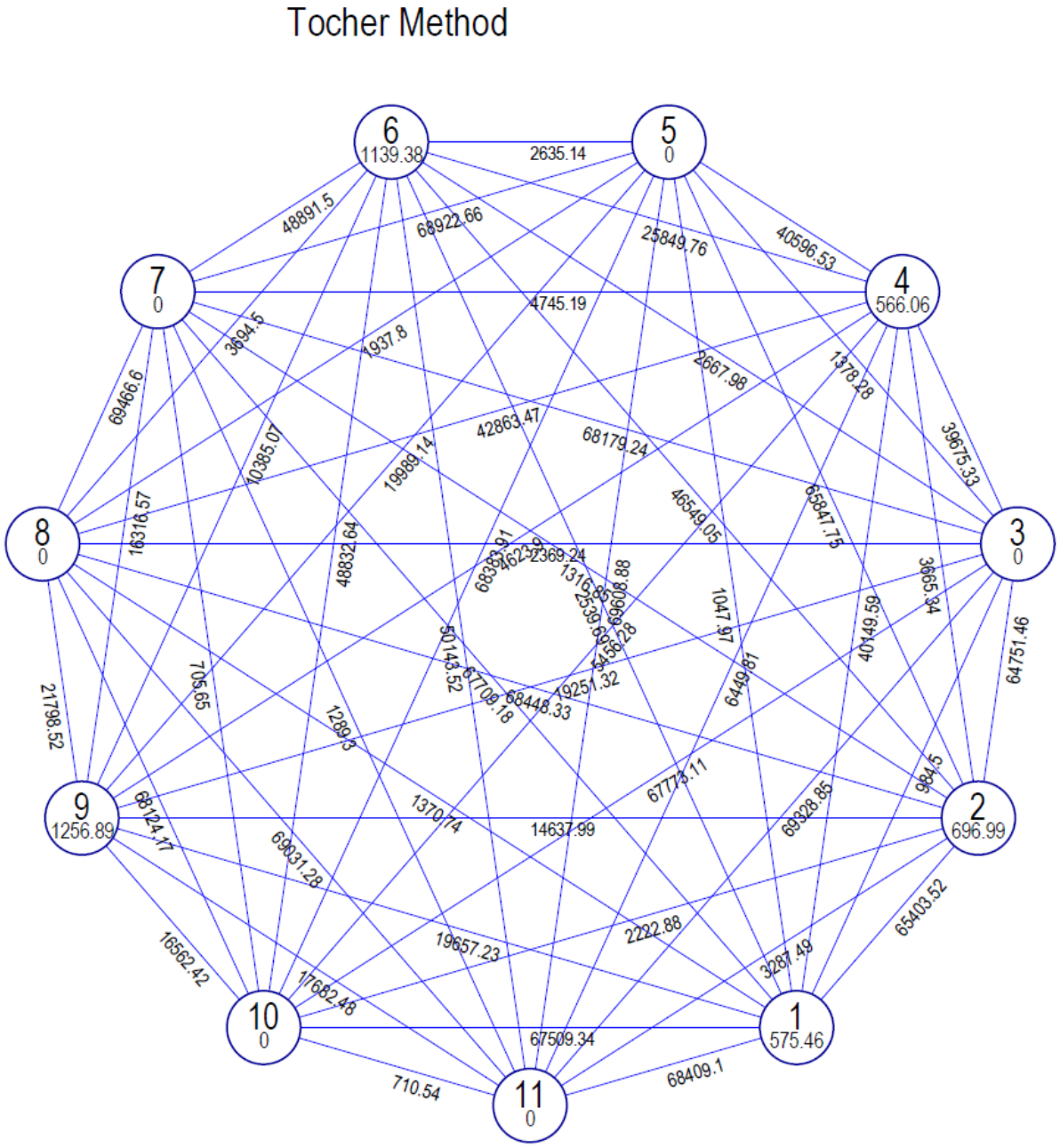



**Fig. 4.4 Dendrogram showing relationship among 100 foxtail millet [*Setaria italica* (L.) Beauv.] genotypes in 11 clusters based on Mahalanobis' $D^2$ values**




**Mahalanobis Euclidean Distance (Not to the Scale)**

**Fig. 4.5 Cluster diagram showing average intra and inter cluster distances**

**Table 4.6 Average intra and inter-cluster distances ($D^2$ values) among 11 clusters of 100 foxtail millet [*Setaria italica* (L.) Beauv.] genotypes**

| Cluster No. | I | II | III | IV | V | VI | VII | VIII | IX | X | XI |
|---|---|---|---|---|---|---|---|---|---|---|---|
| **I** | **575.46** | 65403.52 | 984.50 | 40149.59 | 1047.97 | 2539.69 | 67709.18 | 1370.74 | 19657.23 | 67509.34 | 68409.10 |
| **II** | | **696.99** | 64751.46 | 3665.34 | 65847.75 | 46549.05 | 1316.85 | 68448.33 | 14637.99 | 2222.88 | 3287.49 |
| **III** | | | **0.00** | 39675.33 | 1378.28 | 2667.98 | 68179.24 | 2369.24 | 19251.32 | 67773.11 | 69328.85 |
| **IV** | | | | **566.06** | 40596.53 | 25849.76 | 4745.19 | 42863.47 | 4623.90 | 5456.28 | 6449.81 |
| **V** | | | | | **0.00** | 2635.14 | 68922.66 | 1937.80 | 19989.14 | 68383.91 | 69608.88 |
| **VI** | | | | | | **1139.38** | 48891.50 | 3694.50 | 10385.07 | 48832.64 | 50143.52 |
| **VII** | | | | | | | **0.00** | 69466.60 | 16316.57 | 705.65 | 1289.30 |
| **VIII** | | | | | | | | **0.00** | 21798.52 | 68124.17 | 69031.28 |
| **IX** | | | | | | | | | **1256.89** | 16562.42 | 17682.48 |
| **X** | | | | | | | | | | **0.00** | 710.54 |
| **XI** | | | | | | | | | | | **0.00** |

**Note:** Diagonal values are intra-cluster distances. Off-diagonal values are inter-cluster distances

#### 4.2.1.4 Cluster mean values

The cluster means indicate the average performance of all the genotypes present in a particular cluster. The cluster means values for 18 characters studied were presented in Table 4.7. Wide spectrum of variation was observed in clusters for the characters studied implying that the clusters formed were distinct. The cluster V reported maximum panicle length (19.2), productive tillers / plant (5.33) and highest contents of calcium (39.89), magnesium (21.9), iron (23.54) and manganese (2.78). Highest 1000 grain weight (3), zinc content (4.65) and grain yield / plant (13.48) were noticed in cluster IV. Cluster XI registered highest SCMR at 45 DAS (46.94) and desired earliness for days to 50 % flowering (32.09) and maturity (60.16). Cluster VII registered highest number of grains / ear head (1818) and maximum carbohydrate content (71.71). The clusters II, III, VI and X reported highest SCMR 30 DAS (46.94), plant height (165.9), copper content (1.83) and protein content (16.54) respectively.

The result indicates that selection of genetic resources having desired values for particular trait could be made and utilized in the hybridization programme for improvement of that character. It is observed that no cluster contained at least one germplasm accession with all the desirable traits, which ruled out the possibility of selecting directly one genotype for immediate use. Therefore, hybridization between the selected germplasm accessions from divergent clusters is essential to judiciously combine all the targeted traits. Similar findings were reported by Kavya *et al.* (2017b) and Amarnath *et al.* (2019).

**Table 4.7 Cluster means with respect to yield and its attributes among 100 foxtail millet genetic resources**

| Cluster No. | SCMR at 30 DAS | SCMR at 45 DAS | Days to 50% flowering | Plant height (cm) | Panicle length (cm) | Number of productive tillers /plant | Days to maturity | Number of Grains / ear head | 1000 grain weight (g) | Protein (g/ 100g) | Carbohydrate (g/ 100g) | Calcium (mg/ 100g) | Magnesium (mg/ 100g) | Iron (mg/ 100g) | Zinc (mg/ 100g) | Copper (mg/ 100g) | Manganese (mg/ 100g) | Grain yield/ plant (g) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **I** | 46.63 | 54.76 | 44.84 | 147.02 | 17.69 | 4.17 | 81.92 | 1559.98 | 2.95 | 14.22 | 63.63 | 24.98 | 14.91 | 9.41 | 3.31 | 1.15 | 2.31 | 10.52 |
| **II** | **46.94** | 52.60 | 45.00 | 153.46 | 17.64 | 3.50 | 82.88 | 1814.37 | 2.96 | 14.08 | 61.27 | 22.92 | 15.51 | 11.97 | 3.13 | 1.36 | 2.34 | 13.09 |
| **III** | 43.58 | 59.93 | 46.84 | **165.89** | 18.93 | 2.67 | 80.16 | 1561.54 | 2.79 | 14.86 | **50.29** | **16.21** | 9.71 | 5.93 | 2.58 | 0.88 | 2.03 | 8.79 |
| **IV** | 44.15 | 56.35 | 45.38 | 153.28 | 19.16 | 4.58 | 83.12 | 1758.91 | **3.00** | 14.17 | 63.39 | 23.21 | 13.62 | 13.41 | **4.65** | 1.02 | 2.75 | **13.48** |
| **V** | 40.83 | 51.01 | **49.84** | 151.36 | **19.20** | **5.33** | **85.16** | 1559.82 | 2.65 | 13.47 | 50.98 | **39.89** | **21.90** | **23.54** | 2.68 | 0.89 | **2.78** | 5.12 |
| **VI** | 46.09 | 48.63 | 48.01 | 150.85 | 16.76 | 4.13 | 83.91 | 1600.67 | 2.96 | 13.83 | 59.38 | 24.62 | 14.40 | 15.92 | 3.31 | **1.83** | 2.26 | 10.23 |
| **VII** | 44.73 | 50.66 | 36.09 | 128.11 | 13.53 | 1.48 | 81.91 | **1818.48** | 2.12 | **11.73** | **71.71** | 20.25 | 12.04 | 6.38 | 2.26 | **0.84** | 1.84 | 6.66 |
| **VIII** | 43.63 | **46.41** | **49.84** | 123.16 | **11.40** | 1.97 | 70.16 | **1556.22** | **1.61** | 12.16 | 56.04 | 23.89 | **7.50** | 6.37 | 2.47 | 0.89 | 2.38 | **1.03** |
| **IX** | 45.40 | 54.90 | 45.09 | 153.29 | 17.67 | 4.52 | 81.60 | 1697.03 | 2.91 | 14.26 | 57.29 | 22.00 | 20.41 | 9.54 | 3.70 | 1.44 | 2.47 | 12.44 |
| **X** | **38.33** | 51.96 | 35.09 | 117.21 | 12.53 | 2.28 | 69.91 | 1816.48 | 2.13 | **16.54** | 52.63 | 20.25 | 9.64 | 6.78 | 2.58 | **0.84** | 2.30 | 6.30 |
| **XI** | 46.63 | **65.91** | **32.09** | **109.96** | 14.53 | **1.04** | **60.16** | 1816.66 | 2.50 | 12.89 | 63.02 | 32.12 | 12.00 | **4.41** | **1.62** | 0.98 | **1.69** | 9.47 |

**Note:** Bold figures indicate minimum and maximum values in each character

### 4.2.2 Canonical (vector) root analysis

The canonical root analysis or principal component analysis (PCA) was used to validate the clustering pattern obtained by Mahalanobis $D^2$ statistic. For 100 foxtail millet genetic resources, canonical root analysis was conducted as per the procedure outlined by Rao (1952). Seven canonical roots accounted for 67.371 per cent of total divergence (Table 4.8). The first, second and third roots accounted for 17.239, 10.406 and 10.030 per cent respectively to total variability. The remaining canonical roots *viz*., fourth, fifth, sixth and seventh contributed 9.264, 8.269, 6.557 and 5.606 per cent respectively towards the total variability. These seven canonical roots were retained based on the scree plot and threshold eigen value greater than one (Fig 4.6). The mean values of canonical variates for three roots X, Y and Z were furnished in Table 4.9. Two dimensional (2D) and Three dimensional (3D) picture were constructed by plotting the mean values of vectors as in Fig 4.7 and Fig 4.8 respectively. The amount of contribution of different traits towards canonical vectors total divergence was presented in Table 4.10.

In the vector $Z_1$, traits contributing towards total divergence positively were plant height (0.462), 1000 grain weight (0.379), panicle length (0.365), days to maturity (0.362), grain yield/ plant (0.322), days to 50% flowering (0.215), zinc (0.210), SCMR at 30 DAS (0.197), iron (0.193), magnesium (0.189), number of productive tillers /plant (0.163), manganese (0.162), copper (0.093), number of grains / ear head (0.067), carbohydrate (0.063) and protein (0.019), while the rest of the characters contributed negatively to the total diversity.

For the vector $Z_2$, number of grains / ear head (0.438), copper (0.301), grain yield/ plant (0.233), iron (0.110), plant height (0.105), SCMR at 30 DAS (0.081), days to maturity (0.056) and panicle length (0.052) contributed poitively to the genetic diversity. While the remaining characters contributed negatively to the total diversity.

In the vector $Z_3$, the traits *viz.*, SCMR at 45 DAS (0.423), 1000 grain weight (0.323), SCMR at 30 DAS (0.298), panicle length (0.244), carbohydrate (0.239), protein (0.129), grain yield/ plant (0.115), number of productive tillers /plant (0.095), calcium (0.067) and days to maturity (0.012) had contributed positively to diversity. However the remaining traits showed negative contribution towards divergence.

Zinc (0.341) and manganese (0.337) together contributed positively maximum to the diversity in vector $Z_4$, followed by number of grains / ear head (0.322), SCMR at 45 DAS (0.315), grain yield/ plant (0.296), 1000 grain weight (0.145), SCMR at 30 DAS (0.084), magnesium (0.075), carbohydrate (0.058), iron (0.028) and calcium (0.024) towards total divergence positively. While the remaining characters showed contribution negatively towards divergence.

In the vector $Z_5$, traits contributing towards total divergence positively were carbohydrate (0.526), days to 50% flowering (0.251), SCMR at 30 DAS (0.228), grain yield/ plant (0.145), zinc (0.135), manganese (0.094), calcium (0.059), plant height (0.044) and number of grains / ear head (0.014). While the rest of the characters contributed negatively to the total diversity.

For the vector $Z_6$, calcium (0.647), iron (0.468), copper (0.44), SCMR at 30 DAS (0.150), carbohydrate (0.106), grain yield/ plant (0.085), 1000 grain weight (0.062), number of productive tillers /plant (0.05), days to maturity (0.025) and manganese (0.009) contributed positively towards genetic diversity. However the remaining characters contributed negatively to the total divergence.

