

**MORPHOLOGICAL CHARACTERIZATION
AND DIVERGENCE STUDIES IN BARNYARD
MILLET (*Echinochloa frumentacea* L.)**

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B.Sc. (Ag.)

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



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AND DIVERGENCE STUDIES IN BARNYARD
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BY

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B.Sc. (Ag)

**THESIS SUBMITTED TO THE
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CHAIRPERSON: Dr. A. TRIVIKRAMA REDDY



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2021

DECLARATION

I, **Mr. G.NEHRU**, hereby declare that the thesis entitled **“MORPHOLOGICAL CHARACTERIZATION AND DIVERGENCE STUDIES IN BARNYARD MILLET (*Echinochloa frumentacea L.*)”** 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 :

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Date :

I.D. No. MAM-2019/006

CERTIFICATE

Mr. **G. NEHRU** has satisfactorily prosecuted the course of research and that thesis entitled “**MORPHOLOGICAL CHARACTERIZATION AND DIVERGENCE STUDIES IN BARNYARD MILLET (*Echinochloa frumentacea L.*)**” 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 entitled “**MORPHOLOGICAL CHARACTERIZATION AND DIVERGENCE STUDIES IN BARNYARD MILLET [*ECHINOCHLOA FRUMENTACEA (L.)*]**” 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. NEHRU** 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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LIST OF ABBREVIATIONS AND SYMBOLS

<	:	Less than
>	:	more than
%	:	Per cent
σ^2	:	Variance
σ	:	Standard deviation
CD	:	Critical Difference
CV	:	Coefficient of variation
cm	:	Centimetre
df	:	Degrees of Freedom
<i>et al.</i> ,	:	And others
Fig.	:	Figure
g	:	Gram
GAM	:	Genetic advance as percent of mean
G	:	Genotypic path coefficient
GCV	:	Genotypic Co-efficient of Variation
ha	:	Hectare
kg	:	Kilogram
LSD	:	Lattice square design
m	:	Metre
Mt	:	Miloin tonnes
MSS	:	Mean sea sum of square
MSL	:	Mean sea level
M ha	:	Million hectares
No.	:	Number
P	:	Phenotypic path coefficient
P	:	Phenotypic path coefficient
<i>per se</i> :	:	As such with mean
PCA	:	Principal Component Analysis
PCV	:	Phenotypic co-efficient of variation
r_g	:	Genotypic correlation coefficient

r_p	:	Phenotypic correlation coefficient
SE	:	Standard Error
<i>via</i>	:	Through
<i>viz.,</i>	:	Namely
$\overline{X}$	:	Mean
2D	:	Two dimensional
3D	:	Three dimensional

ABSTRACT

Author : **G. NEHRU**

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The present research investigation on “Morphological Characterization and Divergence Studies in Barnyard Millet [*Echinochloa Frumentacea (L.)*]” was conducted during *kharif*, 2020 at Regional Agricultural Research Station, Nandyal, with sixty four germplasm accessions in lattice square design with two replications.

Morphological characterization of germplasm accessions revealed the existence of wide range of variation among 22 DUS traits studied. For plant growth habit, it was dominant for erectness, for basal tillers all the germplasm are low (<4), medium duration for days to 50% flowering, medium type was dominant for flag leaf blade length and width, medium was dominant for peduncle length, non-pigmented was dominant for pigmentation at internode, pyramidal was dominant for inflorescence shape, green color was dominant for inflorescence color, open was dominant for panicle compactness, for spikelet arrangements one side was dominant, straight was dominant for lower raceme shape, slender was predominant for lower raceme thickness, absent of branching was predominant for lower raceme branching, culm branching, all the germplasm accessions were branched, medium was dominant for lower raceme length, for panicle length medium was dominant, for plant height tall was dominant, grey white was dominant for grain color, medium was dominant for 1000 seed weight, lodging was absent for all the germplasm accessions.

The results of ANOVA indicated the existence of highly significant differences among the germplasm accessions indicating ample genetic variability in the germplasm for all the 18 quantitative traits studied.

Based on *per se* performance, promising germplasm accessions viz., TNEf-216, TNEf-215, TNEf-218 and TNEf-202 that recorded higher values for majority of the traits viz., days to 50% flowering and days to maturity (earliness), basal tillers, peduncle length, flag leaf blade length, flag leaf blade width, plant height, panicle weight / plant, 1000 seed weight, lower raceme length, grain yield / plant, phosphorus, calcium, iron, zinc, phosphorus were identified.

A perusal to the analysis of various genetic parameters viz., genetic variability, heritability and genetic advance as per cent of mean revealed higher values of GCV, PCV, heritability and genetic advance as per cent of mean for the traits basal tillers and lower raceme length implying their amenability for improvement through simple selection strategies. Moderate GCV and PCV values coupled with high heritability and genetic advance as per cent of mean was registered for the traits, days to 50% flowering, peduncle length, panicle length, 1000 seed weight, panicle weight per plant, grain yield per plant, zinc and protein indicating the prevalence of both additive and non-additive gene actions and hence genetic improvement can be achieved by intercrossing among the accessions followed by selection for this trait.

Diversity in the germplasm accessions was assessed through D² analysis and canonical root analysis. The results of D² analysis showed formation of eight non-overlapping distinct clusters with maximum number of accessions in cluster I (57) and cluster II, III, IV, V, VI, VII and VIII were mono genotypic clusters with single accession per cluster. Minimum inter-cluster distance was reported between clusters IV and VI. Maximum inter-cluster distance was observed between cluster VI and VII, IV and VI in the decreasing order of magnitude indicating the presence of diversity in the material which can be utilized for future hybridization programme.

About 75.9 per cent of total genetic divergence was accounted through canonical root analysis. Based on the results of divergence studies and *per se* performance together, the promising accessions TNEf-216, TNEf-215, TNEf-218 and TNEf-202 were identified which can be used as 'potential parents' in future hybridization programmes.

The correlation studies between grain yield and its attributes in sixtyfour accessions of barnyard millet revealed positively significant association of grain yield / plant with most of the traits viz., basal tillers, 1000 seed weight, panicle weight per plant and peduncle length implying that these traits may be employed as selection criterion for developing high yielding cultivars. The path coefficient analysis revealed that traits viz., panicle weight / plant, iron, calcium, panicle length and 1000 seed weight established true relationship with grain yield per plant by exhibiting positive associations and positive direct selection for these traits.

Thus as a whole, the studies conclude that the germplasm accessions viz., TNEf-216, TNEf-215, TNEf-218 and TNEf-202 were promising for majority of the traits and might serve as 'potential parents' in future hybridization programmes. The traits, basal tillers and lower raceme length with higher estimates of variability parameters can be improved through simple selection strategies. Association studies through correlation and path analysis revealed that the traits panicle weight per plant and 1000 seed weight showed high positive direct effects on grain yield implying the scope of direct selection for these traits in genetic improvement of barnyard millet.

Chapter - I

INTRODUCTION



Chapter-1

INTRODUCTION

Millets refers to any small seeded cereal crops or forage grasses used for food, feed, biofuel, forage and brewing. These are most popularly called as Nutri-cereals as they provide most of the nutrients require for better functioning of human body. It mainly includes jowar, bajra, finger millet, foxtail millet, kodo millet, litte millet, proso millet and barnyard millet. These are short-term, warm season crops, resistance to pests and diseases, good productivity even during water scarcity (Sarita and Ekta Singh, 2016). These millets are often referred to as famine crops as these are the crops that yields even in famine conditions. Utilization of millets as food crops represents an interesting opportunity to contribute for filling the gap in food supply. The millets have always been regarded as less important due to which not much efforts were made into improving their productivity as crops, utilization as important staple foods, and processing and food technology development. Hence to sustain food and nutritional security of consumers and livelihood security of rural households, there is a need for reconsideration of millets research in terms of present and future demand.

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 (oodalu) constitute the 'Small millets' or Minor millets. These are often regarded as 'heritage crops' owing to their cultivation from times immemorial for their stability in yield levels. The grains of small millets, being nutritionally important than rice and wheat, provide a cheap source of proteins, minerals, vitamins, fiber, antioxidants and energy to poorest of the poor.

Barnyard millet is also known as Madira or Jhangora or Sawan, is an ancient millet crop grown in warm and temperate regions of the world and widely cultivated in Asia, particularly India, China, Japan, and Korea. The major barnyard millet producing states in India are Uttarakhand, Madhya Pradesh, Karnataka, Uttar Pradesh and North East region of India. The cultivated species of barnyard millet are Indian barnyard millet (*Echinochloa frumentacea*) and Japanese barnyard millet (*Echinochloa esculenta*). It is the fourth most produced minor millet, providing food security to many poor people across the world. Globally, India is the biggest producer of barnyard millet, both in terms of area (0.146 m ha^{-1}) and production (0.147 mt) with average productivity of 1034 kg/ha during the last 3 years (IIMR, 2018).

At present barnyard millet cultivation is increased due to its highly rich nutritious grains and presence of strong antioxidative compounds. Its grain contains 11.2 g/100g Proteins, 10.1 g/100g crude fibre, 4.4 g/100g minerals and 15.2mg/100g iron. (Anonymous, 2010). The barnyard millet contains 3.6% fat, 68.8% carbohydrate and 398 kcal/100 g energy. The total dietary fiber content was high (12.6%) including soluble (4.2%) and insoluble (8.4%) fractions. The presence of dietary fibre leads to low glycemic index (GI) that releases sugars very slowly in blood that's why they are highly suitable for diabetic patients (Ugare *et al.* 2014). Indian barnyard millet contains between 51.5% to 59.5% starch.

Studies on morphological characterization are useful to evaluate the extent of traits phenotypic diversity in the germplasm. They hold vast potential for their objective utilization in the breeding programme. Further they serve as an essential tool in selecting varieties or lines based on agronomical, morphological, genetic or physiological characters. The genetic material collected from different locations may possess wide spectrum of genetic variability that can be utilized in systematic crop breeding programme.

For the initiation of any crop improvement programme, prevalence of wide spectrum of genetic variability in the population is a requisite in selection of desired genotype. The variability in the population is further partitioned into heritable and non-heritable component for the assessment of true breeding behaviour of the genotype. The genetic variability estimated by various genetic parameters viz., genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance. These parameters aid the breeder towards the preparation of effective selection strategies in crop breeding.

Prevalence of genetic diversity is a prime requisite in any crop improvement programme. Multivariate analysis through D^2 statistic, provides a quantitative estimate of association between geographic and genetic diversity based on the generalized distance (Mahalanobis, 1936). It enables to discriminate between different cultivars according to the diversity prevalent in the germplasm collections and thus assist in the selection of genetically divergent parents for their exploitation in hybridization programme. In addition, principal component analysis may be used to classify the relationships between the traits in multi-trait systems and for identifying the patterns of data by reducing the number of dimensions. It

also provides an insight into the process contributing differences in yield among the genotypes, a vital aspect in identification and selection of top ranking genotypes out of diverse germplasm base.

Grain yield of a crop is a polygenic character is influenced by many of its contributing characters governed by polygenes as well as environmental factors. An understanding in the inheritance of yield and its attributes, heritability, expected genetic advance and association between the component trait and yield is vital for designing effective selection procedure in evolving high yielding genotypes. However, the inheritance of quantitative traits is often influenced by variation in other character which may be due to pleiotropy or genetic linkage. Therefore 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 identify cause and effect relationship between different pairs of characters.

Keeping the aforesaid points in view, the present investigation in Barnyard millet is attempted with the objectives for unlocking the genetic variation through characterization of the germplasm and identification of promising genotypes suited for designing breeding strategies in order to develop bio-fortified cultigens.

OBJECTIVES

1. Morphological characterization of germplasm using IBPGR descriptors.
2. To study the genetic divergence in Barnyard millet germplasm for yield and its attributes and quality traits.
3. To estimate variability, heritability and genetic advance for yield and its attributes and quality traits in germplasm.
4. To study the association and path effects of yield attributes and quality traits on grain yield in Barnyard millet.

Chapter - II

REVIEW OF LITERATURE

Chapter II

REVIEW OF LITERATURE

The literature available on Barnyard Millet (*Echinochloa Frumentacea* (L.)) related to present study has been comprehensively reviewed under the following headings. As sufficient literature is not available for some quality parameters, results were justified using literature from other millet crops like foxtail millet, finger millet, pearl millet, proso millet and little millet.

- 2.1 Morphological characterization of germplasm
- 2.2 Genetic divergence
- 2.3 Genetic parameters
- 2.4 Correlation analysis
- 2.5 Path analysis

2.1 Morphological characterization of germplasm

Characterization of germplasm accessions provide pivotal information for the breeding of crop and in the management of genetic resources. Information on characterization of a genotype offers valuable information for practical genotype identification and hypothesizing phylogenetic relationships that may pave the way for effective exploitation of genetic resources. Literature pertaining to characterization and assessment of variation in the germplasm accessions has been reviewed and presented in the following sections.

Nilavarasi *et al.* (2020) evaluated 11 barnyard millet genotypes in randomized block design with three replications to characterize based on their morphological characters viz., Plant growth habit, the number of basal tillers, Culm branching, Plant height (cm), Lodging, Flag leaf length, Flag leaf width, Flag leaf altitude, Inflorescence colour, Stigma colour, Peduncle length (cm), Lower raceme length (cm), Lower raceme thickness, Lower raceme branching, Seed shattering and Seed shape. Morphological variations exist in collected germplasm is due to the variation in genetic makeup and these differences in morphological traits were helpful in recognition of individual barnyard millet cultures.

Kuraloviya *et al.* (2019) evaluated 29 barnyard millet germplasm accessions in randomized block design (RBD) in two replications along with check variety, Germplasm accessions were characterized for 15 qualitative traits namely, growth habit viz.,

decumbent (17), erect (11), prostate (2), plant pigmentation are differ from present (21) or absent (9) of pigmentation , leaf pigmentation, colour of inflorescence are of three types green (7), light purple (17), dark purple (6) inflorescence shape, compactness of inflorescence are three types open (14), intermediate (10), compact (6), shape of lower raceme are of three types straight (4), curved (18), slender (8), branching of lower raceme absent (30), spikelet arrangement are of two types around (27), and one side (3), culm branching, blade pubescence, degree of lodging at maturity, senescence, four seed colours straw white (2), brownish grey (2), grey (6), grey + straw white (15) and grain shape concave (30) variation exists for qualitative traits in barnyard millet.

Renganathan *et al.* (2017) performed cluster analysis in 40 barnyard millet germplasm lines for 15 quantitative and qualitative traits. The findings showed that growth habitat viz., erect (85%), decumbent (3%), Prostate (12%), colour of inflorescence are of three types green (75%), light purple (15%), dark purple (15%), three types of inflorescence shape viz., cylindrical (45%), pyramidal (30%), globose to elliptic (25%), compactness of inflorescence are three types viz., open (23%), intermediate (23%), compact (56%), three types of lower raceme shape straight (23%), curved (23%), slender (56%), branching of lower raceme classify into two absent (38%), present (62%).

Ahmed *et al.* (2017) studied 246 foxtail millet germplasm qualitatively using IBPGR descriptors for plant characters, leaf characters, inflorescence characters and seed characters. Plant characters viz., growth habits – Erect (93.1%) and erect geniculate (6.9%); three classes of plant pigmentations – green (95.5%), pigmented (4.1%) and deep purple (0.4%); Leaf character viz., leaf colour - green (93.9%) and pigmented (6.1%); Inflorescence characters viz., four types of inflorescence lobes – Short (65%), long (32.5%), absentia of lobes (2%), large and thick (0.5%); Four kinds of lobes compactness - medium (50%), loose (28%), compact (20%) and spongy (2%); Seed characters viz., four seed shapes – Cylindrical (77.2%), pyramidal (17.8%), globose to elliptic(2.5%) and ovate (2.5%); five seed colours - white (58.10%), black (13.4%), orange (11.8%), yellow (12.6%) and light yellow (4.1%) were noticed.

Nehra *et al.* (2016) characterized 49 inbred lines of pearl millet for 29 morphological traits using DUS descriptors. The traits viz., anthocyanin coloration of first leaf sheath categorized as present (27%) and absent (73%) ; plant node pigmentation classified as green (22%), brown (22%) and purple (55%); Spike shapes grouped as cylindrical (59%), conical (37%), candle (2%) and lanceolate (2%) ; seed colours as grey

(43%), deep grey (27%), yellow (22%) and (8%) cream seed color; seed shapes as globular (67%) and obovate (33%) were studied.

Sapkota *et al.* (2016) evaluated 16 agro-morphological traits of 10 foxtail millet accessions using IBPGR descriptor. Variation was observed in terms of tip of cotyledon leaf, anthocyanin pigmentation, colour of the plant and leaf, growth habit of the plants, panicle shape, lobe characteristics of the panicle and inflorescence. All the accessions were reported erect in habit and had white anther colour.

Amgai *et al.* (2011) studied five landraces of Nepalese foxtail millet based on IBPGR descriptor. Accordingly, two kinds of growth habit – erect (4) and erect geniculate (1); two types of blade pubescence – essentially glabrous (4) and medium pubescence (1) ; two types of senescence – actively growing (3) and dead (2) were observed.

Reddy *et al.* (2009a) observed in 1993 finger millet germplasm accessions and noted two plant colours viz., green (65%) and pigmented (35%); two types of growth habit – erect (77.92%) and decumbent; eight types of inflorescence shapes viz., top curved (46.26%), incurved, fisty, short open, long open, compact, pendulous and laxa; five grain colours - light brown (71.65%), reddish brown , dark brown , ragi brown and white.

Reddy *et al.* (2007) characterized morphologically 842 prosomillet's global germplasm accessions and noticed three growth habits viz., decumbent (74.5 %), erect and erect-geniculate; three kinds of sheath pubescence - medium (40.5%), sparse and dense; three types of leaf pubescence dominant (51.0 %), medium and dense ; Wide spectrum of grain colours viz., light brown (42.1 %), straw, white, light red, dark olive green, dark red , olive green , dark brown, dark green , brown and black.

Reddy *et al.* (2006) studied 1535 foxtail millet germplasm accessions and reported four growth habits viz., decumbent, erect (96.5%), erect geniculate and prostrate; three leaf colours – green (80.7%), yellow and pigmented; two types of culm branching –medium to high (56%) and rest reported less; three types of lobe compactness – compact (64.4%), medium and loose; six types of grain colours viz., yellow (88.38%), black, combination of black and white, dark grey, light grey and red.

2.2 Genetic divergence:

Knowledge on the nature and magnitude of genetic variability present in the crop species will assist in formulating a successful breeding programme. Assessment of genetic

diversity in germplasm collection can facilitate classification and identification of diverse genotypes. Precise information on the nature and degree of genetic divergence helps the plant breeder in choosing the diverse parents for specific utilization in hybridization. D^2 statistic is a powerful tool in quantifying the degree of genetic divergence at the genotypic level and provides measure of association between geographic distribution and genetic diversity based on generalized distance (Mahalanobis, 1928). Rao (1952) suggested the application of this technique for the assessment of genetic diversity in plant breeding.

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.

Harshal *et al.* (2021) studied 41 barnyard millet genotypes in randomized block design with three replications. Diversity as revealed D^2 analysis into 12 clusters indicated that days to 50% flowering, days to maturity, plant height at maturity, productive tillers per plant, 1000 seed weight, protein, calcium, fat, iron and zinc content could be selected as parents for hybridization programme from cluster III, IV, V, VI, VII, VIII, IX, X, XI and XII.

Prabu *et al.* (2020) studied to evaluate the phenotypic diversity and stability of barnyard millet germplasm for yield and its attributing traits. Diversity as revealed by D^2 analysis indicated that the trait grain yield had contributed maximum towards the diversity followed by days to maturity. The accessions M5P1, M36P1 and M37P1 exhibited the highest mean values for grain yield per plant, but no significance difference was found comparing checks. Stability analysis revealed that none of the accessions were showed stable performance, indicated that influence of environmental factors played a major role.

Renganathan *et al.* (2020) studied the importance of barnyard millet in the current scenario and discuss the up-to-date status of genetic and genomics research and the research gaps to be worked upon by suggesting directions for future research to make barnyard millet a potential crop in contributing to food and nutritional security.

Laxmi Rawat *et al.* (2020) evaluated barnyard millet with respect to yield, yield contributing traits and against grain smut disease at high hills of Uttarakhand. During three consecutive seasons i.e. Kharif- 2017, Kharif- 2018 and Kharif- 2019, in which seven advance breeding lines and three check varieties viz., PRJ 1 (local check), VL 207 (zonal

check) and DHBM 99-3 (national check), selected from core set of barnyard millet germplasm maintained under ICAR- All India Coordinated Research Project on Small Millets at College of Forestry, Ranichauri, Uttarakhand. These two lines (URJ-4 and PRJ 1©) are of immense value for plant breeders in further crop improvement programme for developing grain smut resistant barnyard millet high yielding variety (s).

Rao *et al.* (2000) studied genetic diversity in 28 genotype of barnyard millet indicated that genotypic coefficient of variation and genetic advance were high for grain yield, fodder yield and plant height. High heritability was estimated for days to flower, days to maturity and grain yield.

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.

Dhanalakshmi *et al.* (2019) evaluated the nature of genetic diversity existing in 99 barnyard millet genotypes including two commercial check varieties viz., MDU1 and CO (KV) 2 under sodic soil condition. Mahalanobis D^2 analysis grouped the genotypes into 13 clusters with respect to 12 biometrical traits. They revealed that the traits grain yield per plant and plant height contributed maximum to the genetic diversity. PCA revealed that the traits plant height, flag leaf length, lower raceme length and ear length contributed maximum towards variability in PCA axis I and II. Thus, selection of genotypes as parents from these genetically diversified clusters for breeding programmes could result in heterotic hybrids and could generate good amount of genetic variability in barnyard millet genotypes under the sodic soil condition.

Manimekalai *et al.* (2018) studied genetic diversity among 61 barnyard millet genotypes from southern India, was investigated using 10 morpho-nutritional traits. A large variability was observed for morpho-agronomic and grain nutritional traits including for the important traits such as flowering (49.50–82.00 cm), plant height (58.17–152.38 cm), grain yield (12.52 g–41.25 g), Fe (11.05–21.51 mg/100 g) and Zn (2.46–5.91 mg/100 g).

They revealed that genetic relationships among the southern India barnyard millet genotypes, it can be helpful in planning the utilization patterns and management of barnyard millet germplasm existing in southern India.

Trivedi *et al.* (2017) evaluated 178 accessions of barnyard millet in the mountain ecosystem of the Central Himalayan Region is known for its diversity of crops under rain-fed conditions in an augmented block design (ABD). Significant variability was noted in days to 50% flowering, days to 80% maturity, 1000 seed weight and yield potential of the germplasm.

Mahanthasha *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.

Wallace *et al.* (2015) studied 89 accessions of the barnyard millet core collection (Upadhyaya *et al.*, 2014), along with six additional accessions chosen from the ICRISAT gene bank total of 95 accessions: 65 from *E. colona* and 30 from *E. crus-galli*. To enhance the use of this germplasm and genomic research in barnyard millet improvement, they report that genetic characterization of this core collection using whole-genome genotyping-by-sequencing.

Joshi *et al.* (2015) studied 49 land races of barnyard millet were collected from five districts of Madhya Pradesh during 2008-09 and 2009-10 and evaluated for agro-morphological traits and grain smut. They revealed strong positive association between length of lower raceme and 1000 grain weight was recorded, while strong negative correlation between length of lower raceme and days to 50% flowering and between days to 50% flowering and 1000 grain weight was observed. Positive correlation between 1000 grain weight and grain yield per plant was also noted. Five land races namely -RBM 57, 77, 78, 81 and 82 were completely free and RBM 58 was resistant to grain smut.

Ugare *et al.* (2014) studied nutrient composition, glycemic index and health benefits of barnyard millet in type II diabetics. The millet had 10.5% protein 3.6% fat, 68.8% carbohydrate and 398 kcal/100 g energy. The total dietary fibre content was high (12.6%) including soluble (4.2%) and insoluble (8.4%) fractions. Low glycemic index of the grains both dehulled (50.0) and dehulled and heat treated (41.7) was recorded. The

feeding intervention of 28 days revealed a significant reduction in glucose (139.2 to 131.1 mg/ dl), LDL-C (from 167.7 to 162.9 mg/dl), VLDL-C (from 24.0 to 23.2 mg/dl), ratio of TC: HDL (from 4.7 to 4.6) and LDL: HDL (from 3.2 to 3.1) in the experimental diabetic groups. They concluded that the dehulled and heat treated barnyard millet is beneficial for type-II diabetics.

Arunachalam *et al.* (2012) evaluated eighteen breeding lines in three diverse environments of Tamil Nadu namely Coimbatore, Madurai and Chettinad. Among the three locations, Coimbatore and Chettinad turned out to be high and low yielding environment respectively. The variance analysis inferred that the performance of barnyard millet lines was influenced by the growing environment. They revealed that early maturing genotypes were poor yielders and vice versa. Based on the result it is suggested that, focused breeding efforts are required to identify high yielding stable barnyard millet genotypes.

Gupta *et al.* (2009) evaluated 194 accessions of barnyard millet collected from different eco-geographical regions of India were evaluated for 14 quantitative traits during kharif 2003 and 2005 in augmented block design with two checks. These accessions were grouped into 5 groups differed significantly in their mean values for quantitative traits and magnitude of correlation among traits indicates origin based association. The plotting of first and second principal component axes scores suggests that presence of three distinct morphotypes in the present study. These morphotypes are quite similar to three botanical varieties viz., var. robusta, var. intermedia and var. stolonifera in their morphological traits, while botanical variety *laxa* was completely absent.

Mahalanobis D² Analysis:

Vanniarajan and Chandirakala (2020) studied genetic diversity studies among fifty-three genotypes of Barnyard millet in Randomized Block Design with two replications. The clustering of the genotypes based on the quantitative characters was done by using the D² method. Out of 12 clusters formed, the maximum inter-cluster distance was found between cluster V and cluster VIII, indicating high diversity between the genotypes present in these two clusters. Cluster VIII included the genotypes, which showed significantly higher mean for grain yield and maximum value for many of the yield contributing traits and grain yield/ plant.

Arya *et al.* (2018) studied 35 barnyard millet genotypes for genetic diversity. All thirty-five genotypes were grouped by using Mahalanobis D² stastistic into 6 clusters

irrespective of geographical diversity, indicating no parallelism between geographic and genetic diversity. The cluster pairs exhibiting very high inter-cluster distances were cluster IV and VI, cluster IV and V, cluster II and IV, cluster III and VI, cluster I and IV and cluster III and IV. Crossing between genotypes of clusters IV with genotypes of cluster VI and those genotypes of cluster V would be fruitful for obtaining transgressive segregants for developing high yielding and better quality barnyard millet varieties.

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.

Sao *et al.* (2016) carried out genetic divergence analysis through Mahalanobis 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 Mahalanobis 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.

Brunda *et al.* (2015) investigated genetic diversity in 78 foxtail millet genotypes through Mahalanobis 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.

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.

Karad *et al.* (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 genotypes 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 mono genotypic 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 character iron content contributed maximum towards divergence followed by plant height, days to physiological maturity and days to 50% flowering.

Anantharaju and Meenakshiganesan (2008) grouped 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.

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 Euclidean² 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.

Ramya *et al.* (2017b) conducted principal component analysis in 60 inbred lines of pearl millet for 11 quantitative traits. The PCA identified four principal 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.

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.

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.

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.

Reddy *et al.* (2009b) 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.

2.3 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 in achieving higher yields. The phenotype of quantitative trait is a combined product of genotype, environment and their interaction. Therefore the success of any breeding activity depends on the extent of genetic variability available for utilization in crop improvement.

2.3.1 Genetic variability:

The success of genetic improvement in any character depends on the nature of variability present for that character. Hence, an insight into the magnitude of variability present in the gene pool of a crop is of utmost important to a plant breeder for starting judicious plant breeding program. However, the phenotypic expression of complex character like yield is a combination of genotype, environment and their interaction. This implies the need to partition the overall variability into heritable and non-heritable components by utilizing appropriate statistical techniques.

High PCV and GCV for a trait is an index of greater variability in the population for that character. The magnitude of heritability coupled with nature and extent of variability in the breeding material offers valuable information that paves the way for effective genetic improvement through selection.

Anuradha *et al.* (2021) studied barnyard millet genotypes and noted estimates of high PCV and moderate GCV for number of productive tillers per plant.

Williams *et al.* (2019) studied genetic variability for salinity tolerance in 32 barnyard millet accessions was assessed based on the morpho-physiological parameters governing salt tolerance viz., germination percentage, relative germination rate, root length, shoot length, seedling length, vigour index, relative salt injury rate and relative water content. They revealed that salt tolerant genotypes maintained higher relative water content and enzyme activity under salt stress, which is the underlying mechanism for salt tolerance.

Subbulakshmi *et al.* (2018) analyzed the genetic variability of 54 pearl millet hybrids for 13 traits and reported that PCV was greater than GCV for all the characters

studied indicating little influence of environment. High PCV and GCV was obtained for plant height, single plant yield, single head grain weight, crude fiber, beta carotene content, iron and zinc, indicating that selection for these traits will lead to genetic improvement.

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

Amarnath *et al.* (2018a) investigated 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.

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.

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 these traits might be chosen for crop 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.

Mahanthesh *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.

Das *et al.* (2016) assessed 48 germplasm lines of finger millet and reported PCV and GCV values were high for main ear length and grain yield per plant while it was moderate for number of basal tillers per plant, number of leaves on the main tillers, number of productive tillers per plant and total number of finger on the main ear.

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. Straw weight showed high GCV during Autumn. 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.

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.

Karad *et al.* (2013) studied 65 finger millet accessions to determine the extent of genetic variability. The genotypic and phenotypic coefficients of variation were high for the characters iron percent, fodder yield per plant, grain yield per plant, number of productive tillers per plant, ear head per plant, finger length, average fingers per head and test weight.

Wolie *et al.* (2013) evaluated 88 finger millet germplasm and observed high PCV and GCV values for number of tillers per plant, number of ears per plant, number of fingers per plant, finger length, biomass yield, grain yield, lodging and blast severity suggesting the possibility of improving these traits through selection.

Prasanna *et al.* (2013a) accessed 40 foxtail millet genotypes and noticed that very high PCV and GCV values were recorded for number of basal tillers and grain yield per plant.

Ganapathy *et al.* (2011) assessed 230 finger millet germplasm accessions and found PCV and GCV was high for productive tillers per plant, moderate for days to 50% flowering, plant height, finger numbers per ear, finger length and grain yield per plant and low for days to maturity.

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 1000-grain weight.

Haradari *et al.* (2011b) investigated 1000 finger millet germplasm and observed that PCV and GCV values were high for plant height, number of productive tillers, grain yield per plant while it was low for days to 50 *per cent* flowering and maturity.

Prabu *et al.* (2008) evaluated 150 finger millet germplasm accessions and noted that phenotypic and genotypic coefficient of variation were high for number of leaves and finger breadth, moderate for number of fingers and low for the remaining traits *viz.*, days to 50% flowering, plant height, number of tillers, leaf length, leaf breadth, days to maturity, finger length, 1000-grain weight and single plant yield.

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

Hanson *et al.* (1956) defined heritability in the broad sense as the ratio of genotypic variance to the total genetic variance in the non-segregating populations. 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. Johnson *et al.*, (1955) reported that estimates of both heritability and genetic advance are more useful in the choice of selection method rather than heritability or genetic advance alone. High heritability coupled with high genetic advance indicates additive gene effect (Johnson *et al.*, 1955) and improvement could be made for that character by simple selection based on the phenotypic performance. 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 (Verma *et al.*, 1987).

Anuradha *et al.* (2021) studied barnyard millet genotypes and noted high heritability was observed for days to 50 % flowering followed by days to maturity.

Vikram *et al.* (2020) analysed using 40 mutants along with two check varieties CO(Kv) 2 and MDU1 of barnyard millet during Kharif 2019. High heritability was recorded by traits such as number of basal tillers, days to fifty percent flowering, flag leaf length, plant height, number of racemes, number of productive tillers, number of leaves in main tiller, single ear head weight and single plant yield.

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.

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.

Jyothisna *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.

Jyothisna *et al.* (2016 c) studied 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.

Johar (2015) studied in 34 exotic Italian 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.

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.

Wolie *et al.* (2013) studied 88 finger millet germplasm and noticed that high heritability coupled with high expected genetic advance as percent of mean was obtained for number of ears per plant, number of fingers per plant, finger length and days to heading, biomass yield, 1000 kernel weight, lodging susceptibility and blast severity indicating the presence of more additive gene effects for potential crop improvement and so these characters could be improved by selection.

Karad *et al.* (2013) estimated 65 finger millet accessions and noticed high heritability coupled with high genetic advance for fodder yield per plant, days to 50% flowering, days to maturity and plant height advocated high genetic progress for them.

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.

Ganapathy *et al.* (2011) evaluated 230 finger millet germplasm accessions and reported that high heritability coupled with high genetic advance for days to 50% flowering, plant height, productive tillers per plant, finger numbers per ear, finger length and seed yield per plant, indicating the predominance of additive gene effects, in

controlling these traits, early and simple selection could be exercised due to fixable additive gene effects.

Nirmalakumari *et al.* (2010a) studied 109 little millet germplasm accessions and observed that high heritability coupled with high genetic advance was noted for grain yield, number of productive tillers, total number of tillers, grain yield, flag leaf length, flag leaf width and panicle length. This indicated that the heritability is due to additive gene effects and can be improved by simple selection.

Prabu *et al.* (2008) assessed 150 finger millet germplasm accessions and observed that the characters *viz.*, number of fingers, number of tillers and single plant yield showed high heritability coupled with high genetic advance indicating that additive genes were responsible to contribute more for these characters and selection on the basis of phenotype provides ample scope for genetic improvement.

Bezaweletaw *et al.* (2006) analyzed 66 finger millet accessions and reported that traits finger length and finger width possessed high heritability coupled with high genetic advance, a consequence of additive gene action reflecting the efficiency of selection for the improvement of these traits.

John (2006) evaluated 20 finger millet genotypes and noted that number of productive tillers per plant, number of fingers per ear, test weight, total dry matter production and harvest index possessed high heritability coupled with high estimates of genetic advance suggesting the role of additive gene action and amenability for selection at phenotypic level.

2.4 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.

Anuradha *et al.* (2021) performed correlation studies on barnyard millet. Correlation for grain yield and fodder yield can be taken up via selection of days to 50% flowering and days to maturity which are highly correlated in positive direction.

Vikram *et al.* (2020) performed correlation analysis using 40 mutants along with two check varieties CO(Kv)2 and MDU1 of barnyard millet during Kharif 2019. Correlation studies showed that number of productive tillers, single ear head weight and plant height possess significant positive correlation with yield at both genotypic and phenotypic level.

Prabu *et al.* (2020) performed correlation analysis using forty genotypes of barnyard millet in high altitude region. Correlation analysis evinced that grain yield per plant had positive significant correlation with plant height, days to flowering, days to maturity, number of nodes, stem diameter, length of flag leaf, width of flag leaf, length of inflorescence, width of inflorescence, length of lower racemes, number of racemes and thousand grain weight. The trait length of peduncle alone expressed negative significance with grain yield.

Rao *et al.* (2000) studied correlation in 28 genotypes of barnyard millet indicated tillers per plant and ear length had positive significant correlation with fodder yield and all the three had positive association with yield. Days to flower, days to maturity and plant height had negative correlation with yield.

Jyothi *et al.* (2020) performed correlation studies in kodo millet revealed that the grain yield per plot had positive association with tillers per plant, panicle length, panicle per plant, days to flowering, days to maturity, fodder yield, test weight. Hence improving of grain yield can be achieved by improving these traits.

Vishnuprabha and Vanniarajan (2018) carried out correlation analysis for five traits in 25 genotypes of barnyard millet comprising five parents and their 20 F1 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.

Gohel *et al.* (2018) performed correlation analysis for 30 different genotypes of finger millet, Grain weight per main ear ($r_g=0.847$, $r_p=0.831$), harvest index ($r_g=0.883$, $r_p=0.697$), number of productive tillers per plant ($r_g=0.795$, $r_p=0.685$), biological yield per plant ($r_g=0.463$, $r_p=0.434$) and panicle length ($r_g=0.318$, $r_p=0.294$) positive association towards grain yield per plant at phenotypic and genotypic level.

Anusha *et al.* (2018) carried out correlation analysis in 22 pearl millet genotypes for 12 characters. 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.

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.

Bhasker *et al.* (2017) performed correlation studies with 13 parental lines (5 lines and 8 testers) and their 40 hybrids of pearl millet. Significant genotypic correlations were observed for panicle length, productive tillers per plant, panicle diameter, fodder yield per plot and plant height with grain yield per plant.

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.

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.

Sood *et al.* (2016) performed correlation analysis on barnyard millet (*Echinochloa* spp.) global germplasm collection in 2011 and 2012 in augmented and alpha lattice design respectively. The correlation coefficients indicated that grain yield had high significant and positive association with flag leaf width and culm thickness during both years, whereas negative association of grain yield was observed with basal tillers and peduncle length.

Nandini *et al.* (2016) carried out correlation analysis for seven quantitative traits in 542 F3 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 plant, 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.

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.

Joshi *et al.* (2015) studied 49 land races of barnyard millet were collected from five districts of Madhya Pradesh during 2008-09 and 2009-10 and evaluated for agro-morphological traits and grain smut. They revealed strong positive association between length of lower raceme and 1000 grain weight was recorded, while strong negative correlation between length of lower raceme and days to 50% flowering and between days to 50% flowering and 1000 grain weight was observed. Positive correlation between 1000 grain weight and grain yield per plant was also noted. Five land races namely -RBM 57, 77, 78, 81 and 82 were completely free and RBM 58 was resistant to grain smut.

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.

2.5 Path analysis

Knowledge of inter-relationship between yield and yield components is vital for efficient selection of desirable segregants. Unlike the correlation coefficient values which measures the extent of relationship, path co-efficient (Wright, 1921; Dewey and Lu, 1959) measure the magnitude of direct and indirect effects of characters on complex dependent character like grain yield. Path analysis takes into account the cause and effect relationship between the variables by partitioning the association into direct and indirect effects through other independent variables. It also enables the breeders to judge best about the important component characters during selection programme.

Vikram *et al.* (2020) conducted path analysis using 40 mutants along with two check varieties CO(Kv)2 and MDU1 of barnyard millet during Kharif 2019. Path analysis showed that traits like number of basal tillers, single ear head weight and panicle length had high direct effect on yield. Thus, selection of these traits would be rewarding for yield improvement in barnyard millet.

Prabu *et al.* (2020) conducted path analysis using forty genotypes of barnyard millet in high altitude region. The path coefficient estimation indicated that stem diameter had exposed high magnitude of direct effect on grain yield. Hence, the direct selection based on the flawless relationship between grain yield and these traits would benefit in selecting high yielding genotypes.

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.

Gohel *et al.* (2018) conducted path analysis with 30 different genotypes of finger millet. Path coefficient analysis revealed that grain weight per main ear (0.534) had the highest direct positive effect towards the grain yield followed by number of productive tillers per plant (0.353), panicle length (0.166), days to flowering (0.133), harvest index (0.124), biological yield per plant (0.081), leaf blade length (0.011).

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.

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.

