DUS CHARACTERIZATION AND DIVERSITY ANALYSIS OF INBRED LINES IN PEARL MILLET (*Pennisetum glaucum* (L.) R. Br.)

BY

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DECLARATION

I, **Mr. I.PRAVEEN KUMAR**, hereby declare that the thesis entitled "**DUS CHARACTERIZATION AND DIVERSITY ANALYSIS OF INBRED LINES IN PEARL MILLET (*Pennisetum glaucum* (L.) R. Br.)**" 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 : Tirupati
Date : 17.10.2022

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CERTIFICATE

Mr. **I. PRAVEEN KUMAR** has satisfactorily prosecuted the course of research and that thesis entitled "**DUS CHARACTERIZATION AND DIVERSITY ANALYSIS OF INBRED LINES IN PEARL MILLET (*Pennisetum glaucum* (L.) R. Br.)**" 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.

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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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Everyone is not mentioned, but no one is forgotten.

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LIST OF SYMBOLS AND ABBREVIATIONS

$\overline{X}$	:	Grand mean
%	:	Per cent
1000 GW	:	1000 Grain Weight
AICPMIP	:	All India Coordinated Pearl Millet Improvement Project
AICRP	:	All India Coordinated Research Project
ANOVA	:	Analysis of variance
ARS	:	Agricultural Research Station
CD	:	Critical Difference
cm	:	Centimeter
$cm^2\ g^{-1}$	:	Centimeter square $gram^{-1}$
CV	:	Co-efficient of Variation
DAS	:	Days After Sowing
df	:	Degrees of freedom
DF	:	Days to 50% Flowering
DFY	:	Dry Fodder Yield $Plant^{-1}$
DM	:	Days to Maturity
DUS	:	Distinct, Uniformity, Stability
et al.	:	And others
Fig.	:	Figure
g	:	Gram
GA	:	Genetic Advance
GAM	:	Genetic Advance as per cent of Mean
GCV	:	Genotypic Co-efficient of Variation
GFY	:	Green Fodder Yield $Plant^{-1}$
GYP	:	Grain Yield $Plant^{-1}$
h^2_{bs}	:	Heritability in broad sense

ha	:	Hectare
HI	:	Harvest Index
i.e.	:	That is
ICAR	:	Indian Council of Agricultural Research
Kg	:	Kilogram
LBL	:	Leaf Blade Length
LBW	:	Leaf Blade Width
LSL	:	Leaf Sheath Length
M	:	Meter
NN	:	No of Nodes Plant^{-1}
NPT	:	Number of Productive Tillers Plant^{-1}
^{o}C	:	Degree Celsius
PCV	:	Phenotypic Co-efficient of Variation
per se	:	As such with mean
PH	:	Plant Height
PH	:	Plant Height
PPV&FR	:	Protection of Plant Varieties and Farmer's Right
PW	:	Panicle Weight
RBD	:	Randomized Block Design
r_g	:	Genotypic correlation coefficient
r_p	:	Phenotypic correlation coefficient
S. No.	:	Serial Number
SCMR 45	:	SPAD Chlorophyll Meter Reading at 45 DAS
SCMR 65	:	SPAD Chlorophyll Meter Reading at 65 DAS
SE(d)	:	Standard Error of difference
SE(m)	:	Standard Error of mean
SG	:	Spike Girth

SL	:	Spike Length
SLA 45	:	Specific Leaf Area at 45 DAS
SLA 65	:	Specific Leaf Area at 65 DAS
SPAD	:	Soil Plant Analytical Development
TH	:	Threshing
Via	:	Through
viz.,	:	Namely
WUE	:	Water Use Efficiency
σ^2	:	Variance
σ^2_g	:	Genotypic variance
σ^2_p	:	Phenotypic variance

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ABSTRACT

The present investigation was conducted at Agricultural Research Station (ARS), Perumallapalle, Tirupati during *rabi*, 2021 to characterize pearl millet inbred lines for DUS traits and to identify potential germplasm lines by estimating genetic parameters (variability, heritability and genetic advance), genetic divergence, character association and path coefficient.

DUS characterization of 70 pearl millet genotypes using 28 DUS traits revealed existence of abundant diversity for these characters. In the present studied pearl millet inbred lines appreciable differences were observed for the traits *viz.,* anthocyanin pigmentation, leaf sheath length, leaf blade length, leaf blade width, spike stigma pigmentation, anther colour, plant node pubescence, number of nodes plant^{-1}, node pigmentation, internode pigmentation, spike length, anthocyanin pigmentation of glume, spike bristle, spike bristle colour, bristle appearance, spike girth, number of productive tillers plant^{-1}, plant height, spike shape, spike-density, seed color, seed shape and 1000 seed weight. Based on the DUS descriptors inbred lines were characterized effectively which would be useful for their documentation and registration. These descriptors would aid in explicit identity of inbred lines and help in maintenance of their purity in field for use in future breeding programmes.

The analysis of variance carried out among 70 germplasm lines for 21 yield and yield attributes revealed significant differences for all the characters indicating the presence of considerable amount of genetic variability for the characters in the studied material.

The characters such as grain yield plant^{-1}, 1000 grain weight panicle weight, green fodder yield plant^{-1}, dry fodder yield plant^{-1} and harvest index showed higher estimates of PCV and GCV indicating ample amount of variation among germplasm lines for these traits. Thus, direct selection for these traits would result in further improvement of grain yield. High

heritability coupled with high genetic advance as per cent of mean was observed for days to 50 % flowering, spike length, spike girth, number of productive tillers plant^{-1}, plant height, 1000 grain, panicle weight, green fodder yield plant^{-1}, dry fodder yield plant^{-1}, threshing percentage, harvest index and grain yield plant^{-1} indicating the predominance of additive gene action and direct selection would be effective for improvement of these traits.

D^2 analysis grouped 70 inbred lines into 12 clusters. Among all the characters studied, 1000 grain weight, days to 50% flowering and number of productive tillers plant^{-1} contributed relatively maximum towards the total genetic divergence. Inter cluster distance was observed maximum between cluster VI and XII followed by cluster X and XII, cluster III and XII and cluster IV and XII representing that germplasm lines belonging to these clusters are more divergent.

Correlation studies revealed that characters *viz.,* panicle weight followed by green fodder yield plant^{-1}, dry fodder yield plant^{-1}, number of productive tillers plant^{-1}, spike girth, plant height, leaf blade length, number of nodes plant^{-1}, 1000 grain weight, spike length, harvest index, threshing percentage, leaf blade width and specific leaf area at 45 DAS had significant positive association with grain yield plant^{-1} indicating simultaneous selection of these traits would result in improvement of grain yield.

Further, path analysis estimates in the present investigation revealed that panicle weight followed by threshing percentage, green fodder yield plant^{-1} had true relationship with grain yield plant^{-1} by establishing significant positive association and high positive direct effect on grain yield plant^{-1}. Low residual effects at both phenotypic and genotypic level demonstrated that choice of traits in the present study were able to explain most of the effects on grain yield.

Superior inbred lines PPBi-3, PPBi-46, PPBi-47, PPBi-50 and PPBi-59 identified in the present study could be utilized for the development of composites.

Chapter - I

Introduction

Chapter – I

INTRODUCTION

Pearl millet (*Pennisetum glaucum* (L.) R. Br., 2n = 14) is an annual, C_4 cereal crop with high photosynthetic efficiency and belongs to the family Gramineae. It has its origin in central tropical Africa and is cosmopolitan throughout Africa and India's dry and semi-arid regions. Cumbu, black millet, spiked millet and candle millet are popular names while sajja is the local name in Andhra Pradesh. It is naturally cross pollinated (Allogamous) and the adaptation for cross pollination is Protogyny. Wind is the primary pollinator (anemophily).

Pearl millet is widely cultivated staple grain crop in India next to rice, wheat, maize and sorghum. It is grown solely by subsistence and small-scale farmers with little resources. It is a multipurpose coarse cereal crop cultivated for grain, fodder and stover in various conditions across the world. It can adapt well to drought and unfavorable agro-ecological circumstances and is capable of quick and strong development and is thus planted in marginal regions with low soil fertility, less and unpredictable rainfall and high temperatures, and hence regarded as climate resilient.

Pearl millet is commonly known as a poor man's food and important among nutritious cereals. The composition of grains (per 100g) reveals carbohydrates (67.5g), protein (11.6g), fat (5g), fiber (1.2g), mineral matter (2.3g), calcium (42mg) and phosphorus (296mg). The grain consists high amount of vitamins (thiamine, riboflavin and niacin) and minerals (P, K, Mg, Fe, Zn, Cu and Mn). It being rich source of energy is comparable to rice, wheat, maize and sorghum. Protein content of pearl millet is higher than barley (11.5%), maize (11.1%), sorghum (10.4%) and rice (7.2%). It has a low glycemic index (GI), which helps in weight loss and aids in cholesterol reduction (ICAR - AICRP on pearl millet, 2018).

Pearl millet is majorly grown in Rajasthan, Uttar Pradesh, Gujarat, Haryana, Karnataka, Maharashtra and Andhra Pradesh. In India, Pearl millet is cultivated in 7.65 million hectares with a production of 10.86 million tones and 1420 kg/ha productivity. In Andhra Pradesh, pearl millet is cultivated in 0.31 lakh hectares with a production of 0.71 lakh tones and a productivity of 2281 kg/ha (Directorate of Economics and Statistics, 2021).

It has been reported by Ramarao *et al*., in 2019 that pearl millet production is likely to become more challenging because of predicted intense drought stress, rise in temperature, and greater disease incidences and its production must be increased at a much faster rate. This increasing production must result through enhancement in productivity since there is little scope to enhance production by expanding pearl millet cultivation. No doubt, enormous progress has been made in India to improve productivity by developing high-yielding cultivars and their improved agronomic management. The accomplishments of pearl millet breeding are often referred to as one of the greatest success stories in Indian agriculture (Yadav *et al*., 2021). However, its biological potential has not been fully realized and recurring downy mildew epidemics in pearl millet hybrids in India prompted to intensify efforts on genetic diversification of hybrid parental lines. The replacement of old hybrids with new ones that necessitates continuous development of high yielding diverse trait based inbred lines that can be used as hybrid parents (A & R lines) for breeding pearl millet cultivars.

As a result of the growing usage of pearl millet inbred lines, it is essential to characterize, analyze and catalogue, so that they are utilized in crop improvement programs. Apart from that, there is a need for the protection of inbred lines under Protection of Plant Varieties Act, which involves varietal testing for distinctness, uniformity and stability. DUS is the foundation for the issue of protection to new plant varieties under “The Protection of Plant Varieties and Farmers’ Rights Act”, 2001 (AICPMIP, 2006).

Knowledge of multiple estimations of genetic parameters is required for better utilization of the genetic variation present in the base material for any improvement in features of economic value. The efficacy of selection is known by the proportion of heritable variability. In the prediction of projected genetic gain in the trait with selection of best individual genotypes from the base population, the information on heritability combined with genetic advance is more relevant than information on heritability alone.

The measurement of genetic diversity by means of biometrical procedures such as Mahalanobis D^2 statistics plays a pivot role in choice of divergent parents for hybridization to exploit maximum heterosis and to access relative contribution of different characters towards genetic diversity.