In the vector $Z_7$, traits contributing towards total divergence positively were magnesium (0.565), SCMR at 30 DAS (0.282), number of productive tillers /plant (0.233), grain yield/ plant (0.121), iron (0.088), calcium (0.052), panicle length (0.043) and SCMR at 45 DAS (0.039). While the rest of the characters showed negative contribution towards divergence.

**Table 4.8. Canonical vectors for 18 characters in 100 foxtail millet genetic resources.**

| **Parameter** | **$Z_1$** | **$Z_2$** | **$Z_3$** | **$Z_4$** | **$Z_5$** | **$Z_6$** | **$Z_7$** |
|---|---|---|---|---|---|---|---|
| Eigene Value (Root) | 3.103 | 1.873 | 1.805 | 1.668 | 1.488 | 1.180 | 1.009 |
| % Var. Exp. | 17.239 | 10.406 | 10.030 | 9.264 | 8.269 | 6.557 | 5.606 |
| Cum. Var. Exp. | 17.239 | 27.645 | 37.675 | 46.939 | 55.208 | 61.765 | 67.371 |
| **Character** | | | | | | | |
| SCMR at 30 DAS | 0.197 | 0.081 | 0.298 | 0.084 | 0.228 | 0.150 | 0.282 |
| SCMR at 45 DAS | -0.024 | -0.208 | 0.423 | 0.315 | -0.297 | -0.049 | 0.039 |
| Days to 50% flowering | 0.215 | -0.144 | -0.163 | -0.478 | 0.251 | -0.122 | -0.119 |
| Plant height (cm) | 0.462 | 0.105 | -0.101 | -0.070 | 0.044 | -0.131 | -0.102 |
| Panicle length (cm) | 0.365 | 0.052 | 0.244 | -0.078 | -0.114 | -0.172 | 0.043 |
| No. of productive tillers /plant | 0.163 | -0.348 | 0.095 | -0.334 | -0.164 | 0.050 | 0.233 |
| Days to maturity | 0.362 | 0.056 | 0.012 | -0.286 | -0.023 | 0.025 | -0.188 |
| No. of grains / ear head | 0.067 | 0.438 | -0.150 | 0.322 | 0.014 | -0.109 | -0.180 |
| 1000 grain weight (g) | 0.379 | -0.050 | 0.323 | 0.145 | -0.113 | 0.062 | -0.083 |
| Protein (g/100g) | 0.019 | -0.171 | 0.129 | -0.002 | -0.480 | -0.043 | -0.554 |
| Carbohydrate (g/100g) | 0.063 | -0.118 | 0.239 | 0.058 | 0.526 | 0.106 | -0.148 |
| Calcium (mg/100g) | -0.037 | -0.314 | 0.067 | 0.024 | 0.059 | 0.647 | 0.052 |
| Magnesium (mg/100g) | 0.189 | -0.064 | -0.246 | 0.075 | -0.321 | -0.170 | 0.565 |
| Iron (mg/100g) | 0.193 | 0.110 | -0.383 | 0.028 | -0.218 | 0.468 | 0.088 |
| Zinc (mg/100g) | 0.210 | -0.403 | -0.290 | 0.341 | 0.135 | -0.118 | -0.047 |
| Copper (mg/100g) | 0.093 | 0.301 | -0.053 | -0.088 | -0.179 | 0.440 | -0.188 |
| Manganese (mg/100g) | 0.162 | -0.363 | -0.337 | 0.337 | 0.094 | 0.009 | -0.230 |
| Grain yield/ plant (g) | 0.322 | 0.233 | 0.115 | 0.296 | 0.145 | 0.085 | 0.121 |

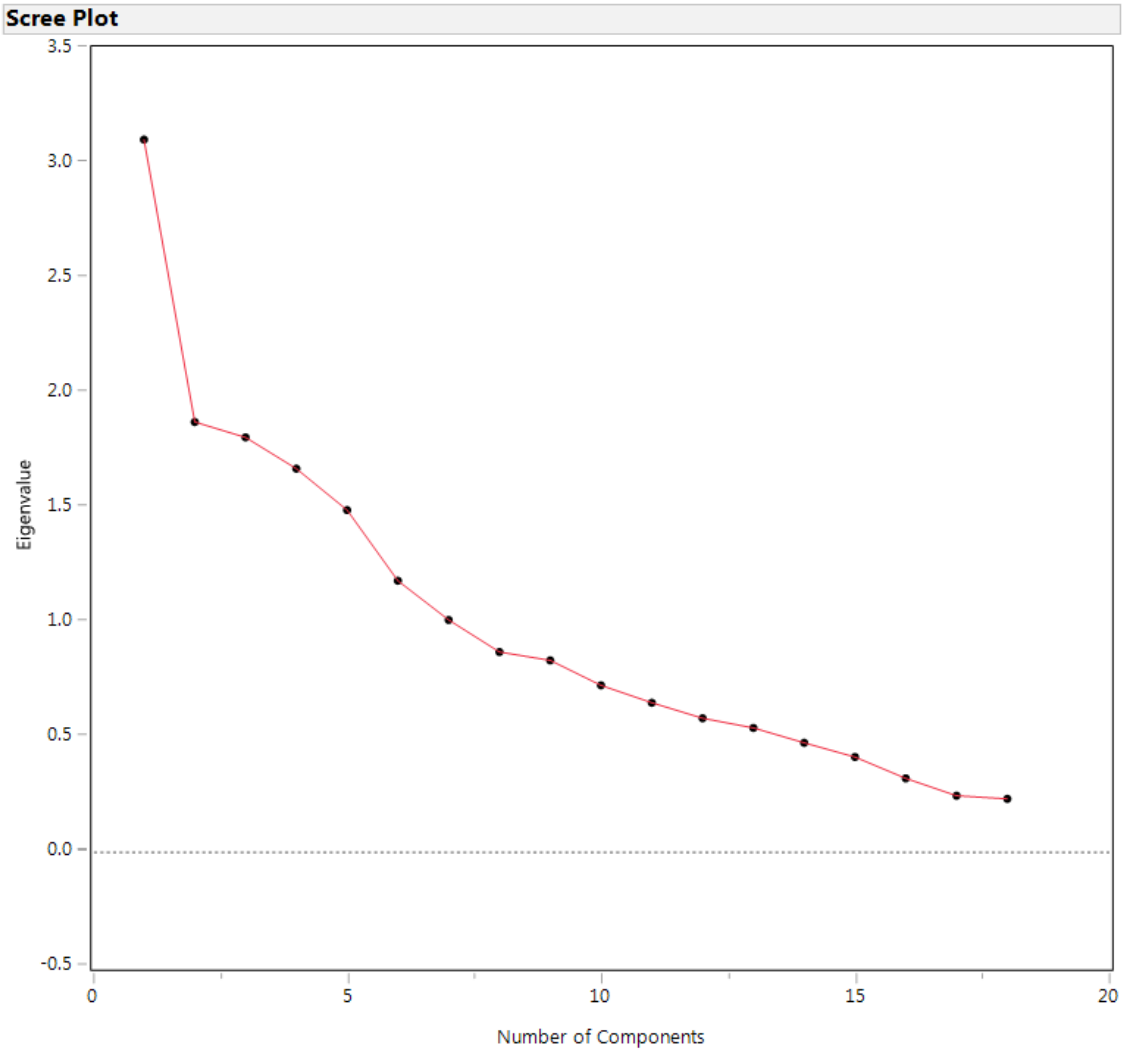



**Fig 4.6 Scree plot showing the eigen value variation for 18 quantitaive traits in 100 foxtail millet genetic resources**

The PCA analysis thus, identified that the maximum contributing traits towards the existing variability as plant height, 1000 grain weight, panicle length, days to maturity, grain yield/ plant, days to 50% flowering and zinc. In PCA analysis magnitude of relative contribution of a particular trait towards total variability is important rather than the sign (+/-) which only indicate the direction of variability.

The means of principal component variates / canonical variates of all the studied 100 foxtail millet genotypes belonging to first three Principal Component vectors were estimated and tabulated in Table 4.9. Using these means of principal component variates, two dimensional (2D) and three dimensional (3D) scattered diagram were obtained (Fig 4.7 and 4.8). This 2D and 3D plot shows that the genotypes numbered 1 and 42 *i.e.* SiA 3409 and SiA 3222 were scattered relatively away from other genotypes confirming the Tocher's clustering where these two genotypes are falling in independent monogenotypic clusters *viz.*, cluster V and XI, respectively. Further this kind of distribution of genotypes in different clusters and scatter diagrams indicate that they are divergent from each other and may be utilized in hybridization programme which may result in heterotic $F_1$s and transgressive segregants subjected to have good *per se* performance for all the desirable characters. Similar studies confirming $D^2$ analysis (Tocher's method) using PCA were earlier done by many researchers in various crops including foxtail millet, Kumar *et al.* (2015) in paddy; Rani *et al.* (2014) in finger millet; Amarnath *et al.* (2018c) and Ayesha *et al.* (2018) in foxtail millet.

**Table 4.9 Mean values of canonical vectors for 100 foxtail millet genetic resources**

| S. No. | Genotype | X Vector | Y Vector | Z Vector |
|---|---|---|---|---|
| 1 | SiA 3222 | 224.579 | 777.792 | -226.917 |
| 2 | SiA 3323 | 254.342 | 784.604 | -248.926 |
| 3 | SiA 3657 | 266.393 | 789.259 | -239.025 |
| 4 | SiA 2745 | 268.821 | 791.530 | -241.780 |
| 5 | SiA 2579 | 270.778 | 791.081 | -244.933 |
| 6 | SiA 3627 | 249.883 | 696.322 | -216.297 |
| 7 | SiA 4061 | 247.416 | 788.775 | -241.236 |
| 8 | SiA 4036 | 245.757 | 672.076 | -203.398 |
| 9 | SiA 2662 | 262.225 | 788.507 | -241.725 |
| 10 | SiA 2737 | 266.601 | 790.869 | -245.230 |
| 11 | SiA 3611 | 271.025 | 791.388 | -249.862 |
| 12 | SiA 4155 | 268.880 | 787.866 | -241.814 |
| 13 | SiA 2849 | 251.919 | 676.679 | -206.243 |
| 14 | SiA 3577 | 264.389 | 738.860 | -229.244 |
| 15 | SiA 3701 | 257.113 | 787.894 | -249.547 |
| 16 | SiA 3559 | 259.145 | 785.238 | -239.139 |
| 17 | SiA 3851 | 269.522 | 788.578 | -244.623 |
| 18 | SiA 4016 | 247.912 | 692.668 | -211.986 |
| 19 | SiA 4179 | 259.526 | 790.696 | -241.705 |
| 20 | SiA 3498 | 262.575 | 789.923 | -250.696 |
| 21 | SiA 4107 | 274.271 | 792.971 | -249.439 |
| 22 | SiA 2674 | 259.497 | 783.367 | -235.508 |
| 23 | SiA 2697 | 259.454 | 775.244 | -233.342 |
| 24 | SiA 3516 | 239.343 | 672.101 | -202.679 |
| 25 | SiA 3496 | 258.832 | 790.848 | -248.347 |
| 26 | SiA 3580 | 247.212 | 682.505 | -219.996 |
| 27 | SiA 3971 | 238.096 | 672.222 | -206.666 |
| 28 | SiA 3038 | 235.240 | 669.956 | -196.537 |
| 29 | SiA 3588 | 249.003 | 674.444 | -203.639 |
| 30 | SiA 3737 | 261.997 | 781.631 | -241.296 |
| 31 | SiA 3462 | 243.165 | 674.380 | -200.718 |
| 32 | SiA 2671 | 262.374 | 784.046 | -237.111 |
| 33 | SiA 3492 | 265.338 | 787.285 | -245.917 |
| 34 | SiA 3429 | 241.528 | 687.215 | -217.607 |
| 35 | SiA 4063 | 254.364 | 783.831 | -237.191 |
| 36 | SiA 3793 | 243.634 | 673.021 | -203.295 |
| 37 | SiA 805 | 256.212 | 787.746 | -243.582 |
| 38 | SiA 3855 | 259.798 | 787.387 | -239.830 |
| 39 | SiA 3420 | 227.164 | 667.035 | -196.377 |
| 40 | SiA 4167 | 231.859 | 672.314 | -203.478 |

**Table 4.9 Contd…**

| S. No. | Genotype | X Vector | Y Vector | Z Vector |
|---|---|---|---|---|
| 41 | SiA 2864 | 234.117 | 669.727 | -198.974 |
| 42 | SiA 3409 | 216.235 | 667.889 | -205.558 |
| 43 | SiA 4027 | 246.117 | 675.679 | -210.138 |
| 44 | SiA 3423 | 227.301 | 669.917 | -205.010 |
| 45 | SiA 4181 | 263.909 | 778.128 | -235.763 |
| 46 | SiA 1244 | 243.748 | 724.795 | -218.279 |
| 47 | SiA 4044 | 244.664 | 668.279 | -214.885 |
| 48 | SiA 3643 | 241.245 | 676.113 | -196.937 |
| 49 | SiA 2713 | 239.824 | 676.326 | -202.768 |
| 50 | SiA 2757 | 267.826 | 787.956 | -237.201 |
| 51 | SiA 2681 | 246.430 | 703.116 | -209.561 |
| 52 | SiA 3511 | 268.675 | 794.699 | -251.397 |
| 53 | SiA 3674 | 244.804 | 668.388 | -207.676 |
| 54 | SiA 3827 | 243.948 | 675.256 | -195.615 |
| 55 | SiA 3908 | 238.987 | 674.826 | -198.210 |
| 56 | SiA 3697 | 245.003 | 672.500 | -199.571 |
| 57 | SiA 4009 | 235.616 | 670.383 | -198.472 |
| 58 | SiA 3965 | 234.859 | 668.062 | -202.074 |
| 59 | SiA 3972 | 230.969 | 667.382 | -199.954 |
| 60 | SiA 3756 | 237.973 | 670.679 | -208.664 |
| 61 | SiA 4013 | 245.608 | 670.726 | -210.653 |
| 62 | SiA 3754 | 257.220 | 780.092 | -236.463 |
| 63 | SiA 3413 | 254.346 | 783.406 | -247.267 |
| 64 | SiA 3435 | 253.798 | 728.858 | -224.791 |
| 65 | SiA 4045 | 231.774 | 670.078 | -200.924 |
| 66 | SiA 3499 | 252.332 | 758.028 | -234.650 |
| 67 | SiA 3436 | 239.699 | 667.290 | -199.927 |
| 68 | SiA 3560 | 246.766 | 670.481 | -204.260 |
| 69 | SiA 4114 | 237.907 | 670.686 | -193.722 |
| 70 | SiA 3419 | 245.080 | 677.275 | -202.981 |
| 71 | SiA 3465 | 230.388 | 668.732 | -194.305 |
| 72 | SiA 4068 | 237.405 | 671.571 | -197.100 |
| 73 | SiA 3749 | 238.896 | 666.189 | -192.649 |
| 74 | SiA 4141 | 236.516 | 668.800 | -194.475 |
| 75 | SiA 2667 | 244.240 | 671.231 | -193.569 |
| 76 | SiA 3422 | 245.474 | 692.043 | -210.878 |
| 77 | SiA 3894 | 242.401 | 673.975 | -199.044 |
| 78 | SiA 3282 | 241.969 | 786.065 | -236.933 |
| 79 | SiA 3639 | 269.107 | 791.604 | -240.181 |
| 80 | SiA 2856 | 249.636 | 783.615 | -235.097 |