Bhasker *et al.* (2017) conducted path analysis with 13 parental lines (5 lines and 8 testers) and their 40 hybrids of pearl millet. The path coefficient analysis at genotypic level revealed that the characters viz., fodder yield per plot had exhibited largest direct effect on grain yield per plant followed by panicle length, 1000 grain weight and number of productive tillers per plant.

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.

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.

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.

Nandini *et al.* (2016) performed path analysis for nine characters in 542 F₃ 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 characters 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.* (2016) conducted path analysis in 44 foxtail millet genotypes for 12 quantitative traits and reported that direct effect of 1000 grain weight on grain yield per plant was positive which indicated the true relationship of this trait and a direct selection through this trait will be effective. The indirect effect of number of panicles, panicle length (cm), number of productive tillers and straw yield through 1000 grain weight was positive and moderate to high implying that direct selection for 1000 grain weight will lead to simultaneous indirect selection of these traits for increased grain yield per plant.

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.

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.

Nazni and Karuna (2016) studied with the objectives to study the different method of chemical treatment in barnyard millet bran and the treated bran and raw bran was analysed for the antinutritional and proximate composition. They revealed that chemical treated bran the calcium hydroxide and hot water treated barnyard millet bran get decrease

the antinutrient factors such as trypsin inhibitor, lipase activity, phytates etc., when compare to raw barnyard millet bran.

Sood *et al.* (2016) conducted path analysis on barnyard millet (*Echinochloa* spp.) global germplasm collection in 2011 and 2012 in augmented and alpha lattice design respectively. Path analysis indicated high direct effects of panicle exertion, flag leaf sheath length, flag leaf width and days to maturity in 2011; and flag leaf width and raceme number in 2012 and these high direct estimates were biased due to multicollinearity. Culm thickness and raceme number are important trait for indirect selection.

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.

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.

Dhamdhare *et al.* (2013) carried out path analysis in 29 finger millet germplasm lines for 17 quantitative traits and reported that total biomass, harvest index, number of tillers per plant, flag leaf area and days to 50% flowering showed positive direct effect on yield while thousand grain weight showed positive indirect effect on yield through ear weight.

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.

Tyagi *et al.* (2011) performed path analysis in 57 foxtail millet accessions for nine agronomic 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.

Nandini *et al.* (2010) carried out path analysis for nine quantitative traits in F₂ generation of seven crosses in finger millet. The results revealed that high positive direct effect of weight of main ear, 1000 seed weight accounts maximum to make up the total grain yield compared to other strongly associated yield attributing traits. Other traits like total number of tillers per plant and productive tillers exerted variable positive or negative direct or indirect effect through other traits and thus, respectively intensified or reduced the total intrinsic association towards yield.

Nirmalakumari *et al.* (2010b) conducted path analysis for seven traits in 741 germplasm accessions of foxtail millet and reported on grain yield, positive direct effects of the traits viz., number of productive tillers, days to 50% flowering and panicle length as high, negligible and moderate respectively. This indicates that, greater yield advantage could be achieved by using germplasm with more productive tillers, medium panicle length and medium duration.

Rao *et al.* (2000) studied path analysis in 28 genotypes of barnyard millet indicated highest direct effects of ear length followed by fodder yield and days to flower on grain yield, whereas tillers per plant had highest direct effects on fodder yield followed by days to maturity and plant height. Considering the genetic parameters, association and path analysis, ear length and fodder yield had a great influence on grain yield.

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 present study were presented in this chapter.

3.1 LOCATION

The present Study on “ Morphological Characterization And Divergence Studies In Barnyard Millet [*Echinochloa Frumentacea (L.)*] ” was carried out in black cotton soils during *Kharif*, 2020 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 (Plate 3.1).

3.2 MATERIAL

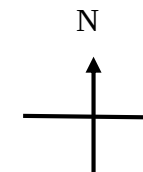
The experimental material utilized for the present study comprised of sixtyfour barnyard millet germplasm accessions obtained from various collections maintained at Centre of Excellence in Millets, Tamil Nadu Agricultural University, Athiyandal and AICRP on Small millets UAS, GKVK, Bengaluru. The details of the germplasm accessions are presented in Table 3.1.

3.3 METHODS

3.2.1 FIELD LAYOUT

Sixty four barnyard millet germplasm accessions were sown in lattice square design (LSD) replicated twice during *kharif*, 2020 at RARS, Nandyal. The inter and intra- row spacing of 22.5 x 10 cm, respectively is adopted. 2-3 seeds were dibbled at a depth of 1.5 cm in line with a row length of 3 m. The size of the plot is 31 x 7.5 m².

R1



GECH-634		GECH-997		GECH-633		TNEF-190		GECH-206		GECH-094		GECH-581		GECH-995
GECH-186		GECH-020		GECH-191		TNEF-191		GECH-008		GECH-360		GECH-045		GECH-060
TNEF-213		TNEF-210		TNEF-212		TNEF-214		TNEF-208		TNEF-215		TNEF-209		TNEF-211
TNEF-205		TNEF-202		TNEF-204		TNEF-206		TNEF-200		TNEF-207		TNEF-201		TNEF-203
TNEF-197		TNEF-194		TNEF-196		TNEF-196		TNEF-192		TNEF-199		TNEF-193		TNEF-195
GECH-374		GECH-571		GECH-573		GECH-578		GECH-566		GECH-579		GECH-570		GECH-572
TNEF-219		BMNDL-1(C)		BMNDL-3(C)		BMNDL-2(C)		TNEF-216		TNEF-318(C)		TNEF-217		TNEF-218
GECH-383		GECH-416		GECH-393		GECH-567		GECH-365		GECH-568		GECH-372		GECH-418

R2

GECH-634		GECH-186		GECH-383		BMNDL-1 (C)		TNEF-197		GECH-374		TNEF-213		TNEF-205
GECH-997		GECH-020		TNEF-318 (C)		TNEF-218		TNEF-194		GECH-571		TNEF-210		TNEF-202
GECH-633		GECH-094		GECH-393		GECH-416		TNEF-196		TNEF-211		TNEF-212		TNEF-204
GECH-995		GECH-060		GECH-418		TNEF-219		TNEF-195		GECH-572		GECH-573		TNEF-203
GECH-206		BMNDL-3(C)		GECH-365		TNEF-216		TNEF-192		GECH-566		TNEF-208		TNEF-200
BMNDL-2(C)		GECH-360		GECH-568		GECH-8		TNEF-199		TNEF-198		TNEF-215		TNEF-207
TNEF-190		GECH-191		GECH-567		TNEF-191		GECH-579		GECH-578		TNEF-206		TNEF-214
GECH-581		GECH-045		GECH-372		TNEF-217		TNEF-193		GECH-570		TNEF-209		TNEF-201

FIELD LAYOUT FOR 8x8 LATTICE SQUARE DESIGN

3.1 Experimental field view



Vegetative Stage



Flowering Stage

Table 3.1 Details of 64 Barnyard millet germplasm accessions utilized for study

S.NO	Germplasm accession	Parentage/ Collection/Source
1	GEch-8	Dholi
2	GEch-45	Dholi
3	GEch-20	Dholi
4	GEch-60	NBPGR DS 67/82/22-2-83 (From GE ch 751)
5	GEch-94	Dholi
6	GEch-186	Almora
7	GEch-191	Almora
8	GEch-360	Almora
9	GEch-365	Almora
10	GEch-372	Almora
11	GEch-416	Almora
12	GEch-418	NBPGR Bihar (from GE ch 759)
13	GEch-393	Almora
14	GEch-383	Almora
15	GEch-567	Bihar
16	GEch-568	Bihar
17	GEch-566	Orissa
18	GEch-570	Orissa
19	GEch-571	Orissa
20	GEch-572	Orissa
21	GEch-573	Orissa
22	GEch-374	Almora
23	GEch-578	Rewa
24	GEch-579	Rewa
25	GEch-206	Almora
26	GEch-581	Rewa
27	GEch-997	India
28	GEch-995	India
29	GEch-633	Madhya Pradesh, Rewa
30	GEch-634	Madhya Pradesh, Rewa
31	TNEf-190	TNAU, Athiyandal
32	TNEf-191	TNAU, Athiyandal

S.NO	Germplasm accession	Parentage/ Collection/Source
33	TNEf-192	TNAU, Athiyandal
34	TNEf-193	TNAU, Athiyandal
35	TNEf-194	TNAU, Athiyandal
36	TNEf-195	TNAU, Athiyandal
37	TNEf-196	TNAU, Athiyandal
38	TNEf-197	TNAU, Athiyandal
39	TNEf-198	TNAU, Athiyandal
40	TNEf-199	TNAU, Athiyandal
41	TNEf-200	TNAU, Athiyandal
42	TNEf-201	TNAU, Athiyandal
43	TNEf-202	TNAU, Athiyandal
44	TNEf-203	TNAU, Athiyandal
45	TNEf-204	TNAU, Athiyandal
46	TNEf-205	TNAU, Athiyandal
47	TNEf-206	TNAU, Athiyandal
48	TNEf-207	TNAU, Athiyandal
49	TNEf-208	TNAU, Athiyandal
50	TNEf-209	TNAU, Athiyandal
51	TNEf-210	TNAU, Athiyandal
52	TNEf-211	TNAU, Athiyandal
53	TNEf-212	TNAU, Athiyandal
54	TNEf-213	TNAU, Athiyandal
55	TNEf-214	TNAU, Athiyandal
56	TNEf-215	TNAU, Athiyandal
57	TNEf-216	TNAU, Athiyandal
58	TNEf-217	TNAU, Athiyandal
59	TNEf-218	TNAU, Athiyandal
60	TNEf-219	TNAU, Athiyandal
61	BMNDL-1	Nandyal local
62	BMNDL-2	PLS from local
63	BMNDL-3	PLS from local
64	TNEf-318	TNAU, Athiyandal

3.2.2 METHODS OF RECORDING OBSERVATIONS

3.2.2.1 GERMPLASM CHARACTERIZATION

Eighteen morphological traits on five randomly tagged plants per replication were recorded as per National test guidelines for Distinctiveness, Uniformity and Stability (DUS) testing given by Protection of Plant Varieties and Farmers' Rights Authority (PPV & FRA). Based on tagged plants, the phenotypic appearance of trait is known. For the assessment of DUS, the characteristics and their states as given in Table 3.2 of characteristics shall be used. Notes (1 to 9) shall be given for each state of expression for different characteristics for the purpose of electronic data processing.

Table 3.2 Characteristics of germplasm accessions studied

S.No	Characteristics	States	Scores/ Noter	Stage of observation	Type of assessment
1	Plant Growth habit	Erect	1	15	VG
		Decumbent	5		
		Prostrate	7		
2	Basal tiller: Number	Low (<4)	3	26	MS
		Medium (4-7)	5		
		High (>7)	7		
3	Days to 50% flowering	Early (<40)	3	51	MG
		Medium (40-50)	5		
		Late (>50)	7		
4	Plant pigmentation (at internodes and leaf sheath)	Absent	1	59	VG
		Present	9		
5	Flag leaf blade: Length(cm)	Short (<15)	3	59	MS
		Medium (15.0-30.0)	5		
		Long (30.1-45.0)	7		
		Very long (>45.0)	9		
6	Flag leaf blade: Width (cm)	Narrow (<2.0)	3	59	MS
		Medium (2.0-3.0)	5		
		Wide (>3.0)	7		

7	Peduncle: Length(cm)	Short (<10.0)	1	59	MS
		Medium (10.0-20.0)	3		
		Long (>20.0)	5		
8	Inflorescence: Shape	Cylindrical	3	59	VG
		Pyramidal	5		
		Globose-Elliptical	7		
9	Inflorescence: colour	Green	1	59	VG
		Light purple	5		
		Dark purple	7		
10	Panicle: Compactness	Open	3	67	VG
		Intermediate	5		
		Compact	7		
11	Spikelets: Arrangements on the rachis	One side	3	67	VS
		Around	7		
12	Lower racemes: Shape	Straight	3	67	VS
		Curved	7		
13	Lower raceme: Thickness	Slender	3	67	VS
		Thick	7		
14	Lower raceme: Branching	Absent	1	67	VS
		Present	9		
15	Culm: Branching	Absent	1	67	VG
		Present	9		
16	Lower raceme: Length (cm)	Short (<3)	3	67	MS
		Medium (3.0-5.0)	5		
		Long (>5.0)	7		
17		Short (<15.0)	3	67	MS

	Panicle: Length (cm)	Short to medium (15.0-20.0)	4		
		Medium (20.1- 25.0)	5		
		Long (>25.0)	7		
18	Plant: Height (cm)	Dwarf (>40)	3	83	MS
		Semi dwarf (40.0-80.0)	5		
		Tall (80.0-120.0)	7		
		Very Tall (>120.0)	9		
19	Lodging	Absent	1	83	VS
		Present	9		
20	Grain: Colour	Straw white RHS NO 163D	2	83	VG
		Light Grey RGS NO 156B	4		
		Grey RHS NO 156A	5		
21	Grain: Shape	Concave	1	95	VG
		Oval	2		
22	1000 seed weight (g)	Low (<2.0)	3	95	MG
		Medium (2.0- 3.0)	5		
		High (>3.0-4.0)	7		
		Very high (>4.0)	9		

Decimal code for the growth stage

Stage code	General Description
15	Two- Four leaf stage
26	Vegetative stage
51	50% flowering
59	Complete flowering
67	Dough stage
83	Maturity
95	Post harvest

Type of Assesement :

MG: Single measurment of a group of plants or parts of plants.

MS: Measurement of a number of individual plants or parts of plants.

VG: Visual assessment by a single observation of a group of plants or plants parts.

VS: Visual assessment observation of individual plants or parts of plants.

Legend:

(*) Characteristics that shall be observed during every growing season on all varieties and shall always be included in the variety, except when the state of expression of any of these characters is rendered impossible by a preceding phenological characteristic or by the environmental conditions of the testing region. Under such exceptional situation, adequate explanation shall be provided.

3.3.1 Plant growth habit

The growth habit of plant may be erect, decumbent which is similar to erect but spaced between tillers and prostate which is widely separated between tillers.

3.3.2 Number of basal tillers

Number of tillers at ground level or from the basal nodes.

Low (<4), Medium (4-7), High (>7).

3.3.3 Days to 50% flowering*

It refers to the total number of days taken from the date of sowing to complete exertion of the panicle tip above the flag leaf sheath in 50 per cent of the total plants in the net plot and is accordingly classified as early (< 40), medium (40-50) and late (>50).

3.3.4 Plant pigmentation at internode and leaf sheath

The plant pigmentation at internode and leaf sheath is determined based on the observation of internode and leaf sheath of tagged plants which may be present or absent.

3.3.5 Flag leaf: Blade length (cm)

It is measured from the ligule to tip of flag leaf during flowering stage and is classified as short (< 15cm), medium (15-30 cm), long (> 30.1-45.0 cm) and very long (>45.0).

3.3.6 Flag leaf: Blade width (cm)

It is calibrated at the widest point of flag leaf and is categorized as narrow (< 2.0 cm), medium (2.0-3.0 cm) and wide (> 3.0 cm).

3.3.7 Peduncle Length (cm)

It is measured from the uppermost node to the base of inflorescence and is categorized as Short (<10.0 cm), Medium (10.0-20.0 cm) and Long (>20.0 cm).

3.3.8 Inflorescence shape

The shape of the inflorescence may be Cylindrical, pyramidal and Globose-Elliptic.

3.3.9 Inflorescence colour

The colour of the inflorescence may be Green, Light purple and Dark purple.

3.3.10 Panicle compactness

It refers to the arrangement of lobes on the inflorescence and may be grouped as Open, intermediate and compact.

3.3.11 Spikelet arrangement

It refers to the arrangement of rachis on the racemes and may be categorized as One side (Rachis visible clearly) and around rachis (rachis not visible clearly).

3.3.12 Lower raceme shape

It refers to the shape of lower raceme of the panicle may be categorized as Straight (not slender), Curved (not slender) and slender.

3.3.13 Lower raceme thickness

It refers to the thickness of the lower raceme of the panicle may be categorized as Slender and Thick.

3.3.14 Lower raceme branching

It refers to the branching of the lower raceme of the panicle which may be present or absent.

3.3.15 Culm branching

It refers to the branching ability of main tiller which may be present or absent.

3.3.16 Lower raceme length (cm)

It refers to the length of the lower raceme of the panicle may be categorized as Short (<3), Medium (3.0-5.0), Long (>5.0).

3.3.17 Panicle length (cm)

It is measurement of the length from base to tip of the ear and is classified as short (< 15.0), short to medium (15.1-20.0), medium (20.1-25.0) and long (>25.0).

3.3.18 Plant height at maturity (cm)

The height of the main tiller measured from ground level to tip of inflorescence; in case of decumbent or prostrate plants, length of flowering culm from rooted base, recorded at maturity indicates the plant height. It was classified as Dwarf (< 40.0), semi dwarf (40.0-80.0), tall (80.1-120.0) and very tall (>120.0).

3.3.19 Days to maturity *

It refers to the number of days taken by each genotype, between sowing of seed to plant attaining physiological maturity.

3.3.20 Lodging

It refers to bending over of the stems near ground level due to weak stems / huge grain weight which makes them difficult to harvest.

3.3.21 Senescence

The plant may show either senescence or stay green trait at maturity.

3.3.22 Grain colour

The grain may exhibit variations in colour viz., straw white, light white, light grey, and grey.

3.3.23 Grain shape

The grain may exhibit variations in shape viz., concave and oval.

3.3.24 Panicle weight /plant (g)

Weight of the total panicles of tagged plants was recorded.

3.3.25 Test weight (g) / 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.

3.3.26 Grain yield /plant (g)

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

3.3.27 Harvest index

3.2.2.2 BIOMETRICAL TRIATS

Observations on five randomly tagged competitive plants per accession for 16 quantitative traits. viz., Basal tillers, Peduncle length (cm), flag leaf blade length(cm), flag leaf blade width(cm), Plant height (cm), Panicle length (cm), 1000 seed weight (gm), Panicle weight /plant (gm), Harvest Index (%), Lower raceme length (cm), Grain yield/plant (gm), Phosphorus, Calcium, Iron, Zinc mg/100g, Protein %. were recorded in each replication. In addition, two quantitative characters, days to 50 % flowering and days to maturity were recorded on plot basis.

3.4 Biometrical traits

3.4.1 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.

3.4.2 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.

P 3.2 Plant growth habit



Decumbent



Erect

P 3.3 Plant pigmentation at internode or node



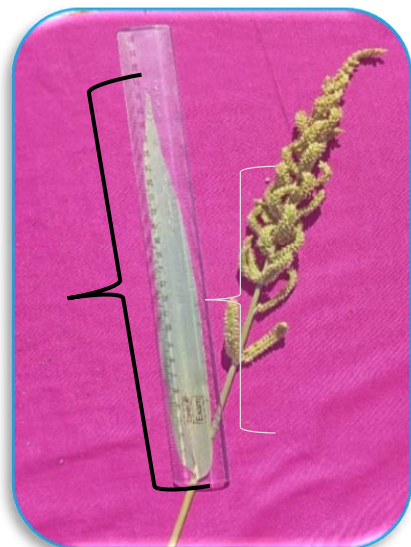
Absent

Present

P 3.4 Flag Leaf Blade Width



P 3.5 Flag Leaf Blade Length



P 3.6 Inflorescence compactness



Open



Intermediate



Compact

P 3.7 Spikelet arrangements On the Rachis



One side



Around

P 3.8 Peduncle length



P 3.9 Panicle length



P 3.10 Inflorescence shape



Cylindrical



Pyramidal

P 3.11 Lower Raceme Shape



Straight



Curved

P 3.12 Culm Branching



Present

P 3.13 Lower Raceme Thickness



Thick



Slender

P 3.14 Lower Raceme Branching



Branched



Unbranched

P 3.15 Inflorescence Colour



Dark Purple



Light Purple



Green

P 3.16 Plant height at Maturity



P 3.17 Grain Colour

Straw white

Light grey

Grey



3.18 Seed Shape



Concave shape

3.4.3 Days to maturity

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

3.4.4 Number of productive tillers/plant

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

3.4.5 Flag leaf: Blade length (cm)

It is measured from the ligule to tip of flag leaf during flowering stage

3.4.6 Flag leaf: Blade width (cm)

It is calibrated at the widest point of flag leaf

3.4.7 Peduncle length (cm)

Measured from top most node to the base of inflorescence.

3.4.8 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.

3.4.10 Grain yield/Plant (g)

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

3.5 Estimation of Nutritional parameters

Estimation of nutritional parameters (protein, Ca, Fe, Zn, and Phosphorous) was done by collecting harvested seed samples from varieties for estimation. 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 ARS, Utukur, Kadapa.

3.5.1 Protein analysis

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

Procedure:

Digestion:

500 mg of sample, 1g of digestion mixture and 10 ml of concentrated H₂SO₄ were carefully added and the samples were digested in a digestion block for 1 h at 375⁰C. The tubes were removed and cooled; distilled water (50ml) was added carefully from sides.

Distillation:

In a 100 ml 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)	:	50 ml
Step 2 (steam digestion time)	:	10 s
Step 3 (distillation time)	:	180 min

Calculations:

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

3.5.2 Minerals estimation:

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

Absorption Spectrophotometer.

3.5.2.1 Estimation of mineral nutrients (Calcium, Iron and Zinc) 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).
- Then, heat the flask at higher temperature until the production of red NO₂ 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 hollow cathode lamps and readings had been recorded.

Calculations:

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

Standard Preparation

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

3.5.2.2 Estimation of Calcium by titration method

A known volume of the solution containing Ca is titrated against 0.01 N EDTA

in the presence murexide 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) murexide 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.

Estimation of Calcium by titration method

Procedure:

- Pipette out 5 ml of aliquat of Sample extracted in clean china dish and f 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.

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

3.6 STATISTICAL ANALYSIS

The data recorded on various characters were subjected to the following statistical analysis. The statistical analysis was performed for the mean data recorded on the five randomly selected plants from each entry from each replication. The statistical software used for analysis of the data is Statistical Analysis Software (SAS) 9.2 version and INDOSTAT 9.1. The data recorded on various characters were subjected to the following statistical analysis.

3.6.1 Analysis of variance

The analysis of variance for each character was calculated as per the standard procedure given by Rao (2007) for simple lattice design.

$$Y_{ij}(m) = \mu + \beta_i + T_m + e_{ij}(m)$$

Where,

$Y_{ij}(m)$ = Performance of the m^{th} genotype in j^{th} plot and i^{th} block

μ = general mean

β_i = effect of i^{th} block

T_m = effect of m^{th} genotype

$e_{ij}(m)$ = random error associated with j^{th} plot, i^{th} block and m^{th} genotype

ANOVA Table for Simple Lattice Design

Source of variation	Degrees of Freedom	Sum of Squares	Mean Sum of Squares	F –ratio
Replications	$r-1$	RSS	$M_r = \sigma_e^2 + \sigma_r^2$	M_r/M_e
Treatments (Unadj.)	$t-1$	TrSS	$M_t = \sigma_e^2 + \sigma_g^2$	M_t/M_e
Blocks within replications (adj.)	$r(k-1)$	BSS	$M_b = \sigma_e^2 + \sigma_B^2$	M_b/M_e
Error	$(k-1)(rk-k-1)$	ESS	$M_e = \sigma_e^2$	
Total	(rk^2-1)	TSS		

The analysis of variance (ANOVA) for each character was carried out as indicated below:

Where,

r = Number of replications

k = Number of plots in a block

t = Number of genotypes / treatments = k^2

d.f = Degrees of freedom

SS = Sum of squares

MSS	=	Mean sum of squares
σ^2_e	=	Error variance
σ^2_g	=	Variance due to genotypes
σ^2_b	=	Variance due to blocks
σ^2_r	=	Variance due to replications
M _r	=	Mean sum of squares due to replications
M _b	=	Mean sum of squares due to blocks
M _t	=	Mean sum of squares due to treatments
M _e	=	Mean sum of squares due to error

3.6.2 Parameters of variability

3.6.2.1 Mean ($\bar{X}$)

The mean value of each character was worked out by dividing the total sum of values with corresponding number of observations.

$$\bar{X} = \frac{\sum_{i=1}^n X_i}{n}$$

Where,

$\bar{X}$ = Sample mean

X = Individual value

n = Number of observations

3.6.2.2 Range

The lowest and highest values of each character were recorded.

3.6.2.3 Standard error of mean (S.E. (m))

Standard error of mean was calculated with the help of error mean squares from the analysis of variance table given as under:

$$\text{S. E. (m)} = \frac{\sqrt{\text{MS}_e}}{r}$$

S.E. = Standard error

MS_e = Error mean sum of squares

r = Number of replications

3.6.2.4 Critical difference (CD)

For every character, the critical difference was the difference of any two mean values. In order to compare the critical difference treatment means was calculated using the following formula:

$$\text{S. E. (d)} = \frac{\sqrt{2\text{MS}_e}}{r}$$

$$\text{CD at 5 or 1\%} = \frac{\sqrt{2\text{MS}_e}}{r} \times 't'$$

Where,

't' is the tabulated value at error degree of freedom at 5 or 1% level of significance as the case may be.

3.6.2.5 Coefficient of variation (C.V)

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

a) Genotypic coefficient of variation (GCV)

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

b) Phenotypic coefficient of variation (PCV)

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

The genotypic and phenotypic coefficients of variation were categorized as per the method suggested by Sivasubramanian and Menon (1973):

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

3.6.2.6 Heritability (broad sense)

Heritability in broad sense is the ratio of genotype variance to the total variance. It is the portion of total variability or phenotypic variability which is heritable and due to the genotype. It was calculated by the formula given by Burton and Devane (1953)

$$\text{Heritability (h}^2\text{)} = \frac{V_G}{V_P} \times 100$$

The calculated heritability was classified into three groups as suggested by Johnson *et al.* (1955):

Classification	Heritability
Low	0-30%
Moderate	30-60%
High	> 60%

3.6.2.7 Genetic advance (GA)

Genetic advance refers to the expected gain in the next generation by selection of superior individuals under certain amount of selection pressure. The genetic advance was calculated based on formula given by Johnson *et al.* (1955 a).

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

Where,

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

σ_p = Phenotypic standard deviation

h^2 = Heritability in broad sense

3.6.2.8 Genetic advance as per cent of mean (GAM)

Genetic advance as per cent of mean was calculated as per the formula

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

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 a).

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

3.7 Studies on Genetic diversity

Genetic diversity study was conducted as per Mahalanobis (1936) and Rao (1952) utilizing 18 characters recorded.

3.7.1.1 Mahalanobis D² analysis

Mahalanobis (1936) D² statistic was used for assessing the genetic divergence among the test genotypes involving quantitative characters. The generalized distance between any two populations is given by the formula:

$$D^2 = \sum \sum_{ij} \sigma_{ai} \sigma_{aj}$$

Where,

D² = Square of generalized distance

ij = Reciprocal of the common dispersal matrix

$\sigma_{ai} = (\mu_{i1} - \mu_{i2})$

$\sigma_{aj} = (\mu_{j1} - \mu_{j2})$

μ = General mean

Since, the formula for computation requires inversion of higher order determinant, transformation of the original correlated unstandardized characters (X's) to standardized uncorrelated variables (Y's) was done to simplify the computational procedure. The D² values were obtained as the sum of squares of the differences between pairs of corresponding uncorrelated (s) values of any two uncorrelated genotypes (Rao, 1952).

3.7.1.2 Cluster of D² values

All n (n-1)/2 D² values were clustered using Tocher's method described by Rao (1952).

3.7.1.3 Intra-cluster distance

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

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

Where,

ΣD_i^2 is the sum of distances between all possible combinations of the genotypes included in a cluster.

n = Number of all possible combinations

3.7.1.4 Inter-cluster distance

The inter-cluster distances were calculated by the formula described by Singh and Chaudhary (1977).

$$\text{Square of the inter cluster distance} = \frac{\Sigma D_i^2}{n_i n_j}$$

Where,

ΣD_i^2 is the sum of distances between all possible combinations ($n_i n_j$) of the genotypes included in the clusters under study.

n_i = Number of genotypes in cluster i

n_j = Number of genotypes in cluster j

In brief, the steps involved for the estimation of D^2 values are as follows (Rao, 1952).

1. Pivotal condensation of error variance and co-variance matrix to obtain inverse matrix.
2. Transformation of original correlated data into un-correlated variables.
3. Calculation of mean values of the transformed characters.
4. Calculation of D^2 values: For each combination, deviation between the means was computed and the D^2 values were computed and arranged in the form of matrix.
5. Determination of group constellations:

As such no standard rules are available for making the clusters because cluster is not a well-defined term. The only criterion appears to be that any two genotypes belonging to the same cluster should at least, on an average, show a smaller D^2 value than those belonging to two different clusters. The D^2 values for all the combinations presented in the matrix form were arranged in increasing order of magnitude and clustering was done according to the method suggested by Tocher (Rao, 1952).

At first, the two most closely associated genotypes were chosen and then third genotype was located which had the smaller average D^2 value as compared to the first

two genotypes. Following this methodology, the subsequent genotypes were chosen which have smaller average D^2 value from the first three genotypes and change in D^2 value within a cluster due to inclusion of additional genotype was computed and so on. The new genotypes were added so long as the increase in average D^2 value became abruptly high, then this genotype was not included in the former groups. The genotypes of first cluster were omitted and rest were treated similarly for constructing new clusters.

6. Intra and inter-cluster distance

The intra-cluster D^2 value was calculated as the sum of $n(n-1)/2$ D^2 values among the genotypes within a cluster divided by $n(n-1)/2$. The single genotype always has zero intra-cluster D^2 value. For calculating the inter-cluster D^2 value, all possible D^2 values between genotypes of two clusters were added and then divided by $n_1 \times n_2$, where n_1 and n_2 represented the number of genotypes in the first and second cluster, respectively. The intra and inter-cluster distances were calculated by taking the square root of respective D^2 value between genotypes of a particular cluster and between genotypes belonging to two clusters, respectively.

7. Clusters mean value

The cluster mean of a particular character is the summation of mean values of the genotypes included in a cluster divided by number of genotypes in the same cluster.

3.7.2 Canonical root analysis

The canonical vector or roots were calculated to represent the traits in three dimensional graphical form (Rao, 1952). The steps involved are as follows

3.7.2.1 Calculation of sum of squares and sum of products

The correlated standard means were transformed into the uncorrelated standardized variables. For each character and combination of characters, sum of squares and sum of products were computed using the transferred variables to obtain the matrix of variables and co-variance (matrix A). From matrix A, matrix $(A)^p$ were derived, where 'p' is the number of characters.

3.7.2.2 Calculation of first vector

The approximation of trial vector was obtained by getting the column totals of matrix $(A)^p$ and then by dividing each of the column totals by the highest quantity among them. The canonical variables were determined by interaction starting with trial vector. The highest element in this vector was found and the procedure was repeated till the elements of the two approximation vectors were same. The vectors were then standardized by dividing them by correlated sum of squares of these vectors. The first root A , was calculated as the p^{th} root of the highest column total of the last approximation.

3.7.2.3 Calculation of second vector

For getting the second vector λ^2 , the original $(A)^p$ matrix was transformed and represented as $(B)^p$. In $(B)^p$ each $(i, j)^{\text{th}}$ element was calculated as follows :

$(i, j)^{\text{th}}$ element = $(A)^p - \lambda_1 X_i^{\text{th}}$ element X_j^{th} element of the first vector.

The procedure followed in case of matrix 'A' was repeated to obtain the second canonical root.

3.7.2.4 Estimation of Z values

From the values of $y_1, y_2, \dots, y_{ij}$ the mean values of characters considered Z_1, Z_2 and Z_3 were calculated as :

$$Z_1 = (y)(V_1); Z_2 = (y)(V_2)$$

(Y) = mean transformed value

V_1, V_2 = the first and second vector, respectively

The mean values of Z_1, Z_2 and Z_3 for the traits were represented in a 3- dimensional diagram.

3.7.2.5 Contribution of vectors towards divergence

Total contribution of all the vectors was given by the sum of diagonal elements in matrix A .

$$\lambda_1 \times 100$$

Per cent contribution of vector '1' (X_1) = $\frac{\lambda_1 \times 100}{\text{Total variance of all the variables}}$

(Characters)

$$\text{Per cent contribution of vector '2' (X}_1\text{)} = \frac{\lambda_2 \times 100}{\text{Total variance of all the variables (Characters)}}$$

Where, λ_s are canonical roots.

3.8 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 and quality traits studied. Correlation coefficients were calculated using the method given by Johanson *et al.* (1955b).

3.8.1 Phenotypic correlation coefficient (r_g)

$$\text{Phenotypic coefficients of correlation (r}_p\text{)} = r(x_i x_j)_p = \frac{\text{Cov}(x_i x_j)_p}{\left[V(x_i)_p \cdot V(x_j)_p \right]^{1/2}}$$

Where,

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

$\text{Cov}(x_i x_j)_p$ = 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.

3.4.4.2 Genotypic correlation coefficient (r_g)

$$\text{Genotypic coefficients of correlation (r}_g\text{)} = r(x_i x_j)_g = \frac{\text{Cov}(x_i x_j)_g}{\left[V(x_i)_g \cdot V(x_j)_g \right]^{1/2}}$$

Where,

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

$\text{Cov}(x_i x_j)_g$ = 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

3.4.4.3 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.

3.4.5 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 Sewall 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:

$$r_{1y} = P_{1y} + r_{12} P_{2y} + r_{13} P_{3y} + \dots + r_{1k} P_{ky}$$

$$r_{2y} = r_{21} P_{1y} + P_{2y} + r_{23} P_{3y} + \dots + r_{2k} P_{ky}$$

$$\begin{matrix} \cdot & \cdot & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot & \cdot \end{matrix}$$

$$r_{ky} = r_{k1} P_{1y} + r_{k2} P_{2y} + r_{k3} P_{3y} + \dots + r_{kk} P_{ky}$$

Where,

r_{1y} to r_{ky} = Correlation coefficients between independent characters

r_{12} to $r_{k-1,k}$ = Correlation coefficients between all possible combinations of independent characters

P_{1y} to P_{ky} = Direct effects of characters 1 to k on character 'y'

The above equations were written in matrix form as under:

$$\begin{pmatrix} A \\ r_{1y} \\ r_{2y} \\ r_{3y} \\ \vdots \\ r_{iy} \end{pmatrix} = \begin{pmatrix} C \\ 1 & r_{12} & r_{13} \dots r_{1i} \\ r_{21} & 1 & r_{23} \dots r_{2i} \\ r_{31} & r_{32} & 1 \dots r_{3i} \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ r_{i1} & r_{i2} & r_{i3} \dots 1 \end{pmatrix} \begin{pmatrix} B \\ P_{1y} \\ P_{2y} \\ P_{3y} \\ \vdots \\ P_{iy} \end{pmatrix}$$

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

where,

$$[C]^{-1} = \begin{pmatrix} C_{11} & C_{12} & C_{13} \dots C_{1i} \\ C_{21} & C_{22} & C_{23} \dots C_{2i} \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ C_{i1} & C_{i2} & C_{i3} \dots C_{ii} \end{pmatrix}$$

Then, direct effects were calculated as follows:

$$P_{1y} = \sum_{i=1}^I \frac{C_{1i}}{r_{1y}}$$

$$P_{2y} = \sum_{i=1}^I \frac{C_{2i}}{r_{2y}}$$

$$P_{iy} = \sum_{i=1}^I \frac{C_{ii}}{r_{iy}}$$

Besides the direct and indirect effects, the residual effect which measures the contribution of the characters not considered in the causal scheme was obtained as follows:

The residual effect was computed by using the formula

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

Where,

R = Residual effect

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

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

The categorization of path coefficients proposed by Lenka and Mishra (1973) was adopted in the present investigation and are as follows:

Value for Direct or Indirect effect	Rate or Scale
0.00 – 0.09	Negligible
0.10 – 0.19	Low
0.20 – 0.29	Moderate
0.30 – 0.99	High
More than 1.00	Very high

Chapter - IV

RESULTS AND DISCUSSION

CHAPTER IV

RESULTS AND DISCUSSION

The present investigation was conducted utilizing 64 Barnyard millet germplasm accessions in *kharif*, 2020 at Regional Agricultural Research Station, ANGRAU, Nandyal, Andhra Pradesh. The data were collected for 22 DUS traits to characterize the germplasm accessions morphologically and 18 quantitative traits to analyse for genetic parameters, genetic divergence, character association and path coefficient analysis in order to know the diverse genotypes that can be utilized as ‘parents’ in hybridization programmes.

The experimental results obtained from the present investigation are presented and discussed under the following heads.

- 4.1 Morphological characterization
- 4.2 Analysis of variance
- 4.3 *Per se* performance
- 4.4 Genetic parameters
- 4.5 Genetic divergence
- 4.6 Correlation analysis
- 4.7 Path coefficient analysis

4.1 MORPHOLOGICAL CHARACTERIZATION

Characterization of germplasm morphologically involves recording the characters visually that are highly heritable and stable across all environments. In modern breeding activities, germplasm characterization is imperative not only for categorization of germplasm accessions but also assists in identification of suitable genotypes for introgression programme.

The results of the present study for 22 DUS traits characterized morphologically in 64 Barnyard millet germplasm accessions based on germplasm qualitatively using IBPGR descriptors for plant characters, are furnished here under (Table 4.1, Fig 4.1& 4.2). These descriptors are highly heritable and easily identifiable.