Grain-yield is a complex character which is affected by several component traits. Understanding such inter-relationship between yield and its constituents will significantly increase breeding program efficiency using the application of proper selection indices. On the other hand correlation coefficients, might occasionally mislead the selection and must be divided into direct and indirect effects. Then path coefficient analysis is used to calculate the direct and indirect impacts of each variable as well as their contribution to yield.

Based on above perspectives, the present research work is composed with the following objectives.

Objectives of investigation:

1. Morphological characterization of pearl millet inbred lines as per DUS descriptors.
2. To estimate genetic variability, heritability and genetic advance for yield and its attributes in pearl millet inbred lines.
3. To assess the genetic diversity for yield and yield attributes.

4. To study the character association among pearl millet inbred lines for yield and yield related traits.
5. To ascertain the direct and indirect contributions of yield attributes towards the seed yield.

Chapter - II

Review of Literature

Chapter - II

REVIEW OF LITERATURE

A complete understanding of the DUS characterization, genetic diversity, extent of variation, heritability of the character, character association, path analysis would help in crop improvement programme. The genetic improvement of economically important traits requires adequate knowledge of their inheritance pattern, genetic variability and relative contribution of genetic and non-genetic components in their expression and inter-relationships.

A brief review of literature in accordance with the objectives of research programme in pearl millet germplasm is previewed here under.

2.1 MORPHOLOGICAL CHARACTERIZATION

Characterization of germplasm accessions provides pivotal information for the breeding of crop and in the management of genetic resources. Information on characterization of a genotype offers valuable knowledge 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 section.

Kumar *et al.* (2005) studied 41 genotypes of pearl millet, including 12 hybrids and their parental lines, and grouped them into two distinct categories based on anthocyanin pigmentation of seedlings under field and controlled conditions of growth. More genotypes (29) developed pigmentation under controlled conditions than in field (14) possibly due to availability of optimum conditions for pigment synthesis. Seedling anthocyanin pigmentation in combination with seed characters such as shape, colour and response to phenol colour reaction could identify 9 genotypes individually and group the rest into 9 categories each with 2-7 genotypes.

Reddy *et al.* (2006) characterized 1535 foxtail millet accessions and based on plant color, accessions were classified into three classes: green, pigmented and deep purple. The majority were green (74.6%), followed by pigmented (23.6%) and deep purple (1.8%). Among the four types of growth habits decumbent, erect, erect geniculate and prostrate 96.5% accessions were erect. Leaf colour of the accessions was classified as green, pigmented or yellow. The majority of the accessions were green (80.7%) followed by yellow (10.6%) and pigmented (8.7%).

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.

Bhattarai *et al.* (2014) classified 537 accessions of finger millet based on ear shape and observed that 280 accessions were semi-compact, 153 were open, 54 accessions were compact and 27 accessions were droopy. For grain color, 133 showed purple brown grain color whereas 128 and 11 accessions showed light brown and copper brown grain color respectively and one accession showed white grain color.

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 shape 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. Large variation among inbreds were found for the quantitative traits like days to 50% flowering (40.33 - 58.55 days), leaf blade length (33.53 -72.13 cm), spike length (13.60 - 24.60 cm), number of productive tillers plant^{-1} (1.60 - 9.57), plant height (115.60 - 160.87 cm) and 1000 grain weight (4.35 - 14.80 g).

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, color of the plant and leaf, growth habit of the plants, panicle shape, lobe characteristics of the panicle and inflorescence. All the accessions were reported to be erect in growth habit and had white anther colour.

Singh *et al*. (2016) characterized pearl millet hybrids and their parents based on morphological descriptors with the objective to identify key diagnostic characters of the genotypes. They selected 24 pearl millet genotypes (7 hybrids and their 17 parental lines) and observations were recorded for 28 morphological and yield characters. All genotypes were classified into different groups based on each character. Nodal pubescence, nodal pigmentation, spike shape, spike density, spike tip sterility, sheath pubescence and spikelet glum colour distinguished all the 24 genotypes by assigning them key diagnostic features that would certainly help the plant breeders, seed growers and seed certification agencies to use these diagnostic characters. Hybrids HHB 216, HHB 226 and HHB 117 could be differentiated by bristle length, spikelet glume colour and spike tip sterility.

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.

Amarnath *et al.* (2019) done DUS characterization for 50 foxtail millet germplasm accessions and grouped them based on six quantitative traits. The results revealed that germplasm accessions had enormous genetic diversity.

Ankit *et al.* (2020) characterized 92 accessions of finger millet and recorded that most of the accessions exhibited erect growth (50%), droopy ears (27.14%), dark green glume (58.70%), non-pigmented leaf juncture (67.30%) and non-culm stem branching (67.39%). Majority of germplasm entries exhibited non branched fingers (88.40%). Among branched fingers predominance was for thumb position (63.04 %). It was noted that seeds of majority of genotypes had brown color (55.43 %).

Kalagarey *et al.* (2020) characterized 31 pearl millet genotypes using DUS descriptors and revealed that most of the DUS traits showed at least two classes except for six traits like leaf sheath pubescence, stigma pigmentation, node pubescence, number of nodes, panicle bristle and panicle bristle appearance which showed no classification. This indicated the presence of diversity for observed morphological traits among the genotypes.

2.2 GENETIC VARIABILITY PARAMETERS

Genetic variability is essential for initiating an effective and successful breeding programme. Variability in a population is measured by phenotypic and genotypic variances. Since the variances are influenced by magnitude of the units of measurement of different traits, a measure of coefficient of variation (CV), which is independent of the unit of measurement, is more useful in comparison between different phenotypes. The coefficient of variation expressed in phenotypic and genotypic levels i.e, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) are used to compare the variability observed among the different characters.

Genetic improvement in pearl millet is possible through selection of characters which show the significant amount of GCV, PCV, heritability (H) and genetic advance (GA). Genotypic coefficient of variation does not give the idea of total heritable variation. The relative amount of heritable portion of

variation can be assessed through heritability estimation. Heritability analysis gives an idea about the effectiveness with which selection can be practiced for the genetic improvement of a particular character based on phenotypic performance.

Magnitude of heritability indicates the reliability with which the genotype will be recognized by its phenotypic expression. Heritability coupled with genetic advance as per cent of mean (GAM) will bring out the genetic gain expected from selection than heritability alone (Herbert W Johnson, Robinson and Comstock, 1955). Previous reports related to GCV, PCV, heritability and genetic advance (as per cent of mean) in pearl millet were summarized below.

Singh *et al.* (2014) evaluated 24 lines (7 hybrids and 17 parental lines) and observed high GCV, heritability and GAM for grain yield plant^{-1}, dry fodder weight plant^{-1}, fresh fodder weight plant^{-1}, productive tillers plant^{-1} and plant height.

Bika *et al.* (2015) conducted variability studies with 30 genotypes for green fodder yield and its related characters and revealed high GCV and PCV for dry matter yield, green fodder yield, while high heritability conjugated with high GAM for spike length, green fodder yield and dry matter yield.

Bind *et al.* (2015) recorded close proximity between GCV and PCV for grain yield plant^{-1}, panicle length and dry matter yield plant^{-1} and high heritability coupled with high GAM for grain yield plant^{-1}, panicle length, dry matter yield plant^{-1}, days to 50% flowering and green fodder yield plant^{-1} in their study involving 36 fodder pearl millet genotypes.

Yaqoob *et al.* (2015) studied 25 pearl millet accessions and noticed high GCV and PCV for grain yield. Moderate to high heritability was noticed for days to heading and days to maturity; very high heritability for 1000-grain weight and grain yield. High heritability amalgamated with high GAM was noticed for grain yield.

Naveen *et al*. (2016) observed moderate to high PCV and GCV for SCMR, plant height, number of productive tillers plant^{-1}, ear head length and grain yield plant^{-1}, while greater magnitude of broad sense heritability coupled with higher GAM for SCMR, plant height, number of productive tillers plant^{-1}, ear head length and grain yield plant^{-1} in their study involving 250 pearl millet recombinant inbred lines.

Bhasker *et al.* (2017a) studied 56 pearl millet genotypes comprising of 40 F_1s, 4 male sterile lines and 12 pollinators for genetic variability, heritability and genetic advance and recorded high GCV, PCV and heritability coupled with maximum GAM for plant height, productive tillers plant^{-1}, panicle length and fodder yield.

Nehra *et al.* (2017) studied 49 pearl millet inbred lines and observed higher PCV and GCV for number of productive tillers, thousand grain weight, green fodder yield, dry fodder yield and seed yield, while high heritability coupled with high GAM was recorded for number of productive tillers plant^{-1}, thousand grain weight, dry fodder yield, green fodder yield and grain yield; high heritability with moderate to low GAM was observed for days to 50% flowering, spike girth, spike length and plant height.

Jagdeep and Ashok Kumar (2018) investigated genetic variability for 50 advance inbred lines of pearl millet and revealed the existence of higher PCV for all the characters than its corresponding GCV. High estimates of coefficient of variation along with high to moderate heritability and genetic advance as per cent over mean was observed for grain yield panicle^{-1} and dry fodder yield indicating the predominance of additive genetic variance for these characters. Likewise, moderate heritability with moderate genetic advance was observed for grain yield and plant height, while high heritability, low genetic advance and low variability for panicle length and days to 50% flowering indicating prevalence of non-additive genetic variance.

Thomas *et al*. (2018) studied 22 pearl millet genotypes for genetic variability. The estimates of genotypic coefficient of variation were much

lesser than that of phenotypic coefficient of variation for all the traits indicating the role of environmental influence for characters studied. High heritability combined with high genetic advance as per cent of mean was observed for green fodder yield plant^{-1}, dry matter yield plant^{-1} and crude protein content.

Kaushik *et al.* (2018) studied 48 maintainer lines of pearl millet and observed slightly lower GCV than PCV indicating the slight influence of environment on the expression of all the characters. High heritability with high GAM was observed for number of productive tillers plant^{-1}, plant height, 1000-grain weight and grain yield plant^{-1} suggesting the prevalence of additive gene action in their inheritance.

Patel *et al.* (2019) investigated 30 genotypes including hybrids and advance lines of pearl millet and recorded high GCV and PCV values for most of the traits studied. Higher PCV values was seen for number of effective tillers plant^{-1}, grain yield plant^{-1}, harvest index and test weight. Pertaining to heritability and GAM, high values were obtained for plant height, dry fodder yield, ear head girth, ear head length, grain yield, test weight and harvest index.

Priyanka *et al.* (2019) in their study with 42 genotypes of pearl millet, revealed the existence of higher values of PCV, GCV, heritability and GAM for grain yield plant^{-1}, green fodder yield plant^{-1}, iron content, green fodder yield plant^{-1}and zinc content.

Rashita *et al.* (2019) included 42 maintainer and 17 restorer pearl millet lines in their genetic studies and reported high heritability and GAM for spike length, spike girth, plant height, 1000-seed weight and single plant yield. However, they recorded higher PCV than GCV for all the traits studied.