**Table 4.9 Contd…**

| S. No. | Genotype | X Vector | Y Vector | Z Vector |
|---|---|---|---|---|
| 81 | SiA 3291 | 229.259 | 783.656 | -240.843 |
| 82 | SiA 3430 | 258.441 | 790.464 | -242.172 |
| 83 | SiA 4020 | 260.009 | 784.786 | -235.350 |
| 84 | SiA 2663 | 241.162 | 672.985 | -197.123 |
| 85 | SiA 3554 | 263.390 | 759.893 | -233.366 |
| 86 | SiA 3753 | 242.749 | 671.731 | -203.416 |
| 87 | SiA 2844 | 248.393 | 675.389 | -207.203 |
| 88 | SiA 4180 | 248.893 | 672.515 | -195.753 |
| 89 | SiA 4005 | 251.105 | 742.313 | -229.605 |
| 90 | SiA 2850 | 269.314 | 782.594 | -239.365 |
| 91 | SiA 3513 | 241.164 | 670.983 | -199.657 |
| 92 | SiA 3469 | 256.055 | 779.676 | -241.392 |
| 93 | SiA 3281 | 264.403 | 778.875 | -243.146 |
| 94 | SiA 1266 | 247.329 | 666.601 | -198.675 |
| 95 | SiA 4182 | 241.369 | 673.080 | -204.112 |
| 96 | SiA 3969 | 255.892 | 756.726 | -227.761 |
| 97 | Prasad (C) | 244.823 | 781.937 | -240.260 |
| 98 | SiA 3085 (C) | 262.958 | 765.049 | -234.791 |
| 99 | SiA 3156 (C) | 241.268 | 678.535 | -201.884 |
| 100 | Suryanandi (C) | 229.014 | 669.8 | -2 04.238 |

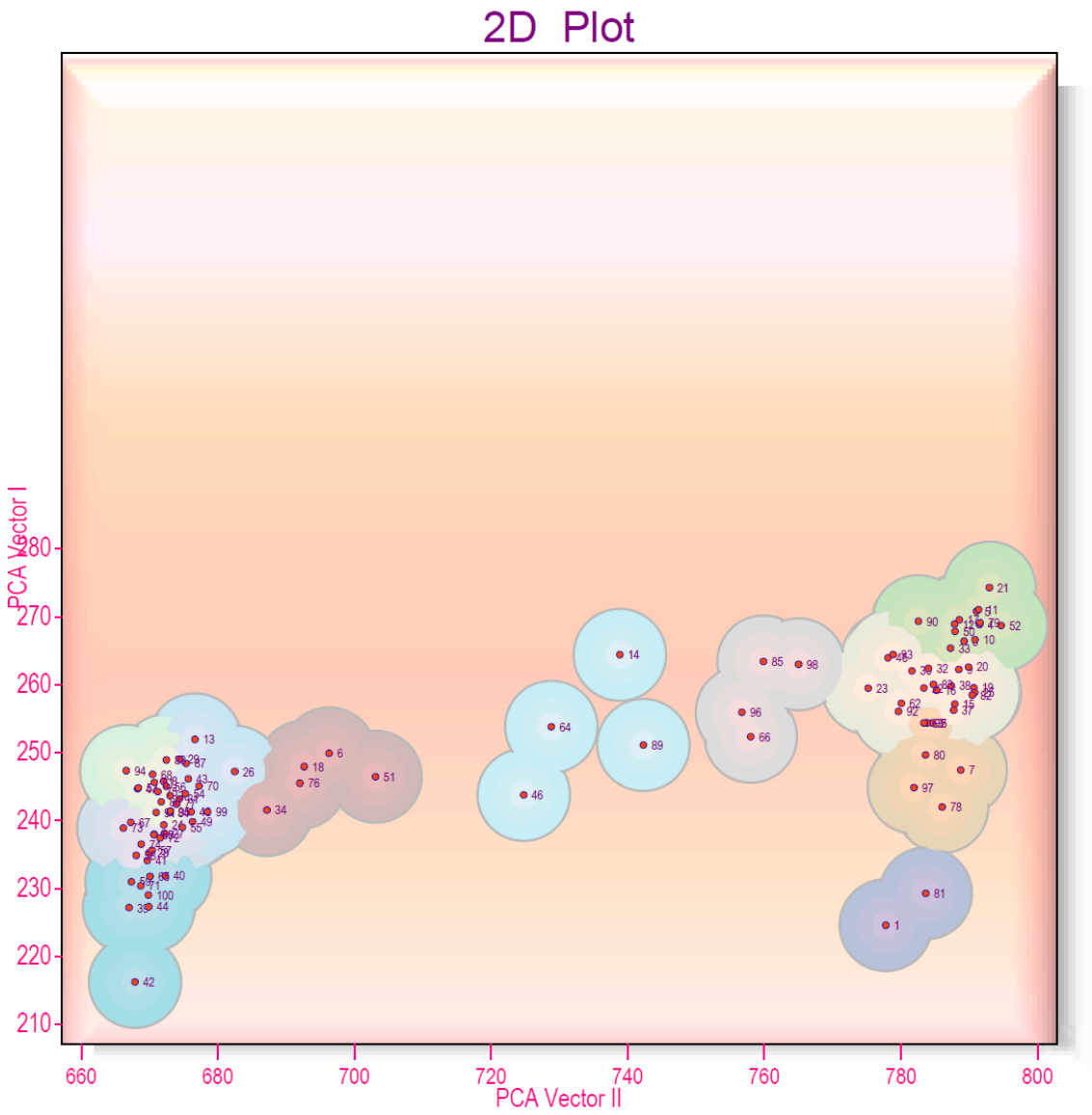



**Fig. 4.7 Two dimensional (2D) graph showing relative positions of 100 foxtail millet [*Setaria italica* (L.) Beauv.] genotypes based on PCA scores**

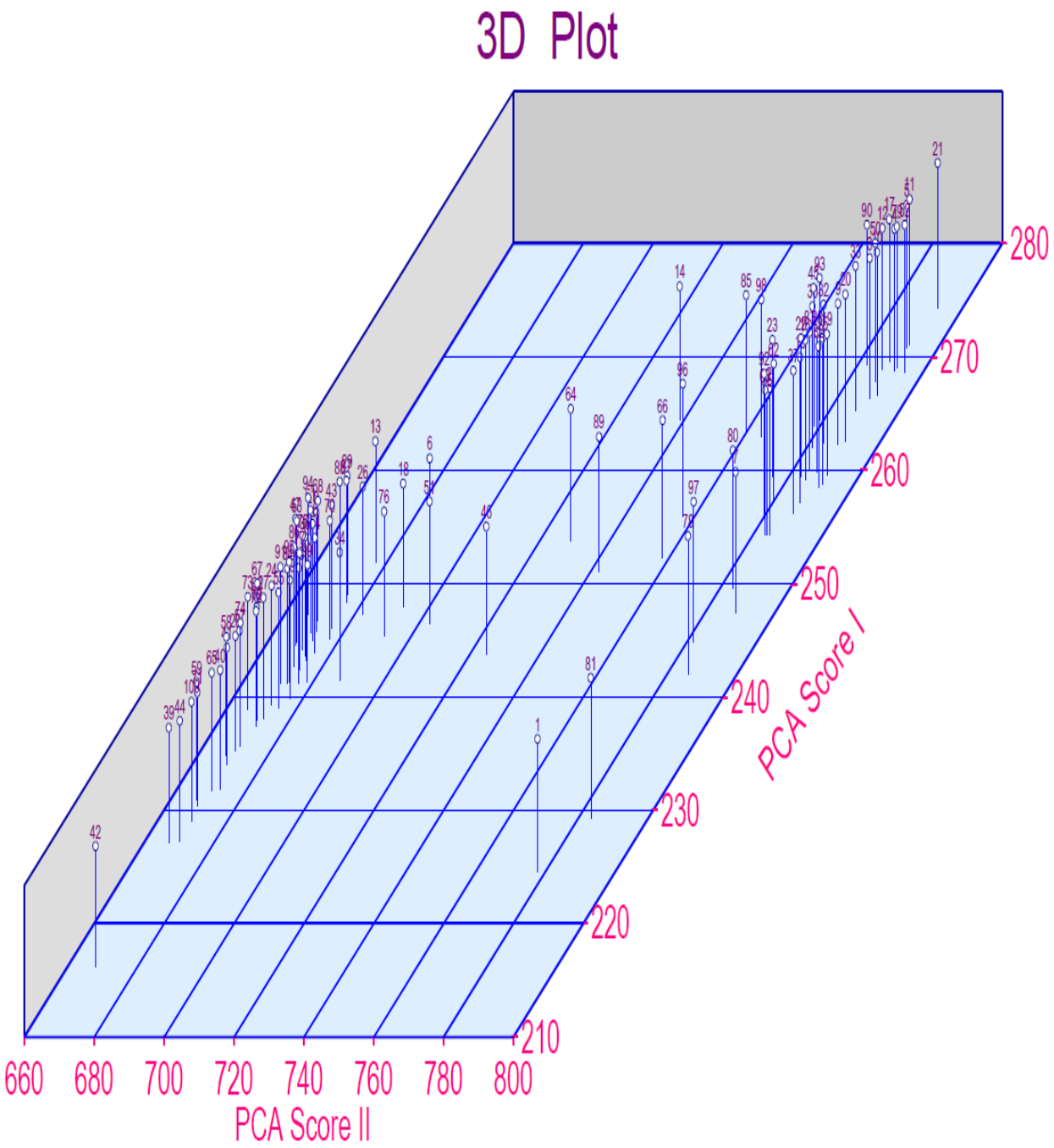



**Fig. 4.8 Three dimensional (3D) graph showing relative positions of 100 foxtail millet [*Setaria italica* (L.) Beauv.] genotypes based on PCA scores**

## 4.2.3 Hierarchial Cluster Analysis

Hierarchial cluster analysis was also done for the 100 foxtail millet genetic resources. The clusters were formed using cluster Euclidean$^2$ distances. The cluster analysis using Euclidean$^2$ distances provides a useful statistical tool for measuring the genetic diversity among genetic resource collections with respect to characters considered together.

### 4.2.3.1 Grouping of genotypes into various clusters

Using the Ward's minimum variance method (Anderberg, 1993), 100 foxtail millet genetic resources were grouped into 11 clusters and their distribution in each cluster at random (Table 4.10) along with the dendrogram was delineated (Fig 4.9). The constellation plot depicting relationship for the 100 genetic resources was also shown (Fig 4.10).

Clustering pattern divulged that majority of genotypes congegrated in cluster III (16) followed by cluster VIII (14), cluster IX (12), cluster VII (11) and cluster V (10). The clusters IV, VI and XI comprised of eight genotypes each. Seven and five genotypes were grouped in clusters X and II, respectively. The cluster I registered as monogenotypic / solitary cluster might have resulted due to geographic barriers preventing gene flow or intensive natural and human selection for diverse and adaptable gene complexes.

### 4.2.3.2 Genetic distance

Estimates of genetic distance matrix was based on 18 metric traits for all pair wise combinations of (100×99)/2 =4950 for the 100 foxtail millet genotypes (data not shown). The observed genetic distance ranged from 2.455 (SiA 3657and SiA 3085) to 12.029 (SiA 3222 and SiA 3580) pair wise combinations reflecting the wide diversity among the genotypes. The low genetic distance within the genotypes points towards their proximity and thus confirms that there is enough genetic diversity for the traits analysed in the genotypes despite their relatedness. The genotypes with high genetic distance can be utilized directly as potent parents in breeding programmes to achieve improved yields.