Table 4.1 Morphological characterization in 64 Barnyard millet germplasm accessions

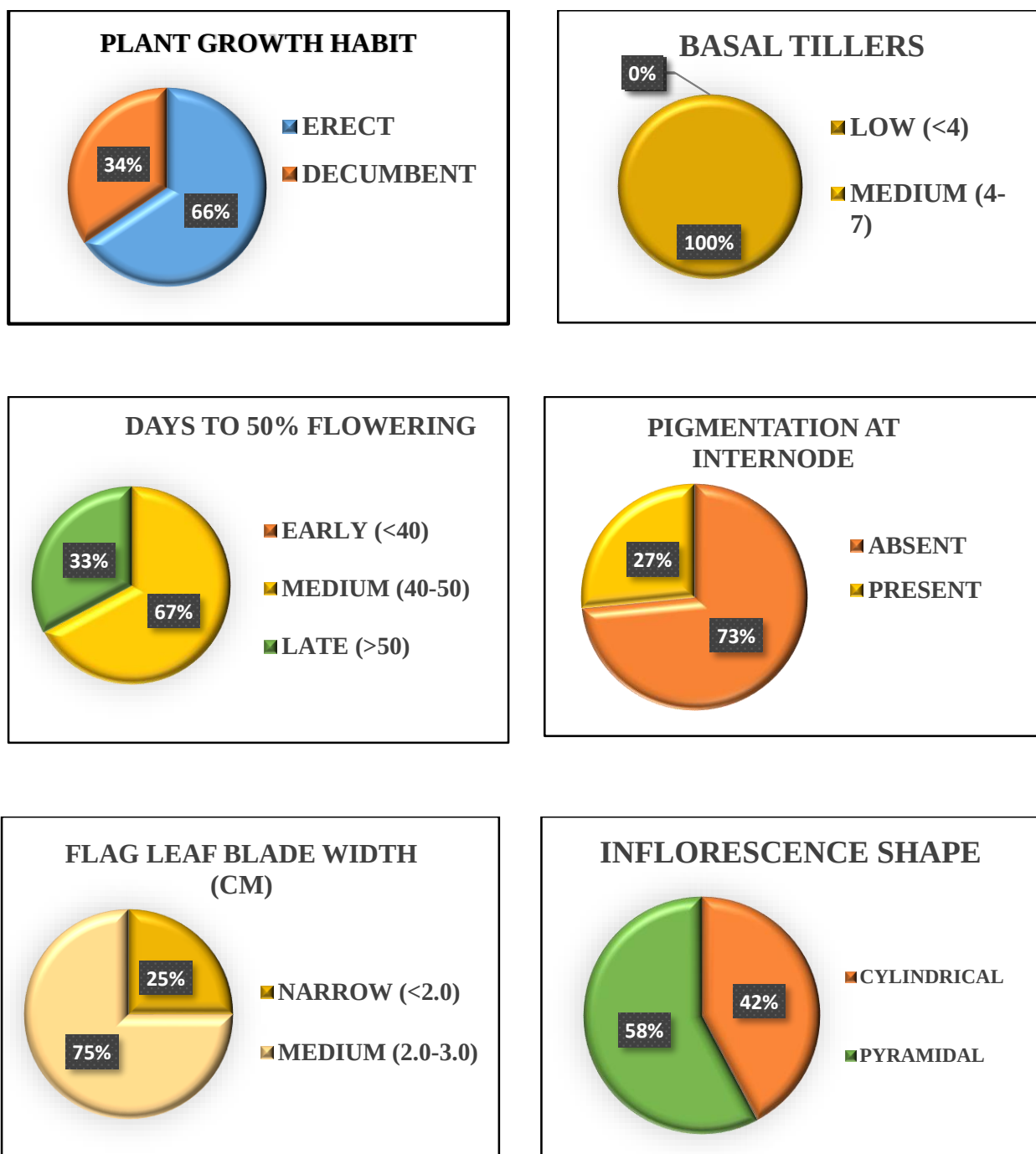
S.NO	NAME OF THE DESCRIPTOR	DESCRIPTOR STATE	NO. OF ACCESSIONS	FREQUENCY (%)
1	Plant Growth Habit	Erect	42	66
		Decumbent	22	34
2	Basal Tiller: Number	Low (<4)	64	100
		Medium (4-7)	0	0
		High (>7)	0	0
3	Days To 50% Flowering	Early (<40)	0	0
		Medium (40-50)	43	67
		Late (>50)	21	33
4	Plant Pigmentation (At Internodes And Leaf Sheath)	Absent	47	73
		Present	17	27
5	Flag Leaf Blade: Length(Cm)	Short (<15)	1	2
		Medium (15.0-30.0)	59	92
		Long (30.0-45.0)	4	6
		Very Long (>45.0)	0	0
6	Flag Leaf Blade: Width (Cm)	Narrow (<2.0)	16	25
		Medium (2.0-3.0)	48	75
		Wide (>3.0)	0	0
7	Peduncle: Length(Cm)	Short (<10.0)	0	0
		Medium (10.0-20.0)	53	83
		Long (>20.0)	11	17
8	Inflorescence: Shape	Cylindrical	27	42
		Pyramidal	37	58
		Globose -Elliptic	0	0
9	Inflorescence: Colour	Green	46	72
		Light Purple	16	25
		Dark Purple	2	3
10	Panicle: Compactness	Open	26	41
		Intermediate	27	42
		Compact	11	17
11	Spikelets: Arrangements On The Rachis	One Side	52	81
		Around	12	19
12	Lower Racemes: Shape	Straight	44	69
		Curved	20	31
13	Lower Raceme: Thickness	Slender	43	67
		Thick	21	33
14		Absent	49	77

	Lower Raceme: Branching	Present	15	23
15	Culm: Branching	Absent	0	0
		Present	64	100
16	Lower Raceme: Length (Cm)	Short (<3)	25	56
		Medium (3.0-5.0)	36	39
		Long (>5.0)	3	5
17	Panicle: Length (Cm)	Short (<15.0)	10	16
		Short To Medium (15.1-20.0)	36	56
		Medium (20.1-25.0)	16	25
		Long (>25.0)	2	3
18	Plant: Height (Cm)	Dwarf (<40)	0	0
		Semi Dwarf (40.0-80.0)	0	0
		Tall (80.1-120.0)	39	61
		Very Tall (>120.0)	25	39
19	Grain: Colour	Straw White	28	44
		Light Grey	30	47
		Grey	6	9
20	Grain: Shape	Concave	64	100
		Oval	0	0
21	1000 Seed Weight (G)	Low (<2.0)	6	9
		Medium (2.0-3.0)	50	78
		High (>3.0-4.0)	8	13
		Very High (>4.0)	0	0
22	Lodging	Absent	64	100
		Present	0	0

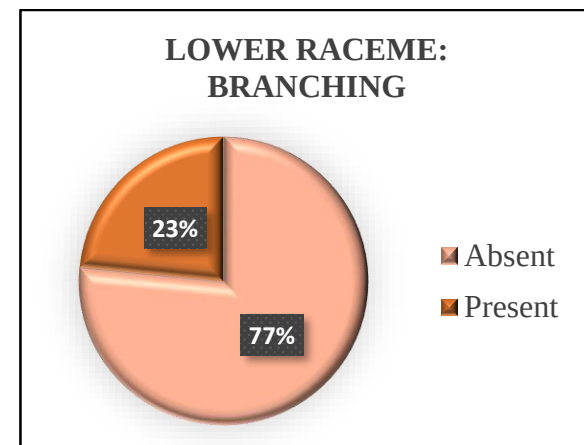
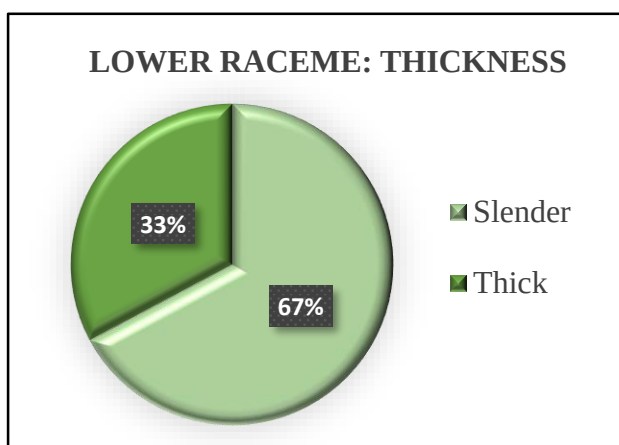
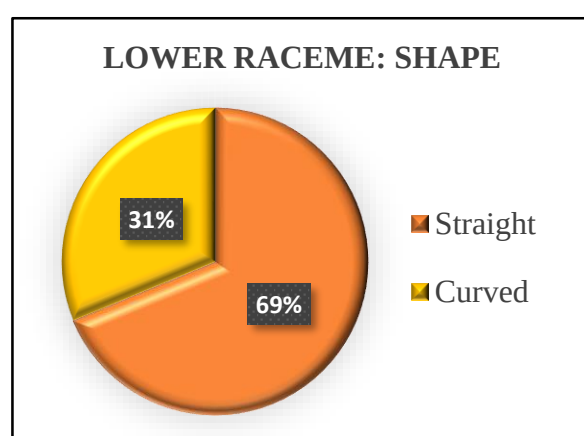
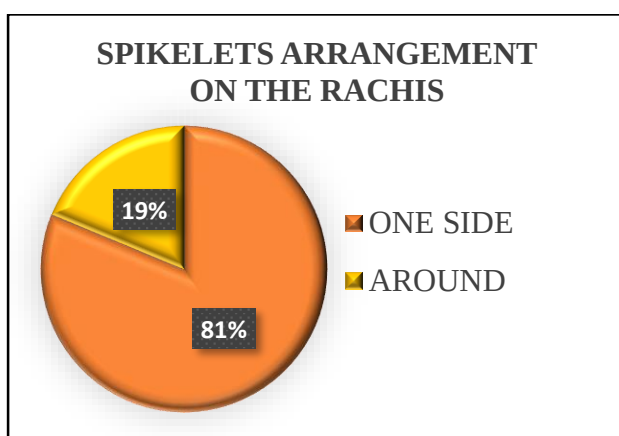
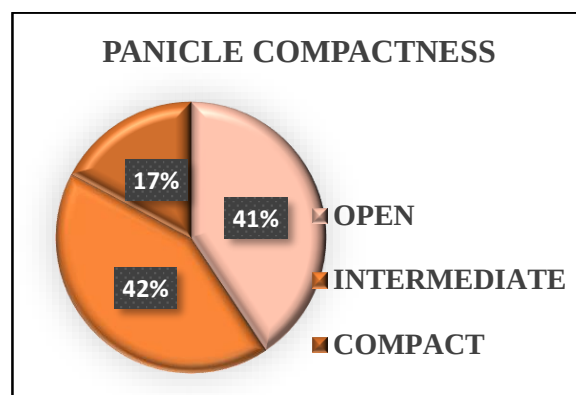
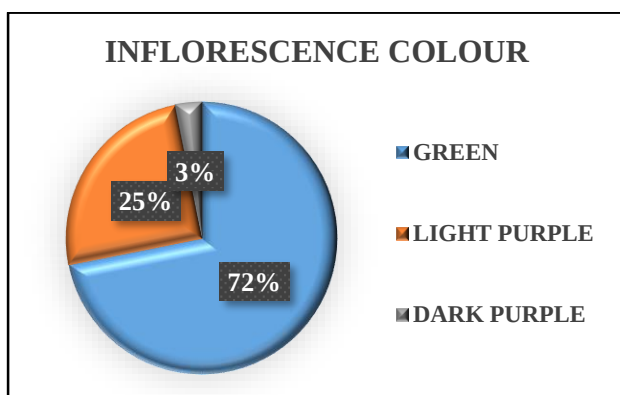
4.1.1 Plant growth habit

Characterization of 64 germplasm accessions, on the basis of growth habit showed that majority of them are erect type (42) over decumbent (22). Similar observations were recorded by Nilavarasi *et al.* (2020) out of 11 barnyard millet genotypes 9 genotypes were recorded erect type growth habit and 2 genotypes are decumbent. Out of 40 genotypes, 34 genotypes are erect growth habit, 1 genotype with decumbent and 5 genotypes with prostate growth habit were reported in barnyard millet by Renganathan *et al.* (2017) and Similarly Kuraloviya *et al.* (2019) has observed 11 are erect, 17 are decumbent and 2 are prostate type of growth habit out of 30 barnyard millet genotypes under study.

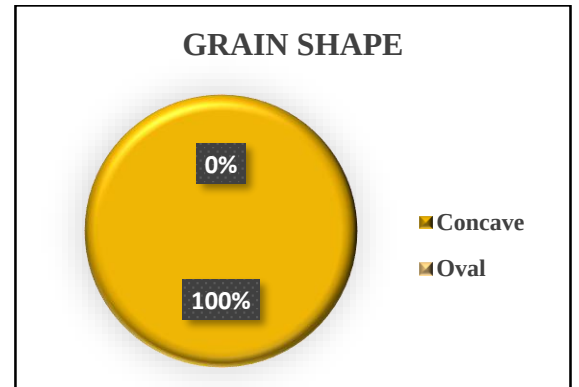
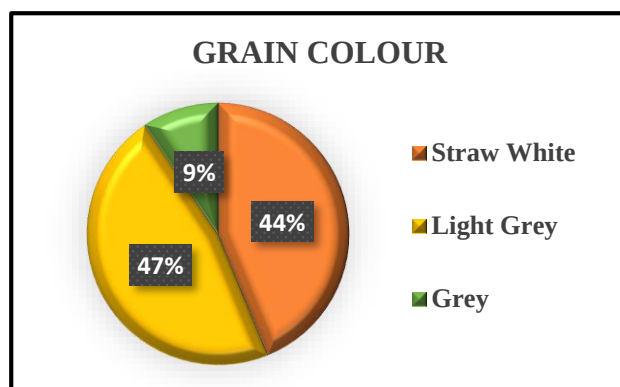
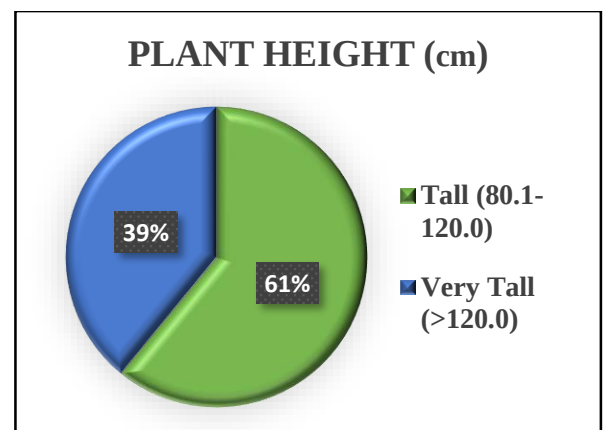
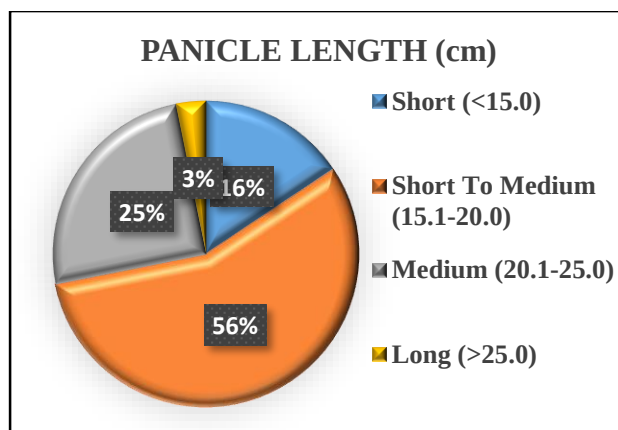
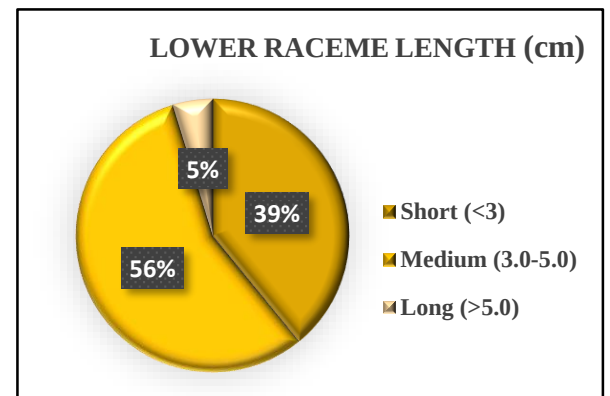
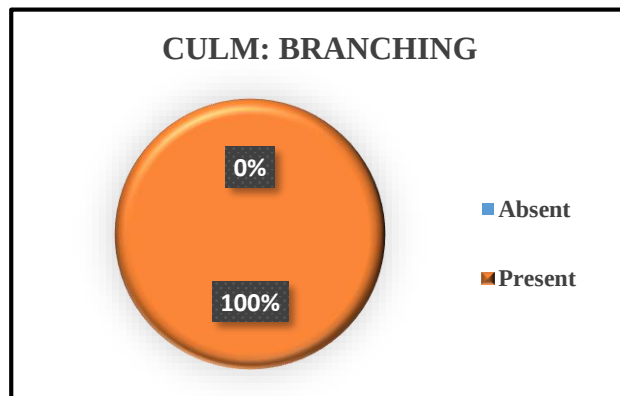
Fig 4.1 Pie diagram depicting variability for various DUS traits among 64 barnyard millet germplasm accessions



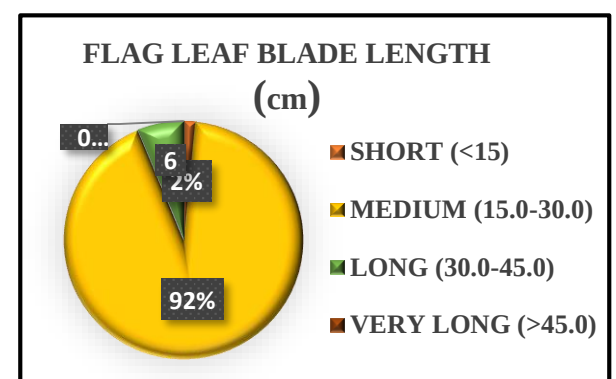
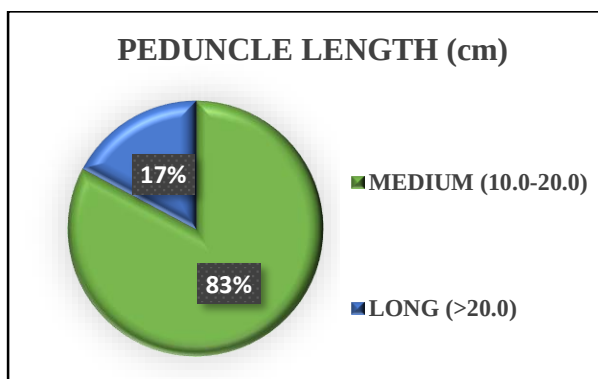
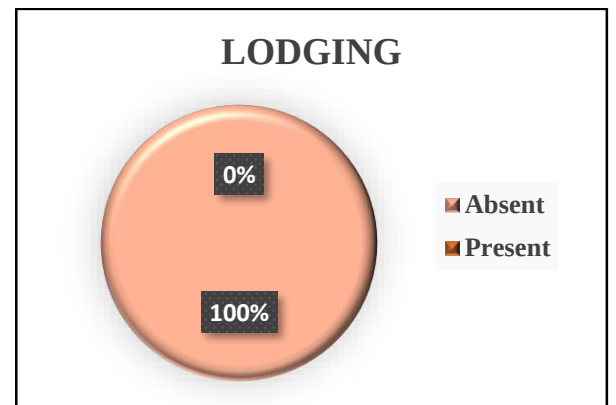
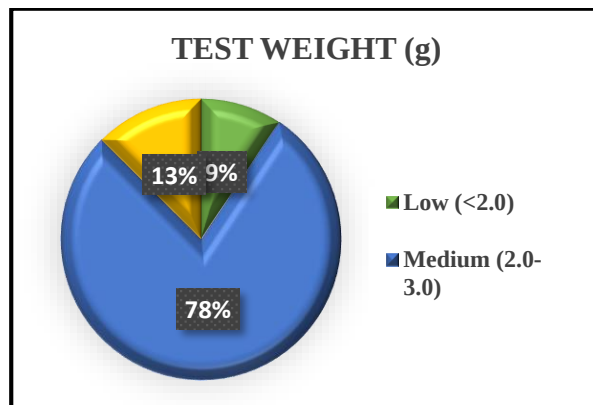
(Fig 4.1 Contd...)



(Fig 4.1 Contd...)



(Fig 4.1 Contd...)



4.1.2 Basal tillers

Basal tillers were categorized into low (<4), medium (4-7) and high (>7) and they are the main contributors to grain yield per plant as number tillers were indication of number of panicles per plant. All the germplasm studied have shown that low tillers (<4) per plant. Similar observations were recorded by Nilavarasi *et al.* (2020), as out of 11 genotypes, 2 genotypes are low, 7 genotypes are with medium and 2 genotypes are with high number of basal tillers in barnyard millet.

4.1.3 Days to 50% flowering

Breeders generally have used days to flowering as a key indicator of maturity duration since this trait provides a good indication of subsequent phenological traits, such as time of maturity in millets. In the present study out of 64 germplasm lines 43 genotypes are grouped under medium flowering group (40-50 DAS) and the remaining are 21 genotypes were grouped under late in flowering category (>50 DAS). Amaranth *et al.* (2018a) has reported that out of 50 germplasm accessions one genotype was early in flowering and 49 genotypes are in medium flowering in foxtail millet.

4.1.4 Plant Pigmentation (At Internodes and Leaf Sheath)

Plant pigmentation is important in growth and development of plant. The genetic material studied are 17 pigmented genotypes and 47 genotypes without pigmentation at internodes and leaf sheath. Similar observations were recorded by Kuraloviya *et al.* (2019), out of 30 genotypes 21 are pigmented and 9 are not pigmented in barnyard millet.

4.1.5 Flag Leaf Blade: Length (cm)

Based on the Flag Leaf Blade Length the genotypes were grouped into short, medium and long. In present study one genotype is Short (<15 cm), 59 are medium (15.0-30.0 cm) and 4 are long (30.1-45.0 cm) for flag leaf blade length. Similar results were obtained by Nilavarasi *et al.* (2020), out of 11 genotypes 2 are having short, 7 are having medium and 2 are having long leaf blade length in barnyard millet

4.1.6 Flag Leaf Blade: Width (cm)

Based on the Flag Leaf Blade Width the genotypes were grouped into Narrow (<2.0 cm), Medium (2.0-3.0 cm), Wide (>3.0 cm). In the present study 48 genotypes are with medium (2.0-3.0 cm) blade width and the remaining 16 genotypes are with narrow (<2.0 cm)

blade width. Similar observation was recorded by Nilavarasi *et al.* (2020), out of 11 genotypes 2 genotypes are with narrow and remaining 9 germplasm lines are with medium flag leaf blade width in barnyard millet.

4.1.7 Peduncle: Length (cm)

Based on the peduncle length the genotypes are grouped into Short (<10.0 cm), Medium (10.0-20.0 cm) and Long (>20.0 cm). In the present study 53 genotypes are with medium and 11 germplasm lines are with long peduncle length. These observations are in consonance with Nilavarasi *et al.* (2020), they have observed that all the 11 genotypes were medium for peduncle in the barnyard millet germplasm.

4.1.8 Inflorescence: Shape

Based on the Inflorescence shape of genotypes are categorized into three types viz., cylindrical, pyramidal and globose elliptical. In the present study 37 genotypes are pyramidal in shape and 27 genotypes are cylindrical in shape. These findings are in consonance with the reports of Kuraloviya *et al.* (2019). In the study Renganathan *et al.* (2017), have reported that out of 40 genotypes 18 are with cylindrical, 12 genotypes inflorescence are with pyramidal and 10 germplasm lines are globose elliptical in barnyard millet.

4.1.9 Inflorescence: Colour

Based on the inflorescence colour the genotypes were grouped into three viz., green, light purple and dark purple. In the present study out of 64 genotypes 46 genotypes are with green colour, 16 germplasm accessions are with light purple and 2 genotypes are with dark purple inflorescence colour. These observations are in consonance with findings of Nilavarasi *et al.* (2020) have observed that out of 11 genotypes, 9 genotypes with green, 1 with light purple and 1 is in dark purple. Similarly Kuraloviya *et al.* (2019), have reported out of 30 genotypes 7 are green, 17 are light purple, and 6 are dark purple colour in barnyard millet.

4.1.10 Panicle: Compactness

Barnyard millet has three types of panicle they are open, intermediate and compact. In the present studies based on the panicle compactness, 26 genotypes are with open, 27 genotypes are with intermediate and 11 germplasm accessions are with compact. These observations are in consonance with Kuraloviya *et al.* (2019), out of 30 genotypes,

14 genotypes with open panicle, 10 genotypes with intermediate compactness and 6 genotypes with compact panicle. Similarly Renganathan *et al.* (2017) have reported that out of 40 genotypes, 9 are with open panicle, 9 genotypes are with intermediate compactness and 22 genotypes are with compact panicle in barnyard millet.

4.1.11 Spikelets: Arrangements on the rachis

Barnyard millet has spikelets arrangements on the rachis are two types viz., one side and around. In the present study in barnyard millet germplasm 52 genotypes are with one side spikelets arrangements on the rachis and 12 genotypes are with around. These observations are in consonance with Kuraloviya *et al.* (2019), out of

30 genotypes 3 genotypes are with one side spikelets arrangements on the rachis and 27 genotypes with around spikelets arrangements on the rachis in barnyard millet.

4.1.12 Lower Racemes: Shape

Lower raceme shape in barnyard millet grouped into straight and curved. The germplasm studied out of 64 genotypes, 44 genotypes are straight lower racemes and 20 genotypes are curved lower racemes shape. These findings are in consonance with Kuraloviya *et al.* (2019), out of 30 genotypes, 4 are straight, 18 are curved and 8 genotypes are slender and Renganathan *et al.* (2017), out of 40 genotypes, 9 genotypes are straight, 9 genotypes are curved and 22 genotypes are with slender shape in barnyard millet.

4.1.13 Lower Raceme: Thickness

The trait lower raceme thickness in the genetic material grouped into slender and thick. Out of 64 germplasm studied 43 genotypes are with slender lower raceme and 21 genotypes are with thick lower raceme. The findings are in consonance with Nilavarasi *et al.* (2020), out of 11 genotypes under study 8 genotypes are with slender and 3 genotypes are with thick lower raceme in barnyard millet.

4.1.14 Lower Raceme: Branching

The trait lower raceme branching in the germplasm grouped into absent and present of lower raceme branching. In present study out 64 germplasm lines, 49 genotypes are with no lower raceme branching and 15 genotypes has lower raceme branching. The findings are in consonance with Nilavarasi *et al.* (2020), out of 11 genotypes tested 9 genotypes has no branching and 2 genotypes is with lower raceme branching. Renganathan *et al.* (2017), 25

genotypes having lower raceme branching and 15 genotypes are with no lower raceme branching in barnyard millet.

4.1.15 Culm: Branching

Culm branching is present in all the germplasm accessions. These findings are in consonance with Nilavarasi *et al.* (2020) and Kuraloviya *et al.* (2019) all the genotypes has culm branching in the barnyard millet in their study.

4.1.16 Lower Raceme: Length (cm)

In barnyard millet lower raceme length grouped into Short (<3 cm), Medium (3.0-5.0 cm) and Long (>5.0 cm) The germplasm studied exhibited 25 genotypes

are with short (<3 cm) lower raceme, 36 genotypes with medium (3.0-5.0 cm) lower raceme length and 3 germplasm lines with long (>5.0 cm) lower raceme length. Similar observations were recorded by Nilavarasi *et al.* (2020) out of 11 genotypes 10 are medium lower raceme length and one with long lower raceme in barnyard millet.

4.1.17 Panicle Length (cm)

Panicle length is the important trait in millets as length is the direct indication number of grains in the panicle. Panicle length in barnyard millet is characterized into four types short (<15.0 cm), short to medium (15.0-20.0 cm), medium (20.1-25.0 cm) and long (>25.0 cm). Out of 64 genetic material used for studies among them 10 genotypes are with short panicle length, 36 genotypes are with short to medium, 16 genotypes are with medium panicle length and 2 genotypes with long panicle length. Similar results were reported by Vikram *et al.* (2020), among the 40 genotypes they have recorded the panicle length range from (15.53-21.95 cm) i.e., short to medium and medium panicle length in their study.

4.1.18 Plant Height (cm)

In barnyard millet plant height is grouped in four viz., dwarf (>40 cm), semi dwarf (40.0-80.0 cm), tall (80.0-120.0) and Very Tall (>120.0). Out of 64 genotypes studies 39 germplasm lines are tall and 25 genotypes are very tall. Similar observations were recorded by Nilavarasi *et al.* (2020) out of 11 genotypes 2 genotypes are semi dwarf, 3 genotypes are tall, 6 genotypes are very tall in barnyard millet.

4.1.19 Grain Colour

Barnyard millets seed or grain colour is classified into three types straw white, light grey and grey. In the present study genetic material studied showed 28 genotypes are with straw white grain colour, 30 genotypes are with light grey grain and 6 germplasm lines are with grey grain colour. These findings are in consonance with Kuraloviya *et al.* (2019), where in 23 genotypes, 2 genotypes with straw white grain colour, 6 germplasm lines with grey and 15 germplasm accessions with grey + white grain colour in barnyard millet.

4.1.20 Grain: Shape

Barnyard millets grain has two types of seed shape concave and oval. In present study all the germplasm accessions utilized for the study are concave in shape. The findings are in consonance with Nilavarasi *et al.* (2020), Kuraloviya *et al.* (2019) all the genotypes with concave grain shape in their study of barnyard millet.

4.1.21 1000 Seed Weight (or) Test Weight (g)

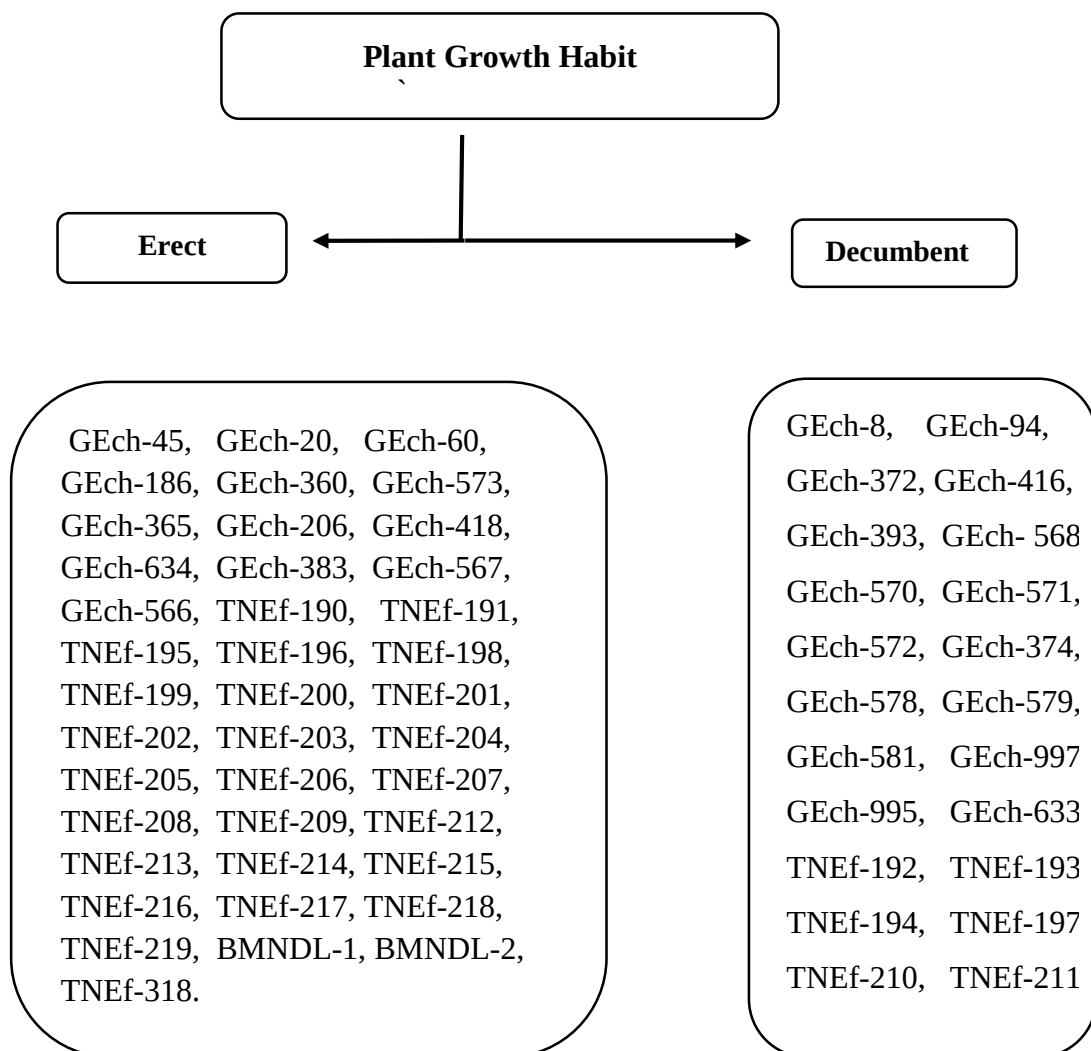
In barnyard millets based on 1000 seed weight seed were grouped into three categories viz., high, medium and low. In the present investigation it was observed 6 genotypes are low (<2.0 g), 50 germplasm lines with medium (2.0-3.0 g) and 8 genotypes are with high test weight (>3.0-4.0 g) in barnyard millet.

4.1.22 Lodging

Lodging is the bending over of the stem near ground level of grain crops, which makes them very difficult to harvest, and it reduces the yield. Breeders prefer the plants that in which lodging is absent or plant that does not show lodging. All the germplasm accessions studied does not show lodging at maturity. Similar findings are reported by Kuraloviya *et al.* (2019).

Morphological characterization of 64 barnyard millet germplasm accessions for 22 DUS traits revealed existence of ample polymorphism for the characters. It was observed that for plant growth habit, erect was majority over decumbent; basal tillers of all the germplasm accessions are low (<4); days to 50% flowering, medium duration was predominant; plant pigmentation at internode, non-pigmentation was dominant over pigmentation; flag leaf blade length, medium was predominant over long; for flag leaf blade width medium was predominant over narrow; for peduncle length, medium was dominant over long; for inflorescence shape pyramidal was dominant over cylindrical; for inflorescence colour green was dominant over light purple and dark purple; for panicle compactness, open was dominant over compact and intermediate; spikelets arrangements on rachies one side was predominant; for lower raceme shape straight was dominant over curved; for lower raceme thickness slender was dominant over thick; for lower raceme branching absent of branching was predominant; for culm branching all the germplasm accessions possess culm branching; lower raceme length, medium was dominant over short and long; for panicle length short to medium was dominant over medium and long; for plant height tall was dominant over very tall; for grain colour grey white was dominant over straw white and grey; for grain shape all the genotypes are concave ; for 1000 seed weight medium was dominant over high and low.

Fig 4.2 Morphological key for identification of 64 Barnyard millet germplasm accessions



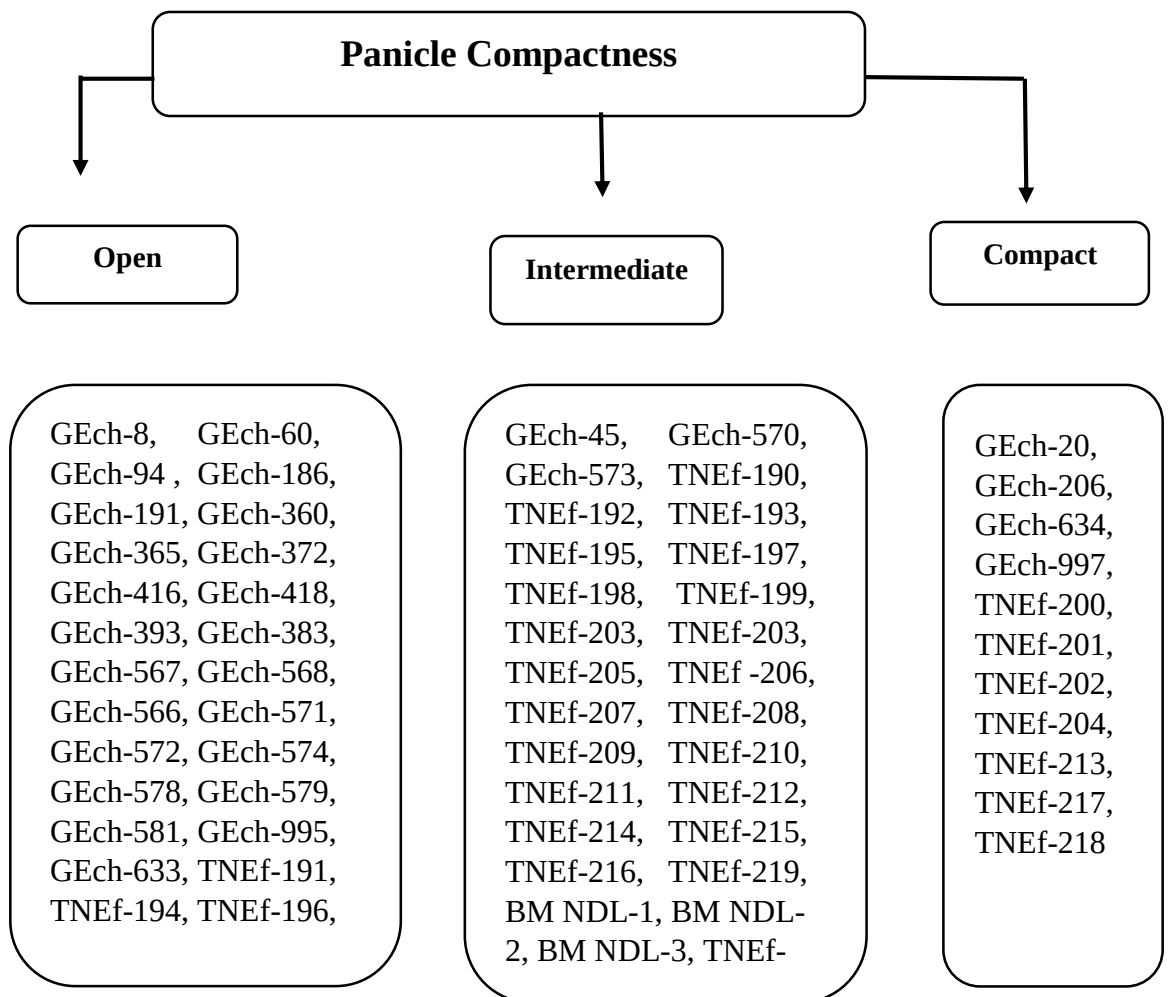
Pigmentation at inter node

Present

Absent

GEch-20, GEch-186,
GEch-365, GEch-418,
GEch-393, GEch-191,
GEch-383, GEch-567,
GEch-372, GEch-568,
GEch-570, GEch-572,
GEch-374, TNEf-195,
TNEf-211, TNEf-214,
TNEf-204,

GEch-8, GEch-45, GEch-60,
GEch-94, GEch-360, GEch-416,
GEch-566, GEch-571, GEch-573,
GEch-578, GEch-579, GEch-206,
GEch-581, GEch-997, GEch-995,
GEch-633, GEch-634, TNEf-190,
TNEf-191, TNEf-192, TNEf-193,
TNEf-194, TNEf-196, TNEf-197,
TNEf-198, TNEf-199, TNEf-200,
TNEf-201, TNEf-202, TNEf-203,
TNEf-205, TNEf-206, TNEf-207,
TNEf-208, TNEf-209, TNEf-210,
TNEf-212, TNEf-213, TNEf-215,
TNEf-216, TNEf-217, TNEf-218,
TNEf-219, BMNDL-1, BMNDL-2,
BMNDL-3, TNEf-318



Spikelet Arrangement on the Rachies

One side

GEch-8, GEch-45, GEch-60, GEch-94,
 GEch-186, GEch-191, GEch-360, GEch-365,
 GEch-372, GEch-416, GEch-418, GEch-383,
 GEch-567, GEch-568, GEch-566, GEch-570,
 GEch-571, GEch-572, GEch-573, GEch-374,
 GEch-578, GEch-579, GEch-206, GEch-581,
 GEch-997, GEch-995, GEch-633, TNEf-190,
 TNEf-191, TNEf-192, TNEf-193, TNEf-194,
 TNEf-195, TNEf-196, TNEf-197, TNEf-
 198, TNEf-200, TNEf-201, TNEf-202, TNEf-
 203, TNEf-204, TNEf-207, TNEf-208, TNEf-
 209, TNEf-210, TNEf-211, TNEf-212, TNEf-
 213, TNEf-214, TNEf-217, TNEf-218, TNEf-
 219

Around

GEch-20,
 GEch-393,
 GEch-634,
 TNEf-199,
 TNEf-205,
 TNEf-206,
 TNEf-215,
 TNEf-216,
 TNEf-219,
 BMNDL-1,
 BMNDL-2,
 BMNDL-3.