Anuradha *et al.* (2020) revealed the preponderance of high PCV for number of productive tillers and moderate GCV for test weight, while high heritability coupled with high GAM was recorded for test weight and fodder yield plant^{-1}.

Annamalai *et al.* (2020) assessed genetic variability in 50 pearl millet germplasm lines and recorded high PCV and GCV for grain yield, number of productive tillers, spike length, 1000 grain weight and plant height while the traits *viz.*, grain yield and plant height recorded high heritability with high GAM.

Dadarwal *et al.* (2020) evaluated 30 maintainer lines of pearl millet and revealed the presence of high heritability with high GAM for days to 50% flowering, plant height, test weight and grain yield plant^{-1}.

Mithlesh *et al.* (2020) revealed high to moderate heritability coupled with moderate to high GAM for the plant height, panicle length, panicle girth, grain yield plant^{-1}, grain iron (Fe) and zinc (Zn) content. Higher PCV values than GCV values was obtained for all the characters studied.

Narasimhulu and Veeraraghavaiah (2020) studied the performance of 16 pearl millet genotypes and observed high heritability coupled with high GAM for grain yield and moderate heritability and high GAM for number of productive tillers. In contrast, high heritability coupled with low GAM and GCV was observed for days to maturity and days to 50% flowering, indicating that the role of non- fixable genetic variation.

Ravindrakumar *et al.* (2020) conducted variability studies composed of 87 hybrids and three checks in pearl millet. They observed high GCV and PCV for number of effective tillers plant^{-1}, harvest index and seed yield plant^{-1}, while low GCV and PCV were observed for days to 50% flowering, days to maturity, plant height and panicle length.

Sai kumar *et al.* (2020) in their study with 10 maintainer and 27 restorer lines revealed the presence of high GCV, PCV, heritability and GAM for panicle length, green fodder yield plant^{-1}, dry fodder yield plant^{-1}, 1000-grain weight, harvest index and grain yield plant^{-1} indicating the preponderance of additive gene action.

Shailja *et al.* (2020) evaluated nine parents and their 36 F_1s developed through half diallel cross and observed high heritability for panicle length,

plant height, days to 50% flowering and grain yield plant^{-1} and high GAM for effective tillers plant^{-1} and grain yield plant^{-1}.

Yadav *et al.* (2020) conducted genetic variability studies for grain iron, zinc, grain yield and its contributing characters and noticed highest PCV and GCV for zinc content, while the lowest for days to maturity. High heritability along with high GAM was noticed for days to 50% flowering, plant height, number of productive tillers plant^{-1}, panicle length, panicle diameter, stover yield plant^{-1}, grain yield plant^{-1}, 1000-grain weight, harvest index, iron content and zinc content.

Narsimhulu *et al.* (2021) studied 95 pearl millet hybrids and recorded highest GCV and PCV values for number of productive tillers plant^{-1} and grain yield, while high heritability along with high genetic advance as percent of mean was recorded for number of productive tillers plant^{-1} and grain yield, indicating the predominance of additive gene effects.

Shashibushan *et al.* (2021) evaluated 40 pearl millet genotypes and observed GCV values were highest for productive tillers plant^{-1} and fodder yield plant^{-1}. Plant height, productive tillers plant^{-1} and grain yield plant^{-1} had highest PCV values. Except for days to maturity all traits had the highest heritability along with high GAM.

Yadav *et al.* (2022) studied 45 pearl millet hybrids and recorded high heritability coupled with high genetic advance as per cent of mean for plant height among hybrids, while other traits show low heritability and low genetic advance as percent of mean.

2.3 GENETIC DIVERGENCE

Genetic divergence is an important factor and also a prerequisite of any hybridization programme because crosses between divergent parents usually produce greater heterosis than those between closely related ones (Moll and Stuber, 1971). Genetic divergence is a result of changes in gene frequencies of different populations due to evolutionary forces.

The concept of D^2 statistics for measuring the divergence between the two populations was introduced by Mahalanobis (1936). Rao (1952) suggested the application of this technique for assessment of genetic diversity in plant breeding. It gives a result based on magnitude of divergence and independent of size of samples. Use of diverse parents in hybridization programme can serve the purpose of combining desirable genes or to obtain recombination. A brief review of work done in this regard in pearl millet is presented below.

Choudhary *et al.* (2013) carried out genetic divergence analysis in 50 genotypes of pearl millet along with three checks using D^2 statistics. Their results revealed that genotypes were grouped into 14 clusters. The genotypes of cluster IX had higher mean value for grain yield plant^{-1}, plant height and test weight and they suggested to use these genotypes as diverse parents in hybridization programme.

Sathya *et al.* (2013) investigated 47 accessions (44 inbred lines and 3 checks) of pearl millet to assess genetic diversity by using multivariate heirarchial clustering analysis and grouped them into eight clusters. Cluster IV had highest number of inbreds (18) followed by cluster I (10) and cluster VI (9). TNBI 43 of cluster V was early to flower and recorded highest mean value for ear head length, number of tillers, ear head girth and grain yield plant^{-1} among 47 genotypes, was suggested for use as a superior parent in hybridization programme to enhance yield potential.

Sumanth *et al*. (2013) evaluated genetic diversity among 42 inbred lines (22 maintainer lines and 20 restorer lines) of pearl millet and grouped the parental lines into three main clusters. Among the three clusters, cluster II was the largest comprising 34 genotypes which is further divided into five sub clusters. Out of five sub clusters in cluster II, the fifth sub cluster itself formed largest group with 25 genotypes consisting 10 restorer lines and 15 maintainer lines. Of the maintainers evaluated, ICMB 88004 alone remained as single apart and highly diverse which can be used for the new male sterile line

development programme. Among the twenty restorer lines, PT 6065, PT 6243, PT 6066, PT 6064, PT 6033 and PT 6029 were highly diversified.

Kumar *et al*. (2015a) assessed genetic divergence among 97 pearl millet genotypes and grouped them into six clusters using D^2 statistics. Mean of characters for each genotype within a cluster was closest to the cluster mean. Plant height, ear diameter and grain yield were found to be best discriminatory characters for better selection of diverse genotypes.

Kumar *et al.* (2015b) studied genetic diversity for 26 genotypes and grouped them into eight clusters. Of the 8 clusters formed, cluster I and II were largest with seven genotypes in each followed by cluster III with 5 genotypes. Cluster IV and VIII had maximum inter-cluster distance whereas minimum inter-cluster distance was recorded between cluster I and cluster VII. The intra-cluster distance was maximum in cluster III followed by cluster II and cluster IV.

Verma *et al.* (2015) estimated genetic diversity among 171 pearl millet germplasm entries and using D^2 clustering grouped them into eight clusters. Plant height, dry fodder yield and grain yield contributed more towards genetic divergence. In addition, the study revealed that genotypes superior to individual trait belongs to different clusters which indicates that none of the clusters contained genotypes with all desirable characters.

Athoni *et al*. (2016) made an attempt to assess the genetic divergence among the 243 germplasm lines by using Mahalanobis D^2 statistics and grouped them into 16 different clusters. Cluster I was the largest with 129 genotypes followed by cluster III (49 genotypes) and cluster V (24 genotypes), while clusters II, VI, VII, VIII, X and XVI were solitary indicating the grouping of more diverse exotic collections in definite groups. Among various characters, seed yield, panicle girth and leaf length contributed maximum towards the divergence.

Jyothi *et al.* (2016) evaluated a total of 221 pearl millet collections and hierarchical clustering method was used for classifying accessions based on agronomic and disease resistance traits, which resulted into three clusters. Clusters I, II and III comprised of 91, 54 and 76 accessions respectively. Among the traits analyzed, plant height, number of nodes plant^{-1}, days to spike emergence, number of tillers, leaf width and leaf length were major contributors towards phenotypic diversity.

Kumari *et al*. (2016) worked out genetic diversity among 30 pearl millet genotypes including three check varieties using D^2 statistics. Genetic divergence analysis grouped the genotypes into 11 clusters. Cluster I was the largest and consisted of 14 genotypes followed by cluster IV with four genotypes and cluster VIII with four genotypes, whereas, clusters II, III, V, VI, VII, IX, X, XI were monogenotypic clusters. Days to maturity and panicle length contributed maximum towards genetic divergence. The maximum inter cluster distance was between cluster IV and cluster XI. Based on divergence study, the genotypes could be selected from the most divergent clusters for hybridization programme.

Sumathi *et al.* (2016) evaluated 100 pearl millet genotypes and grouped into 11 clusters. Cluster VII had 41 genotypes followed by 28 genotypes in cluster III, 14 genotypes in cluster I and three genotypes in cluster XI. The highest inter cluster distance was recorded between cluster VIII and cluster X. The genotypes, PT 2616 and PT 2656 of cluster X had high mean value for plant height, spike length, 1000 seed weight, single ear head weight and grain yield per ear head which could be used for effective hybridization programme to develop hybrid or variety or composite.

Basavaraj *et al.* (2017) conducted genetic diversity studies among 75 restorer lines of pearl millet for nine different productivity traits using Mahalanobis D^2 statistics. Genetically more divergent genotypes were present in clusters II and V. Among the characters studied, panicle weight contributed

highest towards genetic divergence followed by panicle girth and stover weight plot^{-1}.

Ramya *et al*. (2017) conducted divergence analysis among 60 inbred lines including 27 maintainer (B) and 33 restorer (R) lines of pearl millet based on quantitative data of grain yield and its ten component characters. Cluster analysis grouped the inbred lines into eight clusters and the characters *viz.*, plant height, 1000 grain weight, dry matter yield plant^{-1} and number of productive tillers plant^{-1} contributed maximum towards genetic divergence. They noticed maximum inter cluster distance between lines of clusters I, II with cluster VII indicating that lines included in these clusters may have high heterotic response and produce better hybrids when used in pearl millet hybridization.

Employing D^2 analysis, Kaushik *et al.* (2018) divided 48 maintainer lines of pearl millet into seven clusters. Results revealed that cluster II and cluster IV had highest number of genotypes (10 each) followed by cluster I and III (9 each). For days to 50% flowering highest mean value was possessed by cluster IV and lowest mean value by cluster I. Crosses between the genotypes with higher mean values for different traits and of distantly located clusters are likely to produce desirable hybrids in pearl millet.

Utilizing D^2 analysis, Singh *et al.* (2018) examined 40 pearl millet germplasm lines and grouped them into eleven clusters. Based on cluster means, cluster IV had highest mean value for grain yield plant^{-1}. Maximum contribution to genetic divergence was exhibited by number of productive tillers plant^{-1} followed by grain yield plant^{-1}, days to maturity, days to 50% flowering, spike length, plant height, harvest index, test weight and spike girth.

Abdulhakeem *et al.* (2019) evaluated 35 land races of pearl millet for morphological and yield parameters and constructed a dendrogram based on similarity distance and grouped the accessions into four clusters. Cluster III had 14 genotypes followed by 10 genotypes in cluster IV, six genotypes in

cluster II and three genotypes in cluster I. Accession NGB 528 and NGB 589 were grouped together as a distinct unit in cluster II while similar strong association was obtained between NGB 514 and NGB 594 in cluster III.