**Table 4.10 Clustering pattern of 100 foxtail millet [ *Setaria italica* (L.) Beauv.] genotypes by Ward's minimum variance method**

| Cluster No. | No. of genotypes | Name of genotype (s) |
|---|---|---|
| I | 1 | SiA 3222 |
| II | 5 | SiA 3323, SiA 3496, SiA 3409, SiA 3282 and SiA 3291 |
| III | 16 | SiA 3657,SiA 3085 (C),SiA 2662, SiA 4155, SiA 2674, SiA 3737, SiA 3754, SiA 2745, SiA 3639, SiA 2579, SiA 3430, SiA 2737, SiA 3492, SiA 4107, SiA 3851 and SiA 3511 |
| IV | 8 | SiA 3611, SiA 4027, SiA 3701, SiA 3429, SiA 3580, SiA 3498, SiA 4044 and SiA 3674 |
| V | 10 | SiA 3627, SiA 3577, SiA 3588, SiA 3560, SiA 4013, SiA 3554, SiA 2850, SiA 1266, SiA 4005 and SiA 3469 |
| VI | 8 | SiA 3559, SiA 3969, SiA 4180, SiA 3753, SiA 3513, SiA 4182, SiA 2844 and SiA 3281 |
| VII | 11 | SiA 4061, Prasad (C) , SiA 4179, SiA 2856, SiA 3971, SiA 3423, SiA 3965, SiA 3972, Suryanandi (C), SiA 3516 and SiA 3038 |
| VIII | 14 | SiA 4036, SiA 3697, SiA 2671, SiA 4020, SiA 2713, SiA 2663, SiA 3827, SiA 2667, SiA 3908, SiA 4016, SiA 3793, SiA 3422, SiA 2864 and SiA 3436 |
| IX | 12 | SiA 2849, SiA 3462, SiA 3894, SiA 3419, SiA 3643, SiA 4009, SiA 3156 (C), SiA 3465, SiA 4114, SiA 4068, SiA 3749 and SiA 4141 |
| X | 7 | SiA 805, SiA 3756, SiA 3413, SiA 3435, SiA 3499, SiA 3420 and SiA 4045 |
| XI | 8 | SiA 2697, SiA 3855, SiA 4181, SiA 2757, SiA 4063, SiA 1244, SiA 2681 and SiA 4167 |

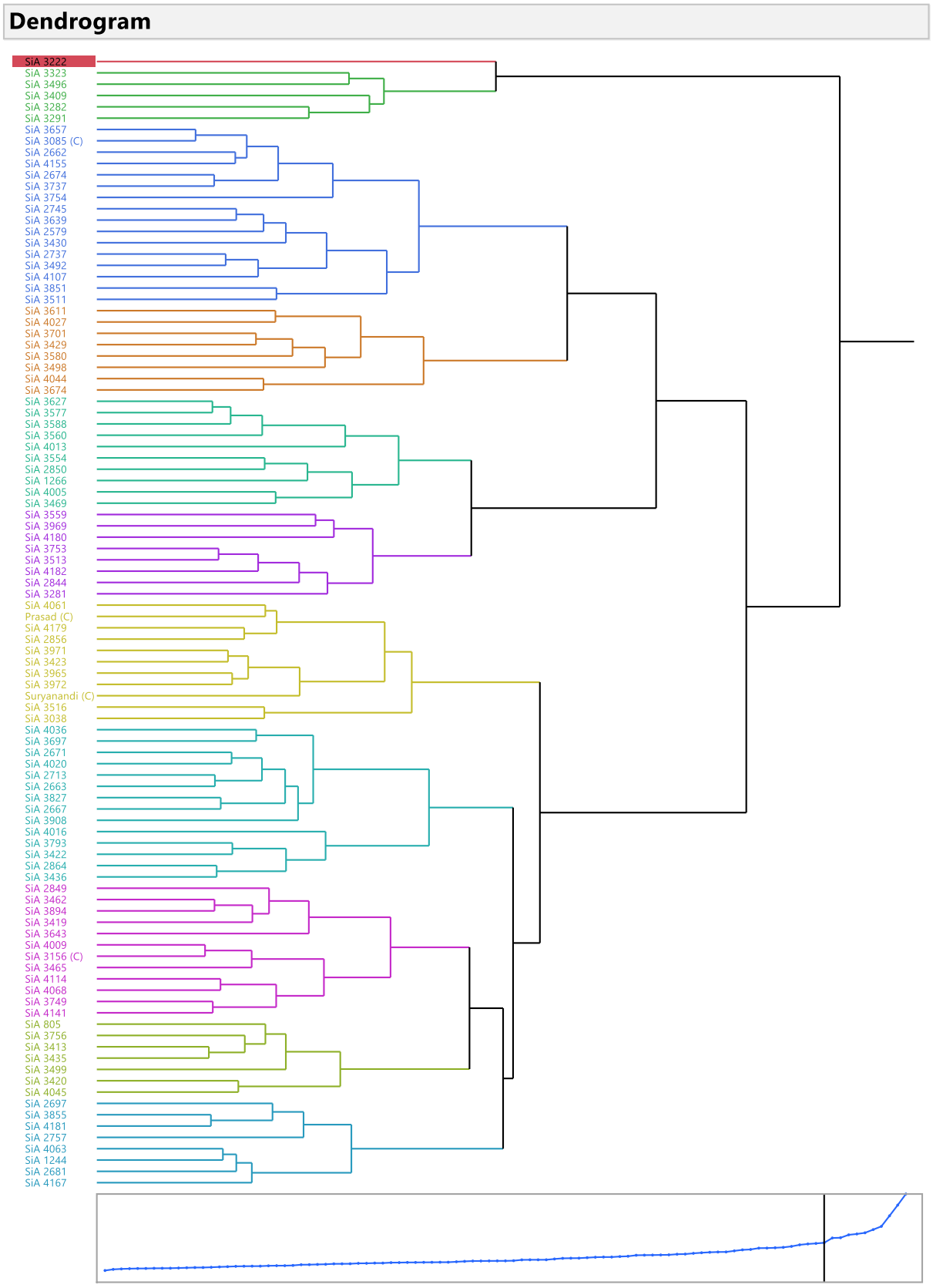



**Fig. 4.9 Dendrogram showing relationship of 100 foxtail millet [*Setaria italica* (L.) Beauv.] genotypes in 11 clusters based on Euclidean$^2$ distance**

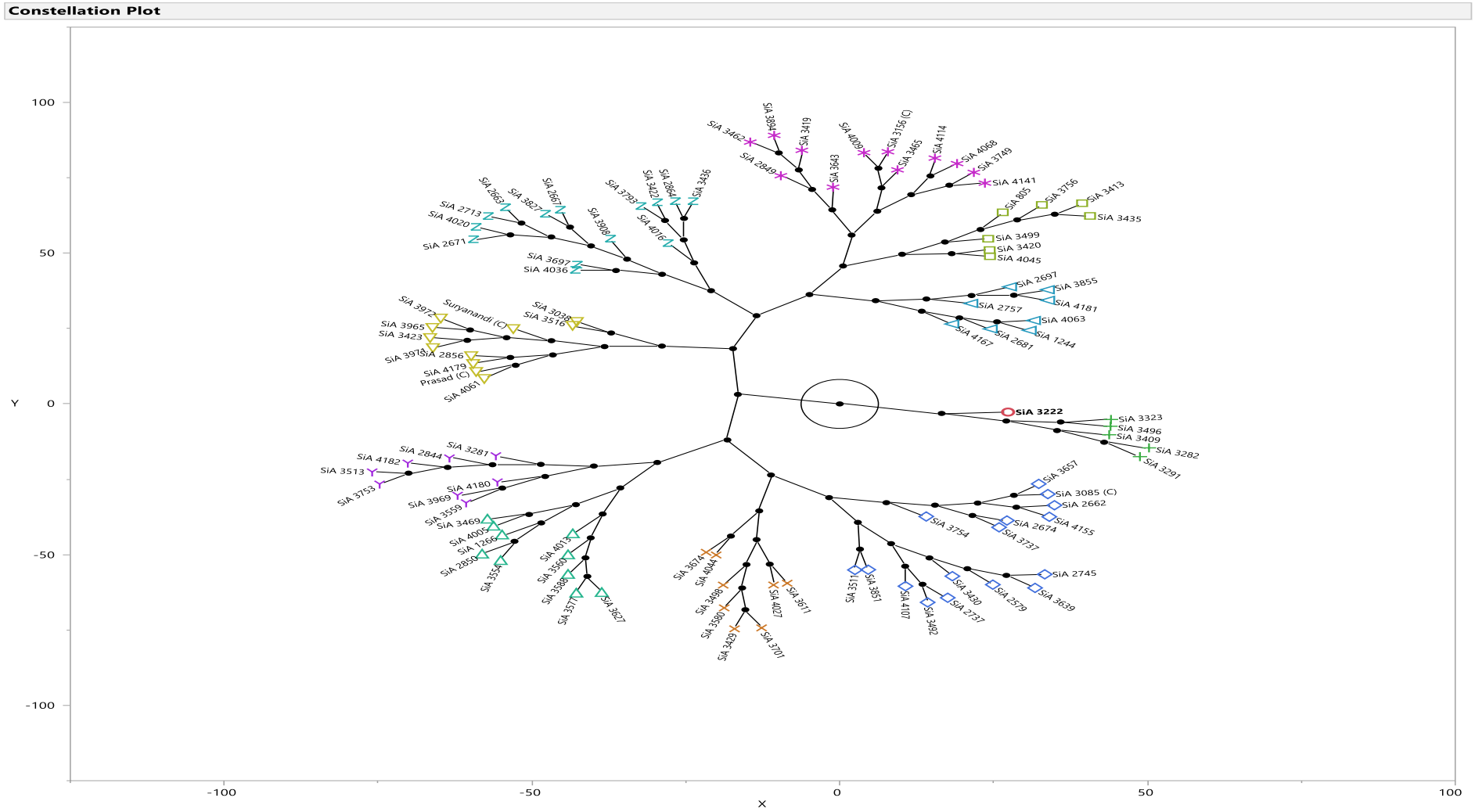



**Fig. 4.10 Constellation plot of 100 foxtail millet [*Setaria italica* (L.) Beauv.] genotypes into 11 clusters based on Euclidean$^2$ distances**

**Table 4.11 Mean values of 11 clusters estimated by Ward's minimum variance method in 100 foxtail millet [*Setaria italica* (L.) Beauv.] genotypes**

| Cluster | SCMR at 30 DAS | SCMR at 45 DAS | Days to 50% flowering | Plant height (cm) | Panicle length (cm) | No. of prod. tillers /plant | Days to maturity | No of Grains / ear head | 1000 grain wt (g) | Protein (g/100g) | Carbohy drate (g/100g) | Calcium (mg/100g) | Magnesium (mg/100g) | Iron (mg/ 100g) | Zinc (mg/ 100g) | Copper (mg/ 100g) | Manga nese (mg/ 100g) | Grain yield/ plant (g) | Mean |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **1** | 46.625 | **65.906** | **32.094** | **109.960** | 14.526 | **1.035** | **60.156** | **1816.662** | 2.501 | **12.886** | 63.022 | **32.122** | 12.003 | **4.411** | **1.622** | 0.983 | **1.688** | 9.469 | **127.093** |
| **2** | **41.848** | 50.111 | 42.694 | 134.940 | **12.366** | 2.401 | 77.956 | 1765.994 | **2.015** | 13.593 | 58.611 | 21.669 | 12.076 | 8.330 | 2.762 | 0.952 | 2.110 | **5.656** | **125.338** |
| **3** | **48.216** | 52.928 | 44.948 | **158.848** | 18.441 | 3.459 | **83.756** | 1812.746 | **3.135** | 13.996 | 59.794 | 23.828 | 14.412 | 14.501 | 2.980 | 1.113 | 2.265 | **15.154** | **131.918** |
| **4** | 45.105 | **49.512** | 46.469 | 150.861 | 17.866 | 4.024 | 82.875 | 1660.770 | 2.762 | 13.228 | 55.845 | 25.396 | 22.272 | **20.720** | 3.119 | 1.856 | 2.443 | 9.963 | **123.060** |
| **5** | 45.479 | 54.429 | 44.719 | 154.944 | 17.926 | 3.977 | 83.681 | 1666.348 | 3.081 | **15.047** | 65.304 | 25.227 | **23.341** | 11.423 | 4.770 | 1.047 | 2.685 | 12.396 | **124.212** |
| **6** | 47.422 | 54.025 | 45.782 | 154.495 | 17.842 | 3.972 | 81.062 | 1646.173 | 2.921 | 13.691 | 65.408 | **21.485** | 11.946 | 10.016 | **5.615** | 0.992 | **3.424** | 12.256 | **122.140** |
| **7** | 47.265 | 52.698 | 42.327 | 137.578 | 15.057 | 3.522 | 79.832 | 1652.522 | 2.891 | 14.312 | 59.268 | 27.504 | 14.691 | 10.602 | 3.140 | 1.330 | 2.258 | 11.426 | **121.012** |
| **8** | 47.062 | 51.965 | **47.523** | 149.650 | 17.868 | 4.632 | 82.299 | 1603.519 | 2.977 | 13.271 | **69.321** | 24.854 | 12.879 | 7.869 | 2.646 | 1.017 | 2.027 | 12.321 | **119.650** |
| **9** | 46.763 | 58.655 | 44.367 | 148.830 | **18.798** | 3.316 | 82.737 | **1561.049** | 2.972 | 14.997 | 62.415 | 22.720 | 12.666 | 7.565 | 2.720 | 1.111 | 2.111 | 9.850 | **116.869** |
| **10** | 42.112 | 55.277 | 45.451 | 145.213 | 17.764 | **5.300** | 81.120 | 1678.254 | 2.790 | 14.459 | **54.205** | 21.775 | 16.598 | 8.693 | 2.821 | **0.890** | 2.238 | 7.759 | **122.373** |
| **11** | 47.117 | 53.653 | 45.250 | 149.714 | 18.621 | 3.985 | 83.656 | 1736.364 | 2.983 | 14.440 | 62.520 | 22.360 | **11.236** | 8.919 | 2.586 | **2.592** | 2.115 | 10.796 | **126.606** |
| **Mean** | **45.910** | **54.469** | **43.784** | **145.003** | **17.007** | **3.602** | **79.921** | **1690.945** | **2.821** | **13.993** | **61.428** | **24.449** | **14.920** | **10.277** | **3.162** | **1.262** | **2.306** | **10.641** | |

**Note:** Bold figures indicate minimum and maximum values in each character

#### 4.2.3.3 Cluster means values

Cluster analysis portrayed a clear differentiation between foxtail millet genotypes. The cluster means computed by Ward's minimum variance method for 18 characters studied (Table 4.11) revealed existence of differences among the clusters The highest cluster mean was recorded in number of grains per ear head (1690.945) and the lowest was in copper (1.262). Maximum cluster mean was recorded in cluster III (131.918) followed by cluster I (127.093). This showed the existence of maximum genetic divergence among the genotypes in these clusters. Based on these parameters, the genotypes were grouped into clusters shown on the dendrogram. The dendogram divided the genotypes into 11 clusters and singleton as shown (Fig 4.9)

Cluster I genotypes were characterized by highest SCMR at 45 DAS, number of grains/ear head, calcium and desired low values for days to 50% flowering and days to maturity. Cluster III, genotypes displayed highest SCMR at 30 DAS, plant height, 1000 grain weight and grain yield/ plant. Cluster V genotypes reported highest protein and magnesium content. Cluster VI genotypes had the highest zinc and manganese content. The genotypes in cluster IV, VIII, IX, X and XI registered highest iron content, carbohydrate content, panicle length, number of productive tillers /plant and copper content respectively.

Genotype SiA 3222, grouped as a singleton can be used widely in breeding programmes to improve the yield levels. The crossing of foxtail millet genotypes in different clusters will provide higher heterotic groups in breeding. Similar result was published by Ayesha *et al.* (2019b) for assessment of genetic diversity in foxtail millet genotypes.

### 4.2.4 Comparison of clusters obtained by Tocher's method and Ward's method

Both Tocher's method ($D^2$ analysis) and Ward's method (Hierarchial cluster analysis) grouped the 100 foxtail millet genotypes into 11 clusters. However, the clusters obtained in the above two methods differ with respect to number and composition of genotypes included in each cluster. In Tocher's method, cluster I was the largest with maximum genotypes (43) followed by clusters II (37 genotypes); cluster VI (6 genotypes); cluster IV (4 genotypes); IX (4 genotypes) and the remaining clusters were solitary or monogenotypic *viz.*, III, V, VII, VIII, X and XI. Whereas in Ward's method, maximum genotypes in cluster III (16 genotypes) followed by clusters VIII

(14 genotypes); Cluster IX (12 genotypes); cluster VII (11 genotypes); Cluster V (10 genotypes); Cluster IV, VI and XI (eight genotypes each); Cluster X (seven genotypes); Cluster II (five genotypes); and Cluster I is solitary. The two clustering methods grouped differently and clustering pattern of genotypes is also not same. It was noted that solitary clusters obtained both in Tocher's method (six) and ward's minimum variance method (One) were monogenotypic and found distant genetically from all other genotypes. The genetic diversity was the outcome of several factors along with geographic diversity; therefore, the selection of genotypes for hybridization should be more based on genetic diversity.