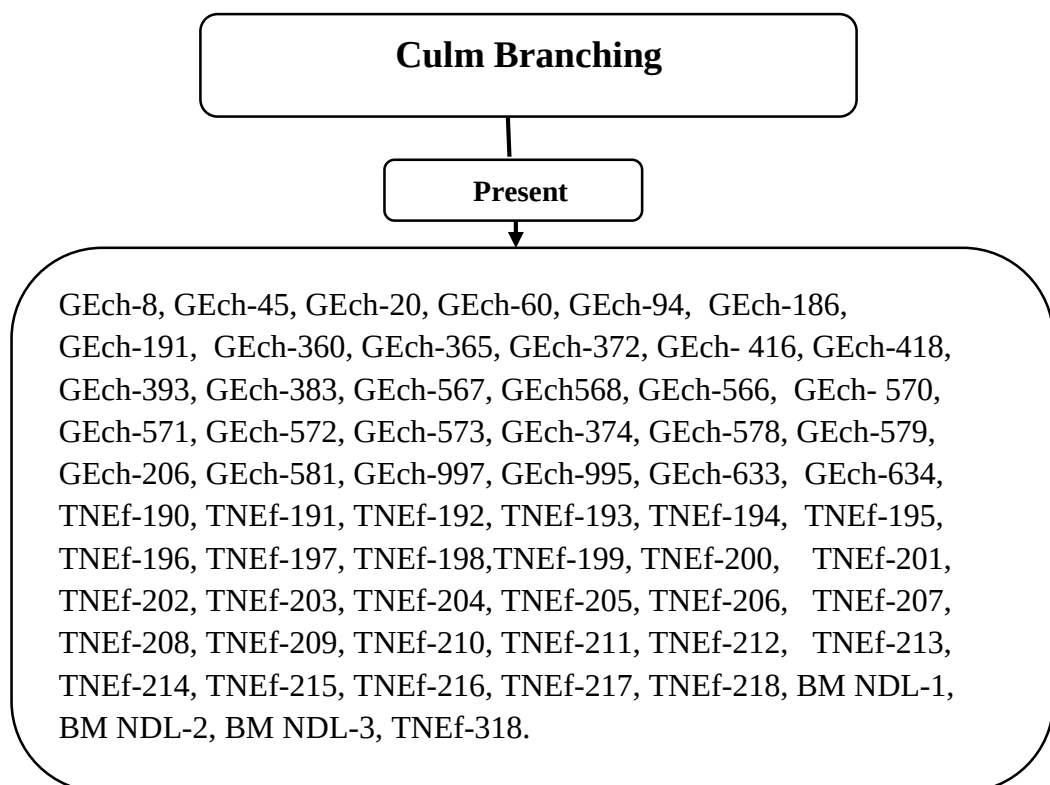
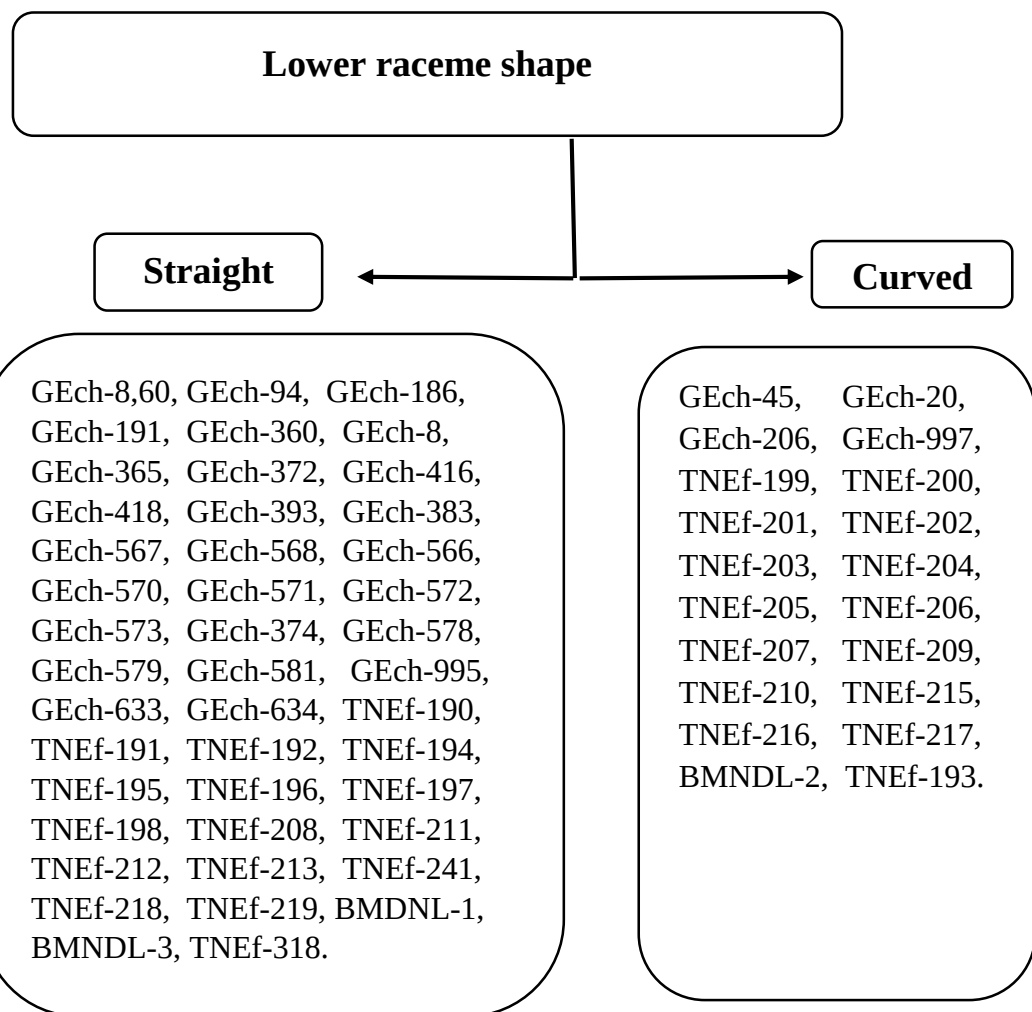
Inflorescence Shape

Cylindrical

GEch-8, GEch-60,
 GEch-186, GEch-191,
 GEch-360, GEch-365,
 GEch-416, GEch-383,
 GEch-567, GEch-568,
 GEch-566, GEch-573,
 GEch-374, GEch-578,
 GEch-581, GEch-995,
 TNEf-195, TNEf-199,
 TNEf-200, TNEf-201,
 TNEf-202, TNEf-204,
 TNEf-205, TNEf-209.

Pyramidal

GEch-45, GEch-20, GEch-94,
 GEch-372, GEch-418, GEch-393,
 GEch-570, GEch-571, GEch-572,
 GEch-579, GEch-206, GEch-997,
 GEch-633, GEch-634, TNEf-190,
 TNEf-191, TNEf-192, TNEf-193,
 TNEf-194, TNEf-196, TNEf-197,
 TNEf-198, TNEf-203, TNEf-206,
 TNEf-207, TNEf-208, TNEf-210,
 TNEf-213, TNEf-214, TNEf-215,
 TNEf-216, TNEf-217, BMNDL-1,
 BMNDL-2, BMNDL-3, TNEf-318



Lower Raceme Thickness

Thick

Slender

GEch-20, GEch-60,
GEch-393, GEch-383,
GEch-568, GEch-206,
GEch-634, TNEf-193,
TNEf-199, TNEf-201,
TNEf-205, TNEf-206,
TNEf-207, TNEf-209,
TNEf-215, TNEf-216,
TNEf-218, TNEf-219,
BMNDL-1, BMNDL-2,
BMNDL-3

GEch-8, GEch-45, GEch-94, GEch-186,
GEch-191, GEch-360, GEch-365, GEch-372,
GEch-416, GEch-418, GEch-567, GEch-566,
GEch-570, GEch-571, GEch-572, GEch-573,
GEch-374, GEch-578, GEch-579, GEch-581,
GEch-997, GEch-995, GEch-633, TNEf-190,
TNEf-191, TNEf-192, TNEf-194, TNEf-195,
TNEf-196, TNEf-197, TNEf-198, TNEf-200,
TNEf-202, TNEf-203, TNEf-204, TNEf-208,
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TNEf-214, TNEf-217, TNEf-318

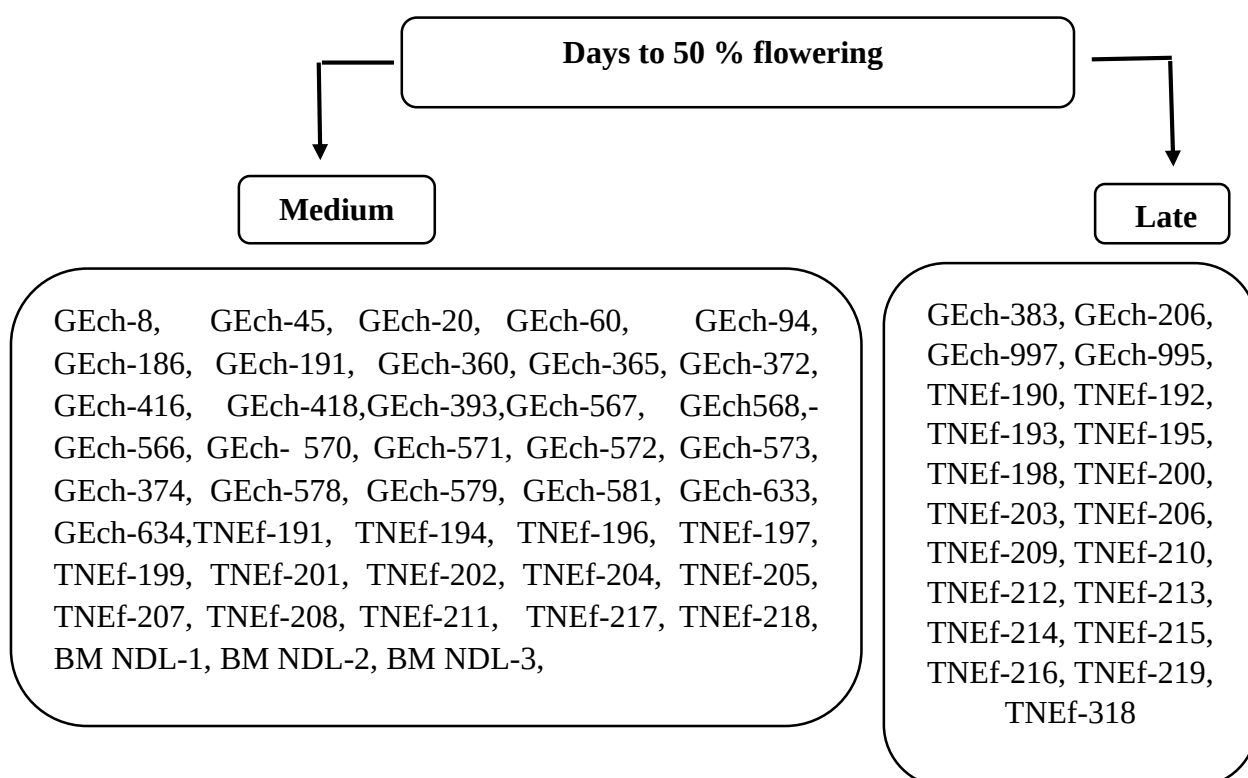
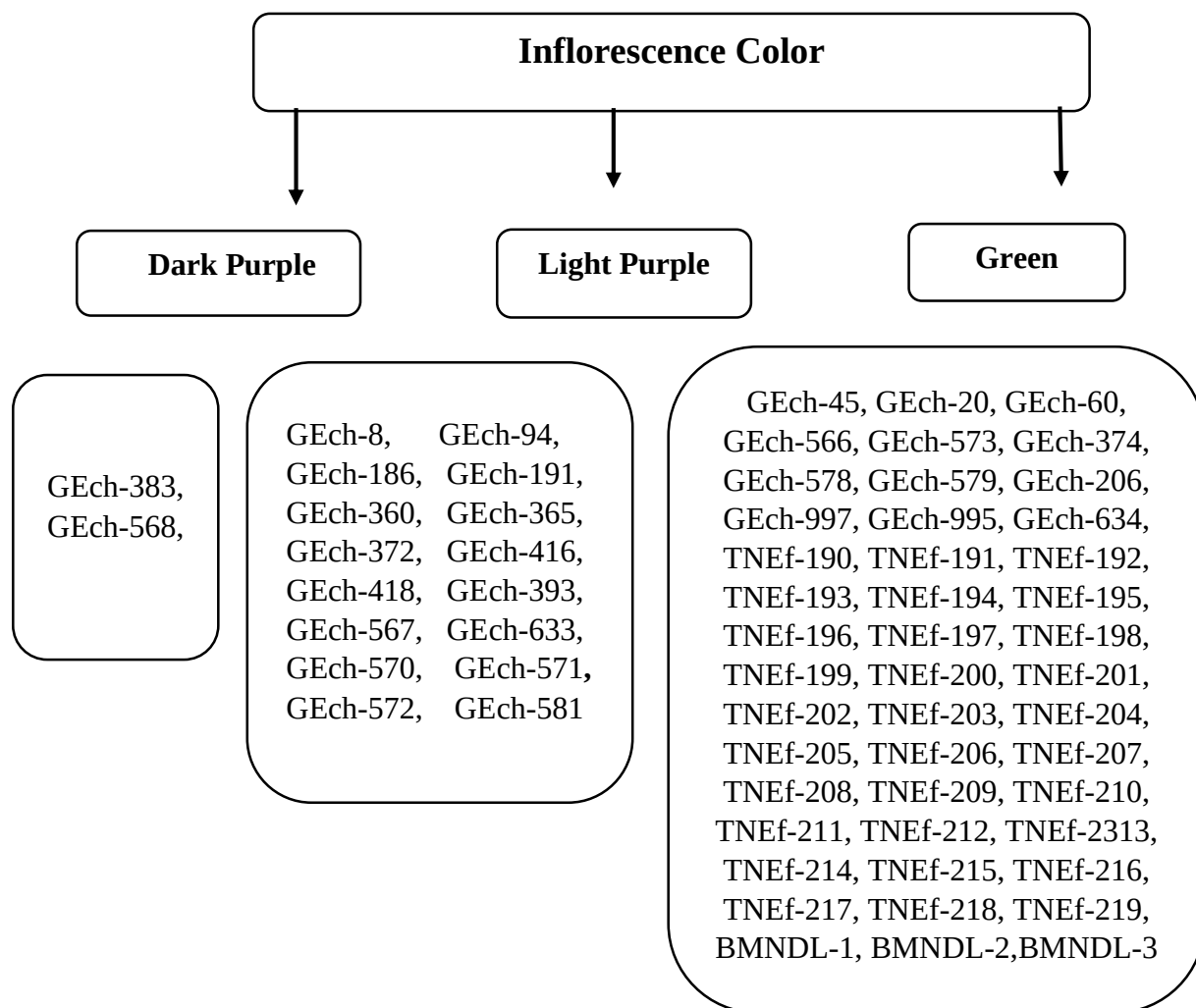
Lower Raceme Branching

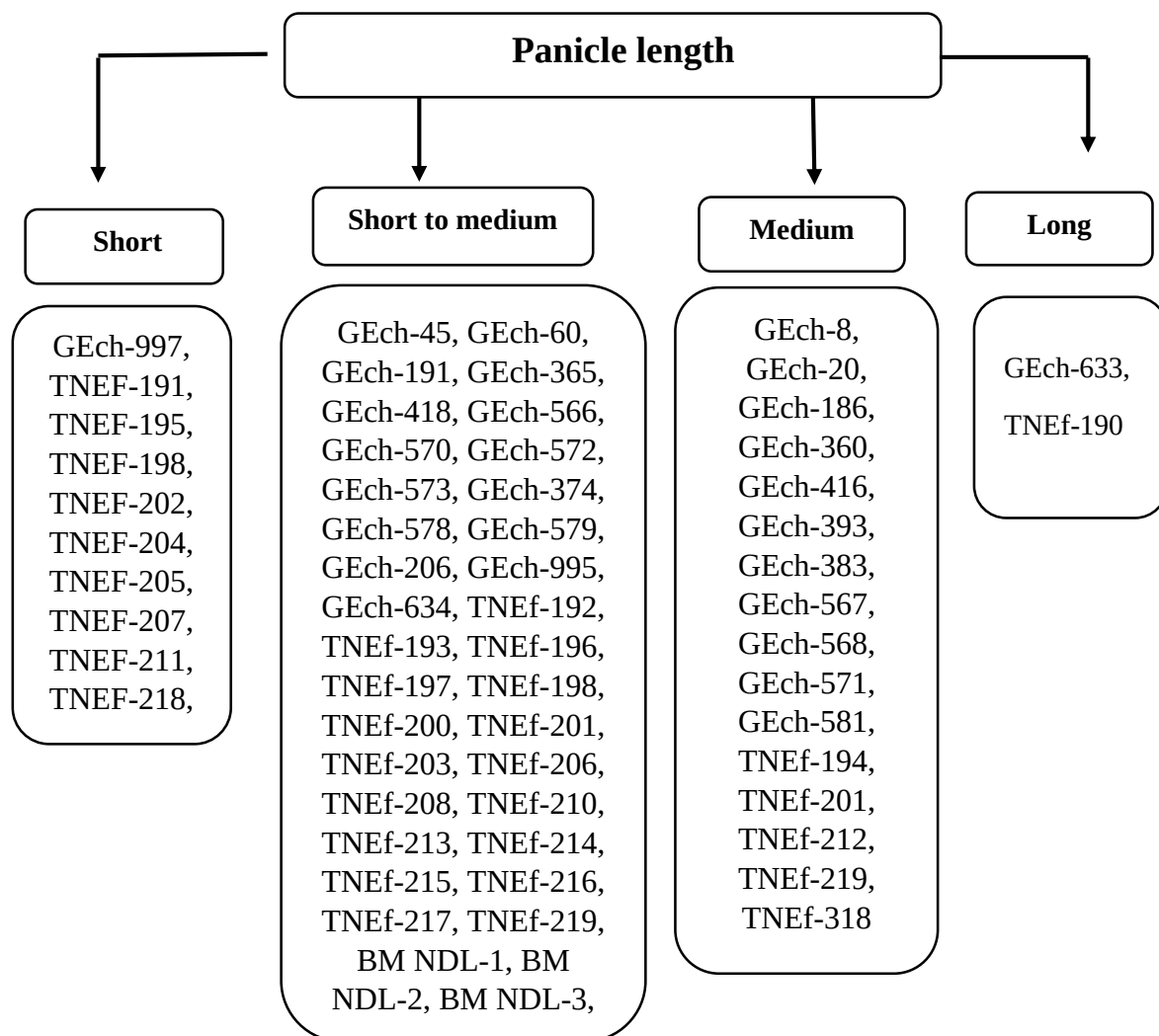
Branched

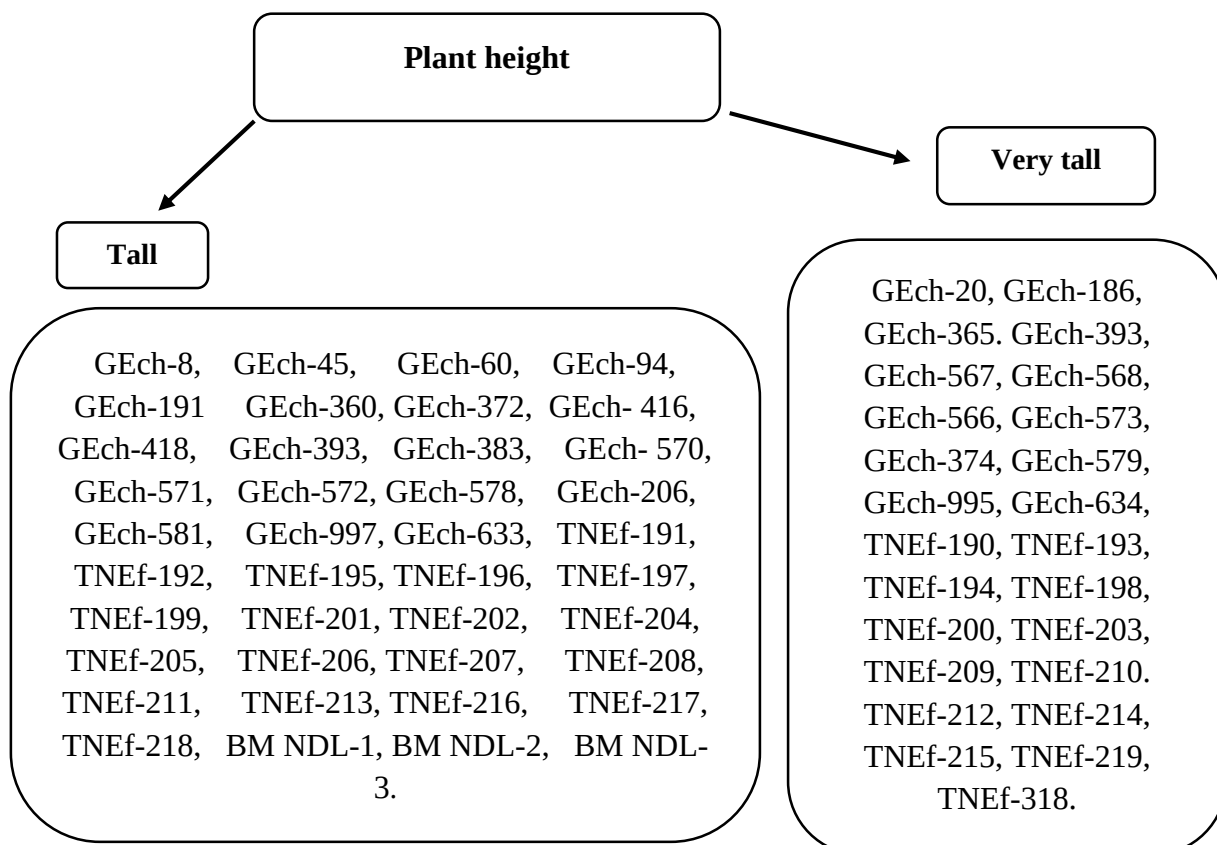
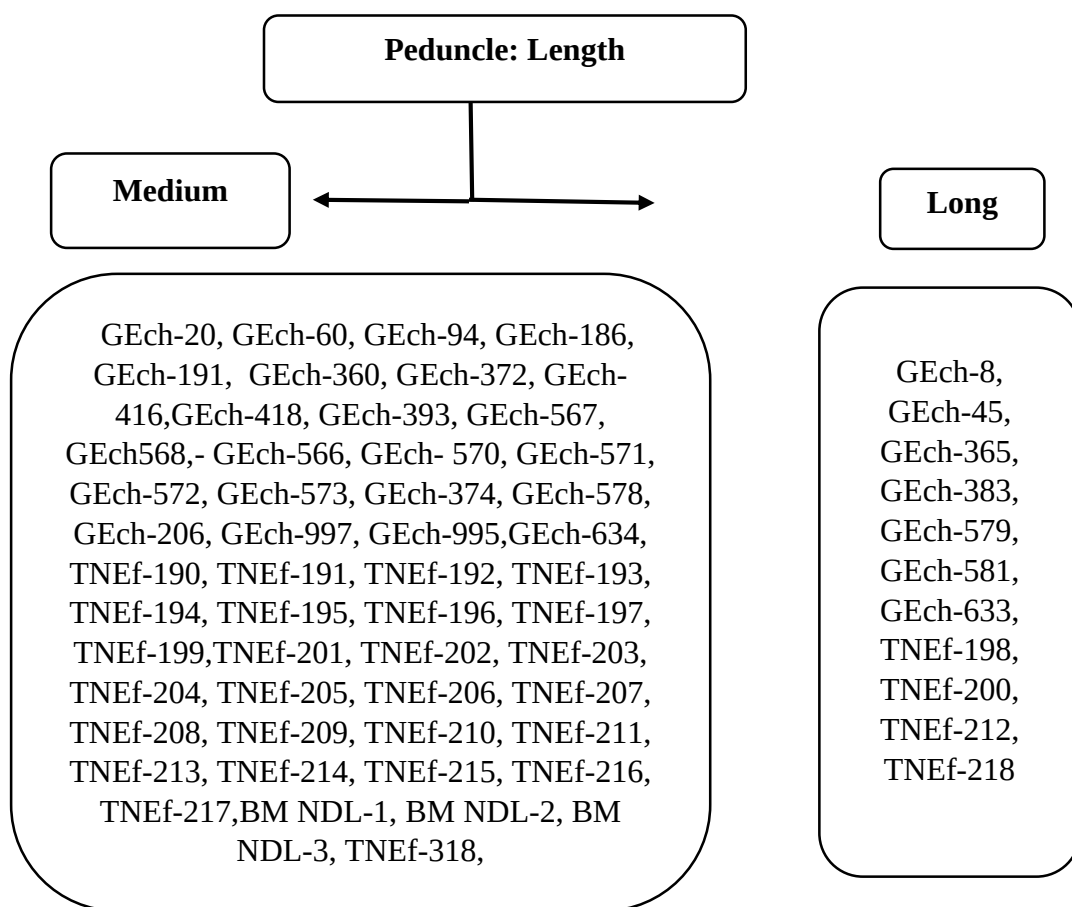
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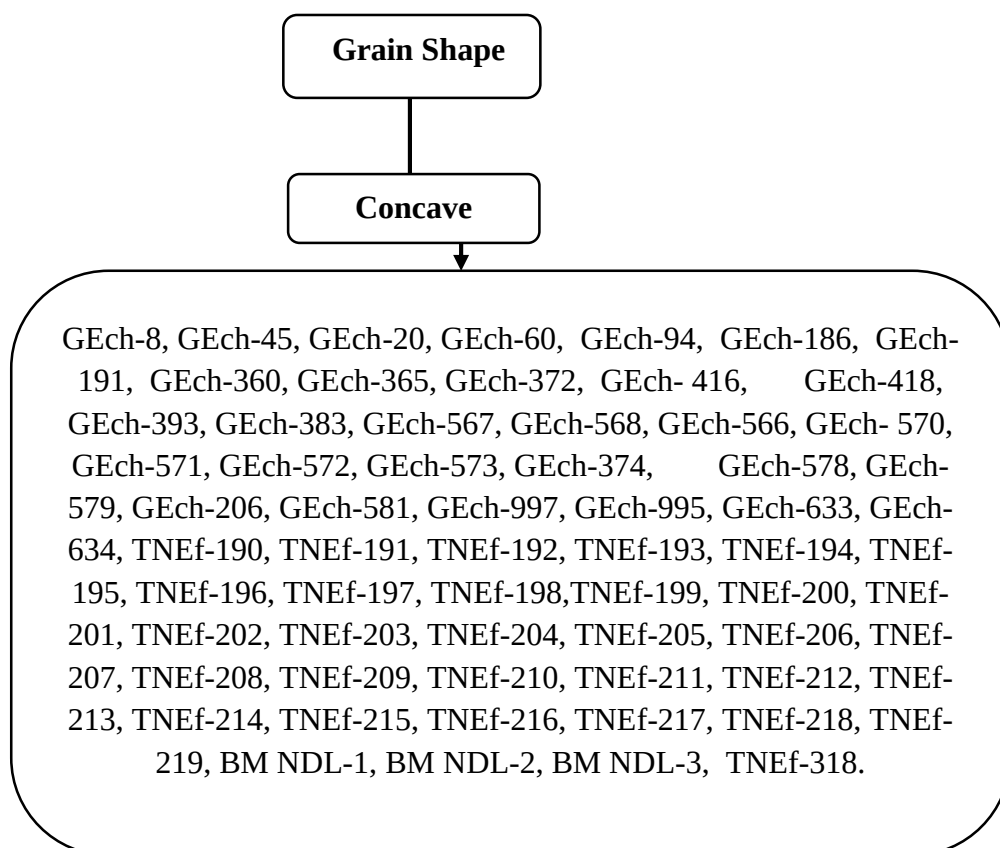
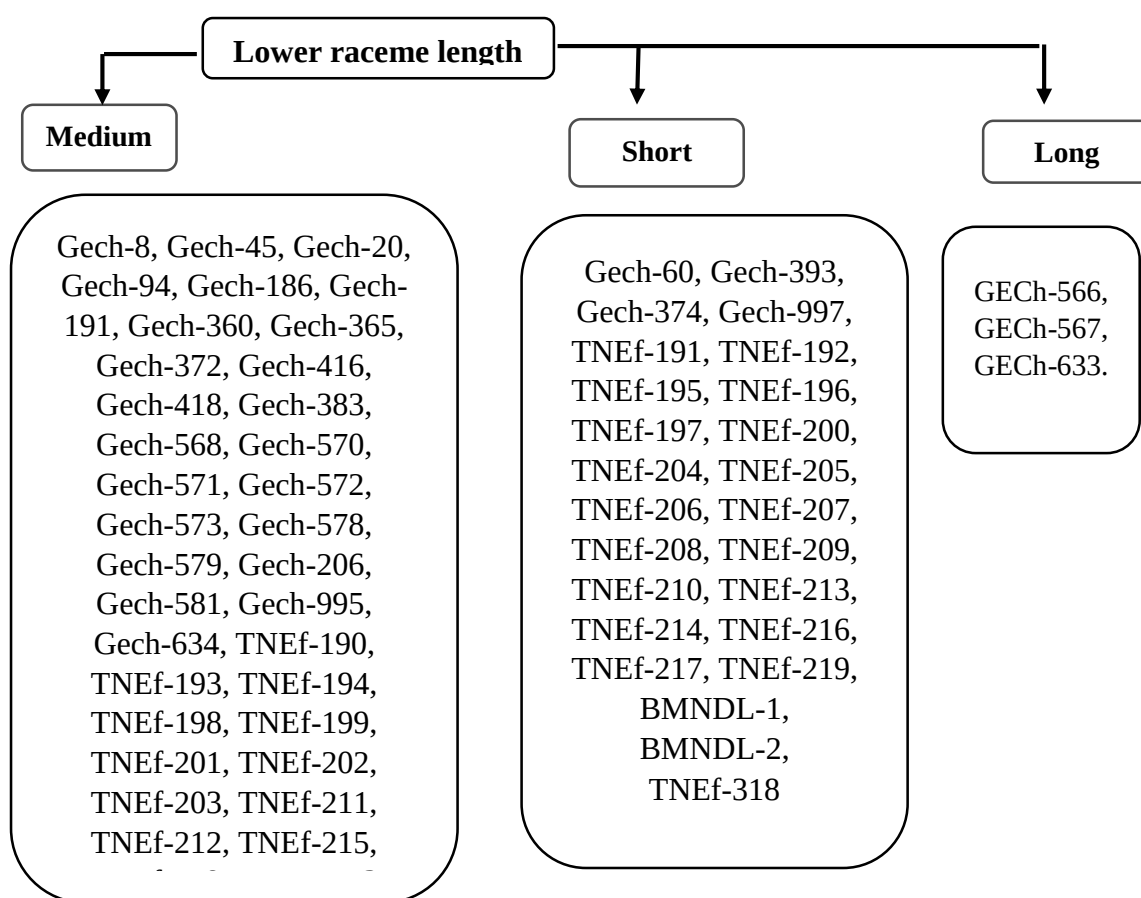
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TNEf-196, TNEf-206,
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BMNDL-1,
BMNDL-2,
BMNDL-3

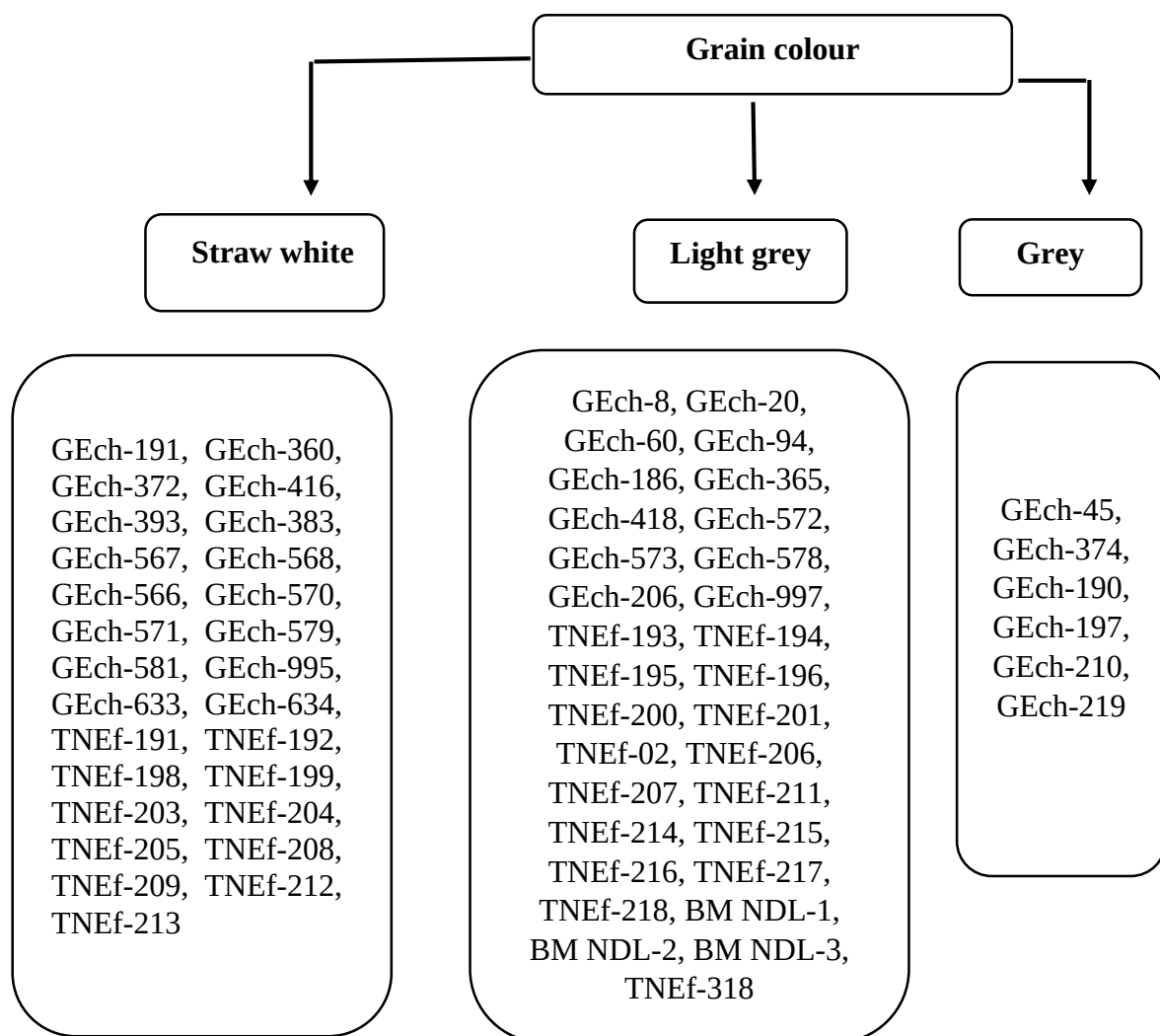
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GEch-568, GEch-566, GEch-570, GEch-571,
GEch-572, GEch-573, GEch-579, GEch-206,
GEch-581, GEch-997, GEch-995, GEch-633,
TNEf-190, , TNEf-191, TNEf-192, TNEf-193,
TNEf-194, TNEf-195, TNEf-197, TNEf-198,
TNEf-199, TNEf-200, TNEf-201, TNEf-202,
TNEf-203, TNEf-204, TNEf-205, TNEf-207,
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TNEf-318

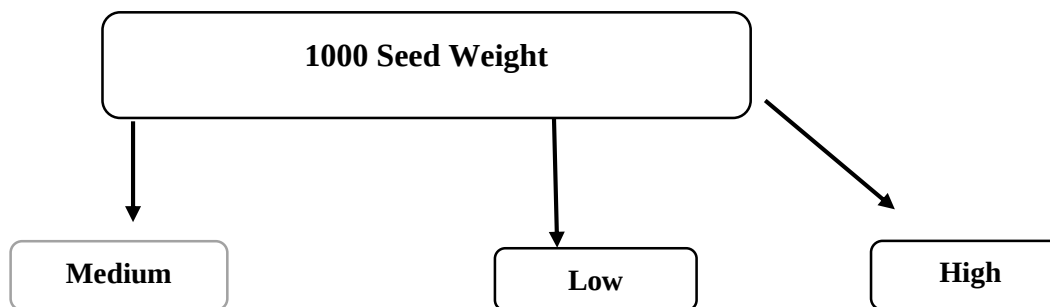












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GEch-581, GEch-997, GEch-995,
GEch-633, GEch-634, TNEf-190,
TNEf-192, TNEf-193, TNEf-195,
TNEf-196, TNEf-197, TNEf-199,
TNEf-200, TNEf-201, TNEf-202,
TNEf-204, TNEf-205, TNEf-206,
TNEf-207, TNEf-208, TNEf-209,
TNEf-210, TNEf-211, TNEf-213,
TNEf-214, TNEf-215, TNEf-216,
TNEf-219, BM NDL-1, BM NDL-2,
BM NDL-3, TNEf-318,

GEch-20,
GEch-191,
GEch-570,
GEch-374,
TNEf-191,
TNEf-212.

GEch-8,
GEch-60,
GEch-566,
TNEf-194,
TNEf-198,
TNEf-203,
TNEf-217,
TNEf-218.

4.2 ANALYSIS OF VARIANCE (ANOVA)

The ANOVA of 64 barnyard millet germplasm accessions for 18 quantitative traits viz., days to 50% flowering, basal tillers, days to maturity, peduncle length, flag leaf blade length, flag leaf blade width, Plant height, Panicle length, 1000 grain weight, Panicle weight /plant, Harvest Index (%), lower raceme length, Phosphorus, Calcium, Iron, Zinc, Protein (%) and grain yield / plant is presented in Table 4.2. The results disclose that the mean sum of squares were highly significant (0.01 significant) for all the characters studied. That indicates considerable extent of variability in the germplasm accessions, which could be utilized in further breeding programmes.

4.3 *Per se* performance

The *per se* performance of 64 barnyard millet germplasm accessions for grain yield and yield attributes are presented in Table 4.3.

4.3.1 Days to 50% flowering:

Days to 50% flowering is foremost grain yield parameter as it rescue the crop from terminal drought stress. The mean for this trait among the genotypes ranged from 41.0 days (Gech-8) to 72.2 days (TNEf-215) with an average of 49.03 days.

4.3.2 Basal tillers

The range of variation for basal tillers varied from 1.0 (TNEf-204) to 3.9 (Gech-995) with an average of 1.99 basal tillers / plant.

4.3.3 Days to maturity

The mean for this trait among the genotypes ranged from 81.0 days (Gech-8) to 112.5 days (TNEf-215) with an average of 89.1 days for the maturity.

4.3.4 Peduncle length (cm)

Peduncle length ranged from 12.33 to 23.97 with general mean of 17.81 cm. The shortest peduncle length among the germplasm studied is recorded TNEf-203 (12.33 cm) and longest peduncle length is TNEf-218 (23.97). Three genotypes GEch-8 (22.15), GEch-581(22.75) and TNEf-212 (21.46) recorded higher mean compared to the general mean and were on par with TNEf-218 (23.97).