Kumar *et al.* (2020a) investigated 48 maintainer (B) and restorer (R) lines of pearl millet and grouped the genotypes into five clusters by using UPGMA. Cluster I possessed genotypes with high panicle length and dry fodder yield. Cluster II comprised only B lines with high panicle girth and late flowering type. While, cluster IV had both 'B' and 'R' lines with early flowering habit and high panicle girth. Clustering of genotypes from different geographical locations into same cluster has confirmed that they are genetically related and possibly from the same progenitor, but could have been separated by geographical or ecological barriers.

Swamynatham *et al.* (2020) conducted genetic divergence studies among 50 pearl millet germplasms using Mahalanobis D^2 statistics for fourteen different traits and grouped the genotypes into sixteen clusters. The maximum inter-cluster distance was observed between cluster XV and XVI followed by clusters V and XV clusters X and XV, clusters XIII and XV, clusters XI and XV and clusters VI and XVI.

Utilizing D^2 analysis, Natwaria *et al.* (2021) evaluated 61 F_1 hybrids and three standard check hybrids and grouped them into 19 clusters. Results of divergence studies indicated the presence of high degree of genetic divergence among the hybrids.

Saikumar *et al.* (2021) conducted divergence analysis among 37 parental lines of pearl millet (10 maintainer and 27 restorer lines) for grain yield and its attributes through Mahalanobis D^2 statistics and grouped them into eight different clusters. Among the characters studied 1000 grain weight contributed maximum (25.53%) towards genetic diversity followed by days to 50% flowering (19.22%), panicle girth (13.21%), panicle length (8.71%), panicle weight (7.81%) and plant height (7.36%).

Kumar *et al.* (2022) examined 90 pearl millet hybrids and grouped them into nine clusters by using Mahalanobis D^2 statistics. Cluster I was the largest with 43 hybrids followed by cluster III (24 hybrids) and cluster II (17 genotypes). In the study, test weight (73.26%) had highest contribution towards total divergence, which was followed by ear head diameter (13.91%), biological yield (3.25%) and days to maturity (3.0%).

Shasibhusan *et al.* (2022) evaluated 40 genotypes of pear millet and grouped them into seven clusters by using Mahalanobis D^2 statistics. Among different clusters the maximum genotypes were observed in cluster V followed by cluster IV and cluster III. Days to flowering was the most important factor in genetic divergence (18.71%), followed by productive tillers $plant^{-1}$ (18.46%), fodder yield $plot^{-1}$ (18.20%), and panicle length (17.30%).

Kalagare *et al.* (2022) investigated 31 genotypes (containing R lines, B lines and land races) of pearl millet to assess genetic diversity by using Mahalanobis D^2 analysis and grouped them into six clusters. Out of six clusters, cluster I possessed maximum genotypes of 23 followed by four genotypes in cluster II.

2.4 CORRELATION ANALYSIS

Correlation studies provide better understanding of yield components which helps the plant breeder during the selection (Robinson *et al.* 1951, Johnson *et al.*1955b). The concept of correlation was given by Galton (1889), which was further elaborated by Fisher (1918). It provides information on the nature and extent of association between any two biometrical traits, it would be possible to bring out genetic upgradation in both the traits of a pair simultaneously. The association between the attributes is measured as “Correlation coefficient”.

Correlation may be positive, negative or zero. If the change is same direction, the correlation is positive and if it is in opposite direction the

correlation is negative. The value is zero when two variables are not related. Positive correlation between desirable characters is favourable to the plant breeder because it helps in simultaneous improvement of both the characters.

Correlation may be phenotypic, genotypic or environmental. Phenotypic correlation is the association between the two phenotypic values which can be directly observed and is subjected to changes in environment. It involves both genetic and non-genetic causes. Genotypic correlation is due to genetic association of two breeding values i.e., additive and (additive × additive) gene effects (Falconer, 1989) and it may be due to either pleiotropy or linkage of genes either in coupling or repulsion phase. Environmental correlation is not strictly due to environmental deviations but merely due to non-genetic deviations. Selection based on component characters is much more useful than selection based on yield *per se* performance. Grain yield of a plant is the net result of several genetic factors and their individual or combined interplay with environmental factors. Hence it is essential to measure the correlations at phenotypic and genotypic levels under different environments.

A brief account on correlation studies already performed in pearl millet was presented here under.

Bikash *et al.* (2013) studied 30 elite hybrids of pearl millet to estimate the association between grain yield and its component characters. Their study revealed that, grain yield was significantly and positively correlated with 1000 grain weight, harvest index, ear girth, number of effective tillers plant^{-1}, dry fodder yield plant^{-1} and biological yield. Ear length had non significant positive association with grain yield.

Ravi (2013) studies on character association analysis with 15 maintainer (B) lines and 61 restorer lines (R) of pearl millet revealed that grain yield plant^{-1}had strong positive association with panicle length, panicle girth and number of productive tillers plant^{-1} while negative association of grain yield was observed with days to 50% flowering and plant height.

Sankar *et al.* (2013) investigated 38 inbred lines of pearl millet and reported positive and significant correlation for 1000 seed weight, spike girth and leaf blade width with grain yield plant^{-1} whereas days to 50% flowering and days to maturity showed significant but negative correlation with grain yield.

Vinodhana *et al.* (2013) studies on character association analysis with 50 pearl millet genotypes revealed that panicle length, panicle diameter, 1000 seed weight and fodder yield had positive and significant association with grain yield. Hence selection towards these components will lead to development of high yielding pearl millet hybrids.

Bhurisingh *et al.* (2014) studied 55 pearl millet genotypes and showed significant and positive correlation of grain yield plant^{-1} with number of productive tillers plant^{-1}, plant height, panicle length, panicle girth, biological yield plant^{-1}, dry fodder yield plant^{-1}, harvest index and test weight at both phenotypic and genotypic levels.

Dapke *et al.* (2014) assessed 12 maintainer (B) and 12 restorer (R) lines of pearl millet for ten quantitative traits. Association studies revealed that grain yield had genotypically significant and positive correlation with ear head length, number of effective tillers, biological yield plant^{-1} and harvest index. Whereas, days to maturity and days to 50% flowering showed highly significant but negative correlation at both genotypic and phenotypic levels with grain yield plant^{-1}.

Kumar *et al.* (2014a) character association studies with 26 pearl millet hybrids traits *viz.*, plant height, panicle length, number of productive tillers plant^{-1} and dry fodder yield plant^{-1} exhibited significant positive phenotypic correlation with grain yield plant^{-1}.

Kumar *et al.* (2014b) studied 97 diverse pearl millet genotypes for character association of eight characters *viz.*, days to 50 percent flowering, plant height, effective tillers plant^{-1}, panicle length, panicle girth, number of

nodes, internode length and grain yield. Their results showed significant and positive correlation of grain yield plant^{-1} with plant height, panicle girth, panicle length, panicle diameter, number of nodes and internode length. Hence, these traits could be considered as suitable selection criteria for the development of high yielding pearl millet genotypes.

Bika and shekhawat (2015) with 30 genotypes including three check varieties, studied character association among characters related to green fodder yield, and concluded that days to 50 percent flowering, plant height, number of tillers plant^{-1}, panicle length and biological yield were having positive and significant correlation with green fodder yield.

Dhendi *et al*. (2015) studies on correlation analysis with 23 genotypes of fodder pear millet revealed that negative and significant association of grain yield with days to 50 percent flowering, days to maturity and biological yield. Similarly, positive and significant association of grain yield with harvest index.

Haq *et al.* (2015) evaluated 10 genotypes of pearl millet to determine the correlation among the yield and yield component characters in randomized completely block design with three replications. Significant and positive correlation coefficient was observed for grain yield with plant height, days to flowering, ear head length, ear head girth, flag leaf area and biomass. Similarly, positive and strong association was found for panicle length with days to flowering and panicle girth.

Yahaya *et al*. (2015) studies on correlation analysis of 90 genotypes consisting of 81 hybrids and nine 9 inbred lines of pearl millet revealed that positive and significant association observed for plant height, panicle length, tillers plant^{-1} and panicle weight with grain yield at genotypic and phenotypic level.

Kumar *et al.* (2016) assessed 50 pearl millet hybrids including three checks to estimate correlation among seed yield plant^{-1} and its ten component

characters. They observed that seed yield plant^{-1} had significant and positive correlation with number of effective tillers plant^{-1} and harvest index. Significant and negative correlation of seed yield plant^{-1} was found with days to 50% flowering and days to maturity at both genotypic and phenotypic levels.

Bhasker *et al*. (2017) conducted a study to determine the correlation among the yield and yield component characters in 13 parental lines (5 lines and 8 testers) and their 40 hybrids of pearl millet and revealed positive and significant correlation for plant height, effective tillers plant^{-1}, panicle length, panicle diameter, 1000 seed weight and biological yield with grain yield.

Dehinwal *et al.* (2017) evaluated 100 inbred lines of pearl millet to study association among the different biometrical and harvest plus traits with grain yield. Grain yield plant^{-1} expressed positive and significant correlation with dry fodder yield followed by ear weight, total tillers plant^{-1}, effective tillers plant^{-1}, spike girth and plant height. There was significant and positive association between many traits indicating that these traits could be improved simultaneously.

Anuradha *et al.* (2018) conducted an experiment to study association of agronomic traits and micronutrients in 130 genotypes of pearl millet. They revealed significant and positive correlation of grain yield with number of productive tillers plant^{-1}, panicle length, panicle diameter and plant height. No significant association was found between grain yield and micronutrient content. Hence it is possible to select simultaneously for higher micronutrient content without hampering grain yield.

Patil *et al.* (2018) determined the correlation of yield and yield component characters in 14 parental populations and 91 hybrids of pearl millet formulated by a diallel cross excluding reciprocals. Strong and significant genotypic and phenotypic correlations were observed between grain yield with panicle girth, plant height and panicle length.

Sharma *et al.* (2018) evaluated 34 inbreds of pearl millet for association of grain yield with component traits. The traits number of effective tillers plant^{-1}, ear length, ear girth and seed density showed positive association with grain yield for which indirect selection can be made in breeding programme to enhance grain yield.

Singh and Chhabra (2018) studied 50 advance inbred lines of pearl millet to analyze genetic variability and character association among them under normal as well as drought situations. They revealed that grain yield plant^{-1} expressed a positive and significant correlation with flag leaf area, number of tillers plant^{-1}, plant height, dry fodder yield, panicle length, grain yield per panicle while it expressed a negative correlation with days to 50% flowering in both normal and drought conditions.

Subbulakshmi *et al.* (2018) conducted correlation studies in 54 hybrids of pearl millet for yield and nutritional traits. Correlation studies revealed that single plant yield has positive significant correlation with the agronomic traits *viz.*, plant height, number of productive tillers, test weight, single head grain weight and quality traits *viz.*, crude fibre, beta carotene and iron; whereas, days to 50% flowering alone recorded negatively significant correlation with single plant yield. It is therefore inferred that simple selection will be effective against positively correlated characters.

Rasitha *et al.* (2019) evaluated 42 B lines and 17 R lines and noticed positive significant correlation of single plant yield with plant height, spike girth and 1000 grain weight. Inter-correlation analysis showed that plant height had a significant positive correlation with spike length and it had significant but negative correlation with number of productive tillers plant^{-1}.