Two important points are to be considered while selecting genotypes for hybridization programmes *viz.,* (i) Choice of the particular cluster from which genotypes are to be used as parents and (ii) selection of particular genotype from selected cluster. The clusters selected should be separated by largest statistical distance *i.e*. maximum divergence. Genotypes from these divergent clusters should be selected based on their *per se* performance for different yield contributing characters. However the selected genotype should be tested for their combining ability and the gene action using other biometrical techniques like Line x Tester or Diallel analysis before using them in any breeding programme.

Based on Tocher's method, it can be inferred that the genetic resources between cluster V (SiA 4044) and cluster XI (SiA 3222) possessing maximum inter cluster distance between them had high degree of genetic diversity and thus may be utilized under inter-varietal hybridization programme (transgressive breeding) for obtaining superior segregants. In selecting genotypes for initiating any breeding programme, one should also consider the *per se* performance of those genotypes for yield and yield contributing characters along with genetic diversity.

Similarly, the clusters obtained using Ward's method indicated that the highest genetic distance of 12.029 was between SiA 3222 and SiA 3580. Genotype SiA 3222, grouped as a singleton can be used widely in breeding programmes to improve the yield levels. The crossing of foxtail millet genotypes in different clusters will provide higher heterotic groups in breeding.

On comparative analysis of the clustering patterns obtained through Tocher's and Ward's methods, it was identified that the crosses SiA 4044 x SiA 3222 (Tocher's method) and SiA 3222 x SiA 3580 (Ward's method) were identified as superior and

therefore, have enormous potential in generating heterotic hybrids or transgressive segregants. However, one should test these genotypes for their combining ability and gene action using different mating designs so that one can decide whether to go for hybrid varieties (in presence of dominance gene action) or to target superior transgressive segregants (in presence of additive gene action).

## 4.3 CHARACTER ASSOCIATION

Yield, a complex and polygenically inherited character is the the end product, resulting from multiplicative interaction of its component traits. A thorough understanding of the interaction of characters amongst themselves provides valuable information for genetic improvement. The efficiency of selection for yield mainly depends on the direction and magnitude of association between yield and its component characters and also among themselves. The change in one character brings about a series of changes in the other characters, since they are interrelated. Therefore, correlation studies are of prime importance in any selection programme as they provide degree and direction of relationship between two or more component traits.

The phenotypic correlation coefficients between grain yield and yield component characters and among themselves were estimated and presented in the Table 4.12. The pictorial representation of correlations and shaded phenotypic matrix are presented in Fig 4.11 and 4.12, respectively. The results are discussed character wise hereunder.

### 4.3.1 SCMR at 30 DAS

This character established positively significant phenotypic association with grain yield/ plant (0.3176**), 1000 grain weight (0.2438*), plant height and panicle length (0.2052*). Similar result was obtained by Bheemesh (2017) for panicle length in foxtail millet.

### 4.3.2 SCMR at 45 DAS

It was noted that this trait showed positively significant association with 1000 grain weight (0.2303*) and protein (0.2263*) at phenotypic level. Similar report was published by Bheemesh (2017) for leaf temperature at 45 DAS and grain yield per plant in foxtail millet.

### 4.3.3 Day to 50% flowering

At phenotypic level this character registered positively significant association with days to maturity (0.3074**), number of productive tillers / plant (0.3018**) and plant height (0.4031**). Similar reports were reported by Prasanna *et al.* (2013a), Prasanna *et al.* (2013b), Brunda *et al*. (2015a); Amarnath *et al.* (2018b) for days to maturity, plant height, culm branches, panicle length and number of productive tillers / plant and Ayesha *et al*. (2019c) for days to maturity.

### 4.3.4 Plant height

The traits grain yield/ plant (0.3729**), panicle length (0.5155**), days to maturity (0.5117**), days to 50 % flowering (0.4031**), 1000 grain weight (0.3826**), zinc (0.2477*), iron (0.2415*), magnesium (0.2096*) and SCMR at 30 DAS (0.2052*) showed positively significant association with plant height at phenotypic level. These results are in consonance with the findings of Brunda *et al*. (2015a) for grain yield per plant, panicle length, and test weight; Amarnath *et al*. (2018b) for peduncle length, panicle length, flag leaf blade length, flag leaf blade width, 1000 grain weight and grain yield / plant; Ayesha *et al*. (2019c) for panicle length, test weight, number of productive tillers / plant, carbohydrate and grain yield per plant.

### 4.3.5 Panicle length (cm)

Panicle length recorded highly significant positive phenotypic association with grain yield/ plant (0.2491*), plant height (0.5155**), days to maturity (0.2799**), SCMR at 30 DAS (0.2052*) and 1000 grain weight (0.4950**). This result is in agreement with the findings of Prasanna *et al.* (2013b), Brunda *et al*. (2015a), Kavya (2017c) for 1000 grain weight and grain yield / plant; Amarnath *et al*. (2018b) for flag leaf blade length, flag leaf blade width, 1000 grain weight and grain yield / plant; Ayesha *et al*. (2019c) for test weight, number of productive tillers / plant, carbohydrate and grain yield / plant.

### 4.3.6 Number of productive tillers per plant

This character displayed significant positive correlation with days to 50% flowering (0.3018**) and days to maturity (0.2572**). Similar reports were published by Brunda *et al*. (2015a) for test weight; Ayesha *et al*. (2019c) for test weight, grain yield / plant and carbohydrate content.

### 4.3.7 Days to maturity

At phenotypic level, this trait registered significant positive association with plant height (0.5117**), 1000 grain weight (0.3546**), days to 50 % flowering (0.3074**), panicle length (0.2799**) and number of productive tillers/plant (0.2572**). Similar result was reported by Amarnath *et al*. (2018b) for plant height, panicle length, 1000 grain weight and flag leaf blade length.

### 4.3.8 Number of grains / ear head

This trait showed significant positive phenotypic association with grain yield/ plant (0.3504**). Similar result was reported by Bheemesh (2017) for this character.

### 4.3.9 1000 grain weight

Thousand grain weight registered significant positive phenotypic correlation with grain yield/ plant (0.4414**), panicle length (0.4950**), plant height (0.3826**), days to maturity (0.3546**), SCMR at 30 DAS (0.2438*) and SCMR at 45 DAS (0.2303*). Similar findings were erlier reported by Brunda *et al*. (2015a),Kavya *et al*. (2017c) and Amarnath *et al*. (2018b) for grain yield / plant; Ayesha *et al*. (2019c) for grain yield / plant, carbohydrate content and protein content.

### 4.3.10 Protein (g/100g)

At phenotypic level, this character displayed significant positive association with SCMR at 45 DAS (0.2263*) only. Similar result was published by Ayesha *et al*. (2019c) for carbohydrate content.

### 4.3.11 Carbohydrate (g/100g)

It was observed that this trait lacked significant association positively or negatively with any of the characters at phenotypic level. However, Ayesha *et al*. (2019c) reported positively significant phenotypic association for this trait with panicle length, test weight, grain yield/plant, number of productive tillers/ plant, protein content and plant height.

## Table 4.12 Phenotypic correlations among grain yield and yield contributing characters in foxtail millet [*Setaria italica* (L.) Beauv.]

| S No | Character | SCMR at 30 DAS | SCMR at 45 DAS | Days to 50% flowering | Plant height | Panicle length | No. of prod. tillers /plant | Days to maturity | No of Grains / ear head | 1000 grain wt | Protein | Carbohy drate | Calcium | Magnesi um | Iron | Zinc | Copper | Mangan ese | Grain yield/ plant |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | **SCMR at 30 DAS** | 1.0000 | 0.112 | 0.065 | 0.2052 * | 0.2052 * | 0.027 | 0.121 | 0.016 | 0.2438 * | -0.104 | 0.1316 | 0.0591 | -0.0265 | -0.0549 | 0.0032 | 0.0515 | -0.0328 | 0.3176 ** |
| 2 | **SCMR at 45 DAS** | | 1.0000 | -0.3444 ** | -0.127 | 0.133 | 0.081 | -0.13 | -0.111 | 0.2303 * | 0.2263 * | 0.0018 | 0.0959 | -0.0105 | -0.2160 * | 0.0256 | -0.0931 | 0.0353 | 0.0193 |
| 3 | **Days to 50 flowering** | | | 1.0000 | 0.4031 ** | 0.175 | 0.3018 ** | 0.3074 ** | -0.158 | -0.006 | -0.026 | 0.0582 | 0.0081 | -0.0086 | 0.0353 | 0.1176 | -0.0459 | 0.0775 | -0.0282 |
| 4 | **Plant height** | | | | 1.0000 | 0.5155 ** | 0.058 | 0.5117 ** | 0.168 | 0.3826 ** | -0.026 | -0.0194 | -0.1251 | 0.2096 * | 0.2415 * | 0.2477 * | 0.1283 | 0.1866 | 0.3729 ** |
| 5 | **Panicle length** | | | | | 1.0000 | 0.164 | 0.2799 ** | -0.026 | 0.4950 ** | 0.051 | 0.0592 | -0.1279 | 0.1448 | 0.0613 | 0.0458 | 0.1002 | -0.0398 | 0.2491 * |
| 6 | **No. of prod. tillers /plant** | | | | | | 1.0000 | 0.2572 ** | -0.315 | 0.178 | 0.12 | -0.0123 | 0.1323 | 0.1698 | 0.0143 | 0.0490 | -0.0515 | 0.0640 | 0.0038 |
| 7 | **Days to maturity** | | | | | | | 1.0000 | 0.016 | 0.3546 ** | 0.073 | 0.1047 | -0.0857 | 0.1264 | 0.1945 | 0.0216 | 0.1454 | 0.0157 | 0.1860 |
| 8 | **No of Grains / ear head** | | | | | | | | 1.0000 | -0.004 | -0.025 | -0.0797 | -0.2022 * | 0.0414 | 0.1251 | -0.0489 | 0.0847 | 0.0178 | 0.3504 ** |
| 9 | **1000 grain wt** | | | | | | | | | 1.0000 | 0.175 | 0.1586 | 0.0505 | 0.1069 | 0.0674 | 0.1584 | 0.0616 | 0.0848 | 0.4414 ** |
| 10 | **Protein** | | | | | | | | | | 1.0000 | -0.1555 | 0.0524 | -0.0003 | -0.0161 | 0.0095 | 0.0013 | 0.0267 | -0.1159 |
| 11 | **Carbohydrate** | | | | | | | | | | | 1.0000 | 0.1242 | -0.1914 | -0.1945 | 0.1261 | -0.0738 | 0.0329 | 0.1429 |
| 12 | **Calcium** | | | | | | | | | | | | 1.0000 | -0.0894 | 0.1234 | 0.0817 | -0.0552 | 0.0764 | -0.0627 |
| 13 | **Magnesium** | | | | | | | | | | | | | 1.0000 | 0.2572 ** | 0.2776 ** | -0.0151 | 0.0802 | 0.0820 |
| 14 | **Iron** | | | | | | | | | | | | | | 1.0000 | 0.0980 | 0.2524 * | 0.1981 * | 0.1722 |
| 15 | **Zinc** | | | | | | | | | | | | | | | 1.0000 | -0.1490 | 0.6812 ** | 0.1241 |
| 16 | **Copper** | | | | | | | | | | | | | | | | 1.0000 | -0.0624 | 0.0704 |
| 17 | **Manganese** | | | | | | | | | | | | | | | | | 1.0000 | 0.0607 |
| 18 | **Grain yield/ plant** | | | | | | | | | | | | | | | | | | 1.0000 |

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

### 4.3.12 Calcium (mg/100g)

This character displayed no significant phenotypic association either positively or negatively with any of the traits. Similar result was reported by Ayesha *et al*. (2019c) for this trait.

### 4.3.13 Magnesium (mg/100g)

The trait magnesium content registered significant positive phenotypic correlation with zinc (0.2776**), Iron (0.2572**) and plant height (0.2096*).

### 4.3.14 Iron (mg/100g)

The character iron content showed significant positive phenotypic association with magnesium (0.2572**), copper (0.2524*), plant height (0.2415*) and manganese (0.1981*). Similar report was published by Anuradha *et al.* (2018) for panicle yield / plant, grain yield/plant and 1000 grain weight in pearl millet.

### 4.3.15 Zinc (mg/100g)

At phenotypic level, zinc content registered significant positive correlation with manganese (0.6812**), magnesium (0.2776**) and plant height (0.2477*). Similar result was reported by Anuradha *et al.* (2018) in pearl millet for panicle yield / plant and grain yield/plant.

### 4.3.16 Copper (mg/100g)

The character copper content displayed significant positive phenotypic association with iron (0.2524*) content only. This result is in agreement with findings of Anuradha *et al.* (2018) for plant height, panicle length, grain yield / plant and days to 50% flowering in pearl millet.

### 4.3.17 Manganese (mg/100g)

Manganese content registered significant positive phenotypic association with zinc content (0.6812**) and Iron content (0.1981*). Similar result was reported by Anuradha *et al.* (2018) in pearl millet for plant height, grain yield / plant and iron content.