4.3.5 Flag Leaf Blade Length (cm)

The range variation of flag leaf length varied from 21.40 to 32.02 cm with an average of 26.84 cm. The maximum blade length was recorded for TNEf-213

(32.02) and minimum blade length was recorded for BMNDL-2 (21.40). Eight genotypes viz GEch-186 (31.25), GEch-191 (30.65), GEch-416 (30.55), GEch-579 (31.8), GEch-206 (30.08), GEch-995 (30.00), GEch-634 (30.80), TNEf-203 (30.40) recorded higher mean compared to the general mean and were on par with TNEf-213 (32.02 cm).

4.3.6 Flag Leaf Blade width (cm)

The flag leaf blade width falls within the range of 1.75 to 2.72 cm with an average of 2.19 cm. The maximum and minimum values for this trait were recorded by TNEf-199 and GEch-634 respectively.

4.3.7 Plant height (cm)

The trait ranged from 90.91(TNEf-218) to 158.40 (TNEf-198) cm with an average of 117.64 cm. Seven genotypes GEch-20 (133.91), GEch-573 (140.83), TNEf-190 (142.10), TNEf-193 (142.16), TNEf-203 (134.98), TNEf-210 (139.57), TNEf-214 (133.41) recorded higher mean and were on par with genotype TNEf-198 (158.40).

4.3.8 Panicle length (cm)

The range of panicle length recorded is 13.48 (GEch-997) to 26.31 (TNEf-190) cm with an average of 18.40 cm. Two genotypes GEch-186 (24.35) and GEch-633 (25.7) recorded higher mean and were on par with genotype TNEf-190.

4.3.9 1000 seed weight (g)

Test weight or thousand seed weight in all the germplasm ranged from 1.40 to 3.65 gm with general mean 2.50 gm. The genotype TNEf-318 recorded maximum test weight. Ten genotypes GEch-8 (3.15), GEch-60 (3.20), GEch-360 (3.00), GEch-416 (3.00), GEch-567 (3.00), GEch-633 (2.95), TNEf-194 (3.10), TNEf-198 (3.25), TNEf-203 (3.45) and TNEf-217 (3.25) recorded higher mean weights compared with general mean and on par with genotype TNEf-318 (3.65).

4.3.10 Panicle weight / plant (g)

The panicle weight / plants in all genotypes ranged from 8.00 to 17.00 gm with general mean 10.43 gm. The genotype TNEf-219 recorded maximum panicle weight / plant.

4.3.11 Harvest index (%)

Harvest index in all the genotypes ranged from 30.2 % to 38.9 % with general mean 33.6%. The genotypes TNEf-191 and TNEf-192 recorded maximum harvest index. The genotypes GEch-418 (35.4), GEch-566 (37.0), GEch-572 (37.5), TNEf-194 (35.7), TNEf-198 (37.5), TNEf-210 (35.7) and TNEf-212 (37.8) recorded higher mean compared with general mean and on par with genotype TNEf-191.

4.3.12 Lower raceme length (cm)

The trait ranged from 1.9 to 6.0 cm with general mean 3.3 cm. The maximum and minimum values are recorded by GEch-633 and TNEf-192 respectively.

4.3.13 Grain yield / plant (g)

The main objective in any plant breeding is to improve the yield and its economic importance. The mean for this trait ranged from 6.5 (TNEf-195) to 15.0 (TNEf-219) (g) with an average 8.9 (g). five genotypes GEch-8 (12.7), GEch-573 (11.5), TNEf-200 (12.2) TNEf-202 (12.9) and TNEf-218 (12.9) recorded higher mean compared with general mean and on par with genotype TNEf-219.

4.3.14 Phosphorus (mg / 100g)

The phosphorus content ranged from 253.0 (GEch-191) to 296.0 (TNEf-192) with a mean of 276.0 mg / 100g.

4.3.15 Calcium (mg /100g)

The calcium content ranged from 16.0 mg (TNEf-192) to 24.1 mg (GEch-374) with a mean of 19.6 mg / 100g.

4.3.16 Iron (mg / 100g)

The iron content ranged from 12.5 mg (GEch-581) to 21.2 mg (GEch-571) with a mean of 16.7 mg / 100g.

4.3.17 Zinc (mg / 100g)

The zinc content ranged from 36.2 mg (BM NDL-3) to 56.8 mg (GEch-579, GEch-416) with a mean of 45.5 mg / 100g.

4.3.18 Protein (%)

The protein content ranged from 6.8 (%) (TNEf-215) to 11.9 % (GEch-634) with a mean 8.6 %. Table 4.3

Table 4.2 Analysis of variance for 18 morpho-physiological and biochemical characters studied in barnyard millet germplasm accessions

	DF	Days to 50% flowering	Basal tillers	Days to maturity	Peduncle length (cm)	FLB Length(cm)	FLB Width(cm)
Replications	1	6.498	0.17	6.216	0.028	1.123	0.023
Treatments (unadjusted)	63	106.721 **	0.788 **	106.202 **	12.791 **	12.886 **	0.122 **
Error (r.c.b.)	63	8.680 **	0.057 **	30.618 **	1.217 **	3.146 **	0.018 **
Blocks within Replicated (adj)	14	10.312	0.073	35.729	1.354	3.791	0.022
Among (a)	7	11.495	0.034	39.991	1.771	3.003	0.013
Among (b)	7	9.129	0.112	31.468	0.937	4.579	0.031
Intra block Error	49	8.213	0.053	29.157	1.178	2.962	0.017
Total	127	57.297 **	0.421 **	67.920 **	6.949 **	7.962 **	0.070 **

	DF	Plant height (cm)	Panicle length (cm)	1000 seed weight (g)	Panicle weight / plant (g)	Harvest Index(%)	Lower raceme length (cm)
Replications	1	5.53	0.025	0.057	0.512	3.073	0.107
Treatments (unadjusted)	63	389.058 **	18.084 **	0.459 **	6.365 **	10.119 **	1.707 **
Error (r.c.b.)	63	51.494 **	1.366 **	0.033 **	0.596 **	4.204 **	0.071 **
Blocks within Replicated (adj)	14	50.592	1.833	0.032	0.765	5.529	0.066
Among (a)	7	37.696	2.954 *	0.033	0.622	7.957	0.043
Among (b)	7	63.487	0.712	0.03	0.908	3.1	0.09
Intra block Error	49	51.751	1.233	0.034	0.547	3.826	0.073
Total	127	218.585 **	9.649 **	0.245 **	3.457 **	7.129 **	0.883 **

***, ** Significant at 0.05 and 0.01 levels respectively.**

Table 4.2 Analysis of variance for 18 morpho-physiological and biochemical characters studied in barnyard millet germplasm accessions

	DF	Grain yield/ plant (g)	Phosphorus (mg/ 100g)	Calcium (mg/ 100g)	Iron (mg/ 100g)	Zinc (mg/ 100g)	Protein %
Replications	1	3.971	7.681	0.296	4.423	0.972	0.997
Treatments (unadjusted)	63	5.024 **	192.381 *	11.996 **	8.228 **	86.895 **	3.414 **
Error (r.c.b.)	63	1.138 **	106.989 **	1.660 **	1.297 **	10.480 **	0.476 **
Blocks within Replicated (adj)	14	1.45	151.448	3.416 **	1.355	6.091	0.637
Among (a)	7	0.405	52.24	3.616 **	1.621	5.139	1.127 *
Among (b)	7	2.494 *	250.656 *	3.216 *	1.089	7.043	0.146
Intra block Error	49	1.049	94.287	1.159	1.281	11.734	0.430
Total	127	3.088 **	148.567 *	6.777 **	4.760 **	48.312 **	1.937 **

***, ** Significant at 0.05 and 0.01 levels respectively.**

Table 4.3 *Per se* performance of 64 barnyard millet germplasm accessions for yield and yield attributes

Sl. No.	GENOTYPE	Days to 50% flowering	Basal tillers	Days to maturity	Peduncle length (cm)	FLB Length (cm)	FLB Width (cm)	Plant height (cm)	Panicle length (cm)	1000 seed weight (g)	Panicle weight /plant (g)	Harvest Index (%)	Lower raceme length (cm)	Grain yield/plant (g)	Phosphorus mg/100g	Calcium mg/100g	Iron mg/100g	Zinc mg/100g	Protein %
1	Gech-8	41.0	2.5	81.0	22.2	29.0	2.1	115.1	22.9	3.2	13.2	30.9	4.5	12.7	283.0	21.4	19.2	37.6	8.0
2	Gech-45	43.5	1.4	83.5	21.0	28.6	2.3	109.6	18.7	2.7	11.0	34.0	3.8	8.6	274.0	17.5	18.9	38.7	11.3
3	Gech-20	49.5	1.8	89.5	16.8	29.1	2.4	133.9	20.3	1.4	11.0	33.1	4.0	8.6	262.0	16.7	17.3	36.6	11.8
4	Gech-60	42.5	1.1	82.5	15.0	24.4	2.3	98.5	18.0	3.2	8.9	31.7	2.4	9.5	272.5	16.6	20.3	38.4	8.0
5	Gech-94	42.0	1.7	82.0	17.1	26.5	2.6	117.9	21.0	2.8	12.0	32.1	4.1	10.1	279.5	18.4	18.4	37.6	8.9
6	Gech-186	47.0	3.3	87.0	19.2	31.3	2.6	133.2	24.4	2.9	10.7	32.0	3.6	9.3	294.0	17.6	19.3	42.4	7.9
7	Gech-191	46.5	1.7	86.5	19.9	30.7	2.1	113.0	18.1	1.6	8.3	32.8	3.5	9.4	253.0	19.6	19.5	45.4	8.9
8	Gech-360	49.0	2.0	89.0	19.8	28.7	2.3	108.3	21.3	3.0	9.3	31.1	4.0	9.1	284.0	22.7	20.0	48.5	8.4
9	Gech-365	42.5	2.3	82.5	20.9	26.9	2.3	129.5	19.4	2.5	11.8	38.5	3.1	9.4	278.0	21.1	18.3	52.2	8.3
10	Gech-372	42.5	2.2	82.5	18.3	28.7	2.1	107.4	16.2	2.8	9.2	31.5	3.6	10.3	288.0	23.4	15.8	54.4	7.9
11	Gech-416	49.0	2.2	89.0	14.2	30.6	2.4	118.5	22.4	3.0	10.7	32.3	3.1	9.3	263.0	23.8	15.3	56.8	8.9
12	Gech-418	44.0	1.3	84.0	14.8	29.9	2.0	114.6	20.0	2.1	9.8	35.4	3.3	8.9	255.5	20.6	16.3	42.6	11.3
13	Gech-393	49.0	2.7	89.0	18.0	27.6	2.3	128.9	20.1	2.5	9.9	34.5	2.7	8.6	261.5	22.8	15.9	45.6	8.9
14	Gech-383	51.5	2.0	91.5	20.2	27.6	2.3	115.8	20.2	2.1	10.0	33.4	3.1	8.6	283.5	22.7	19.5	54.9	7.5
15	Gech-567	48.5	2.3	88.0	19.8	28.3	2.3	125.9	21.1	3.0	10.2	33.4	5.3	8.8	276.0	18.6	19.4	40.1	8.0
16	Gech-568	46.5	1.7	86.0	19.4	24.6	2.4	127.3	22.2	2.1	10.7	34.1	4.4	8.3	264.0	19.5	16.2	54.0	9.4
17	Gech-566	44.5	1.3	84.0	19.7	23.2	1.9	129.4	17.1	3.3	10.3	37.0	5.6	8.0	272.0	18.5	15.4	50.4	8.9
18	Gech-570	43.0	2.2	83.0	17.6	25.2	1.9	116.4	19.3	1.8	10.0	31.9	3.8	7.7	263.0	17.3	14.7	38.5	8.9

Table 4.3 *Per se* performance of 64 barnyard millet germplasm accessions for yield and yield attributes

Sl. No	GENOTYPE	Days to 50% flowering	Basal tillers	Days to maturity	Peduncle length (cm)	FLB Length (cm)	FLB Width (cm)	Plant height (cm)	Panicle length (cm)	1000 seed weight (g)	Panicle weight /plant (g)	Harvest Index (%)	Lower raceme length (cm)	Grain yield/plant (g)	Phosphorus mg/100g	Calcium mg/100g	Iron mg/100g	Zinc mg/100g	Protein %
19	Gech-571	42.0	3.0	82.0	18.5	24.9	1.9	117.9	22.2	2.4	11.0	30.9	4.5	8.7	267.5	18.9	21.2	55.3	8.2
20	Gech-572	49.0	2.5	89.0	18.5	29.3	1.8	115.2	18.5	2.8	10.3	37.5	3.1	8.0	272.5	22.2	15.3	54.3	8.2
21	Gech-573	46.5	2.3	86.5	16.8	29.5	2.2	140.8	18.1	2.5	14.6	32.7	4.6	11.5	267.5	23.7	13.0	38.9	7.9
22	Gech-374	47.5	3.1	87.5	16.6	26.5	2.2	122.1	17.4	1.9	9.0	30.7	2.3	9.5	272.0	24.1	13.9	45.8	8.2
23	Gech-578	43.0	3.4	84.0	18.2	24.8	2.1	113.3	16.4	2.2	9.1	33.0	4.8	8.8	275.5	22.6	20.0	52.4	11.9
24	Gech-579	42.0	2.8	82.0	20.6	31.8	2.0	124.2	18.6	2.0	11.2	38.4	3.5	8.9	276.0	22.2	14.1	56.8	8.8
25	Gech-206	56.0	1.2	96.0	16.2	30.1	1.9	112.6	18.4	2.6	10.1	32.2	3.4	7.8	282.0	18.7	14.7	48.1	9.9
26	Gech-581	41.5	2.4	82.0	22.8	24.1	1.8	106.5	21.4	2.6	10.4	32.5	4.0	8.0	286.0	21.6	12.5	38.3	8.4
27	Gech-997	54.5	2.4	94.5	15.5	26.8	2.5	104.0	13.5	2.8	10.8	31.6	2.2	9.8	263.0	19.6	15.9	38.7	8.0
28	Gech-995	55.5	3.9	95.5	19.5	30.0	1.8	121.5	18.4	2.2	12.7	31.5	4.3	10.4	281.5	21.6	16.5	52.3	7.7
29	Gech-633	42.5	2.7	82.5	20.2	24.4	2.0	118.5	25.7	3.0	11.2	31.4	6.0	9.0	284.0	18.1	18.3	54.1	8.5
30	Gech-634	48.0	3.1	89.0	19.7	30.8	2.7	131.2	19.3	2.8	10.3	31.6	3.0	7.9	288.5	19.8	16.2	40.9	11.9
31	TNEf-190	54.0	1.8	94.0	16.9	28.2	2.2	142.1	26.3	2.1	8.7	32.0	4.0	7.3	290.0	21.1	17.6	48.2	6.9
32	TNEf-191	44.0	1.5	84.0	18.6	26.5	2.1	116.5	13.9	1.6	10.2	38.9	2.2	7.9	296.0	18.5	14.9	44.7	8.2
33	TNEf-192	44.0	1.5	84.0	16.0	26.5	2.1	116.5	16.3	2.0	9.3	38.9	1.9	7.9	296.0	16.0	14.9	44.7	8.2
34	TNEf-193	56.5	1.5	96.5	17.5	25.0	2.0	142.2	15.1	2.4	9.4	31.0	3.0	7.1	285.5	16.6	17.5	39.4	6.9
35	TNEf-194	49.0	2.3	89.0	14.9	27.3	2.6	134.6	22.2	3.1	10.3	35.7	4.1	8.0	276.5	17.2	17.3	43.1	7.5
36	TNEf-195	57.0	1.3	98.0	16.8	26.5	2.0	109.7	14.1	2.9	8.9	32.2	2.0	6.5	267.0	19.7	18.7	43.3	7.6

Table 4.3 *Per se* performance of 64 barnyard millet germplasm accessions for yield and yield attributes

Sl. No.	GENOTYPES	Days to 50% flowering	Basal tillers	Days to maturity	Peduncle length (cm)	FLB Length (cm)	FLB Width (cm)	Plant height (cm)	Panicle length (cm)	1000 seed weight (gm)	Panicle weight /plant (gm)	Harvest Index (%)	Lower raceme length (cm)	Grain yield/plant (gm)	Phosphorus mg/100g	Calcium mgs/100g	Iron mg/100g	Zinc mg/100g	Protein %
37	TNEf-196	48.0	2.3	88.0	17.8	24.5	2.7	110.1	17.7	2.8	11.7	34.3	2.5	8.8	286.5	21.3	13.2	47.7	7.5
38	TNEf-197	42.0	2.8	82.0	17.8	26.7	2.2	106.5	15.1	2.2	9.2	30.4	2.5	7.0	279.0	21.9	14.4	52.0	7.5
39	TNEf-198	58.0	1.2	98.0	20.3	26.2	2.2	158.4	19.0	3.3	10.9	37.5	3.0	8.6	265.0	23.8	15.1	38.9	8.8
40	TNEf-199	48.0	1.4	88.0	13.4	24.7	1.8	112.1	13.8	2.2	9.2	33.3	4.0	6.9	285.0	20.7	16.0	55.3	8.8
41	TNEf-200	69.0	1.4	109.0	23.3	29.2	2.4	121.7	18.3	2.7	14.5	34.3	2.7	12.2	279.5	16.1	16.7	55.6	7.5
42	TNEf-201	45.5	2.3	85.5	12.3	25.9	2.0	97.5	15.5	2.3	8.3	32.1	3.0	8.3	286.5	17.0	17.6	56.1	6.9
43	TNEf-202	43.5	2.3	84.0	14.7	24.7	1.9	98.3	14.0	2.5	14.7	34.6	3.4	12.9	266.0	17.1	16.4	56.6	7.5
44	TNEf-203	54.0	1.8	94.0	17.5	30.4	2.3	135.0	15.6	3.5	9.3	31.7	3.1	8.2	281.5	23.8	18.7	47.9	8.8
45	TNEf-204	44.0	1.0	84.0	12.8	25.5	2.6	100.5	13.7	2.2	8.6	33.6	2.6	7.8	285.5	23.4	14.5	39.1	10.0
46	TNEf-205	45.0	1.9	85.0	15.0	21.5	2.1	99.7	14.8	2.5	8.6	35.0	2.2	9.8	268.5	21.2	18.0	53.5	9.6
47	TNEf-206	59.0	1.6	99.0	18.5	30.0	2.6	114.3	17.8	2.0	10.6	32.6	2.4	8.3	275.5	20.3	18.3	46.2	9.4
48	TNEf-207	44.0	1.4	86.0	16.7	24.0	1.9	91.8	14.0	2.4	10.4	34.6	2.5	8.1	282.5	16.1	18.7	38.7	7.6
49	TNEf-208	46.0	1.1	86.0	16.7	26.9	1.9	106.9	17.5	2.6	8.2	33.0	2.6	7.8	268.0	17.4	18.7	45.0	8.8
50	TNEf-209	62.5	2.1	102.5	17.9	25.5	2.0	131.3	21.5	2.4	11.9	32.1	2.9	10.4	282.5	16.6	18.2	52.5	8.8
51	TNEf-210	56.0	1.5	96.0	14.8	24.9	2.4	139.6	19.3	2.6	10.5	35.7	2.6	8.2	277.5	19.7	16.4	38.1	10.0
52	TNEf-211	43.0	1.5	83.0	19.1	25.6	2.2	92.7	14.4	2.4	9.0	31.2	3.5	6.7	277.0	16.9	16.3	37.1	10.6
53	TNEf-212	58.5	1.7	98.5	21.5	24.6	2.3	129.6	21.1	1.8	10.9	37.8	3.0	8.5	269.0	18.2	19.1	39.7	10.0
54	TNEf-213	56.5	2.2	96.5	18.7	32.0	2.4	108.8	16.2	2.3	10.1	31.5	2.6	7.5	267.5	20.3	13.4	46.3	8.8

Table 4.3 *Per se* performance of 64 barnyard millet germplasm accessions for yield and yield attributes

Sl. No.	GENOTYPES	Days to 50% flowering	Basal tillers	Days to maturity	Peduncle length (cm)	FLB Length (cm)	FLB Width (cm)	Plant height (cm)	Panicle length (cm)	1000 seed weight (g)	Panicle weight /plant (g)	Harvest Index (%)	Lower raceme length (cm)	Grain yield/plant (g)	Phosphorus mg/100g	Calcium mgs/100g	Iron mg/100g	Zinc mg/100g	Protein %
55	TNEf-214	57.0	1.5	97.0	18.9	24.1	2.2	133.4	17.4	3.0	9.1	34.9	2.3	8.3	281.5	17.4	16.1	46.4	9.4
56	TNEf-215	72.5	2.5	112.5	19.0	27.0	2.5	122.2	17.3	2.3	10.9	34.9	3.8	8.8	267.0	18.4	17.0	42.0	6.8
57	TNEf-216	69.0	2.0	109.0	18.9	26.5	2.5	116.1	16.4	2.8	8.1	32.2	2.3	7.2	266.0	17.9	17.3	38.2	7.5
58	TNEf-217	42.0	1.5	82.0	14.6	24.5	2.4	91.8	18.6	3.3	10.8	35.7	2.8	8.5	283.0	16.6	14.6	45.7	7.0
59	TNEf-218	41.0	2.3	81.0	24.0	22.0	2.2	90.9	15.1	3.7	14.9	30.2	5.0	12.9	280.0	22.7	15.1	43.6	7.0
60	TNEf-219	52.0	1.7	92.0	16.1	26.5	2.5	125.7	21.3	2.7	17.0	34.5	2.1	15.0	262.0	19.1	18.1	48.1	8.8
61	BMNDL-1	41.5	1.7	81.5	14.9	24.5	2.3	115.3	15.5	2.3	9.5	35.8	2.7	8.7	266.5	19.2	15.5	38.2	7.9
62	BMNDL-2	48.0	1.4	88.0	15.3	21.4	1.9	105.0	18.7	2.7	9.1	34.8	2.8	8.4	282.0	16.4	14.6	38.3	7.1
63	BMNDL-3	44.5	1.4	84.5	18.4	28.7	2.1	119.5	19.3	2.8	8.0	33.0	3.5	9.9	276.5	17.1	15.2	36.2	7.7
64	TNEf-318	54.0	1.9	94.0	14.5	26.9	2.1	122.6	20.7	2.0	10.3	34.0	2.5	8.0	283.0	17.6	16.5	38.8	11.6
Mean		49.0	2.0	89.1	17.8	26.8	2.2	117.6	18.4	2.5	10.4	33.6	3.3	8.9	276.0	19.6	16.7	45.5	8.6
CV		6.0	12.0	6.2	6.2	6.6	6.2	6.1	6.4	7.3	7.4	6.1	8.1	12.0	3.7	6.6	6.8	7.1	8.0
SEm		2.1	0.2	3.9	0.8	1.3	0.1	5.1	0.8	0.1	0.5	1.4	0.2	0.8	7.3	0.9	0.8	2.3	0.5
CD at 5%		5.9	0.5	11.1	2.2	3.5	0.3	14.3	2.3	0.4	1.5	4.1	0.5	2.1	20.7	2.6	2.3	6.5	1.4
CD at 1%		7.8	0.6	14.7	2.9	4.7	0.4	19.1	3.1	0.5	2.1	5.4	0.7	2.8	27.5	3.4	3.0	8.6	1.8
Minimum		41.0	1.0	81.0	12.3	21.4	1.8	90.9	13.5	1.4	8.0	30.2	1.9	6.5	253.0	16.0	12.5	36.2	6.8
Maximum		72.5	3.9	112.5	24.0	32.0	2.7	158.4	26.3	3.7	17.0	38.9	6.0	15.0	296.0	24.1	21.2	56.8	11.9

Table 4.4 Range, Mean, Coefficients of variation, Heritability (broad sense) and Genetic advance as per cent of mean for 18 characters in 64 barnyard millet germplasm accessions.

SI. No.	Characters	Range		Mean	Coefficient of variation (%)		Heritability (broad sense)%	Genetic advance as % of mean
		Minimum	Maximum		PCV	GCV		
1	Days to 50% flowering	41.00	72.50	49.03	15.49	14.27	85	27.11
2	Basal tillers	1.00	3.90	1.99	32.60	30.3	86.4	58.06
3	Days to maturity	81.00	112.50	89.10	9.28	6.89	55.2	10.56
4	Peduncle length (cm)	12.33	23.97	17.81	14.85	13.50	82.6	25.28
5	FLB Length(cm)	21.4	32.02	26.84	10.54	8.22	60.7	13.2
6	FLB Width(cm)	1.75	2.72	2.19	12.05	10.3	73.7	18.29
7	Plant height (cm)	90.91	158.4	117.64	12.61	11.04	76.6	19.9
8	Panicle length (cm)	13.48	26.31	18.40	16.94	15.71	86	30.00
9	1000 seed weight (g)	1.4	3.65	2.50	19.78	18.39	86.4	35.22
10	Panicle weight /plant (g)	8.00	17.00	10.43	17.87	16.27	82.9	30.52
11	Harvest Index (%)	30.23	38.92	33.55	7.97	5.12	41.3	6.78
12	Lower raceme length (cm)	1.86	6.01	3.30	28.56	27.39	92	54.11
13	Grain yield/plant (g)	6.50	14.95	8.88	19.76	15.69	63.1	25.67
14	Phosphorus (mg/100g)	253.00	296.00	275.99	4.43	2.36	28.5	2.60
15	Calcium (mg/100g)	15.95	24.05	19.58	13.33	11.60	75.7	20.79
16	Iron (mg/100g)	12.50	21.20	16.72	13.04	11.12	72.8	19.55
17	Zinc (mg/100g)	36.20	56.80	45.53	15.32	13.57	78.5	24.77
18	Protein (%)	6.82	11.93	8.61	16.19	14.07	75.5	25.19

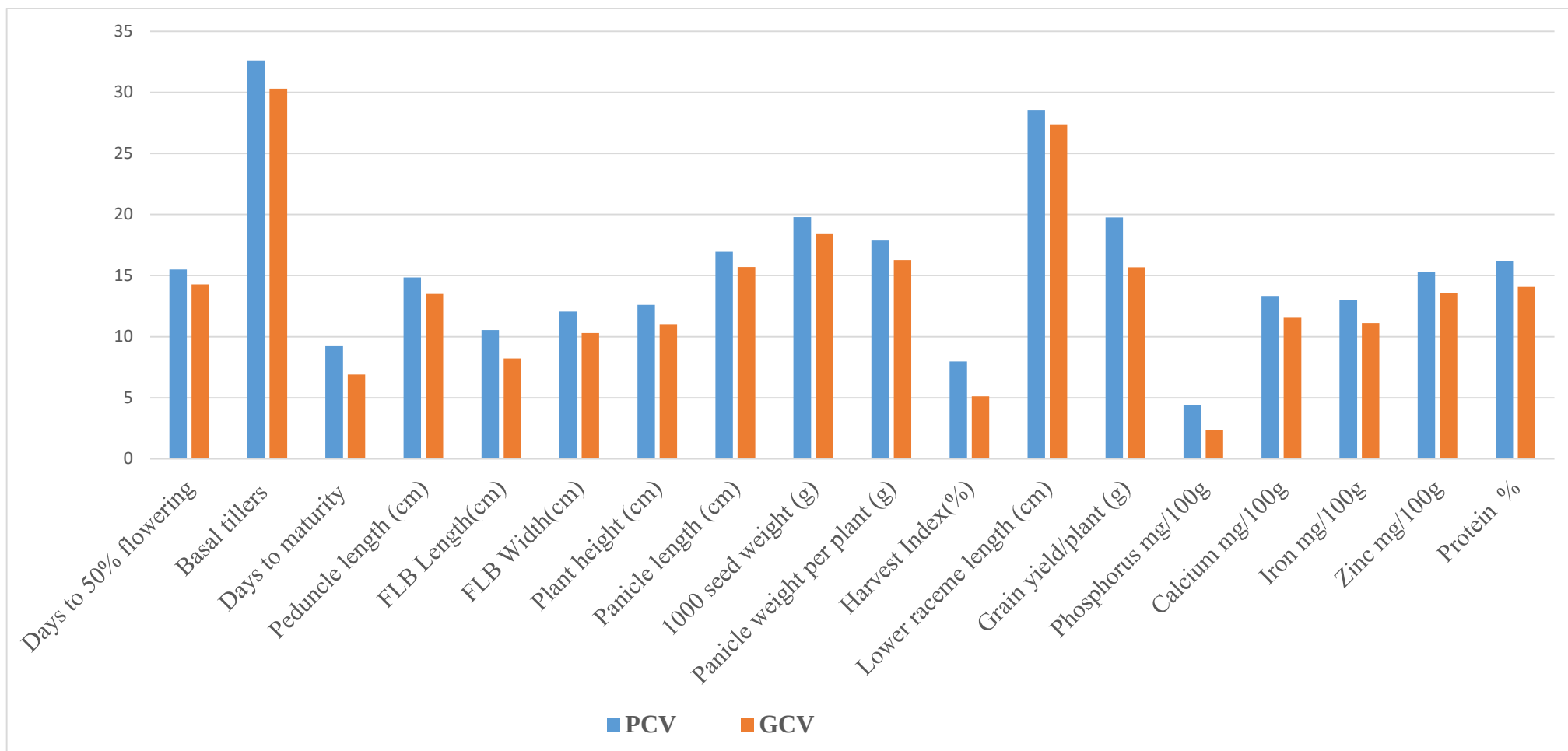


Fig. 4.3 Phenotypic and Genotypic coefficients of variation for the 18 characters

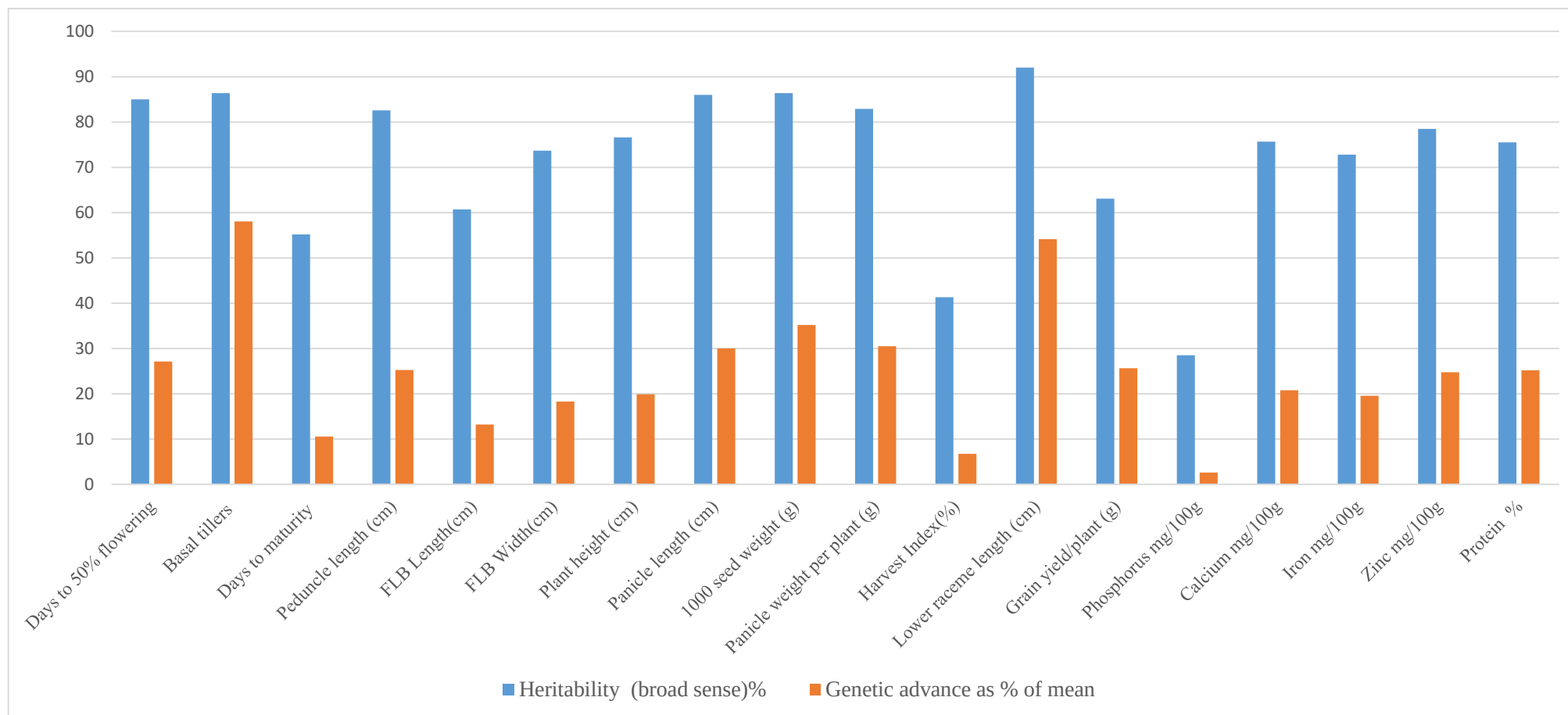


Fig 4.4 Pattern of Heritability and Genetic advance as per cent mean for various traits in barnyard millet germplasm accessions

4.4 STUDY OF GENETIC PARAMETERS

Estimation of genetic parameters like range, variability, co-efficient of variation, heritability and genetic advance in the context of trait characterization is an essential component in developing high yielding genotypes. The extent of variation for a character in a germplasm accession is studied along with the magnitude of heritable portion of variation. The co-efficient of variation is an efficient statistical measure for estimation of range of variability present in various characters of the population. However, the extent of heritable variation cannot be assessed with genetic co-efficient of variation alone. The heritable estimates along with genotypic co-efficient of variation (GCV) provide a deeper understanding of the amount of genetic advance to be expected by phenotypic selection (Burton and Devane 1953). The genetic gain in conjunction with heritability estimates should form a criterion for phenotypic selection (Johnson *et al.* 1955). Information on genetic parameters assists the plant breeder in formulating suitable selection indices for crop improvement. In the present investigation, results of genetic parameters studied were presented in Table 4.4; Fig 4.3 & 4.4.

4.4.1 Range

Range ascertains variation limits of germplasm accessions for the character utilized in breeding programmes. In the present study, the extent of variability for 18 quantitative traits like days to 50% flowering (41.0-72.5 days), basal tillers (1.00-3.90), days to maturity (81.0-112.5 days), peduncle length (12.33-23.97 cm), flag leaf blade length (21.4-32.02 cm), flag leaf blade width (1.75-2.72 cm), plant height (90.91-158.4 cm), panicle length (13.48-26.31 cm), 1000 seed weight (1.4-3.65 g), panicle weight / plant (8.0-17.0 g), harvest index (30.23-38.92 %), lower raceme length (1.86-6.01 cm), grain yield / plant (6.50-14.95 g), phosphorus (253.0-296.0 mg /100g), calcium (15.95-24.05 mg /100g), iron (12.50-21.20 mg/100g), zinc (36.20-56.80 mg/100g), protein (6.82-11.93 g / 100g).

4.4.2 Variability

Phenotypic coefficient of variation (PCV) is the resultant of combined action of genotype and environment over a genotype. Genotypic coefficient of variation (GCV), a component of total variation reflects the heritable portion. In the present study, the GCV values ranged from (2.36-30.3) where as PCV values showed limits from (4.43-32.60). As the PCV estimates were slightly higher than corresponding GCV estimates for the characters studied, it indicates that the characters were less influenced by the environment. Therefore, phenotypic selection would be effective for the improvement of the characters.

4.4.2.1 High GCV and PCV

The traits, number of basal tillers / plant (30.3 and 32.60) and lower raceme length (27.39-28.56) recorded higher GCV and PCV values respectively indicating that these characters contributed to the total variability. Similar results were obtained by findings of Prasanna *et al.* (2013a), Mahanthesha *et al.* (2017a), Shingane *et al.* (2017), Wolie *et al.* (2013) and Sharma *et al.* (2018) for number of basal tillers per plant.

4.4.2.2 Moderate GCV and PCV

Moderate GCV and PCV values were observed for the traits days to 50% flowering (14.27 and 15.49), peduncle length (13.50 and 14.85), flag leaf blade width (10.3 and 12.05), plant height (11.04 and 12.61), panicle length (15.71 and 16.94), 1000 seed weight (18.93 and 19.78), panicle weight/plant (16.27 and 17.87), grain yield/plant (15.69 and 19.76), calcium (11.60 and 13.33), iron (11.12 and 13.04), zinc (13.57 and 15.32) and protein (14.07 and 16.19). Similar results were obtained by Ganapathy *et al.* (2011) for grain yield per plant and plant height. Brunda *et al.* (2014) for panicle length, panicle weight and test weight.

4.4.2.3 Low GCV and PCV

GCV and PCV values were low for the traits viz., days to maturity (6.89 and 9.28), harvest index (5.12 and 7.97), and phosphorus (2.36 and 4.43) indicating that the variability for these characters among the germplasm accessions was meager. Similar findings were reported by Reddy *et al.* (2013), Prabhu *et al.* (2008) and Ganapathy *et al.* (2011) for days to maturity.

4.4.2.4 Low GCV and moderate PCV

Low GCV and moderate PCV values were observed for the trait flag leaf length (8.22 and 10.54). Similar results were obtained by Prabu *et al.* (2008).

4.4.3 Heritability (h^2)

Heritability is a good measure of the transmission of characters from parents to their offsprings (Falconer, 1996). It is the ratio of genotypic variance to the phenotypic variance or total variance and is generally expressed in *per cent*. Genotypic coefficient of variation along with heritability should be considered in plant breeding programs as they would provide a better picture of the amount of genetic advance to be expected by the phenotypic selection (Burton and Devane, 1952).

Heritability values ranged from low to high for phosphorus (28.5 %) and basal tillers, 1000 seed weight (86.4 %) respectively. It was observed that the characters viz., days to 50% flowering (85 %), days to maturity (55.2 %), peduncle length (82.6 %), flag leaf blade length (60.7 %), flag leaf blade width (73.7 %), plant height (76.6 %), panicle length (86 %), 1000 grain weight (86.4%), panicle weight / plant (82.9 %), lower raceme length (92 %), grain yield / plant (63.1 %), calcium (75.7 %), iron (72.8 %), zinc (78.5 %), and protein (75.5 %) exhibited high heritability values indicating that these characters are least influenced by environmental effects and selection may be rewarding. Contrarily the traits, harvest index (41.3 %) showed moderate values of heritability indicating that these characters are relatively more influenced by environmental effects and genetic improvement for them through selection is rather difficult.

4.4.5 Genetic advance as *per cent* of mean

High values of genetic advance as *per cent* of mean was recorded for days to 50% flowering, basal tillers, peduncle length, panicle length, 1000 seed weight, lower raceme length, grain yield per plant, calcium, zinc and protein implying that these characters are governed by additive genes and selection for them will be rewarding. On the other hand, moderate values of genetic advance as *per cent* of mean were noted for days to maturity, flag leaf blade length, flag leaf blade width, plant height, iron and low values of genetic advance as *per cent* of mean were noted for harvest index, phosphorus indicating that these traits are under the control of non - additive gene action and selection may be ineffective.

High heritability value alone provides no indication of the amount of genetic progress that would result from selection of the better individuals. Heritability values coupled with genetic advance are more reliable and useful genetic parameters in predicting the genetic gain under selection than heritability estimates alone (Kundu *et al.* 2008). High heritability and high genetic advance as *per cent* of mean was reported for the traits basal tillers, days to 50% flowering, peduncle length, panicle length, 1000 seed weight, lower raceme length, grain yield / plant, zinc and protein indicating the role of additive gene action in governing these traits and direct selection would be rewarding for crop improvement. Similar works were reported by Anuradha *et al.* (2021), Ganapathy *et al.* (2011), Karad *et al.* (2013) and Brunda *et al.* (2014) for days to 50% flowering. John (2006) and Wolie *et al.* (2013) for 1000 seed weight. Prabhu *et al.* (2008), Nirmalakumari *et al.* (2010a) and Brunda *et al.* (2014), for panicle length, number of tillers per plant and grain yield per plant.