Kumar *et al.* (2020a) investigated 24 maintainer (B) and 24 restorer (R) lines of pearl millet and revealed positive and significant correlation of grain yield plant^{-1} with plant height, panicle weight and dry fodder yield plant^{-1}. Grain yield plant^{-1} exhibited neither positive nor negative correlation with micronutrient concentration suggesting improvement in yield without

compromising nutrient content. Significant but negative association between grain yield plant^{-1} and panicle weight with days to flowering is an added advantage in pearl millet cultivation to fit into multiple cropping system of arid and semi-arid environments.

Kumar *et al.* (2020b) made an attempt to estimate correlation among the yield and yield attributes in 87 hybrids of pearl millet along with three checks. Character association studies indicated that seed yield plant^{-1} had significant and positive correlation with harvest index, number of effective tillers plant^{-1}, biological yield plant^{-1}, test weight and negatively correlated with days to 50% flowering and days to maturity at phenotypic level which is desirable for development of hybrids with high grain yield and early maturity.

To study the genetic variability parameters and character association in pearl millet Annamalai *et al.* (2020) evaluated 50 pearl millet genotypes for 13 different biometrical traits. Character association studies revealed that grain yield was highly significant and positively correlated with spike length (0.69), 1000 grain weight (0.56), number of productive tillers (0.53), number of tillers plant^{-1} (0.49) and peduncle length (0.42).

Dadarwal *et al.* (2020) evaluated 30 maintainer lines of pearl millet to study correlation and path analysis for grain yield and its yield contributing characters. They reported that grain yield plant^{-1} had significant and positive association with ear head length, ear head girth, 1000 grain weigh and biological yield plant^{-1} at genotypic as well as phenotypic level and harvest index at phenotypic level only.

Pallavi *et al.* (2020) evaluated 49 parental lines of pearl millet for extent of genetic variability and correlation for grain yield and its attributing characters and they reported that grain yield showed a significant positive correlation with plant height and ear length.

Anuradha *et al.* (2021) evaluated 16 pearl millet genotypes including one check variety (ABV 04). Character association studies indicated that grain yield showed negative association with panicle diameter.

Patil *et al.* (2021) made an attempt to estimate correlation coefficients among the grain yield and yield contributing characters in 14 parental lines (4 lines and 10 testers) and their 40 hybrids of pearl millet. Positive and significant correlations were observed for 1000 seed weight followed by fodder yield plant^{-1}, harvest index, earhead girth, number of effective tillers plant^{-1}, earhead length and plant height. While, negative association with days to 50% flowering at both genotypic and phenotypic level with grain yield plant^{-1}.

Shasibhusan *et al.* (2021) evaluated 40 genotypes of pearl millet and noticed that at both the genotypic and phenotypic levels, grain yield plant^{-1} demonstrated a strong significant positive association with attributes such as fodder yield plot^{-1}, productive tillers plant^{-1}, panicle length and panicle diameter.

Kumar *et al.* (2022) conducted correlation studies in 18 hybrids of pearl millet and the results revealed that grain yield plant^{-1} exhibited significant positive association with panicle diameter followed by panicle length and plant height and exhibited non-significant association with days to 50% flowering.

Yadav *et al.* (2022) investigated 45 pearl millet hybrids and revealed that direct selection for higher values of harvest index, plant height, biological yield plant^{-1} and number of effective tillers plant^{-1} will improve seed yield plant^{-1} based on correlation studies.

2.5 PATH COEFFICIENT ANALYSIS

For rational improvement of yield and its components, knowledge of character association, cause and effect relationship, direct and indirect effects of component characters on grain yield provides a basis in framing suitable

selection methods. Simple correlation does not give the direct and indirect effects towards yield. Therefore, path coefficient analysis is a useful method of estimating the direct and indirect contribution of attributes on yield.

The concept of path analysis was initially suggested by Wright (1921) but was applied for first time in plant breeding by Dewey and Lu (1959). A path coefficient is simply a standardized partial regression coefficient. It measures the direct and indirect effects of independent variable on dependent variable and allows partitioning of the total correlation coefficient between two variables into direct and indirect components. Path analysis assists breeders in giving due weightage to important yield components while exercising selection.

A brief review of path analysis of yield and yield components reported in pearl millet which will certainly helpful for varietal improvement programme is presented here under.

Chaudhary *et al.* (2012) carried out path coefficient analysis among 60 pearl millet genotypes for nine quantitative characters. They showed that ear head length, harvest index, number of nodes plant^{-1} and fodder yield plant^{-1} were the most important characters manifesting large positive direct effects on grain yield. Positive association of fodder yield plant^{-1}, harvest index and number of nodes plant^{-1} with grain yield and also their large direct effect on grain yield suggested that maximum emphasis should be given on these traits in selection for improvement of grain yield.

Govindaraj and Selvi (2012) examined 61 indigenous germplasm lines of pearl millet and found that maximum direct effect on grain yield plant^{-1} was contributed by crude fat content followed by days to maturity, panicle girth and number of productive tillers. Panicle girth and 1000 grain weight showed positive and significant indirect effects on grain yield.

Ravi (2013) conducted an experiment with fifteen maintainer (B) lines and sixty one restorer (R) lines for path coefficient analysis and the results

revealed that 1000 grain weight, specific leaf area and harvest index showed positive direct effect on grain yield. Similarly, days to maturity and fodder yield showed negative indirect effects on grain yield.

Dapke *et al.* (2014) assessed 12 maintainer (B) and 12 restorer (R) lines of pearl millet for ten quantitative traits. Path analysis revealed high positive direct effect on grain yield plant^{-1} by ear head length, number of effective tillers, biological yield plant^{-1}, days to 50% flowering and harvest index. While, plant height, days to maturity and flag leaf area had direct negative effect on grain yield plant^{-1}.

Kumar *et al.* (2014b) studies on path analysis found that panicle length and plant height exhibited the highest positive and significant direct effect on grain yield at genotypic level. Hence, these traits could be considered as suitable selection criteria for the development of high yielding pearl millet hybrids.

Bakhit and Elgasim (2015) conducted a study in 18 pearl millet genotypes to determine the direct and indirect effects of sixteen characters as yield components on grain yield through path coefficient analysis. The results indicated that panicle length had highest direct effect on grain yield plant^{-1}, followed by number of productive tillers plant^{-1} and panicle girth. The highest indirect effects on grain yield plant^{-1} were showed by 1000 seed weight through number of productive tillers plant^{-1} and number of seeds per panicle through panicle girth.

Rakesh *et al.* (2015) evaluated 50 genotypes of pearl millet to study extent of association between the yield and its component characters including direct and indirect effects. Their results revealed that plant height followed by days to 50% flowering, 1000 grain weight, panicle length, panicle diameter and number of productive tillers had high positive direct effects towards grain yield plant^{-1}. Whereas, days to maturity and fodder yield plot^{-1} exhibited direct but negative effect on grain yield plant^{-1}.

Naveen *et al.* (2016) conducted path analysis among 250 recombinant inbred lines (RILs) of pearl millet. They noticed that number of productive tillers plant^{-1}, single ear head weight had high positive and direct effect on grain yield plant^{-1}. High indirect effect on grain yield was exerted by single ear head weight. 1000 grain weight also influences grain yield through moderate indirect effect *via* number of productive tillers plant^{-1}.

Sowmiya *et al.* (2016) studied inter-relationship analysis in F_3 and F_4 seggregating generations for ten quantitative traits in pearl millet. Their results indicated that traits *viz.*, single ear head grain weight, number of productive tillers plant^{-1} had positive and direct effect towards grain yield plant^{-1}. Single ear head grain weight showed positive indirect effect through days to maturity, plant height, number of productive tillers plant^{-1} and ear head girth.

Sumathi *et al.* (2016) evaluated 100 pearl millet genotypes and path coefficient analysis revealed that, a very high positive direct effect on grain yield was exhibited by days to 50% flowering, spike girth, single ear head weight and 1000 seed weight. Selection based on early maturity would also be effective because it shows highly negative direct effect on grain yield.

Bhasker *et al*. (2017b) conducted an experiment with 13 parental lines (5 lines and 8 testers) and their 40 hybrids in pearl millet and reported biological yield had exhibited high direct effect and positive association on grain yield followed by panicle length, 1000 seed weight, effective tillers plant^{-1} and plant height at genotypic level. Based on the path analysis effective tillers plant^{-1}, panicle length, 1000 seed weight and biological yield plant^{-1} are the main yield contributing characters in pearl millet

Dehinwal *et al.* (2017) evaluated 100 advanced inbred lines of pearl millet under rainfed conditions. The results revealed that high positive direct effects on grain yield plant^{-1} was exerted by dry fodder yield followed by total tillers plant^{-1}, ear weight and effective tillers plant^{-1}. Days to 50% flowering and leaf width had negative direct effects on grain yield plant^{-1}. Therefore, selection for higher yield will be useful if it is based on traits such as dry fodder yield, ear weight, total tillers plant^{-1} and effective tillers plant^{-1}.

Lahham *et al.* (2017) assessed 15 hybrids of pearl millet for path coefficient studies. The results revealed that number of tillers plant^{-1}, plant height and number of leaves plant^{-1} had a direct effect on green fodder yield. Whereas, plant height also had an indirect effect through number of tillers and number of leaves plant^{-1}, therefore they can be used as selection criterion for improving green fodder yield.

Nehra *et al.* (2017) evaluated 49 pearl millet inbred lines to estimate path coefficient for yield and its contributing quantitative characters. Their results revealed that plant height followed by 1000 grain weight, spike length and number of productive tillers plant^{-1} had high positive direct effect towards grain yield plant^{-1}. Days to 50% flowering had negative phenotypic and genotypic direct effect on grain yield plant^{-1}. Number of productive tillers plant^{-1} and green fodder yield also had indirect contribution towards grain yield *via* plant height and 1000 grain weight.

Sathya *et al.* (2017) conducted an experiment with 200 recombinant inbred lines (RILs) during two consecutive seasons of *kharif,* 2013 and *summer,* 2013. Path coefficient analysis showed positive direct effect of number of productive tillers plant^{-1}, single ear head weight, single ear head grain weight, 1000 grain weight, chlorophyll content and beta-carotene content on grain yield plant^{-1} in both seasons. Moreover, single earhead weight showed positive indirect effect towards grain yield plant^{-1} through days to 50% flowering, number of productive tillers plant^{-1} and 1000 grain weight.

Talawar *et al.* (2017) evaluated 52 germplasm lines of pearl millet for eight quantitative characters and noticed that plant height, panicle girth and panicle length had exhibited high positive direct effects on grain yield plant^{-1}. Therefore, these characters could be considered as main components for selection in a breeding programme for higher grain yield.

Govintharaj *et al.* (2018) investigation with 116 forage type hybrid parents (seed (B) and pollinator (R) parents) revealed that total green forage yield had highest positive direct effect on dry forage yield followed by plant

height. Among forage quality traits, metabolizable energy had highest direct effect on *in vitro* organic matter digestibility in both the cuts. Crude protein and cellulose contents also had positive direct effects on *in vitro* organic matter digestibility in both the cuts.