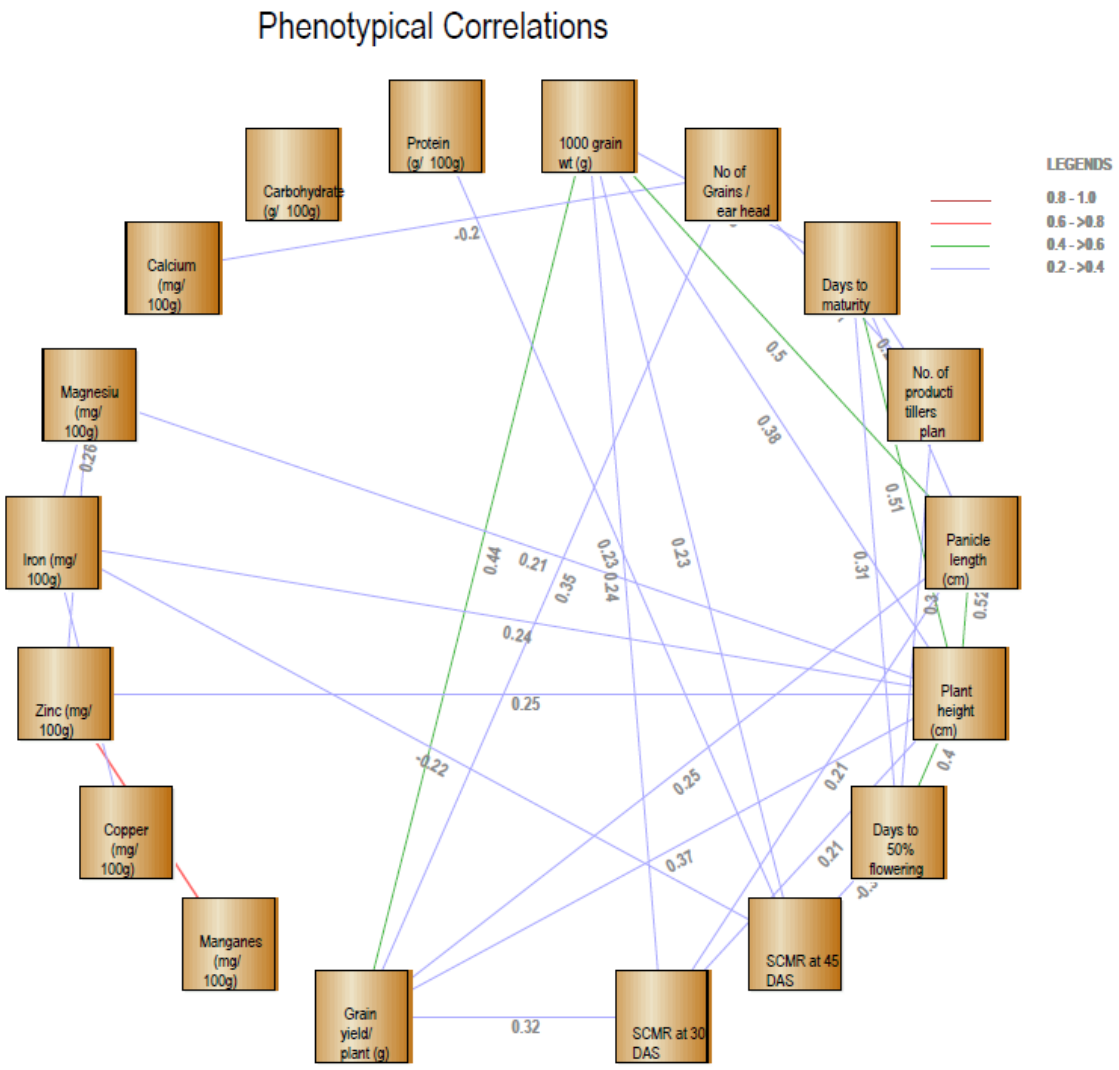



**Fig. 4.11 Pictorial representation of phenotypic correlations among the studied traits in foxtail millet [*Setaria italica* (L.) Beauv.]**

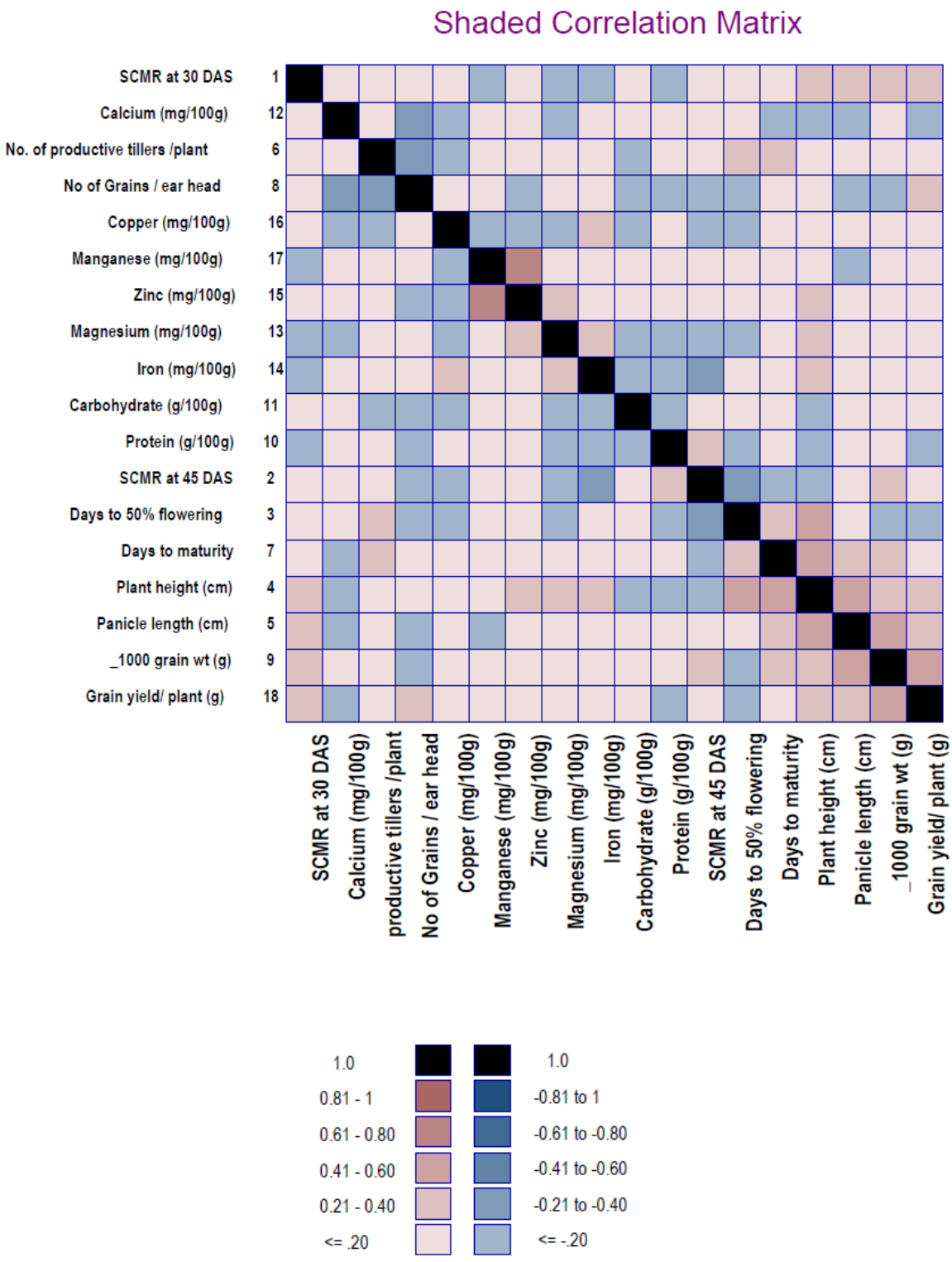



**Fig. 4.12 Shaded phenotypic correlation matrix for all the characters studied in foxtail millet [*Setaria italica* (L.) Beauv.]**

### 4.3.18 Grain yield/ plant

Grain yield/ plant showed significant positive phenotypic association with SCMR at 30 DAS (0.3176**), plant height (0.3729**), panicle length (0.2491*), number of Grains / ear head (0.3504**) and 1000 grain weight (0.4414**). Similar result was recorded by Amarnath *et al.* (2018b) for plant height, peduncle length, panicle length, flag leaf blade length , flag leaf blade width and 1000 grain weight; Ayesha *et al.* (2019c) for plant height, panicle length, number of productive tillers / plant, test weight and carbohydrate content.

The perusal of the results revealed a positive significant phenotypic association with SCMR at 30 DAS (0.3176**), plant height (0.3729**), panicle length (0.2491*), number of grains / ear head (0.3504**) and 1000 grain weight (0.4414**) at phenotypic level. This means that these traits are predominantly governed by additive gene action and hence selection for these traits will lead to simultaneous improvement in grain yield.

Inter-character associations at phenotypic level had shown positively significant contribution of SCMR at 30 DAS with grain yield/ plant (0.3176**), 1000 grain weight (0.2438*), plant height and panicle length (0.2052*); SCMR at 45 DAS with 1000 grain weight (0.2303*) and protein (0.2263*) ; day to 50% flowering with days to maturity (0.3074**), number of productive tillers / plant (0.3018**) and plant height (0.4031**); plant height with grain yield/ plant (0.3729**), panicle length (0.5155**), days to maturity (0.5117**), days to 50 % flowering (0.4031**), 1000 grain weight (0.3826**), zinc (0.2477*), iron (0.2415*), magnesium (0.2096*) and SCMR at 30 DAS (0.2052*); panicle length with grain yield/ plant (0.2491*), plant height (0.5155**), days to maturity (0.2799**), SCMR at 30 DAS (0.2052*) and 1000 grain weight (0.4950**); number of productive tillers per plant with days to 50% flowering (0.3018**) and days to maturity (0.2572**); days to maturity with plant height (0.5117**), 1000 grain weight (0.3546**), days to 50 % flowering (0.3074**), panicle length (0.2799**) and number of productive tillers/plant (0.2572**); number of grains / ear head with grain yield/ plant (0.3504**); 1000 grain weight with grain yield/ plant (0.4414**), panicle length (0.4950**), plant height (0.3826**), days to maturity (0.3546**), SCMR at 30 DAS (0.2438*) and SCMR at 45 DAS (0.2303*); protein with SCMR at 45 DAS (0.2263*); magnesium with zinc (0.2776**), Iron (0.2572**) and plant height (0.2096*); iron with magnesium (0.2572**), copper (0.2524*), plant height (0.2415*) and manganese (0.1981*); zinc with manganese (0.6812**), magnesium (0.2776**) and

plant height (0.2477*); copper with iron (0.2524*) content only; manganese with zinc content (0.6812**) and iron content (0.1981*); grain yield/ plant with SCMR at 30 DAS (0.3176**), plant height (0.3729**), panicle length (0.2491*), number of grains / ear head (0.3504**) and 1000 grain weight (0.4414**). The prevalence of positive correlation envisages the simultaneous improvement of these characters.

Similar results were reported by Shinde *et al*. (2014) for plant height; Ulaganathan and Nirmalakumari (2014) for 1000 grain weight and flag leaf blade length; Brunda *et al*. (2015a) for plant height and panicle length; Jyothsna *et al*. (2016c) for plant height; Kavya (2017c) for panicle length and 1000 grain weight; Negi *et al*. (2016) for plant height,1000 grain weight; Sapkota *et al.* (2016) for peduncle length, panicle length and flag leaf blade length; Amarnath *et al*. (2018b) for plant height, peduncle length, panicle length, flag leaf blade length , flag leaf blade width and 1000 grain weight; Ayesha *et al*. (2019c) for plant height, panicle length, number of productive tillers / plant, test weight and carbohydrate content.

## 4.4 PATH ANALYSIS

Analysis of correlation coefficients revealed only the relationship between yield and its attributes but did not show the direct and indirect effects of various traits on *per se*. This is because the attributes which are in association do not exist by themselves, but are linked to other components. Path coefficient analysis measures the direct and indirect causes of association as well as depicts the relative importance of each factor involved in contributing to the final product *viz*., yield. The results of path analysis are presented in Table 4.13 and discussed character wise hereunder. The path diagram was given in Fig. 4.13.

### 4.4.1 Directs effects of different characters on grain yield / plant

At phenotypic level, 1000 grain weight (0.3527), number of grains / ear head (0.3196), plant height (0.2170), SCMR at 30 DAS (0.1883), iron (0.1426), number of productive tillers /plant (0.1161), carbohydrate (0.1073) and zinc (0.0944) registered high positive direct effect on grain yield / plant. Conversely, negative direct effect on grain yield / plant by SCMR at 45 DAS (-0.0005), copper (-0.0191), magnesium (-0.0502), calcium (-0.06), panicle length (-0.0609), days to maturity (-0.0892), days to 50% flowering (-0.0914), manganese (-0.0959) and protein (-0.1272). Similar results were reported by Jyothsna *et al.* (2016c), Renganathan *et al.* (2017) and Amarnath *et al.*

(2018b) for plant height; Ayesha (2019c) for number of productive tillers / plant and carbohydrate content.

## 4.4.2 Indirect effects of different characters on grain yield / plant

### 4.4.2.1 SCMR at 30 DAS

SCMR at 30 DAS expressed strong significant positive correlation (0.3176**) on grain yield per plant at phenotypic level. The positive indirect effect of SCMR at 30 DAS on grain yield / plant via 1000 grain wt (0.0459), plant height and panicle length (0.0386), carbohydrate (0.0248), days to maturity (0.0228), SCMR at 45 DAS (0.021), days to 50% flowering (0.0122), calcium (0.0111), copper (0.0097), number of productive tillers /plant (0.0051), number of grains / ear head (0.003) and zinc (0.0006). The negative indirect effects of SCMR at 30 DAS on grain yield / plant through protein (-0.0196), iron (-0.0103), manganese (-0.0062) and magnesium (-0.005). These results were in consonance with the findings of Bheemesh (2017) for SCMR at 45 DAS for this character on grain yield / plant.

### 4.4.2.2 SCMR at 45 DAS

SCMR at 45 DAS exhibited positive and non-significant correlation (0.0193) with grain yield per plant at phenotypic level. The positive and negligible indirect effect of SCMR at 45 DAS on grain yield / plant via days to 50% flowering (0.0002), plant height (0.0001), days to maturity (0.0001), number of grains / ear head (0.0001) and iron (0.0001). The negative indirect effects of SCMR at 45 DAS on grain yield / plant was through protein (-0.0001), 1000 grain weight (-0.0001), panicle length (-0.0001) and SCMR at 30 DAS (-0.0001).

### 4.4.2.3 Days to 50% flowering

Days to 50% flowering expressed non-significant negative correlation (-0.0282) with grain yield per plant at phenotypic level. The positive indirect effect of days to 50% flowering on grain yield / plant via SCMR at 45 DAS (0.0315), number of grains / ear head (0.0144), copper (0.0042), protein (0.0024), magnesium (0.0008) and 1000 grain wt (0.0005). The negative indirect effects of days to 50% flowering on grain yield / plant through plant height (-0.0369), days to maturity (-0.0281), number of productive tillers / plant (-0.0276), panicle length (-0.016), zinc (-0.0108), manganese (-0.0071), SCMR at 30 DAS (-0.0059), carbohydrate (-0.0053), iron (-0.0032) and calcium

(-0.0007). Similar results were published by Tyagi *et al.* (2011) and Amarnath *et al.* (2018b) for panicle length for this character on grain yield per plant.