High heritability coupled with moderate genetic advance as *per cent* of mean was observed for the traits *viz.*, days to maturity, flag leaf blade length, flag leaf blade width, plant height and iron indicating the presence of both additive and non-additive genetic effects and genetic improvement for these characters can be exploited through heterosis breeding.

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 like days to 50% flowering, basal tillers, peduncle length, panicle length, 1000 seed weight, panicle weight per plant, lower raceme length, grain yield per plant, calcium, zinc and protein 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.*, days to maturity, flag leaf blade length, flag leaf blade width, plant height, and iron indicated the existence of both additive and non-additive genetic

effects and therefore, suggested to adopt heterosis breeding for improvement of those characters.

- Low heritability and low genetic advance as *per cent* of mean recorded for the trait phosphorus content.
- Moderate heritability and low genetic advance as *per cent* of mean recorded for the trait harvest index.
- The traits number of basal tillers / plant and lower raceme length 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.

4.5 Genetic divergence

The quantitative assessment of genetic divergence was analysed with Mahalanobis D^2 statistic for yield and its contributing characters. Genetic divergence was computed for 64 barnyard millet germplasm accessions in order to identify diverse genotypes for utilization in hybridization programmes as ‘potential parents’. The results obtained from the study are furnished below.

4.5.1 Mahalanobis generalized distance D^2 values

The correlated unstandardized means of 18 quantitative characters studied were transformed to standardized uncorrelated set of variables by using pivotal condensation method. The statistical distance (Mahalanobis D^2 values) between a pair of germplasm accessions was obtained as sum of squares of differences between pairs of corresponding uncorrelated values of any two germplasm accessions. These values were considered at a time and were used for final grouping of genotypes.

4.5.2 Grouping of germplasm accessions into various clusters

Sixty four germplasm accessions using Tocher’s method (Rao, 1952) were grouped into eight distinct non overlapping clusters (Table 4.5, Fig 4.5) suggesting presence of substantial genetic diversity in the experimental material screened. Of all eight clusters, Cluster I was the largest comprising of large number of accessions (57) and the remaining were mono genotypic clusters II, III, IV, V, VI, VII and VIII containing only single accession each indicating high degree of heterogeneity among the genotypes.

4.5.3 Average inter and intra cluster distances

The average intra-cluster and inter-cluster D^2 values of eight clusters in the Table 4.6 and Fig 4.6. The inter-cluster distances were higher than the intra-cluster distances indicating the presence of wider genetic diversity between the clusters rather than within the clusters. Least intra cluster distance (0) observed in clusters II, III, IV, V, VI, VII and VIII indicated either the close resemblance between the germplasm accessions present in that cluster or presence of single genotype in that cluster. Therefore, germplasm accessions occupying the same cluster have low levels of diversity and selection of parents with in the cluster may not be considered promising (Kumar *et al.* (2010). Inter-cluster distance values varied from 62.03 (cluster IV and cluster VI) to 401.29 (cluster VI and cluster VII). Hence the germplasm accessions between cluster IV (TNEf-216, TNEf-202, TNEf-215) and cluster VII TNEf-218 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. Similar results were reported by Brunda *et al.* (2015), Devaliya *et al.* (2017), Mahanthesha *et al.* (2017b) and Amarnath *et al.* (2019).

4.5.4 Cluster means for various characters

The cluster means for 18 characters per cluster 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 I, reported maximum for protein content (8.75). Cluster II has maximum values for panicle length (25.72), lower raceme length (6), phosphorus content (284 mg) and iron content (18.3). Cluster III has maximum panicle length (29.17). Cluster V recorded highest mean for grain yield per plant (12.9) and zinc content (56.55). Cluster VI recorded highest mean for days to 50% flowering (72.5), flag leaf blade width (2.53), plant height (122.17) and harvest index (34.89). Cluster VII reported maximum for peduncle length (23.97), 1000 seed weight (3.65), panicle weight (14.9), calcium content (22.7) and desired means for days to 50% flowering (41), and plant height (90.91) and days to maturity (81.0). Cluster VIII has highest mean for basal tillers (3.9). The lower values for days to 50% flowering (41), days to maturity (81) i.e earliness were reported in Cluster VII.

The result indicates that selection of germplasm accessions 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 Murugan & Nirmalakumari (2006) and Kavya (2016).

4.5.5 Relative contribution of each character towards diversity:

The number of times that each of the 18 characters appeared in first and its respective *per cent* contribution towards total divergence (Table.4.8 and Figure 4.7). Among all the characters studied, grain yield / plant contributed maximum (16.6%) towards genetic divergence by ranking first 335.1 times followed by panicle weight (15.7% by first ranking 317.0 times), harvest index (13.5% by ranking 272 times), basal tillers (7.4% by ranking 149.0 times), lower raceme length (7.3% by ranking 147.0 times) protein (7.2 ranking by 144.8 times), 1000 seed weight (6.3% by ranking 127.0 times), zinc (6.1% by ranking 122.0 times), peduncle length (4.8% by ranking 97.0 times), flag leaf blade width (4.2% by ranking 84.1 times), calcium (3.7% by ranking 74.6 times), days to maturity, iron (2.3% by ranking 46.4 times), plant height (1.8% by ranking 36.1 times), days to 50% flowering (0.4% by ranking 7.1 times), flag leaf blade length (0.2% by ranking 4.0 times), phosphorus (0.2% by ranking 3.8 times) and panicle length(0.2% by ranking 3.0 times)

The traits viz., days to 50% flowering (0.4%), flag leaf blade length (0.2%), panicle length (0.2%), and phosphorus (0.2%) ranked first 7.1, 4.0, 3.8 and 3.0 times respectively, contributed fewer towards total divergence inferring more homogeneity for the traits in the genetic material evaluated.

Similar results were published by Kumari and Singh (2015), Prabu *et al.* (2020), Manimekalai *et al.* (2018) and Mahanthesha *et al.* (2017b) for grain yield per plant, Dhanalakshmi *et al.* (2019) for lower raceme length.

4.5.7 Canonical root analysis:

The canonical root analysis or principal component analysis (PCA) was used to verify the clustering pattern obtained by Mahalanobis D^2 statistic. For 64 barnyard millet germplasm accessions, canonical root analysis was carried out as per the procedure outlined by Rao (1952). Seven canonical roots accounted for 75.9 per cent of total divergence (Table 4.10). The first, second, third and fourth roots accounted for 20.58, 15.20, 10.46, and 9.7 per cent respectively to total variability. The remaining canonical roots viz., fifth, sixth and seventh contributed 8.16, 6.49 and 5.2 per cent respectively towards the total variability. The mean values of canonical variates for three roots X, Y and Z were furnished in Table 4.11. Two dimensional (2D) and Three dimensional (3D) picture was constructed by plotting the mean values of vectors as in Fig 4.8 and Fig 4.9. The amount of contribution of different traits towards canonical vectors total divergence was presented in Table 4.9.

In the vector Z_1 , traits contributing towards total divergence positively were Days to 50% flowering (0.405), flag leaf blade length (0.111), flag leaf blade width (0.234), plant height (0.311), panicle length (0.219), harvest index (0.393) and protein (0.189) while the rest of the characters contributed negatively to the total diversity.

For the vector Z_2 , days to 50% flowering (0.143), basal tillers (0.206), peduncle length (0.276), flag leaf blade width (0.01766), plant height (0.0339), panicle length (0.227), panicle weight per plant (0.225), lower raceme length (0.466), phosphorus (0.185) and iron (0.229) contributed positively to the genetic diversity. While the traits viz., days to maturity, flag leaf blade length, 1000 grain weight, harvest index, grain yield / plant calcium, zinc and protein had contributed negatively to the diversity.

In the vector Z_3 , the traits viz., days to 50% flowering (0.345), peduncle length (0.139), flag leaf blade width (0.049), panicle weight per plant (0.187), harvest index (0.086), grain yield per plant (0.039), phosphorus (0.437) and zinc (0.172) had contributed positively to diversity. While rest of the characters showed negative contribution towards divergence.

In the vector Z_4 , the traits viz., days to 50% flowering (0.026), days to maturity (0.006), flag leaf blade width (0.487), panicle length (0.236), 1000 seed weight (0.391), lower raceme length (0.016), grain yield per plant (0.533), iron (0.008), zinc (0.053) and

protein (0.075) had contributed positively to diversity. While rest of the characters showed negative contribution towards divergence.

For the vector Z_5 , the traits contributed towards total divergence were days to 50% flowering (0.014), peduncle length (0.633), flag leaf blade length (0.301), 1000 seed weight (0.226), harvest index (0.170), lower raceme length (0.104), grain yield per plant (0.174), phosphorus (0.327), calcium (0.157), iron (0.190) and protein (0.269) had contributed positively to diversity. While rest of the characters showed negative contribution towards divergence.

In the vector Z_6 , the trait days to 50% flowering (0.175), basal tillers (0.552), flag leaf blade length (0.430), flag leaf width (0.160), panicle weight per plant (0.051), grain yield per plant (0.394), calcium (0.017), iron (0.217), zinc (0.089) and protein (0.071) contributed positively to diversity. While rest of the characters showed negative contribution towards divergence.

For the vector Z_7 , the traits flag leaf blade length (0.200), plant height (0.300), panicle length (0.300), 1000 seed weight (0.100), panicle weight per plant (0.300), harvest index (0.100), phosphorus (0.100) and zinc (0.500) contributed positively to diversity. While rest of the characters showed negative contribution towards divergence

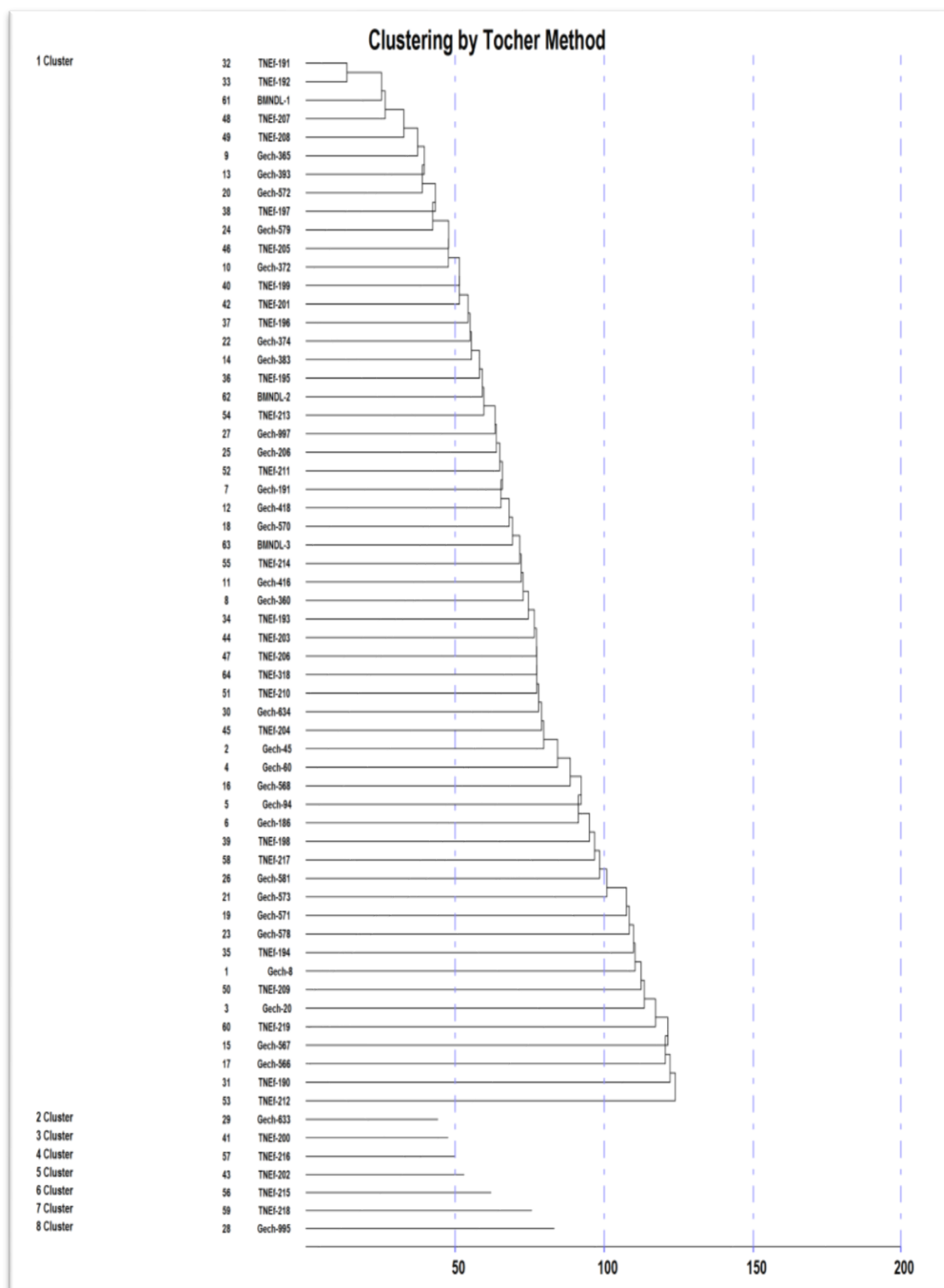
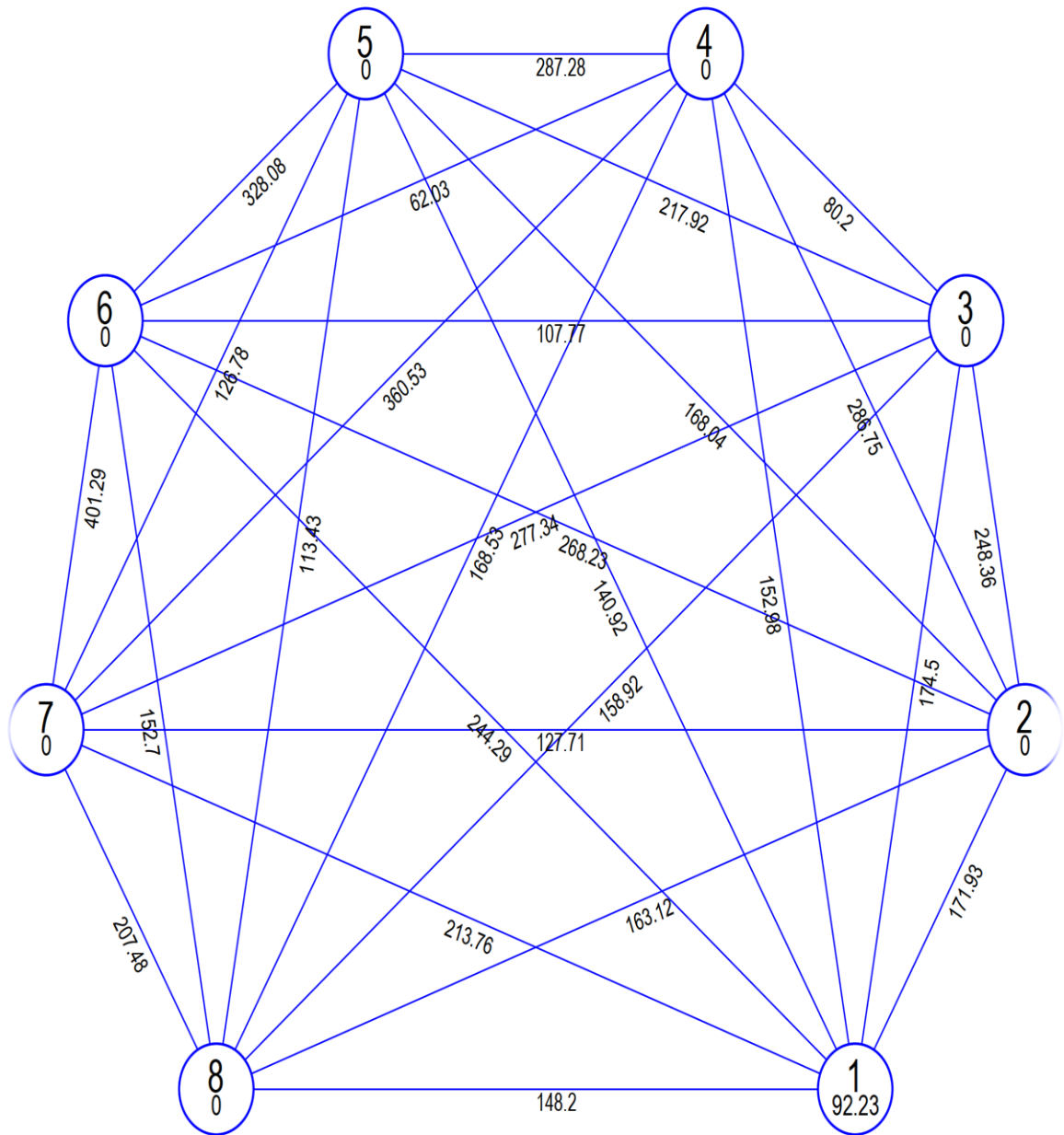


Fig 4.5 Clustering pattern of 64 barnyard millet germplasm accessions by Tochers method

Tocher Method



Mahalanobis Euclidean Distance (Not to the Scale)

Fig 4.6 Cluster diagram showing average intra and inter cluster distance

Table 4.5 Clustering pattern of 64 barnyard millet genotypes by Tocher' method

Cluster No.	No.of genotypes	Genotype(s)
I	57	GEch-8, GEch-45, GEch-20, GEch-60,GEch-94, GEch-186, GEch-191, GEch-360, GEch-365, GEch-372, GEch- 416, GEch-418, GEch-393, GEch-383, GEch-567, GEch-568, GEch-566, GEch- 570, GEch-571, GEch-572, GEch-374, GEch-578, GEch-579, GEch-206, GEch-581, GEch-997, GEch-634, TNEf-190, TNEf-191, TNEf-192, TNEf-193, TNEf-194, TNEf-195, TNEf-196, TNEf-197, TNEf-198, TNEf-199, TNEf-201, TNEf-203, TNEf-204, TNEf-205, TNEf-206, TNEf-207, TNEf-208, TNEf-209, TNEf-210, TNEf-211, TNEf-212, TNEf-213, TNEf-214, TNEf-216, TNEf-217, TNEf-219, BM NDL-1, BM NDL-2, GEch-573,BM NDL-3, TNEf-318.
II	1	GEch-633
III	1	TNEf-200
IV	1	TNEf-216
V	1	TNEf-202
VI	1	TNEf-215
VII	1	TNEf-218
VIII	1	GEch-995

Table 4.6 Average intra and inter cluster distance for the barnyard millet accessions studied

Cluster Distances								
Clusters	I	II	III	IV	V	VI	VII	VIII
I	92.23	171.93	174.5	152.98	140.92	244.29	213.76	148.2
II		0	248.36	286.75	168.04	268.23	127.71	163.12
III			0	80.2	217.92	107.77	277.34	158.92
IV				0	287.28	62.03	360.53	168.53
V					0	328.08	126.78	113.43
VI						0	401.29	152.7
VII							0	207.48
VIII								0

Table 4.7 Cluster means with respect to yield and yield attributes among 64 barnyard millet germplasm accessions.

Cluster Means: Torcher's method																		
Clusters	Days to 50% flowering	Basal tillers	Days to maturity	peduncle length (cm)	FLB Length(cm)	FLB Width(cm)	Plant height (cm)	Panicle length (cm)	1000 seed weight (g)	panicle weight /plant (g)	Harvest Index(%)	lower raceme length (cm)	Grain yield/plant (g)	Phosphorus (mg/100g)	Calcium (mg/100g)	Iron (mg/100g)	Zinc (mg/100g)	Protein (%)
I	48.17	1.94	88.24	17.56	26.92	2.2	118.25	18.46	2.48	10.1	33.66	3.23	8.69	276.13	19.69	16.72	45.12	8.75
II	42.5	2.7	82.5	20.23	24.35	2	118.45	25.72	2.95	11.2	31.43	6.02	9	284	18.05	18.3	54.1	8.53
III	69	1.4	109	23.25	29.17	2.38	121.66	18.3	2.7	14.4	34.25	2.7	12.15	279.5	16.1	16.7	55.55	7.53
IV	68.99	2	108.98	18.9	26.49	2.48	116.05	16.37	2.75	8.1	32.22	2.27	7.25	266	17.9	17.35	38.23	7.5
V	43.5	2.3	84	14.74	24.65	1.88	98.33	14.02	2.45	14.7	34.64	3.4	12.9	266	17.05	16.35	56.55	7.53
VI	72.5	2.5	112.5	18.95	27	2.53	122.17	17.29	2.3	10.9	34.89	3.82	8.75	267	18.35	16.95	41.95	6.83
VII	41	2.3	81	23.97	21.95	2.21	90.91	15.05	3.65	14.9	30.23	5	12.85	280	22.7	15.1	43.6	7
VIII	55.5	3.9	95.5	19.5	30	1.79	121.5	18.38	2.2	12.6	31.55	4.25	10.4	281.5	21.55	16.5	52.25	7.68

Table 4.8 Contribution of yield and its attributes towards total diversity in 64 barnyard millet germplasm accessions.

S.no	Characters	Contribution %	Times ranked 1st
1	Days to 50% flowering	0.4	7.1
2	Basal tillers	7.4	149.0
3	Days to maturity	2.3	46.4
4	Peduncle length (cm)	4.8	97.0
5	Flag Leaf Blade Length (cm)	0.2	4.0
6	Flag Leaf Blade Width (cm)	4.2	84.1
7	Plant height (cm)	1.8	36.1
8	Panicle length (cm)	0.2	3.0
9	Test weight (g)	6.3	127.0
10	Panicle weight /plant (g)	15.7	317.0
11	Harvest Index (%)	13.5	272.0
12	lower raceme length (cm)	7.3	147.0
13	Grain yield per plant (g)	16.6	335.1
14	Phosphorus (mg/100g)	0.2	3.8
15	Calcium (mg/100g)	3.7	74.6
16	Iron (mg/100g)	2.3	46.4
17	Zinc (mg/100g)	6.1	122.0
18	Protein (%)	7.2	144.8

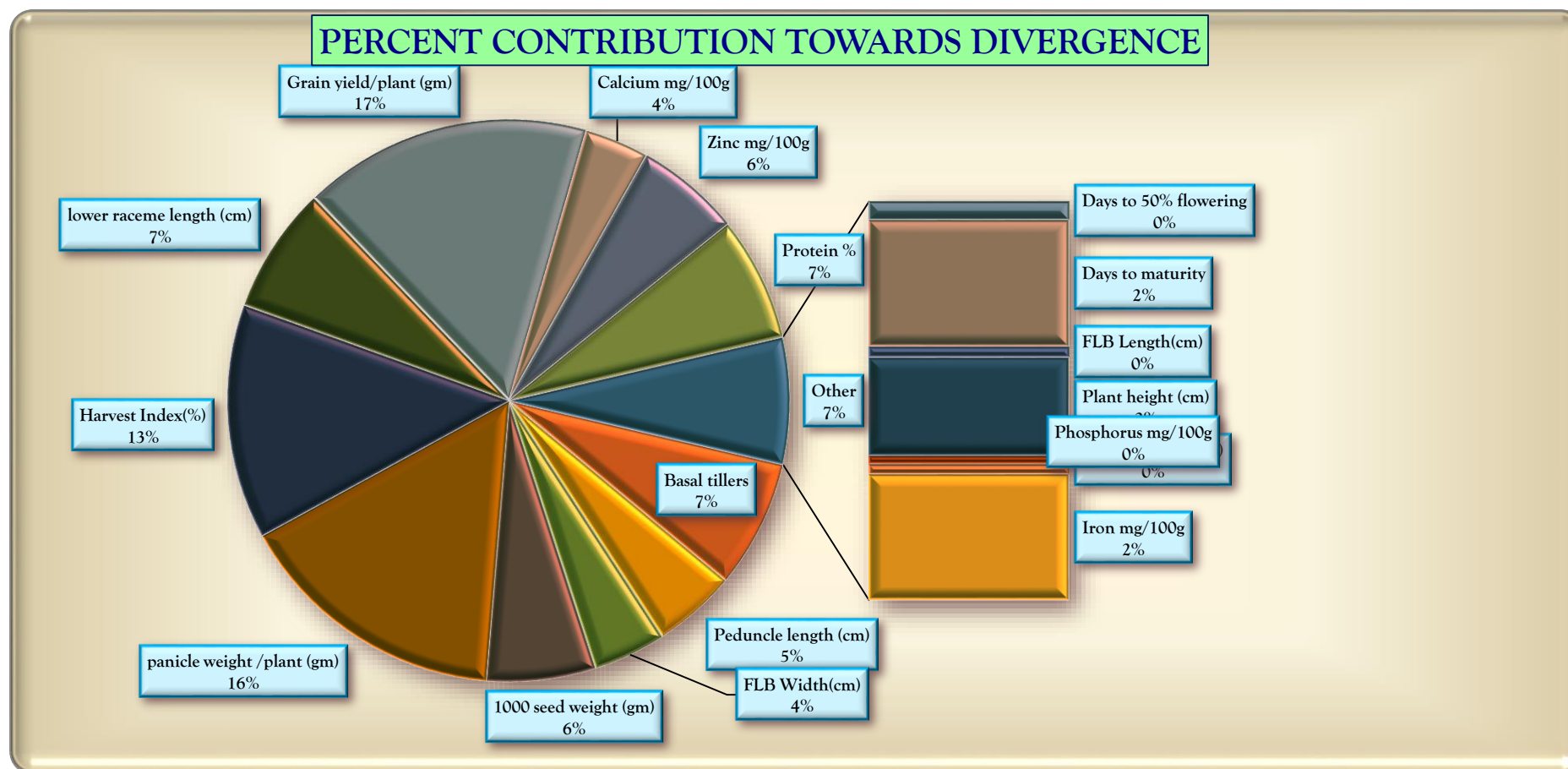


Fig 4.7 Relative contribution of 18 characters to total genetic diversity in 64 barnyard millet germplasm accessions

Table 4.9 Canonical vectors for 18 characters in 64 barnyard millet germplasm accessions

Parameters	Z₁	Z₂	Z₃	Z₄	Z₅	Z₆	Z₇
Eigene Value (Root)	3.70473	2.73658	1.8845	1.75198	1.47025	1.16972	0.9
% Var. Exp.	20.58185	15.20319	10.46943	9.73324	8.16807	6.49842	5.2
Cum. Var. Exp.	20.58185	35.78505	46.25448	55.98772	64.15578	70.65421	75.9
Characters							
Days to 50% flowering	0.40553	0.14318	0.34532	0.02626	0.01383	0.17468	0
Basal tillers	-0.18463	0.20613	-0.0076	-0.31914	-0.0538	0.55239	0
Days to maturity	-0.39136	-0.17318	-0.33946	0.00617	-0.00573	-0.23601	0
Peduncle length (cm)	-0.013	0.27683	0.13999	-0.08948	0.63295	-0.09399	0
Flag Leaf Blade Length (cm)	0.11125	-0.14059	-0.2546	-0.17546	0.30118	0.42982	0.2
Flag Leaf Blade Width (cm)	0.23477	0.01766	0.04979	0.4873	-0.21787	0.15969	0
Plant height (cm)	0.31174	0.03393	-0.26736	-0.19041	-0.10658	-0.18571	0.3
Panicle length (cm)	0.21917	0.22722	-0.32112	0.23562	-0.02406	-0.13507	0.3
Test weight (g)	-0.28102	-0.02969	-0.1274	0.39129	0.22562	-0.16856	0.1
Panicle weight /plant (g)	-0.21117	0.22571	0.18775	-0.06614	-0.28809	0.05128	0.3
Harvest Index (%)	0.39348	-0.11278	0.08662	-0.00875	0.17041	-0.2252	0.1
lower raceme length (cm)	-0.08338	0.46686	-0.24556	0.01618	0.10394	-0.06371	-0.1
Grain yield per plant (g)	-0.1167	-0.09104	0.03925	0.55332	0.174	0.39394	0
Phosphorus (mg/100g)	-0.1728	0.18516	0.43724	-0.00856	0.32679	-0.18849	0.1
Calcium (mg /100g)	-0.03164	-0.46873	-0.0194	-0.23863	0.1569	0.01741	0.1
Iron (mg/100g)	0.04763	0.22991	-0.39911	0.00839	0.18985	0.21672	0
Zinc (mg/100g)	-0.25998	-0.19603	0.17271	0.05257	-0.04862	0.08949	0.5
Protein (%)	0.18902	-0.3485	-0.0497	0.07461	0.2689	0.07093	-0.1

Table 4.10 Canonical root values, per cent of variation and cumulative variation explained for 64 barnyard millet germplasm accessions

Parameters	Z₁	Z₂	Z₃	Z₄	Z₅	Z₆	Z₇
Eigene Value (Root)	3.70473	2.73658	1.8845	1.75198	1.47025	1.16972	0.9
% Var. Exp.	20.58185	15.20319	10.46943	9.73324	8.16807	6.49842	5.2
Cum. Var. Exp.	20.58185	35.78505	46.25448	55.98772	64.15578	70.65421	75.9

Table 4. 11 Mean values of canonical vectors for 64 barnyard millet germplasm accessions.

S. No	Genotype	X Vector	Y Vector	Z Vector
1	Gech-8	3.498	8.382	4.284
2	Gech-45	7.768	4.824	4.366
3	Gech-20	12.916	7.279	3.867
4	Gech-60	6.474	1.984	4.394
5	Gech-94	6.922	7.644	3.136
6	Gech-186	8.306	8.543	4.484
7	Gech-191	9.652	3.384	4.645
8	Gech-360	7.757	5.525	5.016
9	Gech-365	6.646	3.655	6.252
10	Gech-372	3.734	1.387	7.34
11	Gech-416	8.502	2.087	4.779
12	Gech-418	9.684	0.717	3.385
13	Gech-393	9.59	2.765	6.393
14	Gech-383	9.496	4.531	7.518
15	Gech-567	8.537	11.057	3.342
16	Gech-568	9.488	7.851	4.452
17	Gech-566	6.139	8.131	4.711
18	Gech-570	7.292	6.243	5.328
19	Gech-571	4.657	8.791	3.633
20	Gech-572	7.128	2.323	7.98
21	Gech-573	6.775	7.246	5.782
22	Gech-374	7.748	0.971	8.766
23	Gech-578	5.283	5.674	5.295
24	Gech-579	5.856	2.438	7.223
25	Gech-206	10.81	3.714	7.87
26	Gech-581	4.136	5.899	7.341
27	Gech-997	8.876	3.722	9.682
28	Gech-995	6.865	9.463	10.14
29	Gech-633	4.368	13.015	2.946
30	Gech-634	9.227	3.522	6.348
31	TNEf-190	13	7.703	4.216
32	TNEf-191	7.955	0.761	9.631
33	TNEf-192	8.372	0.477	8.543
34	TNEf-193	11.612	5.864	8.537
35	TNEf-194	10.029	8.875	3.463
36	TNEf-195	10.58	1.12	8.753
37	TNEf-196	7.056	4.011	9.506
38	TNEf-197	4.506	0.824	8.462

S.No	Genotype	X Vector	Y Vector	Z Vector
39	TNEf-198	7.218	2.899	7.302
40	TNEf-199	12.955	9.244	13.684
41	TNEf-200	5.465	3.245	7.604
42	TNEf-201	1.957	5.771	9.192
43	TNEf-202	9.821	1.178	6.593
44	TNEf-203	8.739	-1.358	6.474
45	TNEf-204	6.269	-0.664	8.218
46	TNEf-205	13.451	3.924	8.746
47	TNEf-206	5.075	2.972	7.818
48	TNEf-207	8.236	1.036	5.426
49	TNEf-208	12.432	8.324	10.1
50	TNEf-209	13.878	4.078	6.856
51	TNEf-210	6.454	3.584	6.496
52	TNEf-211	14.943	7.961	7.961
53	TNEf-212	10.781	3.091	9.663
54	TNEf-213	11.931	3.239	9.512
55	TNEf-214	16.194	12.923	11.406
56	TNEf-215	15.74	6.724	10.987
57	TNEf-216	4.806	4.074	6.465
58	TNEf-217	-1.178	9.54	9.022
59	TNEf-218	8.693	5.406	8.2
60	TNEf-219	7.336	2.049	5.76
61	BMNDL-1	7.827	4.863	7.876
62	BMNDL-2	7.838	3.764	5.07
63	BMNDL-3	12.781	3.813	7.165
64	TNEf-318	3.498	8.382	4.284

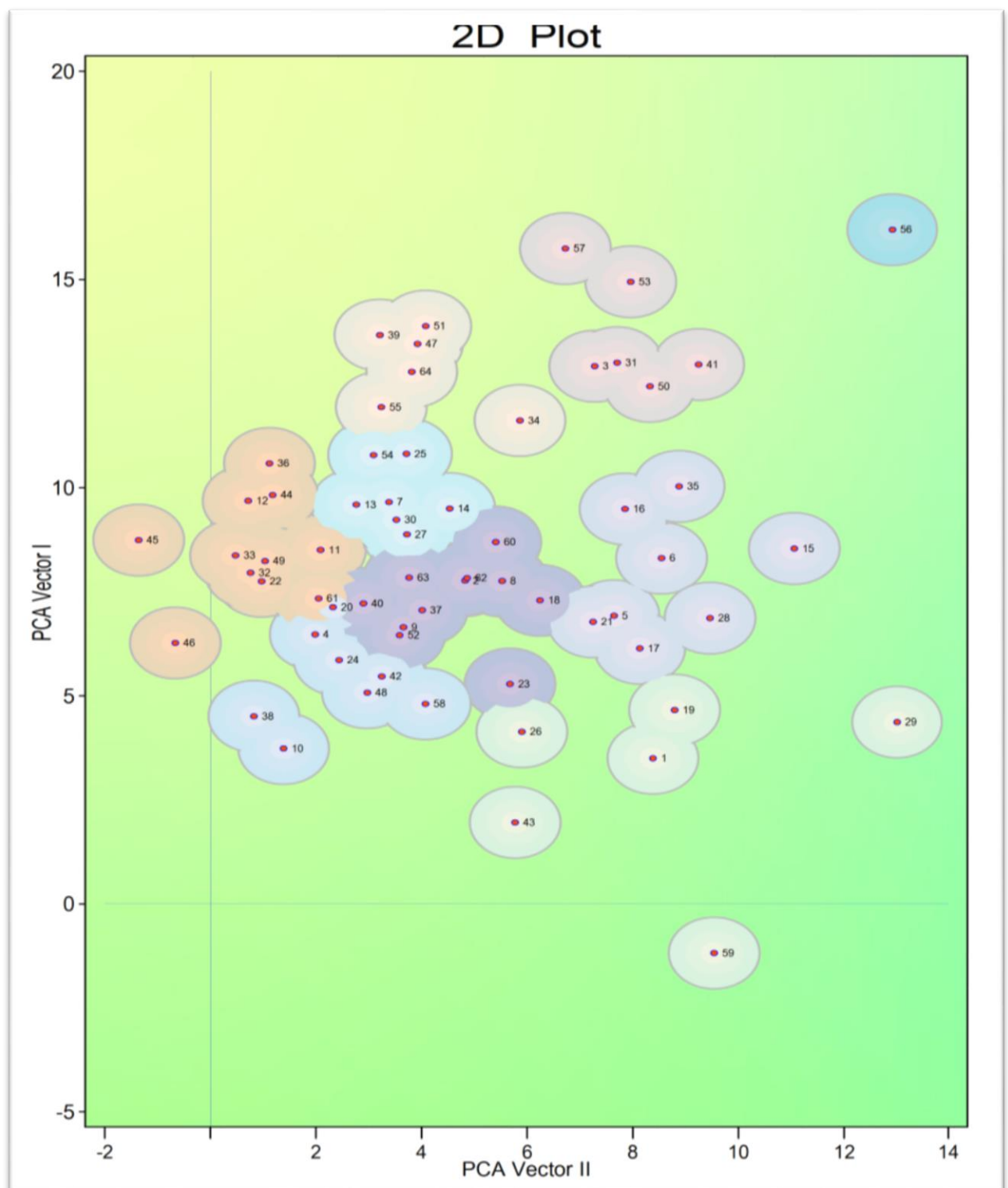


Fig.4.8 Two dimensional (2D) graph showing relative positions of 64 barnyard millet germplasm based on PCA scores

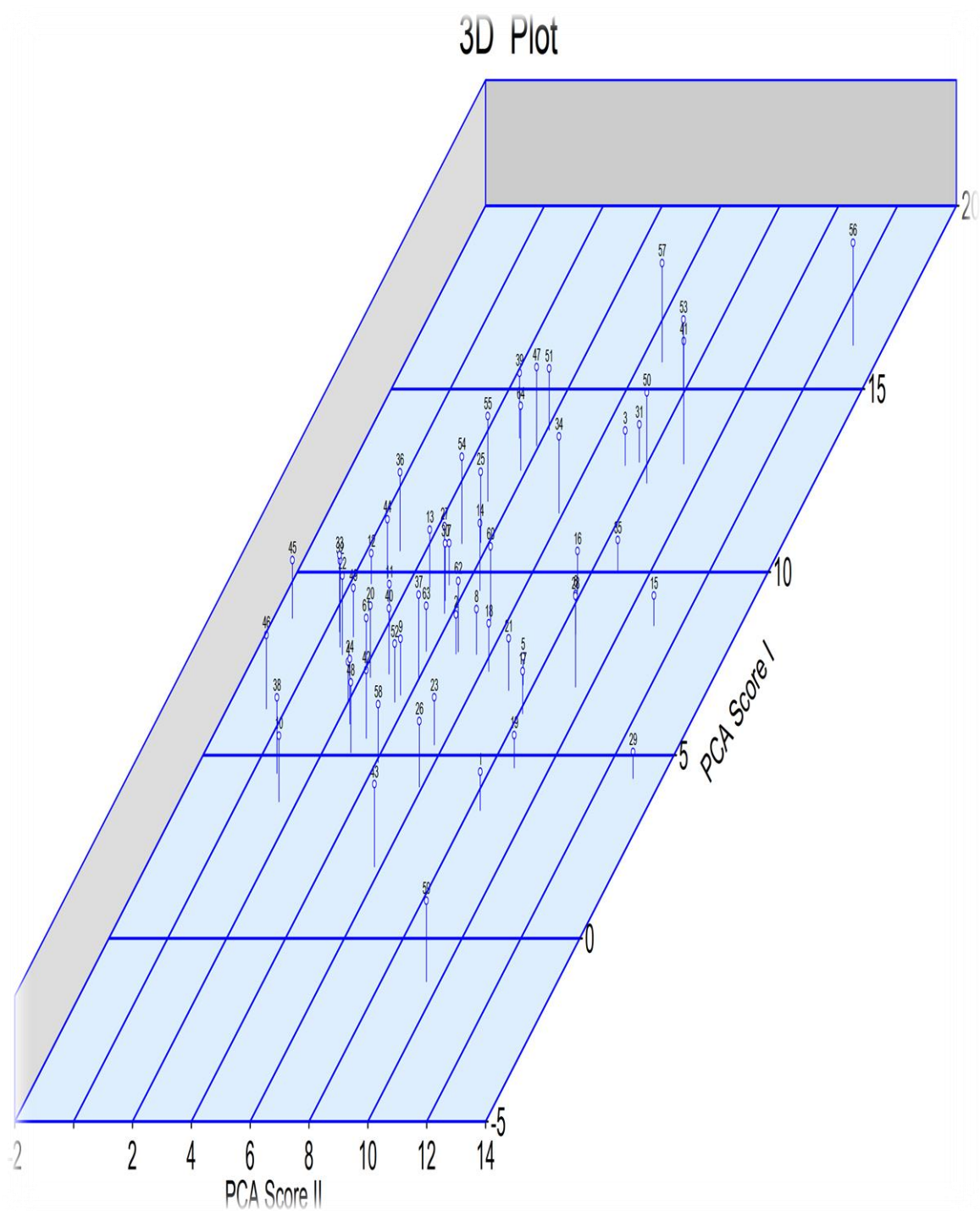


Fig 4.9 Three dimensional (3D) graph showing relative positions of 64 barnyard millet germplasm based on PCA score

4.6 CHARACTER ASSOCIATION

Grain yield is a complex polygenic inherited trait resulting from the interaction of various yield components and hence direct selection of this character may not be useful for the genetic improvement. The efficiency of selection mainly depends on the direction and magnitude of association between yield and its component characters and also among themselves. As the grain yield is interrelated to other characters, the change in one character can bring in series change of other characters. Correlation studies are importance in any selection programme as they provide degree and direction of relationship between two or more characters.