Kaushik *et al*. (2018) studied 48 maintainer (B) lines of pearl millet and noticed that days to 50% flowering, spike length and number of productive tillers plant^{-1} had high significant direct contribution towards grain yield plant^{-1}. They opined that indirect selection based on these characters can be adopted in future breeding programme to enhance grain yield.

Patil *et al*. (2018) examined 14 parental populations and 91 hybrids of pearl millet for path analysis studies. The results indicated that panicle girth and plant height had highest direct effects on grain yield. Days to 50% flowering, 1000 grain weight and number of productive tillers plant^{-1} had the least direct effects on grain yield. The direct effect of panicle girth was greatly reduced by the negative indirect effects of days to 50% flowering and 1000 grain weight. Panicle girth, plant height and panicle length were identified as selection indices for obtaining good parental lines and hybrids in a pearl millet breeding program.

Singh *et al*. (2018) evaluated 40 accessions of pearl millet for five consecutive years (environments) for path coefficient analysis and revealed highest positive direct effect of spike girth, stover yield, harvest index, spike length, number of productive tillers plant^{-1}, plant height and test weight on seed yield in all the environments. They opined that these characters could be given prime importance during the selection programme to improve the seed yield potential of the crop.

Thomos *et al*. (2018) studied 22 pearl millet genotypes for path analysis and indicated that the traits *viz.*, plant height, panicle length, number of productive tillers plant^{-1} and dry matter yield plant^{-1} might be responsible for increasing the green fodder yield plant^{-1} in fodder pearl millet.

Rasitha *et al.* (2019) conducted an experiment to determine the direct and indirect effects of different yield attributes on grain yield in 42 B lines and 17 R lines and revealed that 1000 seed weight followed by number of productive tillers plant^{-1} had high positive direct effect on single plant yield. While, leaf sheath length and spike girth exhibited a moderate negative direct effect on single plant yield.

Annamalai *et al.* (2020) evaluated 50 pearl millet genotypes for 13 different biometrical traits and revealed that number of nodes plant^{-1} and number of tillers plant^{-1} showed high positive and indirect effect on grain yield through number of productive tillers.

Dadarwal *et al.* (2020) evaluated 30 maintainer lines of pearl millet to study correlation and path analysis for grain yield and its yield contributing characters. Path coefficient analysis revealed that the ear head length, biological yield plant^{-1} and harvest index were the most important characters for selection of high yielding genotypes as they exerted highest positive direct effect as well as positive correlation with grain yield plant^{-1}.

Kumar *et al.* (2020b) evaluated eighty seven F_1s of pearl millet along with three checks in randomized block design with two replications. Path coefficient analysis revealed that characters *viz.,* harvest index, biological yield plant^{-1}, test weight and number of effective tillers plant^{-1} had direct positive effect on seed yield plant^{-1}. Path analysis further recorded highest negative direct effect by ear head length followed by days to 50% flowering and number of effective tillers plant^{-1} on seed yield plant^{-1}. They observed low residual effect at phenotypic level which indicated choice of traits in the study were able to explain most of the effects on seed yield.

Shasibhusan *et al.* (2021) conducted an experiment to determine the direct and indirect effects of different yield attributes on grain yield in 40 pearl millet genotypes and revealed that characters like days to 50% flowering, productive tillers plant^{-1}, panicle length, fodder yield plant^{-1} and

panicle diameter showed positive direct effects showing true relationships with grain yield plant^{-1}.

Kumar *et al.* (2022) conducted a study to evaluate the relationship between grain yield and its components using correlation and path analysis studies in 18 hybrids of pearl millet and the results revealed that the highest positive and direct effect on grain yield by days to 50 percent flowering followed by panicle diameter (cm).

Yadav *et al.* (2022) investigated 45 pearl millet hybrids and revealed that biological yield plant^{-1} had the highest direct positive effect on seed yield plant^{-1}, while days to 50% maturity, ear head length, number of tillers plant^{-1}, and 1000 grain weight had the greatest direct negative effect. This implied that seed yield was primarily determined by attributing traits with direct and indirect effects.

Chapter - III

Material and Methods

Chapter III

MATERIAL AND METHODS

The experimental material used and methods followed pertaining to the present investigation entitled **"DUS characterization and diversity analysis of inbred lines in pearl millet (*Pennisetum glaucum* (L.) R. Br.)"** were briefly described here under.

3.1 LOCATION OF THE EXPERIMENTAL SITE

The experiment was carried out during *rabi*, 2021 at Agricultural Research Station, Perumallapalle, Tirupati located at 13°N latitude and 79°E longitude from an altitude of 182.9 m above mean sea level, and situated in southern agro-climatic zone of Andhra Pradesh.

3.2 MATERIAL

The experimental material utilized for the present study comprised of 70 pearl millet inbred lines (S_6 generation) developed at Agricultural Research Station, Perumallapalle, Tirupati. The lists of inbred lines were furnished in the Table 3.1.

3.3 METHODS

3.3.1 Field Layout

The experiment was laid out in a Randomized Block Design with two replications. All the entries were sown in nursery on 6th October, 2021 and transplanted to main field on 22nd October, 2021 at ARS, Perumallapalle. Each genotype was sown in three rows of three meters length with a spacing of 60 cm between rows and 15 cm between the plants within the rows.

Table 3.1 List of 70 inbred lines of pearl millet

S. No.	Inbred lines	Pedigree
1	PPBi-1	XMT-1858/1-1-2-1-1-1
2	PPBi-2	XMT-1858/1-1-2-2-3-2
3	PPBi-3	XMT-1858/2-1-3-4-3-3
4	PPBi-4	86M01/1-1-1-2-1-1
5	PPBi-5	86M01/1-1-3-3-1-2
6	PPBi-6	86M01/1-1-6-4-4-3
7	PPBi-7	86M01/1-1-9-5-1-4
8	PPBi-8	83R/1-1-6-2-1-1
9	PPBi-9	69R/3-1-2-3-2-1
10	PPBi-10	69R/3-1-5-4-2-2
11	PPBi-11	69R/3-1-5-6-5-3
12	PPBi-12	80R/9-1-1-1-1-1
13	PPBi-13	80R/9-1-1-3-1-2
14	PPBi-14	80R/10-1-1-1-1-3
15	PPBi-15	96R/1-1-1-1-4-1
16	PPBi-16	95R/4-1-2-1-4-1
17	PPBi-17	33R/1-1-4-1-2-1
18	PPBi-18	PHB3/2-1-3-4-1-1
19	PPBi-19	PHB3/2-1-3-9-3-2
20	PPBi-20	PHB3/2-1-3-10-2-3
21	PPBi-21	76R/5-1-1-2-1-1
22	PPBi-22	76R/5-1-2-5-1-2
23	PPBi-23	76R/5-1-3-7-3-3
24	PPBi-24	76R/7-1-4-3-1-4
25	PPBi-25	76R/7-1-6-5-3-5
26	PPBi-26	76R/7-1-6-7-1-6
27	PPBi-27	76R/7-1-6-10-4-7
28	PPBi-28	80R/19-1-1-2-3-1
29	PPBi-29	4743/2-1-2-1-1-1
30	PPBi-30	4743/2-1-4-3-1-2
31	PPBi-31	4702/1-1-1-3-3-3
32	PPBi-32	4702/1-1-2-4-4-4
33	PPBi-33	4702/1-1-2-8-1-5
34	PPBi-34	4702/1-1-3-12-1-6
35	PPBi-35	15056/3-1-2-4-4-1

Cont.

Vegetative stage

Flowering stage

Plate 1: Overall view of experimental field

Table 3.1 (cont.).

S. No.	Inbred lines	Pedigree
36	PPBi-36	15056/3-1-3-5-1-2
37	PPBi-37	4743/17-1-1-1-2-1
38	PPBi-38	4743/17-1-4-2-2-2
39	PPBi-39	15025/6-1-4-2-1-1
40	PPBi-40	15025/6-1-4-5-2-2
41	PPBi-41	BFT31/1-1-1-1-2-1
42	PPBi-42	BFT31/1-1-1-6-1-2
43	PPBi-43	BFT31/1-1-2-8-2-3
44	PPBi-44	BFT31/1-1-3-11-2-4
45	PPBi-45	BFT39/2-1-1-2-1-1
46	PPBi-46	BFT39/2-1-2-5-1-2
47	PPBi-47	BFT39/2-1-3-6-3-3
48	PPBi-48	BFT39/2-1-5-10-2-4
49	PPBi-49	BFT39/2-1-6-12-2-5
50	PPBi-50	BFT27/1-1-1-1-1-1
51	PPBi-51	BFT27/1-1-2-4-1-2
52	PPBi-52	BFT27/1-1-3-5-2-3
53	PPBi-53	48R/2-1-3-1-1-1
54	PPBi-54	48R/2-1-5-2-2-2
55	PPBi-55	48R/2-1-6-3-1-3
56	PPBi-56	15063/1-1-1-1-2-1
57	PPBi-57	15063/1-1-6-3-2-2
58	PPBi-58	15063/4-1-1-2-2-3
59	PPBi-59	15063/4-1-3-4-1-4
60	PPBi-60	15063/4-1-4-7-2-5
61	PPBi-61	15063/4-1-5-9-1-6
62	PPBi-62	15063/4-1-6-12-2-7
63	PPBi-63	15063/4-1-7-13-2-8
64	PPBi-64	BFT22/1-1-1-1-1-1
65	PPBi-65	BFT22/1-1-5-6-1-2
66	PPBi-66	BFT22/1-1-6-7-1-3
67	PPBi-67	BFT22/1-1-7-10-1-4
68	PPBi-68	BFT10/2-1-1-2-1-1
69	PPBi-69	BFT5/1-1-5-2-2-1
70	PPBi-70	BFT5/1-1-6-5-2-2

3.3.2 Crop Husbandry

The crop was provided with fertilizers to supply 80:40:30 N:P:K kg ha^{-1}. Half of N and entire P and K were applied as basal dose and second half of N was applied as top dressing after 35 days of sowing. The crop was raised under completely irrigated conditions. All the recommended cultural and agronomic measures were followed during the crop period.

3.4 DATA RECORDING

3.4.1 Morphological Characterization

Twenty eight morphological traits on five randomly tagged plants from each entry in each 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, 2001). Based on mean of 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 were used. Notes (1 to 9) were given for each state of expression for different characteristics for the purpose of electronic data processing.

3.4.2 Quantitative Traits

Observations were recorded on five randomly selected competitive plants in each genotype from each replication for all the quantitative characters except days to 50% flowering and days to maturity which were recorded on plot basis. Treatment means were worked out from the data collected on these five plants for the respective character. The details of data recorded were as follows.

3.4.2.1 Time of spike emergence/Days to 50% flowering

Number of days taken from the date of sowing to emergence of stigma on main tillers in 50 per cent of plants in each genotype of each replication was recorded and were classified as very early (<43 days), early (43-46 days), medium (47-50 days), late (51-54 days) and very late (>54 days).