#### 4.4.2.4 Plant height

At phenotypic level, plant height showed significant positive correlation (0.3729**) with grain yield per plant. The negative indirect effects of plant height on grain yield / plant through SCMR at 45 DAS (-0.0276), calcium (-0.0272), protein (-0.0057) and carbohydrate (-0.0042). The positive indirect effect of plant height on grain yield / plant via panicle length (0.1119), days to maturity (0.1111), days to 50% flowering (0.0875), 1000 grain weight (0.083), zinc (0.0538), iron (0.0524), magnesium (0.0455), SCMR at 30 DAS (0.0445), manganese (0.0405), number of grains / ear head (0.0365), copper (0.0278) and number of productive tillers /plant (0.0125). Amarnath *et al.* (2018b) for number of productive tillers /plant on grain yield per plant.

#### 4.4.2.5 Panicle length

Panicle length exhibited significant positive correlation (0.2491*) on grain yield per plant at phenotypic level. The positive indirect effect of panicle length on grain yield / plant via calcium (0.0078), manganese (0.0024) and number of grains / ear head (0.0016). The negative indirect effects of panicle length on grain yield / plant through plant height (-0.0314), 1000 grain weight (-0.0302), days to maturity (-0.0171), SCMR at 30 DAS (-0.0125), days to 50% flowering (-0.0107), number of productive tillers /plant (-0.01), magnesium (-0.0088), SCMR at 45 DAS (-0.0081), copper (-0.0061), iron (-0.0037), carbohydrate (-0.0036), protein (-0.0031) and zinc (-0.0028). Similar finding was reported by Brunda *et al.* (2015a) and Amarnath *et al.* (2018b) for indirect effect via 1000 grain weight.

#### 4.4.2.6 Number of productive tillers per plant

Number of productive tillers /plant expressed non-significant positive correlation (0.0038) on grain yield per plant at phenotypic level. The negative indirect effects of number of productive tillers /plant on grain yield / plant through number of grains / ear head (-0.0365), copper (-0.006) and carbohydrate (-0.0014). The positive indirect effect of number of productive tillers /plant on grain yield / plant via days to 50% flowering (0.035), days to maturity (0.0299), 1000 grain wt (0.0206), magnesium (0.0197), panicle length (0.019), calcium (0.0154), protein (0.0139), SCMR at 45 DAS (0.0094), manganese (0.0074), plant height (0.0067), zinc (0.0057), SCMR at 30 DAS (0.0032)

and iron (0.0017). These results are in conformity with the findings of Ganapathy *et al.* (2011) and Amarnath *et al.* (2018b) for days to maturity for this character on grain yield per plant.

#### 4.4.2.7 Days to maturity

Days to maturity expressed non-significant positive correlation (0.186) on grain yield per plant at phenotypic level. The positive indirect effect of days to maturity on grain yield / plant via SCMR at 45 DAS (0.0116) and calcium (0.0076). The negative indirect effects of days to maturity on grain yield / plant through plant height (-0.0457), 1000 grain weight (-0.0316), days to 50% flowering (-0.0274), panicle length (-0.025), number of productive tillers /plant (-0.0229), iron (-0.0174), copper (-0.013), magnesium (-0.0113), SCMR at 30 DAS (-0.0108), carbohydrate (-0.0093), protein (-0.0065), zinc (-0.0019), nmber of grains / ear head (-0.0015) and manganese (-0.0014). This result is in consonance with the findings of Prasanna *et al.* (2013a), Ashok *et al*. (2016) and Ayesha *et al.* (2019c) for indirect effects via for days to 50 per cent flowering, plant height and number of productive tillers per plant.

#### 4.4.2.8 Number of Grains / ear head

Number of grains / ear head exhibited significant positive correlation (0.3504**) on grain yield per plant at phenotypic level. The positive indirect effect of number of grains / ear head on grain yield / plant via plant height (0.0537), iron (0.04), copper (0.0271), magnesium (0.0132), manganese (0.0057), days to maturity (0.0053) and SCMR at 30 DAS (0.0051).The negative indirect effects of number of grains / ear head on grain yield / plant through number of productive tillers /plant (-0.1006), calcium (-0.0646), days to 50% flowering (-0.0505), SCMR at 45 DAS (-0.0354), carbohydrate (-0.0255), zinc (-0.0156), panicle length (-0.0083), protein (-0.0078) and 1000 grain weight (-0.0012). Similar result was published by by Bheemesh (2017) for indirect effects via plant height.

**Table 4.13 Phenotypic direct and indirect effects of different traits on grain yield per plant in foxtail millet [*Setaria italica* (L.) Beauv.]**

| S No | Character | SCMR at 30 DAS | SCMR at 45 DAS | Days to 50% flowering | Plant height | Panicle length | No. of prod. tillers /plant | Days to maturity | No of Grains / ear head | 1000 grain wt | Protein | Carbohydrate | Calcium | Magnesium | Iron | Zinc | Copper | Manganese | Grain yield/ plant |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | SCMR at 30 DAS | 0.1883 | 0.0210 | 0.0122 | 0.0386 | 0.0386 | 0.0051 | 0.0228 | 0.0030 | 0.0459 | -0.0196 | 0.0248 | 0.0111 | -0.0050 | -0.0103 | 0.0006 | 0.0097 | -0.0062 | 0.3176 ** |
| 2 | SCMR at 45 DAS | -0.0001 | -0.0005 | 0.0002 | 0.0001 | -0.0001 | 0.0000 | 0.0001 | 0.0001 | -0.0001 | -0.0001 | 0.0000 | 0.0000 | 0.0000 | 0.0001 | 0.0000 | 0.0000 | 0.0000 | 0.0193 |
| 3 | Days to 50 flowering | -0.0059 | 0.0315 | -0.0914 | -0.0369 | -0.0160 | -0.0276 | -0.0281 | 0.0144 | 0.0005 | 0.0024 | -0.0053 | -0.0007 | 0.0008 | -0.0032 | -0.0108 | 0.0042 | -0.0071 | -0.0282 |
| 4 | Plant height | 0.0445 | -0.0276 | 0.0875 | 0.2170 | 0.1119 | 0.0125 | 0.1111 | 0.0365 | 0.0830 | -0.0057 | -0.0042 | -0.0272 | 0.0455 | 0.0524 | 0.0538 | 0.0278 | 0.0405 | 0.3729 ** |
| 5 | Panicle length | -0.0125 | -0.0081 | -0.0107 | -0.0314 | -0.0609 | -0.0100 | -0.0171 | 0.0016 | -0.0302 | -0.0031 | -0.0036 | 0.0078 | -0.0088 | -0.0037 | -0.0028 | -0.0061 | 0.0024 | 0.2491 * |
| 6 | No. of prod. tillers /plant | 0.0032 | 0.0094 | 0.0350 | 0.0067 | 0.0190 | 0.1161 | 0.0299 | -0.0365 | 0.0206 | 0.0139 | -0.0014 | 0.0154 | 0.0197 | 0.0017 | 0.0057 | -0.0060 | 0.0074 | 0.0038 |
| 7 | Days to maturity | -0.0108 | 0.0116 | -0.0274 | -0.0457 | -0.0250 | -0.0229 | -0.0892 | -0.0015 | -0.0316 | -0.0065 | -0.0093 | 0.0076 | -0.0113 | -0.0174 | -0.0019 | -0.0130 | -0.0014 | 0.1860 |
| 8 | No of Grains / ear head | 0.0051 | -0.0354 | -0.0505 | 0.0537 | -0.0083 | -0.1006 | 0.0053 | 0.3196 | -0.0012 | -0.0078 | -0.0255 | -0.0646 | 0.0132 | 0.0400 | -0.0156 | 0.0271 | 0.0057 | 0.3504 ** |
| 9 | 1000 grain wt | 0.0860 | 0.0812 | -0.0021 | 0.1350 | 0.1746 | 0.0627 | 0.1251 | -0.0013 | 0.3527 | 0.0617 | 0.0559 | 0.0178 | 0.0377 | 0.0238 | 0.0559 | 0.0217 | 0.0299 | 0.4414 ** |
| 10 | Protein | 0.0132 | -0.0288 | 0.0033 | 0.0033 | -0.0065 | -0.0152 | -0.0093 | 0.0031 | -0.0222 | -0.1272 | 0.0198 | -0.0067 | 0.0000 | 0.0020 | -0.0012 | -0.0002 | -0.0034 | -0.1159 |
| 11 | Carbohydrate | 0.0141 | 0.0002 | 0.0062 | -0.0021 | 0.0064 | -0.0013 | 0.0112 | -0.0086 | 0.0170 | -0.0167 | 0.1073 | 0.0133 | -0.0205 | -0.0209 | 0.0135 | -0.0079 | 0.0035 | 0.1429 |
| 12 | Calcium | -0.0036 | -0.0058 | -0.0005 | 0.0075 | 0.0077 | -0.0079 | 0.0051 | 0.0121 | -0.0030 | -0.0031 | -0.0075 | -0.0600 | 0.0054 | -0.0074 | -0.0049 | 0.0033 | -0.0046 | -0.0627 |
| 13 | Magnesium | 0.0013 | 0.0005 | 0.0004 | -0.0105 | -0.0073 | -0.0085 | -0.0063 | -0.0021 | -0.0054 | 0.0000 | 0.0096 | 0.0045 | -0.0502 | -0.0129 | -0.0139 | 0.0008 | -0.0040 | 0.0820 |
| 14 | Iron | -0.0078 | -0.0308 | 0.0050 | 0.0344 | 0.0087 | 0.0020 | 0.0277 | 0.0178 | 0.0096 | -0.0023 | -0.0277 | 0.0176 | 0.0367 | 0.1426 | 0.0140 | 0.0360 | 0.0282 | 0.1722 |
| 15 | Zinc | 0.0003 | 0.0024 | 0.0111 | 0.0234 | 0.0043 | 0.0046 | 0.0020 | -0.0046 | 0.0150 | 0.0009 | 0.0119 | 0.0077 | 0.0262 | 0.0093 | 0.0944 | -0.0141 | 0.0643 | 0.1241 |
| 16 | Copper | -0.0010 | 0.0018 | 0.0009 | -0.0024 | -0.0019 | 0.0010 | -0.0028 | -0.0016 | -0.0012 | 0.0000 | 0.0014 | 0.0011 | 0.0003 | -0.0048 | 0.0028 | -0.0191 | 0.0012 | 0.0704 |
| 17 | Manganese | 0.0031 | -0.0034 | -0.0074 | -0.0179 | 0.0038 | -0.0061 | -0.0015 | -0.0017 | -0.0081 | -0.0026 | -0.0032 | -0.0073 | -0.0077 | -0.0190 | -0.0653 | 0.0060 | -0.0959 | 0.0607 |

* Significant at 5% level ;
** Significant at 1% level
Residual Effect = 0.74

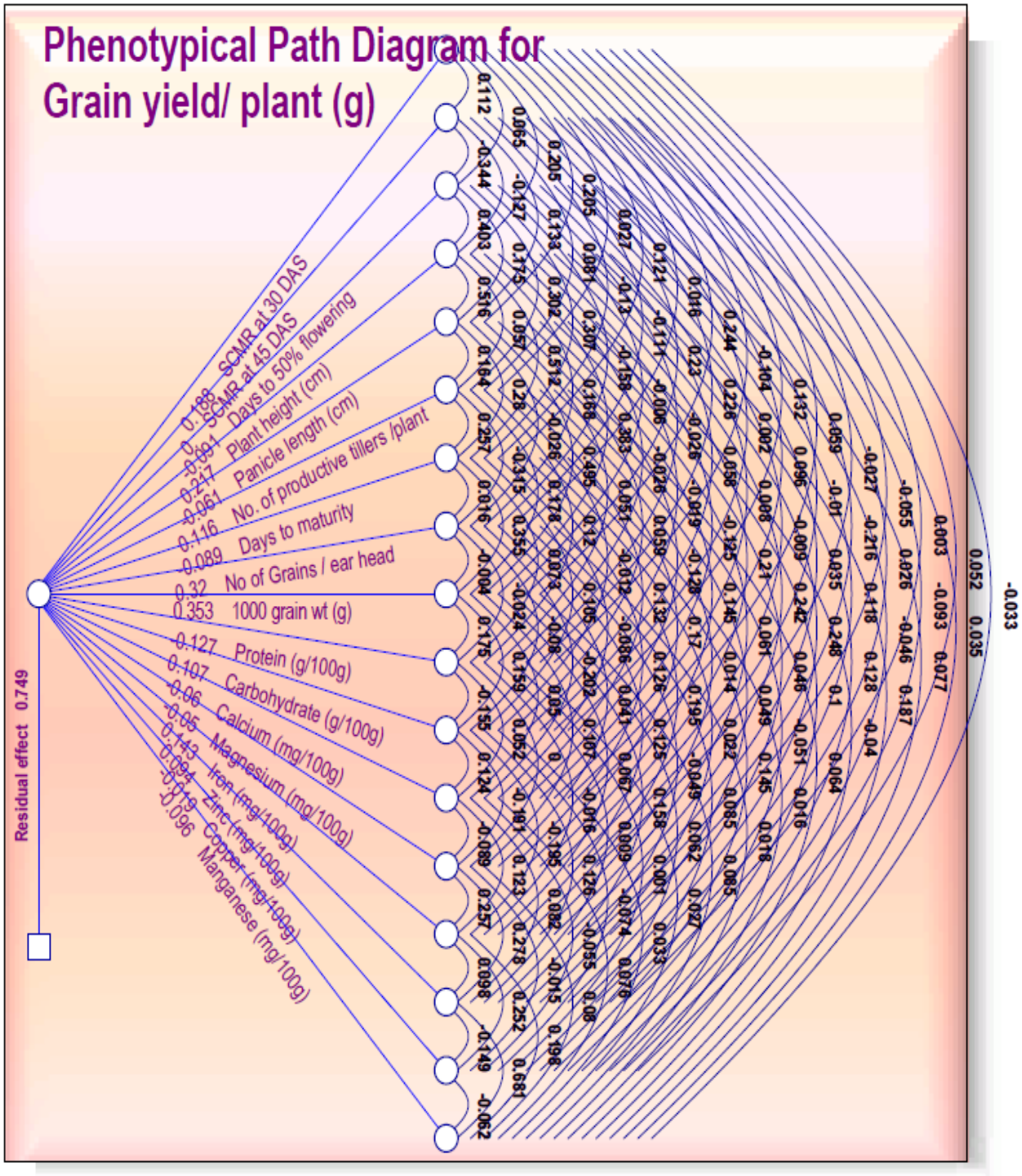



**Fig. 4.13 Phenotypic path diagram for grain yield per plant**

#### 4.4.2.9 1000 grain weight

Thousand grain weight expressed significant positive correlation (0.4414**) on grain yield per plant at phenotypic level. The positive indirect effect of 1000 grain weight on grain yield / plant via panicle length (0.1746), plant height (0.135), days to maturity (0.1251), SCMR at 30 DAS (0.086), SCMR at 45 DAS (0.0812), number of productive tillers /plant (0.0627), protein (0.0617), carbohydrate (0.0559), zinc (0.0559), magnesium (0.0377), manganese (0.0299), iron (0.0238), copper (0.0217) and calcium (0.0178). The negative indirect effects of 1000 grain weight on grain yield / plant through days to 50% flowering (-0.0021) and number of grains / ear head (-0.0013). This result was in consonance with the findings of Shingane *et al.* (2017), Amarnath *et al.* (2018b) and Ayesha *et al.* (2019c).