The phenotypic and genotypic 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 phenotypic correlation and Shaded Phenotypic correlations presented in fig 4.10 and 4.11 and The pictorial representation of genotype and shaded genotypic matrix were presented in fig 4.12 and 4.13 respectively. The magnitude of genotypic correlation coefficients for most of the characters were recorded slightly higher than the corresponding phenotypic correlation coefficients, that indicates the presence of inherent association among various characters and limited influence of environment.

4.6.1 Days to 50% flowering

This trait showed positively significant correlation with days to maturity ($r_p=0.9976^{**}$ and $r_g=0.9998^{**}$), plant height ($r_p=0.3800^{**}$ and $r_g=0.4038^{**}$), flag leaf blade width ($r_p=0.2193^{*}$ and $r_g=0.2556^{**}$) an flag leaf blade length ($r_p=0.1900^{*}$ and 0.2023^{*}) at both phenotypic and genotypic levels. Similar results were reported by Sood *et al.* (2016), Prabu *et al.* (2020) for flag leaf width and flag leaf blade length, Vikram *et al.* (2020) for plant height and Anuradha *et al.* (2021) for days to maturity.

4.6.2 Basal tillers

At phenotypic and genotypic level the trait basal tillers showed positively significant correlation with peduncle length ($r_p=0.2441^{**}$ and $r_g=0.2711^{**}$), flag leaf blade length ($r_p=0.2192^{*}$ and $r_g=0.2401^{**}$) panicle length ($r_p=0.2464^{**}$ and $r_g=0.23316^{**}$), lower raceme length ($r_p=0.3072^{**}$ and 0.334^{**}), calcium ($r_p=0.327^{**}$ and $r_g=0.3472^{**}$), zinc ($r_p=0.3088^{**}$ and $r_g=0.3290^{**}$) and panicle weight ($r_p=0.1986^{*}$ and 0.2276^{**}). The trait grain yield per plant ($r_p=0.182^{**}$ and $r_g=0.2201^{**}$) shows positive correlation at genotypic

level. Similar results by Sood *et al.* (2016) and Prabu *et al.* (2020) for flag leaf blade length, Jyothi *et al.* (2020) and Gohel *et al.* (2018) for panicle length.

4.6.3 Days to maturity

At phenotypic and genotypic level the trait days to maturity shows positive correlation with plant height ($r_p=0.3681^{**}$ and $r_g=0.3939^{**}$), flag leaf blade width ($r_p=0.2131^*$ and $r_g=0.2508^{**}$), and flag leaf blade length ($r_p=0.1870^*$ and $r_g=0.1975^*$). Similar results recorded by Prabhu *et al.* (2020) and Vikram *et al.* (2020) for plant height, Prabu *et al.* (2020), and Sood *et al.* (2016) flag leaf blade width and flag leaf blade width.

4.6.4 Peduncle length

The trait panicle length ($r_p=0.2512^{**}$ and $r_g=0.2717^{**}$), panicle weight / plant ($r_p=0.2925^{**}$ and $r_g=0.3003^{**}$), lower raceme length ($r_p=0.3583^{**}$ and $r_g=0.4114^{**}$), grain yield per plant ($r_p=0.1944^*$ and $r_g=0.2058^*$) and plant height ($r_p=0.1810^*$ and $r_g=0.1796^*$) shows positively significant association with peduncle length. Similar results reported by Prabu *et al.* (2020) and Vikram *et al.* (2020) for plant height. Jyothi *et al.* (2020) for panicle weight / plant and Jyothi *et al.* (2020) and Gohel *et al.* (2018) for panicle length.

4.6.5 Flag leaf blade length

The trait plant height ($r_p=0.2622^{**}$ and $r_g=0.3123^{**}$), panicle length ($r_p=0.2236^*$ and $r_g=0.2402^{**}$), calcium ($r_p=0.2088^*$ and $r_g=0.2736^{**}$) shows positive association with flag leaf blade length. The trait flag leaf blade width ($r_p=0.2090^*$) and protein ($r_g=0.1736^*$) shows positive correlation at phenotypic and genotypic level respectively. Similar results by reported by Prabu *et al.* (2020) and Vikram *et al.* (2020) for plant height, Jyothi *et al.* (2020) and Gohel *et al.* (2018) for panicle length.

4.6.6 Flag leaf blade width

The trait plant height ($r_p=0.1876^{**}$ and $r_g=0.2120^{**}$) shows positive correlation with both at phenotypic and genotypic levels. The trait thousand seed weight ($r_g=0.2008^*$) shows positive correlation at genotypic level. Similar results were reported by Prabu *et al.* (2020) and Vikram *et al.* (2020) for plant height.

4.6.7 Plant height

The trait panicle weight per plant ($r_p=0.4499^{**}$ and $r_g=0.4892^{**}$) and harvest index ($r_p=0.2000^*$ and $r_g=0.2440^{**}$) shows positive association with plant height. Similar results were reported by Jyothi *et al.* (2020) for panicle weight / plant.

4.6.8 Panicle length / plant

The trait panicle weight ($r_p=0.1835^*$ and $r_g=0.2082^*$), lower raceme length ($r_p=0.1890^*$ and $r_g=0.2143^*$) iron ($r_p=0.2340^{**}$ and $r_g=0.2896^{**}$) shows positive association with panicle weight. Similar results were reported by Vishnuprabha and Vanniarajan (2018) for iron and Prabu *et al.* (2020) for lower raceme length.

4.6.9 1000 seed weight

The trait panicle weight ($r_p=0.1858^*$ and $r_g=0.2066^*$), lower raceme length ($r_p=0.1890^*$ and $r_g=0.2143^*$) and grain yield per plant ($r_p=0.2369^*$ and $r_g=0.2923^{**}$) shows positive correlation at phenotypic and genotypic level. The trait phosphorus ($r_g=0.1838^*$) shows positive correlation at genotypic level. Similar results were reported by Prabhu *et al.* (2020) for lower raceme length, Jyothi *et al.* (2020) for panicle weight / plant.

4.6.10 Panicle weight per plant

The trait lower raceme length ($r_p=0.2129^*$ and $r_g=0.2408^{**}$), and grain yield ($r_p=0.7476^{**}$ and $r_g=0.8398^{**}$) shows positive correlation at phenotypic and genotypic level. Similar results by Prabhu *et al.* (2020) for lower raceme length.

4.6.11 Harvest index

The trait plant height ($r_p=0.183^*$ and $r_g=0.284^{**}$) shows positive correlation with harvest index. Prabhu *et al.* (2020), Vikram *et al.* (2020) reported similarly for plant height.

4.6.12 Lower raceme length

The trait 1000 seed weight ($r_p=0.1890^*$ and $r_g=0.2143^*$), panicle length / plant ($r_p=0.1890^*$ and $r_g=0.2143^*$), basal tiller ($r_p=0.3072^{**}$ and 0.3268^{**}) shows the positive correlation at both genotypic and phenotypic level. Jyothi *et al.* (2020) gave similar report for 1000 seed weight and for panicle length and Gohel *et al.* (2018) for panicle length.

4.6.13 Phosphorus

Phosphorus content registered positive correlation at genotypic level with thousand seed weight ($r_g=0.1838^*$).

4.6.14 calcium

Calcium content registered positive correlation with zinc ($r_p=0.2689^{**}$ and $r_g=0.3183^{**}$) flag leaf length ($r_p=0.2088^*$ and $r_g=0.2736^{**}$) and basal tillers ($r_p=0.327^{**}$ and $r_g=0.3472^{**}$). Similar results reported by Rao *et al.* (2000) for basal tillers.

4.6.15 Iron

Iron content registered positive correlation with panicle length ($r_p=0.2340^{**}$ and $r_g=0.2896^{**}$) at both genotypic and phenotypic level. Similar results reported by Gohel *et al.* (2018) for panicle length.

4.6.16 Zinc

Zinc content registered positive correlation with calcium ($r_p=0.2689^{**}$ and $r_g=0.3183^{**}$) and basal tillers ($r_p=0.3088^{**}$ and $r_g=0.3290^{**}$). Similar results reported by Rao *et al.* (2000) for basal tillers.

4.6.17 Protein

Protein content registered positive correlation with flag leaf length ($r_g=0.1736^{*}$) genotypic level.

4.6.18 Grain yield per plant

Grain yield / plant showed basal tillers ($r_p=0.182^{**}$ and $r_g=0.2201^{**}$), 1000 seed weight ($r_p=0.2369^{*}$ and $r_g=0.2923^{**}$), Panicle weight per plant ($r_p=0.7476^{**}$ and $r_g=0.8398^{**}$), Peduncle length ($r_p=0.1944^{**}$ and $r_g=0.2058^{**}$) at both genotypic and phenotypic levels. Similar results were reported by Rao *et al.* (2000) for basal tillers, Jyothi *et al.* (2020) for 1000 seed weight and panicle weight / plant, Amarnath *et al.* (2018b), Negi *et al.* (2016), Nandini *et al.* (2016) and Joshi *et al.* (2015) for 1000 seed weight and Amarnath *et al.* (2018b) for peduncle length.

The perusal of the results revealed a positively significant association of grain yield / plant with majority of traits viz., basal tillers ($r_p=0.182^{**}$ and $r_g=0.2201^{**}$), 1000 seed weight ($r_p=0.2369^{*}$ and $r_g=0.2923^{**}$), Panicle weight per plant ($r_p=0.7476^{**}$ and $r_g=0.8398^{**}$), Peduncle length ($r_p=0.1944^{**}$ and $r_g=0.2058^{**}$) at both phenotypic and genotypic levels. 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 had shown positively significant contribution of Days to 50% flowering with days to maturity ($r_p=0.9976^{**}$ and $r_g=0.9998^{**}$), plant height ($r_p=0.3800^{**}$ and $r_g=0.4038^{**}$), flag leaf blade width ($r_p=0.2193^{*}$ and $r_g=0.2556^{**}$) and flag leaf blade length ($r_p=0.1900^{*}$ and $r_g=0.2023^{*}$); basal tillers with peduncle length ($r_p=0.2441^{**}$ and $r_g=0.2711^{**}$), flag leaf blade length ($r_p=0.2192^{**}$ and $r_g=0.2401^{**}$)

panicle length ($r_p=0.2464^{**}$ and $r_g=0.23316^{**}$), lower raceme length ($r_p=0.3072^{**}$ and 0.334^{**}), calcium ($r_p=0.327^{**}$ and $r_g=0.3472^{**}$), zinc ($r_p=0.3088^{**}$ and $r_g=0.3290^{**}$), panicle weight ($r_p=0.1986^*$ and 0.2276^{**}) and grain yield per plant ($r_p=0.182^{**}$ and $r_g=0.2201^{**}$); days to maturity with plant height ($r_p=0.3681^{**}$ and $r_p=0.3939^{**}$), flag leaf blade width ($r_p=0.2131^*$ and $r_g=0.2508^{**}$), and flag leaf blade length ($r_p=0.1870^*$ and $r_g=0.1975^*$); peduncle length with panicle length ($r_p=0.2512^{**}$ and $r_g=0.2717^{**}$), panicle weight / plant ($r_p=0.2925^{**}$ and $r_g=0.3003^{**}$), lower raceme length ($r_p=0.3583^{**}$ and $r_g=0.4114^{**}$), grain yield per plant ($r_p=0.1944^*$ and $r_g=0.2058^*$) and plant height ($r_p=0.1810^*$ and $r_g=0.1796^*$); flag leaf blade length with plant height ($r_p=0.2622^{**}$ and $r_g=0.3123^{**}$), panicle length ($r_p=0.2236^*$ and $r_g=0.2402^{**}$), calcium ($r_p=0.2088^*$ and $r_g=0.2736^{**}$); flag leaf blade width with plant height ($r_p=0.1876^{**}$ and $r_g=0.2120^{**}$); plant height with trait panicle weight per plant ($r_p=0.4499^{**}$ and $r_g=0.4892^{**}$) and harvest index ($r_p=0.2000^*$ and $r_g=0.2440^{**}$); panicle length / plant with panicle weight ($r_p=0.1835^*$ and $r_g=0.2082^*$), lower raceme length ($r_p=0.1890^{**}$ and $r_g=0.2143^{**}$) and iron ($r_p=0.2340^{**}$ and $r_g=0.2896^{**}$); 1000 seed weight ($r_p=0.1858^{**}$ and $r_g=0.2066^{**}$) with lower raceme length ($r_p=0.1890^{**}$ and $r_g=0.2143^{**}$) and grain yield per plant ($r_p=0.2369^*$ and $r_g=0.2923^{**}$); panicle weight / plant with lower raceme length ($r_p=0.2129^*$ and $r_g=0.2408^{**}$), and grain yield ($r_p=0.7476^{**}$ and $r_g=0.8398^{**}$); harvest index with plant height ($r_p=0.183^*$ and $r_g=0.284^{**}$); lower raceme length with 1000 seed weight ($r_p=0.1890^{**}$ and $r_g=0.2143^{**}$), panicle length / plant ($r_p=0.1890^*$ and $r_g=0.2143^*$), ($r_p=0.3072^{**}$ and 0.334^{**}); phosphorus with thousand seed weight ($r_g=0.1838^*$) at genotypic level; calcium with zinc ($r_p=0.2689^{**}$ and $r_g=0.3183^{**}$); iron with panicle length ($r_p=0.2340^{**}$ and $r_g=0.2896^{**}$); zinc with calcium ($r_p=0.2689^{**}$ and $r_g=0.3183^{**}$); protein with flag leaf length ($r_g=0.1736^*$) at genotypic level.

Similar results were reported by Rao *et al.* (2000) for basal tillers, Jyothi *et al.* (2020) for 1000 seed weight and panicle weight per plant, Amarnath *et al.* (2018b), Negi *et al.* (2016), Nandini *et al.* (2016) and Joshi *et al.* (2015) for 1000 seed weight and Amarnath *et al.* (2018b) for peduncle length

Table 4.12 Phenotypic (P) and genotypic (G) correlations for yield and its attributes in 64 barnyard millet germplasm accessions

Chara- -cters	r	DFE	BT	DTM	PL	FLBL	FLBW	PH	PAL	TSW	PW	HI	LRL	Phs	Ca	Fe	Zinc	Pr	GYP
DFE	r _p	1	-0.1093	0.9976 **	0.0708	0.1900 *	0.2193 *	0.3800 **	-0.0074	-0.0397	0.0327	0.0272	-0.3111 **	-0.1116	-0.1376	0.0628	-0.0390	-0.0862	-0.0887
	r _g	1	-0.1187	0.9998**	0.0994	0.2023*	0.2556**	0.4038**	-0.0083	-0.0581	0.0383	0.0512	-0.3322**	-0.1077	-0.1602	0.0620	-0.0443	-0.0857	-0.0932
BT	r _p		1	-0.1025	0.2441 **	0.2192 *	0.0152	0.0963	0.2464 **	-0.0481	0.1986 *	-0.2447 **	0.3072 **	0.1057	0.3237 **	0.0043	0.3088 **	-0.0863	0.182**
	r _g		1	-0.1158	0.2711**	0.2401**	0.0065	0.0937	0.2316**	-0.0700	0.2276**	-0.3330**	0.3268**	0.1134	0.3472**	0.0171	0.3290**	-0.0951	0.2201**
DTM	r _p			1	0.0658	0.1870 *	0.2131 *	0.3681 **	-0.0173	-0.0420	0.0310	0.0235	-0.3161 **	-0.1059	-0.1404	0.0692	-0.0424	-0.0820	-0.0931
	r _g			1	0.1023	0.1975*	0.2508**	0.3939**	-0.0224	-0.0575	0.0393	0.0443	-0.3447**	-0.0995	-0.1603	0.0701	-0.0487	-0.0826	-0.0936
PL	r _p				1	0.1351	0.0252	0.1810 *	0.2512 **	0.1355	0.2925 **	-0.0218	0.3583 **	0.0975	0.1336	0.0937	0.0243	-0.0396	0.1944**
	r _g				1	0.1657	-0.0098	0.1796*	0.2717**	0.1658	0.3003**	-0.0337	0.4114**	0.1287	0.1436	0.1406	0.0242	-0.0421	0.2058**
FLBL	r _p					1	0.2090 *	0.2622 **	0.2236 *	-0.1410	0.0483	-0.1291	0.0001	-0.0632	0.2088 *	0.0161	0.0669	0.1545	0.0022
	r _g					1	0.1715	0.3123**	0.2402**	-0.1324	0.0084	-0.1016	-0.0154	-0.0908	0.2736**	0.0288	0.0597	0.1736	0.0305
FLBW	r _p						1	0.1876 *	0.1200	0.1455	0.1344	-0.0380	-0.1776 *	-0.0027	0.0802	0.0530	-0.2280 **	0.0946	0.0683
	r _g						1	0.2120	0.1631	0.2008	0.0993	-0.0429	-0.1844	-0.0186	0.0489	0.0917	-0.2596	0.1101	0.1158
PH	r _p							1	0.4499 **	-0.0220	0.1271	0.2000 *	0.1489	-0.0506	0.1346	0.0245	-0.0645	0.1287	-0.0047
	r _g							1	0.4892**	-0.0407	0.1183	0.2440*	0.1397	-0.0450	0.1339	0.0536	-0.0712	0.1350	-0.0756
PAL	r _p								1	0.0816	0.1835 *	-0.0527	0.3972 **	0.0555	-0.0115	0.2340 **	0.0435	0.0737	0.1438
	r _g								1	0.0786	0.2082*	-0.0586	0.4410**	0.0574	-0.0114	0.2896**	0.0479	0.0736	0.1663
TSW	r _p									1	0.1858 *	-0.1302	0.1890 *	0.1617	0.0914	0.0645	-0.0383	-0.2826 **	0.2369**
	r _g									1	0.2066*	-0.1824	0.2143*	0.1838*	0.0690	0.0700	-0.0244	-0.3003**	0.2923**
PW	r _p										1	0.0803	0.2129 *	-0.0644	0.0570	-0.0722	0.1272	-0.1030	0.7476**
	r _g										1	0.0637	0.2408	-0.0574	0.0082	-0.0592	0.1441	-0.1168	0.8398**
HI	r _p											1	-0.1833 *	-0.1307	-0.0775	-0.1722	0.0261	0.0908	-0.0611
	r _g											1	-0.2379**	-0.1615	-0.1406	-0.1786*	0.0353	0.0995	-0.1149
LRL	r _p												1	0.0941	0.1167	0.1263	0.1401	0.0275	0.1507
	r _g												1	0.1041	0.1019	0.1625	0.1346	0.0210	0.1705*
Phs	r _p													1	-0.0149	-0.0181	0.0957	-0.1922 *	-0.1238
	r _g													1	0.0010	-0.0375	0.1061	-0.1965*	-0.1063
Ca	r _p														1	-0.2173 *	0.2689 **	0.0247	0.1203
	r _g														1	-0.2468**	0.3183**	0.0316	0.0963
Fe	r _p															1	0.0667	0.0750	0.0903
	r _g															1	0.0807	0.0973	0.106
Zinc	r _p																1	-0.1609	0.1437
	r _g																1	-0.1658	0.1824*
Pr	r _p																	1	-0.1574
	r _g																	1	-0.1909*
GYP	r _p																		1
	r _g																		1

r_p= Phenotypic correlation; r_g= Genotypic correlation; *, ** Significant at 5% and 1% levels, respectively

DFE Days to 50% Flowering, **BT** Basal tillers, **DTM** Days to maturity, **PL** Peduncle length, **FLBL** Flag leaf blade length, **FLBW** Flag leaf blade width, **PH** Plant height, **PAL** Panicle length, **TSW** 1000 seed weight, **PW** Panicle weight, **HI** Harvest index, **LRL** Lower raceme length, **GYP** Grain yield per plant , **Phs** Phosphorus mg/100g, **Ca** Calcium mg/100g, **Fe** Iron mg/100g, **Zinc** mg/100g, **Pr** Protein.

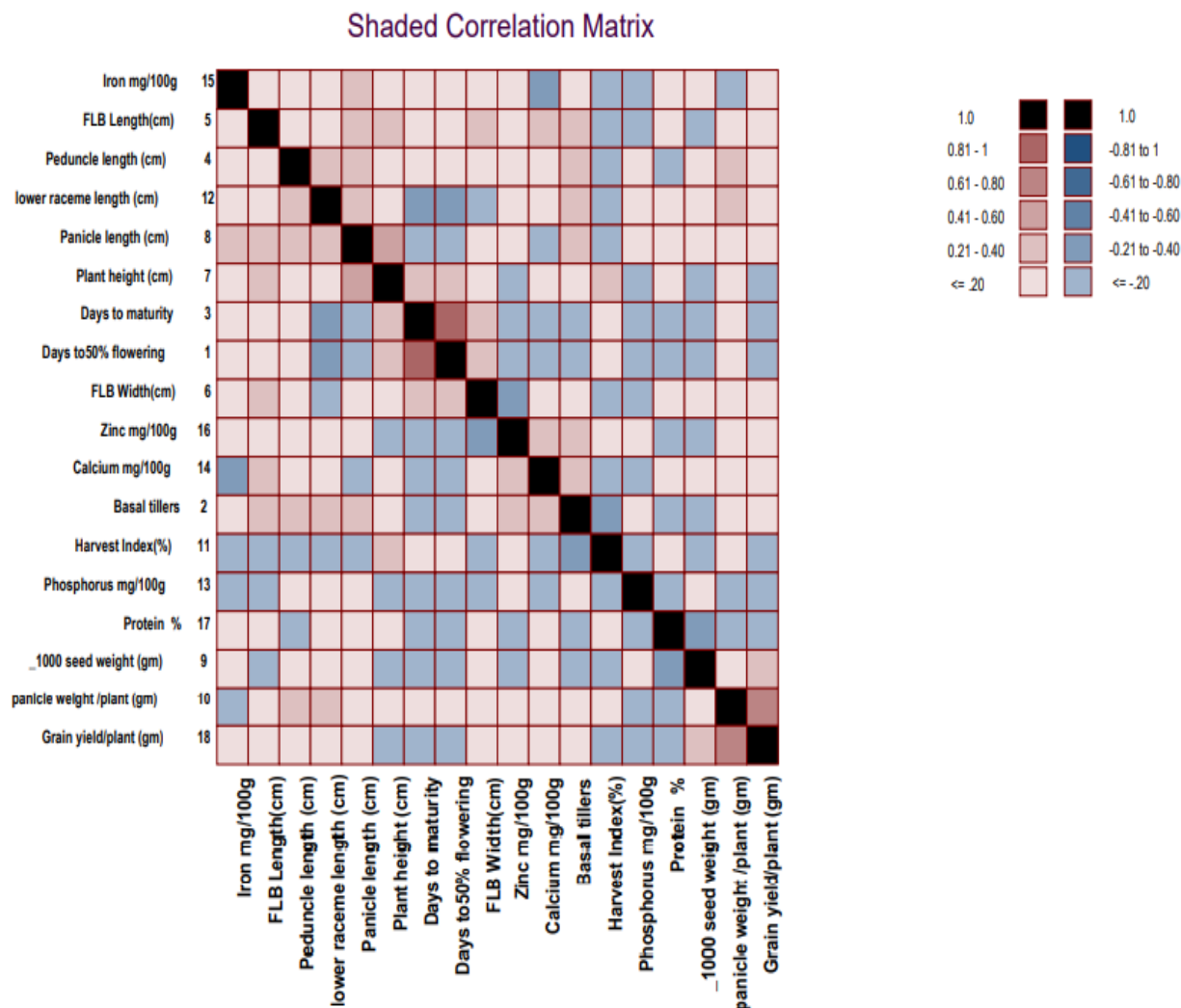


Fig 4.10 Shaded Phenotypic correlation matrix for all the characters studied in barnyard millet germplasm

Phenotypical Correlations

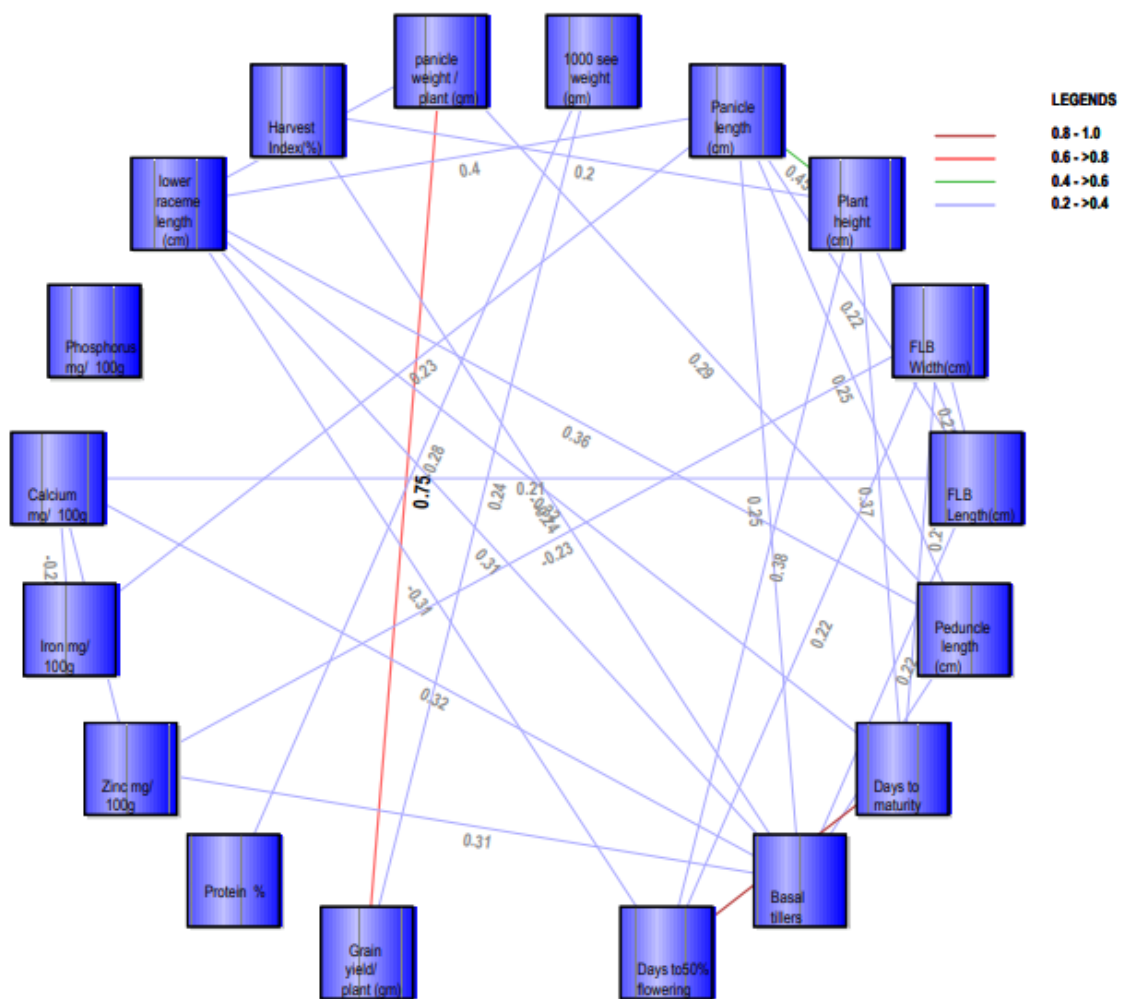


Fig 4.11 Pictorial representation of phenotypic correlation

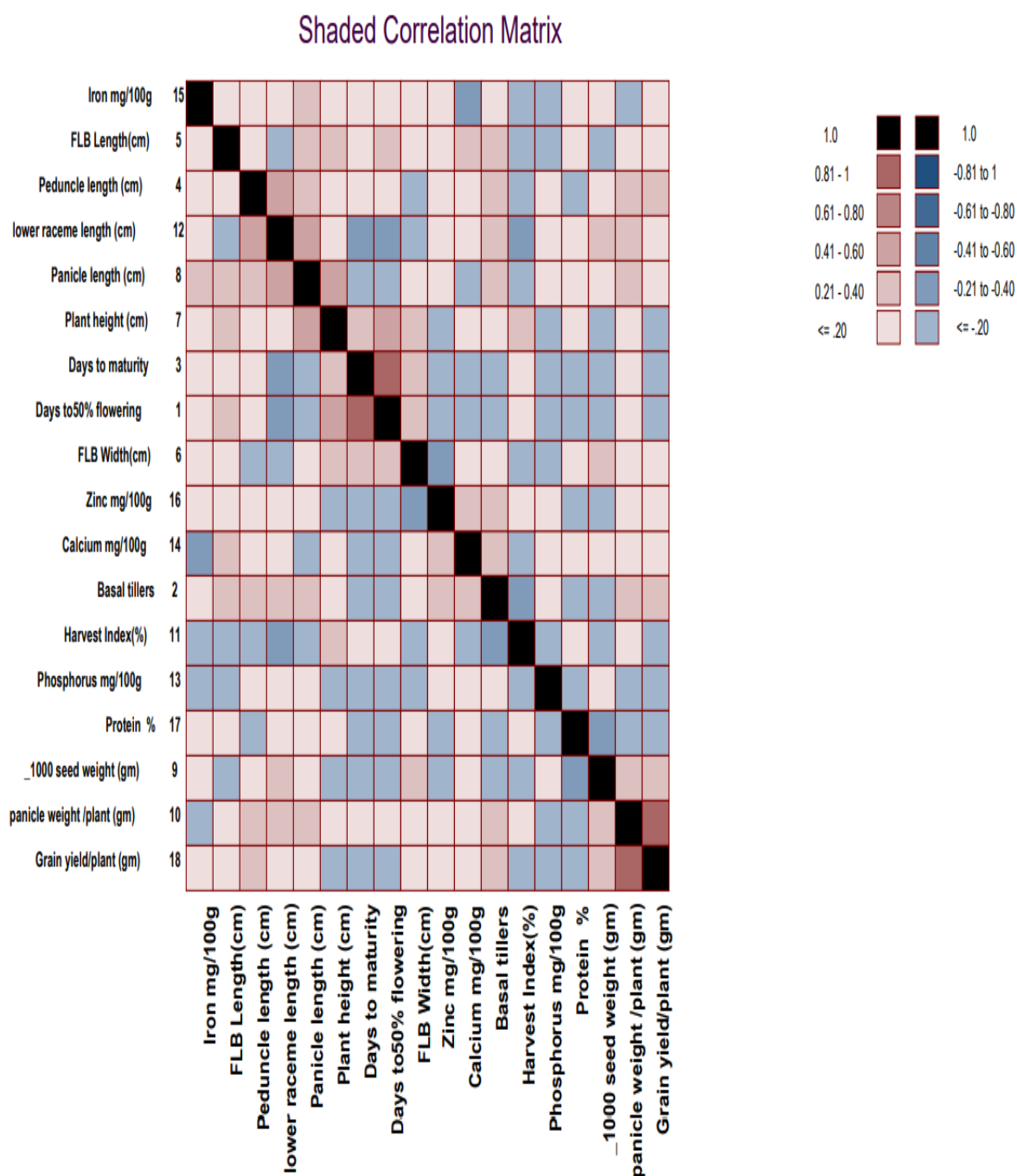


Fig 4.12 Shaded Genotypic correlation matrix for all the characters studied in barnyard millet germplasm

Genotypical Correlations

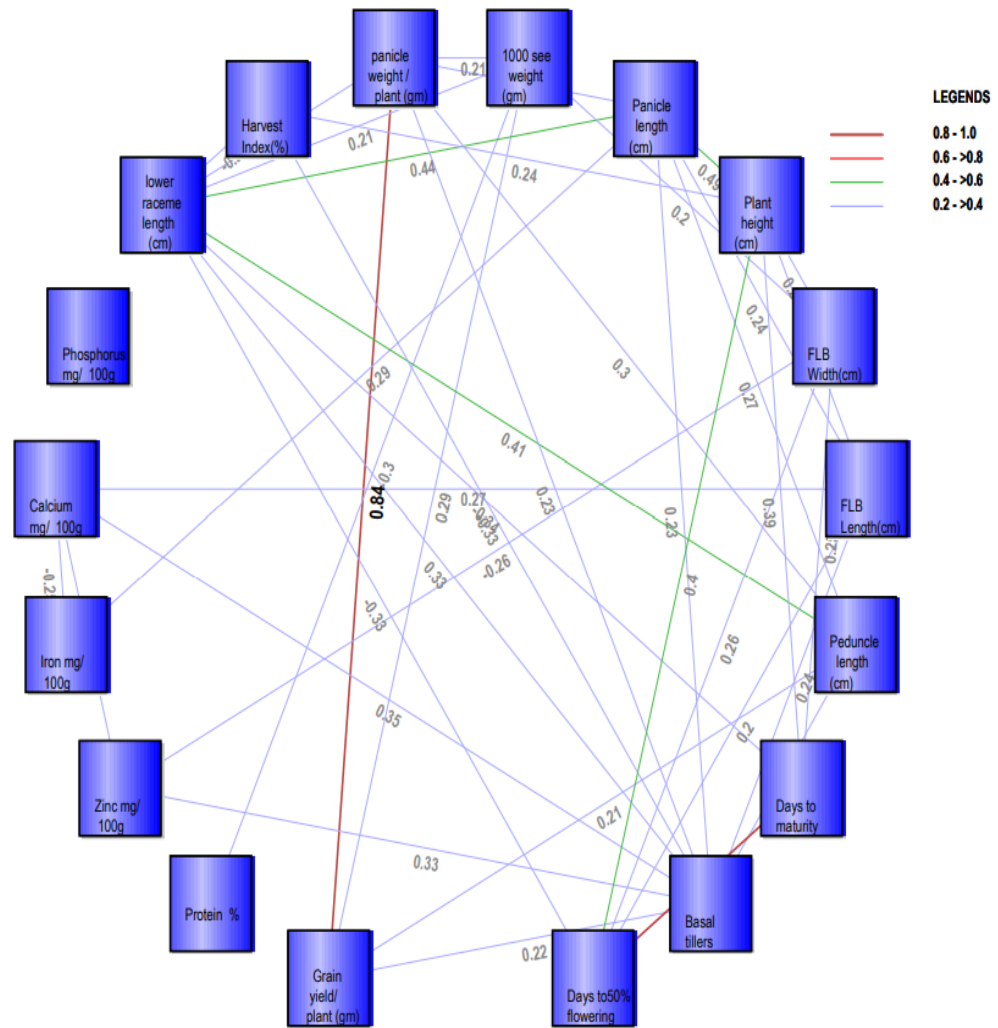


Fig 4.13 Pictorial representation of genotypic correlation

4.7 Path analysis

Analysis of correlation coefficients revealed the relationship between yield and its attributes but did not show direct and indirect effect of various traits on *per se*. Path analysis measures the direct and indirect effect and measures the direct and indirect 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 the table 4.13 and path diagram given in fig 4.14 and fig 4.15

4.7.1 Direct effect of different characters on grain yield / plant

At phenotypic and genotypic levels, panicle length ($P=0.0284$ and $G=0.1026$), 1000 seed weight ($P=0.0773$ and $G=0.0568$), panicle weight per plant ($P=0.7727$ and $G=0.8396$), calcium ($P=0.1055$ and $G=0.1029$), iron ($P=0.1813$ and $G=0.1268$) recorded high positive direct effect on grain yield / plant. Contrarily, negative direct effect on grain yield / plant, peduncle length ($P=-0.0168$ and $G=-0.0545$), plant height ($P=-0.0315$ and $G=-0.1248$), harvest index ($P=-0.0987$ and $G=-0.0905$), lower raceme length ($P=-0.1318$ and $G=-0.0482$), phosphorus ($P=-0.1114$ and $G=-0.1424$), protein ($P=-0.0773$ and $G=-0.1446$) whereas days to 50% flowering ($G=-4.038$), basal tillers ($G=-0.0793$) at genotypic level and days to maturity ($P=-0.9907$), flag leaf blade length ($P=-0.0222$), flag leaf blade width ($P=-0.0539$) and zinc ($P=-0.002$) at phenotypic levels. Similar results were reported by Renganathan *et al.* (2017), Prakash and Vanniarajan (2015), and Vikram *et al.* (2020) for panicle weight / plant. Eric *et al.* (2016), Negi *et al.* (2016), Nandini *et al.* (2010), Shingane *et al.* (2016) and Jadhav *et al.* (2015) for 1000 seed weight. Nirmalakumari *et al.* (2010b) and Vikram *et al.* (2020) for panicle length.

4.7.2 Indirect effect of component characters on grain yield / plant

4.7.2.1 Days to 50% flowering

Days to 50% flowering shows negative and non-significant correlation with grain yield / plant ($P=-0.887$ and $G=-0.0932$), negative indirect effect of days to 50% flowering on grain yield / plant via peduncle length ($P=-0.0012$ and $G=-0.0054$), plant height ($P=-0.012$ and $G=-0.0504$), panicle length ($P=-0.0002$ and $G=-0.0008$), harvest index ($P=-0.0027$ and $G=-0.0046$), calcium ($P=-0.0145$ and $G=-0.0165$). The positive and negligible indirect effects of days to 50% flowering on grain yield / plant through

panicle weight ($P= 0.0253$ and $G= 0.032$), lower raceme length ($P= 0.041$ and $G= 0.016$), phosphorus ($P= 0.0124$ and $G= 0.0153$), iron ($P= 0.0114$ and $G= 0.0079$) and protein ($P= 0.0067$ and $G= 0.0124$). Similar results were reported by Tyagi *et al.* (2011) for panicle length, peduncle length for this trait on grain yield per plant.