Table 3.2 Characteristics of germplasm accessions studied

S. No.	Characteristics	States	Note	Stage of observation	Type of assessment
1.	Plant: Anthocyanin coloration of first leaf sheath	Absent	1	Five leaf stage (8)	VG
		Present	9		
2.	Plant: Growth habit	Erect	1	Spike emergence(45)	VG
		Intermediate	5		
		Spreading	**7**		
3.	Time of spike emergence (50% plants with atleast one spike emerged fully)	Very early (<43days)	1	Spike emergence(45)	VG
		Early (43-46 days)	3		
		Medium (47-50)	5		
		Late (51-54days)	7		
		Very late (>54days)	9		
4.	Leaf: Sheath pubescence	Absent	1	Spike emergence(45)	VG
		Present	9		
5.	Leaf: Sheath length (cm)	Short (<11)	3	Spike emergence(45)	MS
		Medium (11-15)	5		
		Long (>15)	7		
6.	Leaf : Blade length (cm)	Very short (<41)	1	Spike emergence(45)	MS
		Short (41-50)	3		
		Medium (51-60)	5		
		Long (61-70)	7		
		Very long (>70)	9		
7.	Leaf : Blade width (at widest point) (cm)	Narrow (<3)	3	Spike emergence(45)	MS
		Medium (3-4)	5		
		Broad (>4)	7		
8.	Spike: Stigma pigmentation	Absent	1	Stigma emergence(47)	VG
		Present	9		

Cont.

Table 3.2 (cont.).

S.No.	Characteristics	States	Note	Stage of observation	Type of assessment
9.	Spike: Anther colour	Yellow	3	Anther dehiscence(50)	VG
		Brown	5		
		Purple	7		
10.	Plant: Node pubescence	Absent	1	Dough grain (65)	VG
		Present	9		
11.	Plant: Number of nodes	Low (<11)	3	Dough grain (65)	MS
		Medium (11-15)	5		
		High (>15)	7		
12.	Plant: Node pigmentation	Whitish	1	Dough grain (65)	VG
		Green	2		
		Brown	3		
		Red	4		
		Purple	5		
13.	Plant: Internode pigmentation (between 3rd& 4th node from top)	Whitish	1	Dough grain (65)	VG
		Green	2		
		Brown	4		
		Red	6		
		Purple	7		
14.	Spike exertion	Incomplete	1	Dough grain (65)	VS
		Partial	3		
		Complete	5		
15.	Spike: Length (cm)	Very small (<11)	1	Dough grain (65)	MS
		Small (11-20)	3		
		Medium (21-30)	5		
		Long (31-40)	7		
		Very long (>40)	9		
16.	Spike: Anthocyanin pigmentation of glume	Absent	1	Dough grain (65)	VG
		Present	9		

Cont.

Table 3.2 (cont.).

S. No.	Characteristics	States	Note	Stage of observation	Type of assessment
17.	Spike: Bristle	Absent	1	Dough grain (65)	VG
		Present	9		
18.	Spike: Bristle colour	Yellow	1	Dough grain (65)	VS
		Green	2		
		Brown	3		
		Purple	5		
19.	Spike: Bristle appearance	Non prominent (Bristle length <2mm from the ear head)	3	Dough grain (65)	VS
		Prominent (Bristle length > 2mm from the ear head)	5		
20.	Spike: Girth at maximum point (excluding bristles) (cm)	Thin (<1.6)	3	Dough grain (65)	MS
		Medium (1.6-3.0)	5		
		Thick (>3.0)	7		
21.	Plant: Number of productive tillers	Monoculm (<2 tillers)	1	Dough grain (65)	MS
		Low (2-3tillers)	3		
		Medium (4-6tillers)	5		
		High (>6 tillers)	7		
22.	Plant: Height (including spike) (cm)	Very short (<101)	1	Dough grain (65)	MS
		Short (101-150)	3		
		Medium (151-200)	5		
		Tall (201-250)	7		
		Very tall (>250)	9		
23.	Spike: Shape	Cylindrical	1	Maturity(75)	VG
		Conical	2		
		Spindle	3		
		Candle	4		
		Lanceolate	5		
		Dumb-bell	6		

Cont.

Table 3.2 (cont.).

S. No.	Characteristics	States	Note	Stage of observation	Type of assessment
		Club	7		
		Oblanceolate	8		
		Globose	9		
24.	Spike: Tip sterility	Absent	1	Maturity (75)	VS
		Present	9		
25.	Spike: Density	Loose	3	Maturity (75)	VG
		Semi-compact	5		
		Compact	7		
26.	Seed: Colour	Whitish	1	After harvest (00)	VG
		Cream	2		
		Yellow	3		
		Grey	4		
		Deep grey	5		
		Grey brown	6		
		Yellow brown	7		
27.	Seed: Shape	Obovate	3	After harvest (00)	VG
		Elliptical	5		
		Hexagonal	7		
		Globular	9		
28.	Seed: Weight of 1000 grains (g)	Very low(<5)	1	After harvest (00) At 10% moisture content	
		Small(5.0-7.5)	3		
		Medium(7.6-10.0)	5		
		Bold(10.1-12.5)	7		
		Very bold(>12.5)	9		

MG : Measurement by single observation 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 parts of plants

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

3.4.2.2 Days to maturity

It was recorded by counting the number of days taken from sowing to attainment of physiological maturity in each genotype.

3.4.2.3 SPAD Chlorophyll Meter Reading (SCMR)

SCMR was measured on third leaf from the top of the main axis at 45 DAS and 65 DAS using SPAD meter of Minolta Company, NJ, USA.

3.4.2.4 Specific Leaf Area (SLA) (cm^2g^{-1})

Specific leaf area was recorded by taking five leaves from the third leaf of main tiller of each plant. These leaves were cleaned and their leaf area was estimated using a leaf area meter (LICOR model-3100) at 45 DAS and 65 DAS. They were then dried in hot air oven at 80^{o}C and dry weight was recorded. The formula used for calculating SLA was

$$\text{SLA} = \frac{\text{Leaf area } \left(\text{cm}^2\right)}{\text{Leaf dry weight (g)}}$$

3.4.2.5 Leaf sheath length (cm)

It was measured from the uppermost node to the ligule and were categorized as short (<11 cm), medium (11-15 cm) and long (>15 cm).

3.4.2.6 Leaf blade length (cm)

It was measured from the ligule to tip of leaf and were classified as very short (<41 cm), short (41-50 cm), medium (51-60 cm), long (61-70 cm) and very long (>70 cm).

3.4.2.7 Leaf blade width (cm)

It was calibrated at the widest point of flag leaf and were categorized as narrow (<3cm), medium (3-4 cm) and broad (>4 cm).

3.4.2.8 Number of nodes plant^{-1}

Total number of nodes plant^{-1} were counted, recorded and grouped into low (<11), medium (11-15) and high (>15).

3.4.2.9 Spike length (cm)

It was the measurement of the length from base to tip of the panicle and classified as very small (< 11 cm), small (11-20 cm), medium (21-30 cm), long (31-40 cm) and very long (>40 cm).

3.4.2.10 Spike girth (cm)

Measured in centimeters by using vernier calipers and the diameter was taken at maximum point (excluding bristles) of panicle at harvest and were categorized as thin (<1.6 cm), medium (1.6-3.0 cm) and thick (>3.0 cm).

3.4.2.11 Number of productive tillers plant^{-1}

Total number of panicle bearing tillers that arise from the basal portion of the plant were counted for each individual plant at harvest stage and recorded as monoculm (<2 tillers), low (2-3tillers), medium (4-6tillers) and high (>6 tillers).

3.4.2.12 Plant height (cm)

Plant height was measured in centimeters using a scale as the length of the main tiller from ground level to the tip of the panicle at maturity and were classified as very short (<101cm), short (101-150 cm), medium (151-200 cm), tall (201-250cm) and very tall (>250 cm).

3.4.2.13 1000 grain weight (g)

Thousand grains collected from five randomly selected plants were weighed, expressed in grams and grouped into very low (<5 g), small (5.0-7.5 g), medium (7.6-10.0 g), bold (10.1-12.5 g) and very bold (>12.5 g).

3.4.2.14 Panicle weight (g)

The panicles of the five tagged plants were harvested; weighed together and average panicle weight was worked out and expressed in grams.

3.4.2.15 Green fodder yield plant^{-1} (g)

The plant stalks detached of ear head were harvested from each line separately and fresh weight was recorded in grams.

3.4.2.16 Dry fodder yield plant^{-1} (g)

The plant stalks excluding ear head harvested from each line separately were sundried and dry weight was recorded in grams.

3.4.2.17 Threshing (%)

Threshing percentage was calculated as average grain yield to weight of panicle and it is the ability to fill and set grains on panicle.

3.4.2.18 Harvest Index (%)

Harvest Index was expressed as the ratio of the grain yield to biological yield and was calculated as given below.

$$\text{Harvest Index} = \frac{\text{Grain yield}}{\text{Biological yield}} \times 100$$

3.4.2.19 Grain yield plant^{-1} (g)

All the sundried ear heads of a plant were threshed, cleaned and dried to uniform moisture before weighing and recorded in grams.

3.4.3 Qualitative Traits

3.4.3.1 Plant anthocyanin coloration of first leaf sheath

The plant anthocyanin coloration of first leaf sheath was determined based on the observation at five leaf stage of tagged plants which may be present or absent.

3.4.3.2 Plant growth habit

The growth habit of plant may be erect, intermediate which was similar to erect but spaced between tillers and spreading which was widely separated between tillers.

3.4.3.3 Leaf sheath pubescence

Leaf sheath may show either presence of pubescence (bristle-like appearance on surface) or absence of it.

3.4.3.4 Spike stigma pigmentation

The stigma pigmentation of spike is determined based on the observation of stigma of tagged plants which may be present or absent.

3.4.3.5 Spike anther colour

The anther colour is determined based on the observation of anthers of tagged plants which may show various colorations *viz.,* yellow, brown and purple.

3.4.3.6 Plant node pubescence

Plant node may exhibit either presence of pubescence (bristle-like appearance on surface) or absence of it.

3.4.3.7 Plant node pigmentation

Plant nodes may exhibit various colorations *viz.*, whitish, green, brown, red and purple.

3.4.3.8 Plant internode pigmentation

The internode pigmentation of plant was determined based on the observation of portion between third and fourth node from top of tagged plants which may show various colorations *viz.,* whitish, green, brown, red and purple.

3.4.3.9 Spike exertion

It refers to the exerted portion of spike from leaf sheath and were accordingly categorized as incomplete, partial and complete.

3.4.3.10 Anthocyanin pigmentation of glume

The glume pigmentation was determined based on the observation of glumes of tagged plants which may be present or absent.

3.4.3.11 Spike bristle

The bristle may be recorded as present or absent.

3.4.3.12 Spike bristle colour

The bristle may show various colorations *viz.*, yellow, green, brown and purple.

3.4.3.13 Spike bristle appearance

The spike bristle may appear as prominent (Bristle length greater than 2mm from the ear head) or non prominent (Bristle length less than 2mm from the ear head).

3.4.3.14 Spike shape

The shape of the spike may be observed as cylindrical, conical, spindle, candle, lanceolate, dumb-bell, club, oblanceolate and globose.