#### 4.4.2.10 Protein (g/100g)

Protein exhibited non-significant negative correlation (-0.1159) on grain yield per plant at phenotypic level. The positive indirect effect of protein on grain yield / plant via carbohydrate (0.0198), SCMR at 30 DAS (0.0132), days to 50% flowering (0.0033), plant height (0.0033), number of grains / ear head (0.0031) and iron (0.002). The negative indirect effects of protein on grain yield / plant through SCMR at 45 DAS (-0.0288), 1000 grain weight (-0.0222), number of productive tillers /plant (-0.0152), days to maturity (-0.0093), calcium (-0.0067), panicle length (-0.0065), manganese (-0.0034), zinc (-0.0012) and copper (-0.0002). Similar positive indirect effects for days to 50 per cent flowering and carbohydrate were also reported by Kavya *et al.* (2017c), Ayesha *et al.* (2019c).

#### 4.4.2.11 Carbohydrate (g/100g)

Carbohydrate expressed non-significant positive correlation (0.1429) on grain yield per plant at phenotypic level. The positive indirect effect of carbohydrate on grain yield / plant via 1000 grain weight (0.017), SCMR at 30 DAS (0.0141), zinc (0.0135), calcium (0.0133), days to maturity (0.0112), panicle length (0.0064), days to 50% flowering (0.0062), manganese (0.0035) and SCMR at 45 DAS (0.0002). The negative indirect effects of carbohydrate on grain yield / plant through iron (-0.0209), magnesium (-0.0205), protein (-0.0167), number of grains / ear head (-0.0086), copper (-0.0079), plant height (-0.0021) and number of productive tillers /plant (-0.0013). These results were in consonance with the findings of Kavya *et al.* (2017c), Ayesha *et al.* (2019c) for panicle length and test weight.

#### 4.4.2.12 Calcium (mg/100g)

Calcium exhibited non-significant negative correlation (-0.0627) on grain yield per plant at phenotypic level. The positive indirect effect of calcium on grain yield / plant *via* number of grains / ear head (0.0121), panicle length (0.0077), plant height (0.0075), magnesium (0.0054), days to maturity (0.0051) and copper (0.0033). The negative indirect effects of calcium on grain yield / plant through number of productive tillers /plant (-0.0079), carbohydrate (-0.0075), iron (-0.0074), SCMR at 45 DAS (-0.0058), zinc (-0.0049), manganese (-0.0046), SCMR at 30 DAS (-0.0036), protein (-0.0031), 1000 grain weight (-0.003) and days to 50% flowering (-0.0005). Similar results of positive indirect effects were published by Ayesha *et al.* (2019c) for panicle length.

#### 4.4.2.13 Magnesium (mg/100g)

Magnesium expressed non-significant positive correlation (0.082) on grain yield per plant at phenotypic level. The positive indirect effect of magnesium on grain yield / plant *via* carbohydrate (0.0096), calcium (0.0045), SCMR at 30 DAS (0.0013), copper (0.0008), SCMR at 45 DAS (0.0005) and days to 50% flowering (0.0004). The negative indirect effects of magnesium on grain yield / plant through zinc (-0.0139), iron (-0.0129), plant height (-0.0105), number of productive tillers /plant (-0.0085), panicle length (-0.0073), days to maturity (-0.0063), 1000 grain weight (-0.0054), manganese (-0.004) and number of grains / ear head (-0.0021).

#### 4.4.2.14 Iron (mg/100g)

Iron exhibited non-significant positive correlation (0.1722) on grain yield per plant at phenotypic level. The positive indirect effect of iron on grain yield / plant via magnesium (0.0367), copper (0.036), plant height (0.0344), manganese (0.0282), days to maturity (0.0277), number of grains / ear head (0.0178), calcium (0.0176), zinc (0.014), 1000 grain weight (0.0096), panicle length (0.0087), days to 50% flowering (0.005) and number of productive tillers /plant (0.002). The negative indirect effects of iron on grain yield / plant through SCMR at 45 DAS (-0.0308), carbohydrate (-0.0277), SCMR at 30 DAS (-0.0078) and protein (-0.0023). Similar finding was reported by Ayesha *et al.* (2019c) for indirect effect through plant height and days to 50% flowering.

#### 4.4.2.15 Zinc (mg/100g)

Zinc expressed non-significant positive correlation (0.1241) on grain yield per plant at phenotypic level. The positive indirect effect of zinc on grain yield / plant via manganese (0.0643), magnesium (0.0262), plant height (0.0234), 1000 grain weight (0.015), carbohydrate (0.0119), days to 50% flowering (0.0111), iron (0.0093), calcium (0.0077), number of productive tillers /plant (0.0046), panicle length (0.0043), SCMR at 45 DAS (0.0024), days to maturity (0.002), protein (0.0009) and SCMR at 30 DAS (0.0003). The negative indirect effects of zinc on grain yield / plant through copper (-0.0141) and number of grains / ear head (-0.0046). Similar reports were published by Vishnuprabha *et al.* (2018) for iron content.

#### 4.4.2.16 Copper (mg/100g)

Copper showed non-significant positive correlation (0.0704) on grain yield per plant at phenotypic level. The positive indirect effect of copper on grain yield / plant via zinc (0.0028), SCMR at 45 DAS (0.0018), carbohydrate (0.0014), manganese (0.0012), calcium (0.0011), number of productive tillers /plant (0.001), days to 50% flowering (0.0009) and magnesium (0.0003). The negative indirect effects of copper on grain yield / plant through iron (-0.0048), days to maturity (-0.0028), plant height (-0.0024), panicle length (-0.0019), number of grains / ear head (-0.0016), 1000 grain weight (-0.0012) and SCMR at 30 DAS (-0.001).

#### 4.4.2.17 Manganese (mg/100g)

Manganese expressed non-significant positive correlation (0.0607) on grain yield per plant at phenotypic level. The positive indirect effect of manganese on grain yield / plant via copper (0.006), panicle length (0.0038) and SCMR at 30 DAS (0.0031). The negative indirect effects of manganese on grain yield / plant through zinc (-0.0653), iron (-0.019), plant height (-0.0179), 1000 grain weight (-0.0081), magnesium (-0.0077), days to 50% flowering (-0.0074), calcium (-0.0073), number of productive tillers /plant (-0.0061), SCMR at 45 DAS (-0.0034), carbohydrate (-0.0032), protein (-0.0026), number of grains / ear head (-0.0017) and days to maturity (-0.0015).

The residual effect permits precise explanation about the pattern of interaction of other possible components of yield. In other words, residual effect measures the role of the possible independent variables which were not included in the study on the dependent variable. In the present study, the residual effect is 0.749 suggesting there

might be few more important traits contributing to grain yield other than those studied in the present investigation.

From the foregoing results and dicussions on path analysis, it was noted that the traits SCMR at 30 DAS, plant height, number of grains / ear head and 1000 grain weight established true relationship with grain yield per plant by exhibiting positive associations and positive direct effects. Hence, these traits might be considered during selection of genotypes for improving the dependent variable *i.e.* grain yield per plant.


# Chapter – V

# SUMMARY AND CONCLUSIONS

## CHAPTER V

# SUMMARY AND CONCLUSIONS

The present research investigation on "Diversity in morpho-physiological and biochemical components in genetic resources of foxtail millet (*Setaria italica* (L.) Beauv.)" was carried out with 100 foxtail millet genetic resources at Regional Agricultural Research Station, Nandyal, Andhra Pradesh located at 15°29' N latitude and 78°29' E longitude from an altitude of 211.76 m above mean sea level during *kharif*, 2018 in order to study the genetic variability, heritability, genetic advance as per cent of mean, extent of genetic diversity, character association and path analysis for 18 metric traits *viz.*, SCMR at 30 DAS, SCMR at 45 DAS, days to 50 % flowering, plant height, panicle length, number of productive tillers /plant, days to maturity, number of grains / ear head, 1000 grain weight, protein, carbohydrate, calcium, magnesium, iron, zinc, copper, manganese and grain yield/ plant.

The results of ANOVA revealed significant differences for all the characters studied *viz.*, SCMR at 30 DAS, SCMR at 45 DAS, days to 50 % flowering, plant height, panicle length, number of productive tillers /plant, days to maturity, number of grains / ear head, 1000 grain weight, protein, carbohydrate, calcium, magnesium, iron, zinc, copper, manganese and grain yield/ plant implying existence of ample variation in the germplasm accessions studied.

Estimates of PCV were slightly higher than the corresponding GCV values for all the characters studied indicating that the characters were less influenced by the environment and thereby offering ample scope for improvement of the traits through simple phenotypic selection. High PCV and GCV were registered for copper, iron, magnesium, zinc, grain yield/ plant and number of productive tillers /plant indicating existence of large amount of variation among the test genotypes. Moderate PCV and GCV were recorded for calcium, manganese, panicle length and carbohydrate implying comparatively moderate variability for these traits. Moderate PCV and low GCV for protein indicated less variation among the test genotypes studied. On the other hand, low PCV and GCV exhibited by 1000 grain weight, SCMR at 30 DAS, SCMR at 45 DAS, days to 50% flowering, plant height, number of grains / ear head and days to maturity indicated low variation for these traits among the test genotypes studied.

The estimates of high heritability coupled with high genetic advance as per cent of mean were recorded for panicle length, number of productive tillers /plant, carbohydrate, calcium, magnesium, iron, zinc, copper, manganese and grain yield/ plant indicating the predominance of additive gene action in controlling the inheritance of these traits. Hence direct phenotypic selection will be rewarding with respect to these traits. High heritability coupled with moderate genetic advance as per cent of mean were registered by SCMR at 30 DAS, SCMR at 45 DAS, days to 50% flowering, plant height, number of grains / ear head, 1000 grain weight and protein indicating the operation of both additive and non additive gene actions in the inheritance of these traits. High heritability accompanied with low genetic advance as per cent of mean shown by days to maturity implied the operation of both additive and non additive gene actions in the inheritance of the trait.

The traits, number of productive tillers / plant, magnesium, iron, zinc, copper and grain yield/ plant possessed higher estimates of GCV, PCV, heritability and genetic advance as *per cent* of mean implying that these traits were predominantly under the control of additive gene action and genetic improvement can be achieved through simple selection for these traits.

Diversity in the genetic resources was assessed through $D^2$ analysis, canonical root analysis and hierarchial cluster analysis. $D^2$ analysis using Tocher's method showed formation of 11 non-overlapping distinct clusters with maximum number of genetic resources in cluster I (43) followed by cluster II (37), cluster VI with six genetic resources, cluster IV, IX with four genetic resources each and the remaining were monogenotypic clusters III, V, VII, VIII, X and XI containing only single genetic resource. Hence the germplasm accessions between cluster V (SiA 4044) and cluster XI (SiA 3222) possessing maximum inter cluster distance between them had high degree of genetic diversity and thus may be utilized under inter-varietal hybridization programme (transgressive segregation) for obtaining superior segregants. Minimum inter-cluster distance was reported between cluster VII and cluster X with accessions of lesser diversity indicating the need for increase of variability. Intra-cluster distance was reported to be high in case of cluster IX followed by VI indicating that the accessions under cluster IX are more divergent than the accessions under cluster VI.

Similarily hierarchial cluster analysis, done by ward's minimum variance method also showed formation of 11 non-overlapping distinct clusters. Clustering pattern divulged that majority of genotypes congegrated in cluster III (16) followed by

cluster VIII (14), cluster IX (12), cluster VII (11) and cluster V (10). The clusters IV, VI and XI comprised of eight genotypes each. Seven and five genotypes were grouped in clusters X and II, respectively. The cluster I registered as monogenotypic / solitary cluster might have resulted due to geographic barriers preventing gene flow or intensive natural and human selection for diverse and adaptable gene complexes. The maximum genetic distance 12.029 between SiA 3222 and SiA 3580, reflecting the wide diversity among the genotypes. The genotypes with high genetic distance can be utilized directly as potent parents in breeding programmes to achieve improved yields.

Canonical root analysis accounted for 67.371 per cent of total genetic divergence and showed seven canonical roots retained based on the scree plot and threshold eigen value greater than one. The traits plant height, 1000 grain weight, panicle length, days to maturity, grain yield/ plant, days to 50% flowering and zinc contributed maximum to the existing variability. The 2D and 3D scatter diagram confirmed the Tocher's clustering and showed that the genotypes SiA 3409 and SiA 3222, scattered relatively away from other genotypes can be used as 'potential parents' in future hybridization programmes.

The correlation studies between grain yield and its attributes in 100 accessions of foxtail millet revealed positively significant association of grain yield / plant with most of the traits *viz*., SCMR at 30 DAS, plant height, panicle length, number of grains / ear head and 1000 grain weight at phenotypic level implying that these traits may be chosen as selection criterion for developing high yielding cultivars.

The path coefficient analysis revealed that SCMR at 30 DAS, plant height, number of grains / ear head and 1000 grain weight had true relationship with grain yield per plant by establishing significant positive association and positive direct effect at phenotypic levels. The residual effect was also low, validating the accuracy of the results obtained in path coefficient analysis.

Thus as a whole, the studies conclude that the genetic resources *viz*., SiA 3222, SiA 4044 and SiA 3580 were found promising for majority of the traits and might serve as 'potential parents' in future hybridization programmes. The traits, number of productive tillers / plant, magnesium content, iron content, zinc content, copper content and grain yield / plant with higher estimates of variability parameters can be improved through simple selection strategies. Association studies through correlation and path analysis revealed that the trait SCMR at 30 DAS, plant height, number of grains / ear

head and 1000 grain weight had true relationship with grain yield per plant by establishing significant positive association and positive direct effect on grain yield implying the scope of direct selection for these traits in genetic improvement of foxtail millet.

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*Original not seen

**Note:** The literature is cited as per the "Thesis Guidelines" prescribed by Acharya N. G. Ranga Agricultural University, Guntur.