4.7.2.2 Basal tillers

Basal tillers shows positive and significant correlation with grain yield / plant ($P= 0.182^*$ and $G= 0.2201^{**}$), negative indirect effects of basal tillers on grain yield / plant via peduncle length ($P= -0.0041$ and $G= -0.0148$), plant height ($P= -0.003$ and $G= -0.0117$), 1000 seed weight ($P= -0.0033$ and $G= -0.004$), lower raceme length ($P= -0.0405$ and $G= -0.0158$), phosphorus ($P= -0.0118$ and $G= -0.0162$). The positive and negligible indirect effects basal tillers on grain yield / plant through panicle length ($P= 0.007$ and $G= 0.0238$), panicle weight ($P= 0.1534$ and $G= 0.1911$), harvest index ($P= 0.0242$ and $G= 0.0301$), iron ($P= 0.0008$ and $G= 0.0022$), protein ($P= 0.0067$ and $G= 0.0137$). Positive indirect effect of basal tillers via days to 50% flowering ($G= 0.4793$), flag leaf blade length ($G=0.0178$), flag leaf blade width ($G=0.0005$), zinc ($G= 0.0195$) at genotypic level. This results is in consonance with the findings of Shingane *et al.* (2016) for indirect effect via panicle length.

4.7.2.3 Days to maturity

Days to maturity shows negative and non-significant correlation with grain yield / plant ($P= -0.0931$ and $G= -0.0936$), negative indirect effects of days to maturity on grain yield / plant via peduncle length ($P= -0.0011$ and $G=-0.0056$), plant height ($P= -0.0116$ and $G= -0.0492$), panicle length ($P= -0.0005$ and $G= -0.0023$), 1000 grain weight ($P= -0.0032$ and $G= -0.0033$), harvest index ($P= -0.0023$ and $G= -0.004$), calcium ($P= -0.0148$ and $G= -0.0165$). The positive and negligible indirect effects of days to maturity on grain yield / plant via panicle weight ($P= 0.024$ and $G=0.033$), lower raceme length ($P=0.0417$ and $G=0.0166$), phosphorus ($P=0.0118$ and $G=0.0142$), iron ($P=0.0126$ and $G=0.0086$) and protein ($P=0.0063$ and $G=0.0119$). This result is consonance with findings Prasanna *et al.* (2013a), Ashok *et al.* (2016) and Ayesha *et al.* (2019c) for indirect effects via plant height.

4.7.2.4 Peduncle length

Peduncle length shows positive and significant correlation with grain yield / plant ($P=0.01944^*$ and $G=0.02058^*$). The indirect effect of peduncle length on grain yield was positive via panicle length ($P=0.0071$ and $G=0.0279$), 1000 seed weight ($P=0.0105$ and $G=0.0094$), panicle weight ($P=0.02261$ and $G=0.02521$), harvest index ($P=0.0022$ and $G=0.003$), calcium ($P=0.0141$ and $G=0.0148$), iron ($P=0.017$ and $G=0.0178$), protein ($P=0.0031$ and $G=0.0061$). In contrast, the negative indirect effect of peduncle length on grain yield / plant was through flag leaf blade width ($P= -0.0014$ and $G= -0.007$), plant height ($P= -0.0057$ and $G= -0.0224$), lower raceme length ($P= -0.0472$ and $G= -0.0199$) and phosphorus ($P= -0.0109$ and $G= -0.0183$). This result is in consonance with the finding of Shingane *et al.* (2016) for indirect effect via panicle length.

4.7.2.5 Flag leaf blade length

Flag leaf blade length shows positive and non-significant correlation with grain yield / plant ($P=0.0022$ and $G= 0.0305$). The positive indirect effect of flag leaf blade length on grain yield are panicle length ($P= 0.0063$ and $G= 0.0247$), panicle weight ($P= 0.0373$ and $G= 0.007$), harvest index ($P= 0.0217$ and $G= 0.0092$), phosphorus ($P= 0.007$ and $G= 0.0129$), calcium ($P= 0.022$ and $G= 0.0281$), iron ($P= 0.0029$ and $G= 0.0037$). The negative indirect effect of flag leaf blade length on grain yield through peduncle length ($P= -0.0023$ and $G=-0.009$), plant height ($P=-0.0083$ and $G=-0.039$), 1000 seed weight ($P=-0.0109$ and $G=-0.0075$). This results is in consonance with the finding of Shingane *et al.* (2016) for indirect effect via panicle length.

4.7.2.6 Flag leaf blade width

Flag leaf blade width shows positive and non-significant correlation with grain yield / plant ($P= 0.0683$ and $G= 0.1158$). The negative indirect effect of flag leaf blade length on grain yield recorded are plant height ($P= -0.0059$ and $G=-0.0265$) and protein ($P=-0.0073$ and $G=-0.0159$). On the other side positive and negligible indirect effect of flag leaf blade length on grain yield / plant are panicle length ($P= 0.0034$ and $G= 0.0167$), 1000 seed weight ($P=0.0112$ and $G=0.0114$), panicle weight ($P=0.1039$ and $G=0.0834$), harvest index ($P=0.0037$ and $G=0.0039$), lower raceme length ($P=0.0234$ and $G=0.0089$), phosphorus ($P=0.0003$ and $G=0.0026$), calcium ($P=0.0085$ and $G=0.005$), iron ($P=0.0096$ and $G=0.0116$). This result is in consonance with the finding of Shingane *et al.* (2016) for indirect effect via panicle length.

4.7.2.7 Plant height

Plant height shows negative and non-significant correlation with grain yield / plant ($P=-0.0047$ and $G=-0.0756$). The negative indirect effect of plant height on grain yield / plant recorded peduncle length ($P=-0.003$ and $G=-0.0098$), 1000 seed weight ($P=-0.0017$ and $G=-0.0023$), harvest index ($P=-0.0197$ and $G=-0.0221$), lower raceme length ($P=-0.0196$ and $G=-0.0067$), protein ($P=-0.01$ and $G=-0.0195$). The positive and negligible indirect effect of plant height on grain yield / plant recorded panicle length ($P=0.0128$ and $G=0.0502$), panicle weight ($P=0.0982$ and $G=0.0994$), phosphorus ($P=0.0056$ and $G=0.0064$), calcium ($P=0.0142$ and $G=0.0138$), iron ($P=0.0044$ and $G=0.0068$). This result is in consonance with the finding of Shingane *et al.* (2016) for indirect effect via panicle length.

4.7.2.8 Panicle length

Panicle length shows positive and non-significant correlation with grain yield / plant ($P=0.1438$ and $G=0.1663$). The positive and negligible indirect effect of panicle length on grain yield / plant recorded for 1000 seed weight ($P=0.0063$ and $G=0.0045$), panicle weight ($P=0.1418$ and $G=0.1748$), harvest index ($P=0.0052$ and $G=0.0053$), iron ($P=0.0424$ and $G=0.0367$). The negative indirect effect of panicle weight on grain yield / plant via peduncle length ($P=-0.0042$ and $G=-0.0148$), lower raceme length ($P=-0.0523$ and $G=-0.0213$), phosphorus ($P=-0.0062$ and $G=-0.0082$), calcium ($P=-0.0012$ and $G=-0.0012$), protein ($P=-0.0057$ and $G=-0.0106$). This result is in consonance with the finding of Dhamdhere *et al.* (2013) via 1000 seed weight.

4.7.2.9 1000 seed weight

Thousand seed weight shows positive and significant correlation with grain yield / plant ($P=0.2369$ and $G=0.2923$). The positive and negligible indirect effect of 1000 seed weight on grain yield / plant recorded for plant height ($P=0.0007$ and $G=0.0051$), panicle length ($P=0.0023$ and $G=0.0081$), panicle weight ($P=0.1436$ and $G=0.1735$), harvest index ($P=0.0129$ and $G=0.0165$), calcium ($P=0.0096$ and $G=0.0071$), iron ($P=0.0117$ and $G=0.0089$), protein ($P=0.0219$ and $G=0.0434$). The negative indirect effect of 1000 seed weight on grain yield / plant via peduncle length ($P=-0.0023$ and $G=-0.009$), lower raceme length ($P=-0.0249$ and $G=-0.0103$), phosphorus ($P=-0.018$ and $G=-0.0262$). This result is in consonance with the finding of Shingane *et al.* (2016) for indirect effect via panicle length.

4.7.2.10 Panicle weight

Panicle weight shows positive and significant correlation with grain yield / plant ($P=0.7476^{**}$ and $G=0.8398^{**}$). The positive indirect effect of panicle weight on grain yield / plant recorded panicle length ($P=0.0052$ and $G=0.0214$), 1000 seed weight ($P=0.0144$ and $G=0.0117$), phosphorus ($P=0.0075$ and $G=0.0082$), calcium ($P=0.006$ and $G=0.0008$). The negative indirect of panicle weight on grain yield / plant recorded peduncle length ($P=-0.0049$ and $G=-0.0164$), plant height ($P=-0.004$ and $G=-0.0148$), harvest index ($P=-0.0079$ and $G=-0.0058$), lower raceme length ($P=-0.0281$ and $G=-0.0116$), iron ($P=-0.0131$ and $G=-0.0075$). This result is in consonance with the finding of Dhamdhere *et al.* (2013) via 1000 seed weight.

4.7.2.11 Harvest index

Harvest index shows negative and non-significant correlation with grain yield / plant ($P=-0.0611$ and $G=-0.1149$). The positive indirect effect of harvest index on grain yield / plant recorded for peduncle length ($P=0.0004$ and $G=0.0018$), panicle weight ($P=0.062$ and $G=0.0535$), lower raceme length ($P=0.0241$ and $G=0.0115$), phosphorus ($P=0.0146$ and $G=0.023$). The negative indirect effect of harvest index on grain yield / plant recorded for plant height ($P=-0.0063$ and $G=-0.0305$), 1000 seed weight ($P=-0.0101$ and $G=-0.0104$), panicle length ($P=-0.0015$ and $G=-0.006$), calcium ($P=-0.0082$ and $G=-0.0145$), iron ($P=-0.0312$ and $G=-0.0226$), protein ($P=-0.007$ and $G=-0.0144$).

4.7.2.12 Lower raceme length

Lower raceme length shows positive and non-significant correlation with grain yield / plant ($P=0.1507$ and $G=0.1705$). The positive indirect effect of lower raceme length on grain yield / plant via panicle length ($P=0.0113$ and $G=0.0453$), 1000 seed weight ($P=0.0146$ and $G=0.0122$), panicle weight ($P=0.1645$ and $G=0.2022$), harvest index ($P=0.0181$ and $G=0.0215$), calcium ($P=0.0123$ and $G=0.0105$), iron ($P=0.0229$ and $G=0.0206$) was recorded. The negative indirect effect of lower raceme length on grain yield / plant was recorded via peduncle length ($P=-0.006$ and $G=-0.0224$), plant height ($P=-0.0305$ and $G=-0.0047$), phosphorus ($P=-0.0105$ and $G=-0.0148$), protein ($P=-0.0021$ and $G=-0.003$). Similar results of positive indirect effect were published by Ayesh *et al.* (2019c) for 1000 seed weight and panicle length.

4.7.2.13 Phosphorus

Phosphorus shows negative and non-significant correlation with grain yield / plant ($P=-0.1238$ and $G=-0.1063$). The positive indirect effect of phosphorus on grain yield / plant recorded for plant height ($P=0.0016$ and $G=0.0056$), panicle length ($P=0.0016$ and $G=0.0059$), 1000 seed weight ($P=0.0125$ and $G=0.0104$), harvest index ($P=0.0129$ and $G=0.0146$), protein ($P=0.0148$ and $G=0.0284$). The negative indirect effect of phosphorus on grain yield / plant are panicle weight ($P=-0.0498$ and $G=-0.0482$), lower raceme length ($P=-0.0124$ and $G=-0.005$), iron ($P=-0.0033$ and $G=-0.0048$). Similar results of positive indirect effect were published by Ayesh *et al.* (2019c) for 1000 seed weight.

4.7.2.14 Calcium

Calcium shows positive and non-significant correlation with grain yield / plant ($P=0.1203$ and $G=0.0963$). The positive indirect effect of calcium on grain yield / plant recorded for 1000 seed weight ($P=0.0071$ and $G=0.0039$), panicle weight ($P=0.044$ and $G=0.0069$), harvest index ($P=0.0076$ and $G=0.0127$). The negative indirect effect of calcium on grain yield / plant via peduncle length ($P=-0.0022$ and $G=-0.0078$), plant height ($P=-0.0042$ and $G=-0.0167$), panicle length ($P=-0.0003$ and $G=-0.0012$), lower raceme length ($P=-0.0154$ and $G=-0.0049$), iron ($P=-0.0394$ and $G=-0.0313$), protein ($P=-0.0019$ and $G=-0.0046$). Similar results of positive indirect effect were published by Ayesh *et al.* (2019c) for 1000 seed weight.

4.7.2.15 Iron

Iron shows positive and non-significant correlation with grain yield / plant ($P=0.0903$ and $G=0.106$). The positive indirect effect of calcium on grain yield / plant recorded for panicle length ($P=0.0066$ and $G=0.0297$), 1000 seed weight ($P=0.005$ and $G=0.004$), harvest index ($P=0.017$ and $G=0.0162$), phosphorus ($P=0.002$ and $G=0.0053$). The negative indirect effect of iron on grain yield / plant via peduncle length ($P=-0.0016$ and $G=-0.0077$), plant height ($P=-0.0008$ and $G=-0.0067$), panicle weight ($P=-0.0558$ and $G=-0.0497$), lower raceme length ($P=-0.0166$ and $G=-0.0078$), calcium ($P=-0.0229$ and $G=-0.0254$), protein ($P=-0.0058$ and $G=-0.0141$). Similar results of positive indirect effect were published by Ayesh *et al.* (2019c) for panicle length.

4.7.2.16 Zinc

Zinc shows positive and non-significant at phenotypic level and significant at genotypic level correlation with grain yield / plant ($P=0.1437$ and $G=0.1824^*$). The positive indirect effect of zinc on grain yield / plant via plant height ($P=0.002$ and $G=0.0089$), panicle length ($P=0.0012$ and $G=0.0049$), panicle weight ($P=0.0983$ and $G=0.121$), calcium ($P=0.0284$ and $G=0.0328$), iron ($P=0.0121$ and $G=0.0102$), protein ($P=0.0124$ and $G=0.024$). The negative indirect effect of zinc on grain yield / plant via peduncle length ($P=-0.0004$ and $G=-0.0013$), 1000 seed weight ($P=-0.003$ and $G=-0.0014$), harvest index ($P=-0.0026$ and $G=-0.0032$), lower raceme length ($P=-0.0185$ and $G=-0.0065$), phosphorus ($P=-0.0107$ and $G=-0.0151$) was recorded. Similar results were reported by Vishnuprabha *et al.* (2018) for iron content.

4.7.2.17 Protein

Protein shows negative correlation with grain yield / plant ($P=-0.1574$ and $G=-0.1909^*$). The positive indirect effect of protein on grain yield / plant via peduncle length ($P=0.0007$ and $G=0.0023$), panicle length ($P=0.0021$ and $G=0.0076$), phosphorus ($P=0.0214$ and $G=0.028$), calcium ($P=0.0026$ and $G=0.0033$), iron ($P=0.0136$ and $G=0.0123$). The negative indirect effect of protein on grain yield / plant recorded for plant height ($P=-0.0041$ and $G=-0.0169$), 1000 seed weight ($P=-0.0218$ and $G=-0.0171$), panicle weight ($P=-0.0796$ and $G=-0.098$), harvest index ($P=-0.009$ and $G=-0.009$), lower raceme length ($P=-0.0036$ and $G=-0.001$). Similar results of positive indirect effect were published by Ayesh *et al.* (2019c) for panicle length.

From the foregoing results and discussions on path analysis, it was recorded that traits viz., panicle weight / plant, iron, calcium, panicle length and 1000 seed 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.

In the present study, the residual effect was of high magnitude (0.588), suggesting there might be few more important traits contributing to grain yield other than those studied in the present investigation.

Table 4.13 Phenotypic (P) and genotypic (G) Path Coefficient for yield and yield attributes in 64 barnyard millet germplasm accessions

Characters		DFE	BT	DTM	PL	FLBL	FLBW	PH	PAL	TSW	PW	HI	LRL	Phs	Ca	Fe	Zinc	Pr	GYP
DFE	P	0.8543	-0.0018	-0.9883	-0.0012	-0.0042	-0.0118	-0.012	-0.0002	-0.0031	0.0253	-0.0027	0.041	0.0124	-0.0145	0.0114	0	0.0067	-0.0887
	G	-4.0388	0.0094	3.9033	-0.0054	0.015	0.018	-0.0504	-0.0008	-0.0033	0.032	-0.0046	0.016	0.0153	-0.0165	0.0079	-0.0026	0.0124	-0.0932
BT	P	-0.0934	0.0165	0.1016	-0.0041	-0.0049	-0.0008	-0.003	0.007	-0.0037	0.1534	0.0242	-0.0405	-0.0118	0.0342	0.0008	-0.0001	0.0067	0.182*
	G	0.4793	-0.0793	-0.4519	-0.0148	0.0178	0.0005	-0.0117	0.0238	-0.004	0.1911	0.0301	-0.0158	-0.0162	0.0357	0.0022	0.0195	0.0137	0.2201**
DTM	P	0.8522	-0.0017	-0.9907	-0.0011	-0.0041	-0.0115	-0.0116	-0.0005	-0.0032	0.024	-0.0023	0.0417	0.0118	-0.0148	0.0126	0.000	0.0063	-0.0931
	G	-4.039	0.0092	3.9031	-0.0056	0.0146	0.0177	-0.0492	-0.0023	-0.0033	0.033	-0.004	0.0166	0.0142	-0.0165	0.0089	-0.0029	0.0119	-0.0936
PL	P	0.0605	0.004	-0.0652	-0.0168	-0.003	-0.0014	-0.0057	0.0071	0.0105	0.2261	0.0022	-0.0472	-0.0109	0.0141	0.017	0.000	0.0031	0.1944*
	G	-0.4012	-0.0215	0.3994	-0.0545	0.0123	-0.0007	-0.0224	0.0279	0.0094	0.2521	0.003	-0.0199	-0.0183	0.0148	0.0178	0.0014	0.0061	0.2058*
FLBL	P	0.1623	0.0036	-0.1853	-0.0023	-0.0222	-0.0113	-0.0083	0.0063	-0.0109	0.0373	0.0127	0	0.007	0.022	0.0029	0.000	-0.012	0.0022
	G	-0.8167	-0.019	0.771	-0.009	0.074	0.0121	-0.039	0.0247	-0.0075	0.007	0.0092	0.0007	0.0129	0.0281	0.0037	0.0035	-0.0251	0.0305
FLBW	P	0.1874	0.0003	-0.2112	-0.0004	-0.0046	-0.0539	-0.0059	0.0034	0.0112	0.1039	0.0037	0.0234	0.0003	0.0085	0.0096	0.0001	-0.0073	0.0683
	G	-1.0322	-0.0005	0.979	0.0005	0.0127	0.0704	-0.0265	0.0167	0.0114	0.0834	0.0039	0.0089	0.0026	0.005	0.0116	-0.0154	-0.0159	0.1158
PH	P	0.3246	0.0016	-0.3647	-0.003	-0.0058	-0.0101	-0.0315	0.0128	-0.0017	0.0982	-0.0197	-0.0196	0.0056	0.0142	0.0044	0.000	-0.01	-0.0047
	G	-1.6309	-0.0074	1.5376	-0.0098	0.0231	0.0149	-0.1248	0.0502	-0.0023	0.0994	-0.0221	-0.0067	0.0064	0.0138	0.0068	-0.0042	-0.0195	-0.0756
PAL	P	-0.0063	0.0041	0.0172	-0.0042	-0.005	-0.0065	-0.0142	0.0284	0.0063	0.1418	0.0052	-0.0523	-0.0062	-0.0012	0.0424	0.000	-0.0057	0.1438
	G	0.0333	-0.0184	-0.0875	-0.0148	0.0178	0.0115	-0.0611	0.1026	0.0045	0.1748	0.0053	-0.0213	-0.0082	-0.0012	0.0367	0.0028	-0.0106	0.1663
TSW	P	-0.0339	-0.0008	0.0416	-0.0023	0.0031	-0.0078	0.0007	0.0023	0.0773	0.1436	0.0129	-0.0249	-0.018	0.0096	0.0117	0.000	0.0219	0.2369**
	G	0.2347	0.0056	-0.2245	-0.009	-0.0098	0.0141	0.0051	0.0081	0.0568	0.1735	0.0165	-0.0103	-0.0262	0.0071	0.0089	-0.0014	0.0434	0.2923**
PW	P	0.0279	0.0033	-0.0307	-0.0049	-0.0011	-0.0073	-0.004	0.0052	0.0144	0.7727	-0.0079	-0.0281	0.0072	0.006	-0.0131	0.000	0.008	0.7476**
	G	-0.1541	-0.018	0.1532	-0.0164	0.0006	0.007	-0.0148	0.0214	0.0117	0.8396	-0.0058	-0.0116	0.0082	0.0008	-0.0075	0.0086	0.0169	0.8398**
HI	P	0.0232	-0.004	-0.0233	0.0004	0.0029	0.002	-0.0063	-0.0015	-0.0101	0.062	-0.0987	0.0241	0.0146	-0.0082	-0.0312	0.0000	-0.007	-0.0611
	G	-0.2068	0.0264	0.173	0.0018	-0.0075	-0.003	-0.0305	-0.006	-0.0104	0.0535	-0.0905	0.0115	0.023	-0.0145	-0.0226	0.0021	-0.0144	-0.1149
LRL	P	-0.2658	0.0051	0.3132	-0.006	0	0.0096	-0.0047	0.0113	0.0146	0.1645	0.0181	-0.1318	-0.0105	0.0123	0.0229	0.0000	-0.0021	0.1507
	G	1.3418	-0.0259	-1.3456	-0.0224	-0.0011	-0.013	-0.0174	0.0453	0.0122	0.2022	0.0215	-0.0482	-0.0148	0.0105	0.0206	0.008	-0.003	0.1705
Phs	P	-0.0954	0.0017	0.1049	-0.0016	0.0014	0.0001	0.0016	0.0016	0.0125	-0.0498	0.0129	-0.0124	-0.1114	-0.0016	-0.0033	0.0000	0.0149	-0.1238
	G	0.4349	-0.009	-0.3882	-0.007	-0.0067	-0.0013	0.0056	0.0059	0.0104	-0.0482	0.0146	-0.005	-0.1424	0.0001	-0.0048	0.0063	0.0284	-0.1063
Ca	P	-0.1175	0.0053	0.1391	-0.0022	-0.0046	-0.0043	-0.0042	-0.0003	0.0071	0.044	0.0076	-0.0154	0.0017	0.1055	-0.0394	-0.0001	-0.0019	0.1203
	G	0.6472	-0.0275	-0.6257	-0.0078	0.0202	0.0034	-0.0167	-0.0012	0.0039	0.0069	0.0127	-0.0049	-0.0001	0.1029	-0.0313	0.0189	-0.0046	0.0963
Fe	P	0.0536	0.0001	-0.0686	-0.0016	-0.0004	-0.0029	-0.0008	0.0066	0.005	-0.0558	0.017	-0.0166	0.002	-0.0229	0.1813	0.000	-0.0058	0.0903
	G	-0.2504	-0.0014	0.2738	-0.0077	0.0021	0.0065	-0.0067	0.0297	0.004	-0.0497	0.0162	-0.0078	0.0053	-0.0254	0.1268	0.0048	-0.0141	0.106
Zinc	P	-0.0333	0.0051	0.042	-0.0004	-0.0015	0.0123	0.002	0.0012	-0.003	0.0983	-0.0026	-0.0185	-0.0107	0.0284	0.0121	-0.0002	0.0124	0.1437
	G	0.1789	-0.0261	-0.1902	-0.0013	0.0044	-0.0183	0.0089	0.0049	-0.0014	0.121	-0.0032	-0.0065	-0.0151	0.0328	0.0102	0.0594	0.024	0.1824*
Pr	P	-0.0736	-0.0014	0.0812	0.0007	-0.0034	-0.0051	-0.0041	0.0021	-0.0218	-0.0796	-0.009	-0.0036	0.0214	0.0026	0.0136	0.0000	-0.0773	-0.1574
	G	0.3462	0.0075	-0.3222	0.0023	0.0128	0.0078	-0.0169	0.0076	-0.0171	-0.098	-0.009	-0.001	0.028	0.0033	0.0123	-0.0098	-0.1446	-0.1909*

Residual effect (phenotypic)=0.588; Residual effect (Genotypic)=0.424; Diagonal values = Direct values off –Diagonal values = indirect effect ;

*,** Significant at 0.05 and 0.01 levels respectively.

DFE, Days to 50% Flowering, **BT** Basal tillers, **DTM** Days to maturity, **PL** Peduncle length, **FLBL** Flag leaf blade length, **FLBW** Flag leaf blade width, **PH** Plant height, **PAL** Panicle length, **TSW** 1000 seed weight, **PW** Panicle weight, **HI** Harvest index, **LRL** Lower raceme length, **GYP** Grain yield per plant , **Phs**, Phosphorus mg/100g, **Ca** Calcium mg/100g, **Fe** Iron mg/100g, **Zinc** mg/100g, **Pr** Protein %

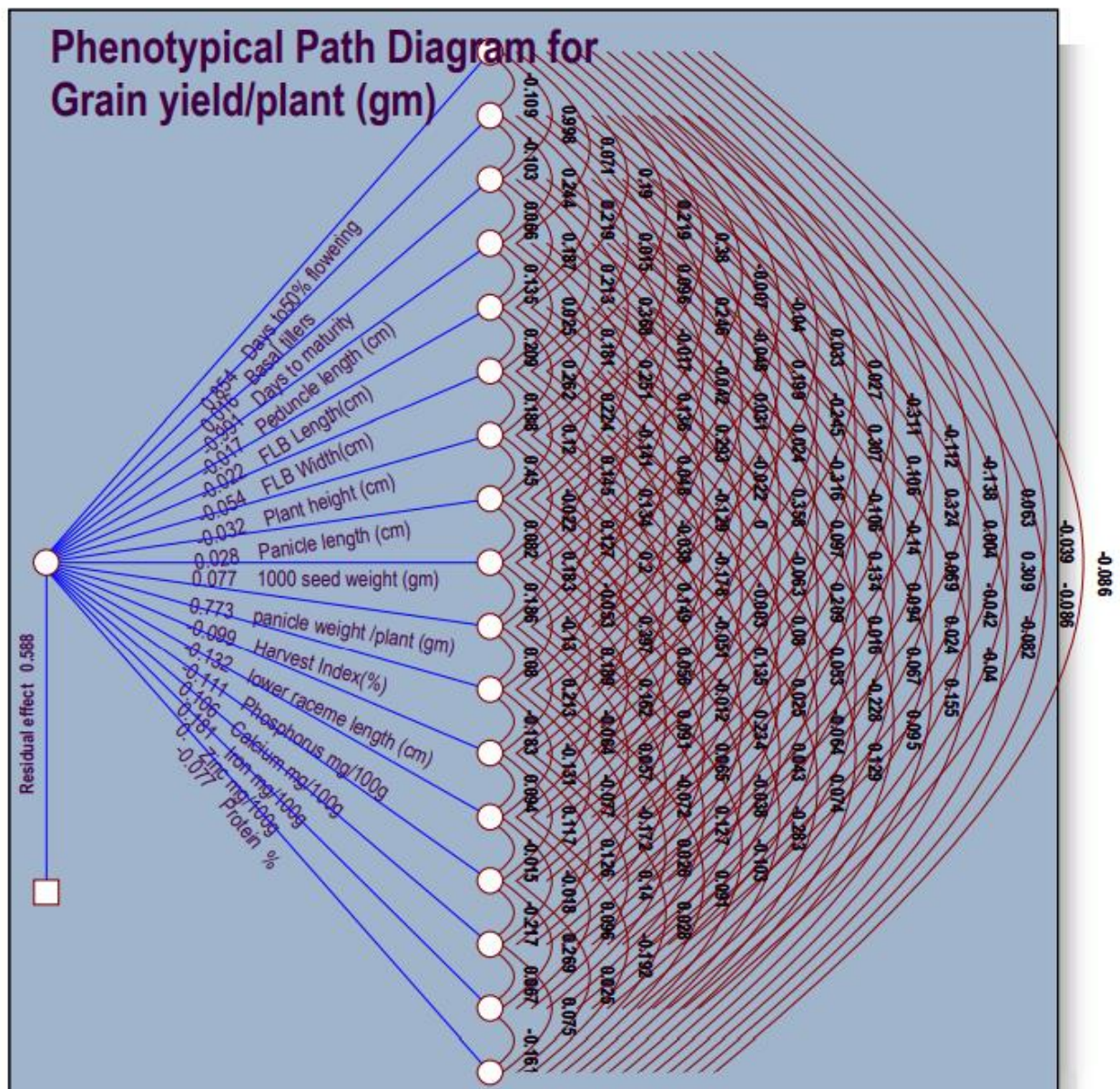


Fig 4.14 phenotypic path diagram for grain yield per plant

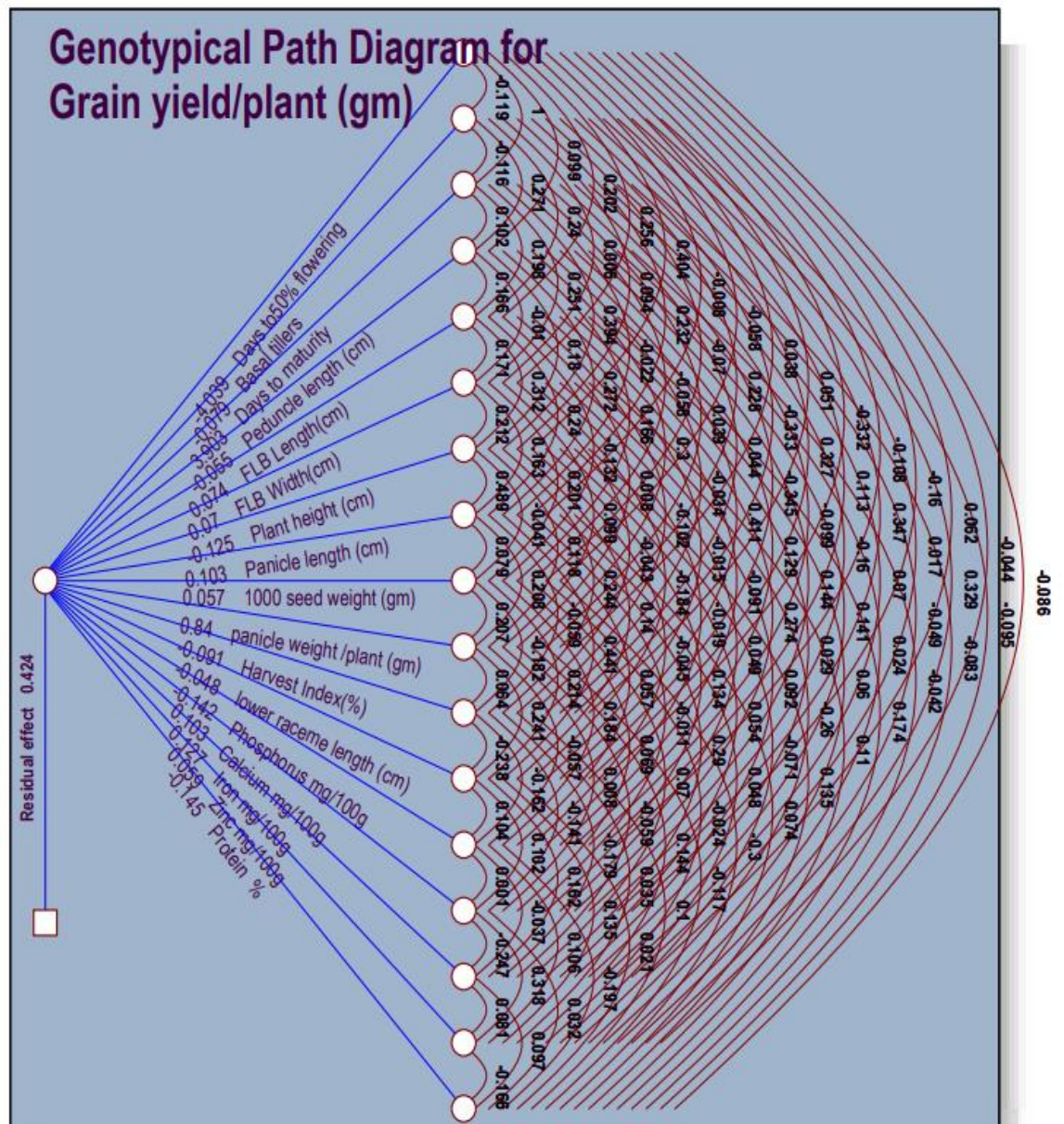


Fig 4.15 Genotypic path diagram for grain yield per plant

Table 4.14 Details of promising barnyard millet germplasm accessions identified

Germplasm accessions identified	High <i>per se</i> performance noticed for characters
TNEf-216	Basal tillers, peduncle length, flag leaf blade length, flag leaf blade width, plant height, 1000 seed weight, iron.
TNEf-202	Basal tillers, plant height (short), panicle weight, harvest index, lower raceme length, zinc.
TNEf-215	Days to 50% flowering and days to maturity (late), peduncle length, flag leaf blade length, flag leaf blade width, plant height, panicle weight / plant, harvest index, lower raceme length, iron.
TNEf-218	Days to 50% flowering and days to maturity (earliness), basal tillers, peduncle length, flag leaf blade length, flag leaf blade width, plant height, panicle weight / plant, 1000 seed weight, panicle weight, lower raceme length, grain yield / plant, phosphorus, calcium.

Chapter - V

SUMMARY AND CONCLUSIONS



CHAPTER-V

SUMMARY AND CONCLUSIONS

The present research entitled “ Morphological Characterization and Divergence Studies in Barnyard Millet [*Echinochloa Frumentacea (L.)*] ” was conducted with sixtyfour barnyard millet germplasm accessions at Regional Agricultural Research Station, Nandyal, Andhra Pradesh during *kharif*, 2020 in order to morphologically characterize the germplasm accessions for twenty two DUS traits and to study the genetic variability, heritability, genetic advance as per cent of mean, extent of genetic diversity, character association and path analysis for 18 quantitative traits viz., days to 50% flowering, basal tillers, days to maturity, peduncle length, plant height, flag leaf blade length, flag leaf blade width, panicle length, harvest index, grain yield / plant, panicle weight / plant, lower raceme length, 1000 seed weight, phosphorus, calcium, iron, zinc and protein.

Morphological characterization of sixty four barnyard millet germplasm accessions for twenty two DUS traits revealed existence of ample polymorphism for the characters. It was observed that for plant growth habit, erect was dominant over decumbent; basal tillers of all the germplasm accessions are low (<4); days to 50% flowering, medium duration was predominant; plant pigmentation at internode, non-pigmentation was dominant over pigmentation; flag leaf blade length, medium was predominant over long; for flag leaf blade width medium was predominant over narrow; for peduncle length, medium was dominant over long; for inflorescence shape pyramidal was dominant over cylindrical; for inflorescence color green was dominant over light purple and dark purple; for panicle compactness, open was dominant over compact and intermediate; spikelet arrangements one rachies one side was predominant; for lower raceme shape straight was dominant over curved; for lower raceme thickness slender was dominant over thick; for lower raceme branching absent of branching was predominant; for culm branching all the germplasm accessions possess culm branching; lower raceme length, medium was dominant over short and long; for panicle length short to medium was dominant over medium and long; for plant height tall was dominant over very tall; for grain color grey white was dominant over straw white and grey; for grain shape all the genotypes are concave ; for 1000 seed weight medium was dominant over high and low.

The ANOVA of sixty four barnyard millet germplasm accessions for 18 quantitative traits viz., days to 50% flowering, basal tillers, days to maturity, peduncle length, flag leaf blade length, flag leaf blade width, Plant height, Panicle length, 1000 grain weight, Panicle weight /plant, Harvest Index (%), lower raceme length, Phosphorus, Calcium, Iron, Zinc, Protein (%) and grain yield / plant implying existence of ample variation in the germplasm accessions studied. Based on *per se* performance, promising germplasm accessions viz., TNEf-216, TNEf-215, TNEf-218 and TNEf-202 that recorded higher values for majority of the traits viz., Days to 50% flowering and days to maturity (earliness), basal tillers, peduncle length, flag leaf blade length, flag leaf blade width, plant height, panicle weight / plant, 1000 seed weight, lower raceme length, grain yield / plant, phosphorus, calcium, iron, zinc, phosphorus.

A perusal to the analysis of various genetic parameters viz., genetic variability, heritability and genetic advance as per cent of mean revealed higher values of GCV, PCV, heritability and genetic advance as per cent of mean for the traits basal tillers and lower raceme length implying their amenability for improvement through simple selection strategies. Moderate GCV and PCV values coupled with high heritability and genetic advance as per cent of mean was registered for the traits, days to 50% flowering, peduncle length, panicle length, 1000 seed weight, panicle weight / plant, grain yield / plant, zinc and protein indicating the prevalence of both additive and non-additive gene actions and hence genetic improvement can be achieved by intercrossing among the accessions followed by selection for this trait.

Diversity in the germplasm accessions was assessed through D² analysis and canonical root analysis. The results of D² analysis showed formation of eight non-overlapping distinct clusters with maximum number of accessions in cluster I (57) and cluster II, III, IV, V, VI. VII and VIII were mono genotypic clusters with single accession per cluster. Minimum inter-cluster distance was reported between clusters IV and VI. Maximum inter-cluster distance was observed between cluster VI and VII, IV and VI in the decreasing order of magnitude indicating the presence of diversity in the material which can be utilized for future hybridization programme.

About 75.9 per cent of total genetic divergence was accounted through canonical root analysis. Based on the results of divergence studies and *per se* performance together, the promising accessions TNEf-216, TNEf-215, TNEf-218 and TNEf-202 were identified that can be used as 'potential parents' in future hybridization programmes.

The correlation studies between grain yield and its attributes in 64 accessions of barnyard millet revealed positively significant association of grain yield / plant with most of the traits viz., basal tillers ($r_p = 0.182^{**}$ and $r_g = 0.2201^{**}$), 1000 seed weight ($r_p = 0.2369^*$ and $r_g = 0.2923^{**}$), Panicle weight per plant ($r_p = 0.7476^{**}$ and $r_g = 0.8398^{**}$), Peduncle length ($r_p = 0.1944^{**}$ and $r_g = 0.2058^{**}$) implying that these traits may be chosen as selection criterion for developing high yielding cultivars. Inter-character associations of important traits such as days to 50% flowering, basal tillers, plant height, peduncle length, flag leaf blade length, flag leaf blade width, 1000 seed weight had shown significant positive association with the traits viz., days to maturity, peduncle length, plant height, panicle weight and lower raceme length. The presence of strong positive correlation envisages the simultaneous improvement of these characters.

The path coefficient analysis revealed that traits viz., panicle weight / plant, iron, calcium, panicle length and 1000 seed weight established true relationship with grain yield per plant by exhibiting positive associations and positive direct selection for these traits.

Thus as a whole, the studies conclude that the germplasm accessions viz., TNEf-216, TNEf-215, TNEf-218 and TNEf-202 were promising for majority of the traits and might serve as 'potential parents' in future hybridization programmes. The traits, basal tillers and lower raceme length with higher estimates of variability parameters can be improved through simple selection strategies. Association studies through correlation and path analysis revealed that the trait panicle weight per plant and 1000 seed weight showed high positive direct effects on grain yield implying the scope of direct selection for these traits in genetic improvement of barnyard 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.