3.4.3.15 Spike tip sterility

The spike tip sterility may be recorded as present or absent.

3.4.3.16 Spike density

It refers to the degree of compactness within the spike and were accordingly categorized as loose, semi-compact and compact.

3.4.3.17 Seed colour

The seed may exhibit variations in colour *viz*., whitish, cream, yellow, grey, deep grey, grey brown and yellow brown.

3.4.3.18 Seed shape

Shape of the seed recorded as obovate, elliptical, hexagonal and globular.

3.5 STATISTICAL ANALYSIS

The mean data of quantitative characters recorded on all the genotypes over two replications were subjected to the following statistical analysis using INDOSTAT 9.2 software.

3.5.1 Analysis of Variance

The variation among 70 genotypes for different characters was tested for significance by using analysis of variance technique (Panse and Sukhatme, 1961).

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

where,

Y_{ij} = Phenotypic observation on 'i'th genotype in 'j'th replication.

μ = General mean

g_i = Effect of i^{th} genotype

γ_j = Effect of j^{th} replication

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

The analysis of variance for each character was carried out as follows:

Source of variation	Degree of freedom	Sum of squares	Mean sum of squares	'F' ratio
Replications	(r-1)	RSS	M_r	M_r/M_e
Genotypes	(t-1)	VSS	M_v	M_v/M_e
Error	(r-1) (t-1)	ESS	M_e	-
Total	(rt-1)	TSS		

Where,

r = Number of replications

t = Number of genotypes

M_r = Mean sum of squares due to replications

M_v = Mean sum of squares due to genotypes

M_e = Mean sum of squares due to error.

The significance of differences among all the genotypes was tested by 'F' test using the error variance by comparing calculated 'F' value with table 'F' value at 1 percent and 5 percent probability levels. The significance test was carried out by referring to standard 'F' table values given by Fisher and Yates (1967). After testing for significance of differences among the means of different genotypes for each character, further computations were done as detailed below.

3.5.2 Estimation of Genetic Parameters

In order to assess and quantify the genetic variability among the genotypes for important yield contributing characters, the following parameters were estimated based on mean sum of squares from ANOVA

3.5.2.1 Components of variance

The genotypic and phenotypic variances were calculated as per the formulae proposed by Burton (1952)

(i) Genotypic variance $\left(\sigma_g^2\right) = \frac{\text{MSS due to genotypes} - \text{MSS due to error}}{\text{Number of replications}}$

(ii) Phenotypic variance $\left(\sigma_p^2\right) = \sigma_g^2 + \sigma_e^2$

σ_g^2 = Genotypic variance

σ_e^2 = Error variance

3.5.2.2 Genotypic and phenotypic coefficient of variation

The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were computed according to Burton (1952).

$$\text{(i) GCV}(\%) = \frac{\sigma_g}{\bar{X}} \times 100$$

$$\text{(ii) PCV}(\%) = \frac{\sigma_p}{\bar{X}} \times 100$$

where,

GCV = Genotypic coefficient of variation

PCV = Phenotypic coefficient of variation

σ_g, σ_p and $\bar{X}$ were genotypic standard deviation, phenotypic standard deviation and general mean of the characters respectively.

Categorization of the range of variation was done as proposed by Sivasubramanian and Madhavamenon (1973)

Less than 10% - Low

10 – 20 % - Moderate

More than 20% - High

3.5.2.3 Broad sense heritability

Heritability in broad sense refers to the proportion of genotypic variance to the total variance of the population. Heritability in broad sense [$h^2_{(b)}$] was calculated by the formula given by Lush (1940).

$$\text{Broad sense Heritability} = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

where,

h^2_b = Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance ($\sigma^2_g + \sigma^2_e$)

σ^2_e = Environmental variance

As suggested by Johnson *et al.* (1955b), heritability estimates were categorized as

Less than 30% - Low

30 – 60 % - Moderate

More than 60% - High

3.5.2.4 Genetic advance

Genetic advance refers to the expected genetic gain or improvement in the next generation by selecting the superior individuals under certain amount of selection pressure. From the heritability estimates, the genetic advance was estimated by the following formula given by Johnson *et al.* (1955a).

$$GA = k\, \sigma_p\, H$$

where,

GA = Genetic advance

σ_p = Phenotypic standard deviation

H = Heritability (broad sense)

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

3.5.2.5 Genetic advance as percent of mean (GA as per cent mean)

Genetic advance as percent of mean was calculated as per the formula.

$$\text{GA as percent of mean} = \frac{GA}{\overline{X}} \times 100$$

where,

GA = Genetic advance

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

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

Less than 10%	-	Low
10 – 20 %	-	Moderate
More than 20%	-	High

3.5.3 Genetic Divergence Analysis

The genetic diversity among 70 inbred lines for 21 traits was estimated by using Mahalanobis generalized distance (D^2).

3.5.3.1 Mahalanobis's D^2 analysis

The data collected on different characters was analyzed by using D^2 statistics given by Mahalanobis (1936) to determine genetic divergence.

3.5.3.2 Test of significance

Variances were calculated for all the 21 characters and test of significance was done. Analysis of covariance for the character pairs was estimated on the basis of mean values (Panse and Sukhatme, 1961). After testing the difference between genotypes for each of the characters, a simultaneous test of significance for differences between the mean values of a number of correlated variables with regard to the pooled effect of 21 characters was carried out using 'V' statistic, which in turn utilized Wilk's '$\wedge$' criterion (Wilks, 1932). The sum of squares and sum of products of error

and error plus variety, variance and covariance matrix were used for this purpose.

The estimation of '$\wedge$' (Wilk's criterion) was done using the following relationship:

$$'\wedge' = \frac{(E)}{(E+V)}$$

where,

$\wedge$ = Wilk's criterion

(E) = Determinant of error matrix

(E + V) = Determinant of error + variety matrix

The significance of '$\wedge$' was tested by

$\chi^2_{pq} = V = - m \log_e \wedge$

where,

m = n - (p + q + 1)/2 with 'pq' degree of freedom

n = Degrees of freedom of error + varieties

p = Number of characters

q = Number of genotypes – 1

$\log_e \wedge = 2.3407 \log_{10} \wedge$

V (Stat) is distributed as χ^2 with 'pq' degrees of freedom.

3.5.3.3 Transformation of correlated variables

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

3.5.3.4 Computation of D^2 values

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

$$D_{ij}^2 = p\Sigma_{t=1} (\overline{Y_{it}} - \overline{Y_{jt}})^2$$

where,

$\overline{Y_{it}}$ = Uncorrelated mean value of 'ith' genotype for 't' character

$\overline{Y_{jt}}$ = Uncorrelated mean value of 'jth' genotype for 't' character

D_{ij}^2 = D^2 value between 'ith' and 'jth' genotypes

3.5.3.5 Testing the significance of D^2 values

The D^2 values obtained for a pair of genotypes was taken as the calculated value of χ^2 and tested against the tabulated χ^2 at 'P' degree of freedom where 'P' is the number of characters considered.

3.5.3.6 Grouping of genotypes into various clusters

Grouping of genotypes into different clusters was done by using Tocher's method as described by Rao (1952). The criterion was that the two varieties belonging to the same cluster at least on an average show a smaller D^2 value than those belonging to different clusters. For this purpose D^2 values of all combinations of each genotype were arranged in ascending order of their magnitude in a tabular form as described by Singh and Choudhary (1977).

To start with, two populations having the smallest distance from each other were considered, to which a third population having smaller D^2 value from the first two populations was added. Similarly, the nearest next fourth population was considered and this procedure was continued. At certain stage when it was felt that after adding a particular population, there was an abrupt increase in the average D^2, that population was not considered for including in that cluster. The groups of the first cluster were then omitted and the rest were treated in similar way. This process was continued till all the populations were included into one or the other cluster. After the formation of the clusters, the average inter and intra cluster distances (divergence) were calculated.

3.5.3.7 Average intra-cluster distance

For the measurement of intra cluster distance, the formula used was

$$\Sigma D_i^2 /n$$

where,

ΣD_i^2 = The sum of distance between all possible combinations (n) of the populations included in a cluster.

3.5.3.8 Average inter - cluster distance

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

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

$$\text{Average inter cluster distance} = \Sigma D_i^2 /n_i n_j$$

where,

ΣD_i^2 = The sum of distance between all possible combinations ($n_i n_j$) of the entries included in the cluster study.

n_i = Number of entries in cluster ‘i’

n_j = Number of entries in cluster ‘j’

3.5.3.9 Contribution of individual characters towards divergence

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

$$X = \frac{(N \times 100)}{M}$$

where,

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

M = All possible combinations of number of genotypic pairs.

3.5.4 Character Association Analysis

Genotypic and phenotypic correlation coefficients were calculated using the method given by Johnson *et al.* (1955b) to determine the degree of association of the characters with yield and also among the yield components.

3.5.4.1 Genotypic correlation coefficient (r_g)

$$r_g(x_i x_j) = \frac{CoV_g(x_i x_j)}{\sqrt{V_g(x_i)\, V_g(x_j)}}$$

where,

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

$V_g(x_i)$ = Genotypic variance of 'i^{th}' character

$V_g(x_j)$ = Genotypic variance of 'j^{th}' character

$Cov_{(g)}(x_i x_j)$ = Genotypic covariance between 'i^{th}' and 'j^{th}' characters.

3.5.4.2 Phenotypic correlation coefficient (r_p)

$$r_p(x_i x_j) = \frac{CoV_p(x_i x_j)}{\sqrt{V_p(x_i).V_p(x_j)}}$$

where,

$V_p(x_i)$ = Phenotypic variance of 'i^{th}' character

$V_p(x_j)$ = Phenotypic variance of 'j^{th}' character

$Cov_{(p)}(x_i x_j)$ = Phenotypic covariance between 'i^{th}' and 'j^{th}' characters.

The significance of correlation coefficients was tested by comparing the genotypic and phenotypic correlation coefficients with table value [Fisher and Yates (1967)] at (n-2) degrees of freedom at 5% and 1% probability levels where, ‘n’ denotes the number of treatments used in the calculations.

3.5.5 Path Coefficient Analysis

Path coefficient analysis was carried out by the procedure originally proposed by Wright (1921) which was subsequently elaborated by Dewey and Lu (1959) to calculate the direct and indirect contribution of various characters to yield. The following set of simultaneous equations were formulated and solved for estimating various direct and indirect effects.

$r_{1y} = p_{1y} + r_{12}p_{2y} + r_{13}p_{3y} + \ldots\ldots\ldots\ldots + r_{1i}p_{iy}$

$r_{2y} = r_{21}p_{1y} + p_{2y} + r_{23}p_{3y} + \ldots\ldots\ldots\ldots.... + r_{2i}p_{iy}$

. . . . . .

. . . . . .

$r_{iy} = r_{i1}p_{1y} + r_{i2}p_{2y} + r_{i3}p_{3y} + \ldots\ldots\ldots\ldots\ldots + p_{iy}$

where,

r_{1y} to r_{iy} = Coefficient of correlation among causal factors.

p_{1y} to p_{iy} = Direct effects of characters ‘1’ to i on character ‘y’.

The above equations were written in matrix forms as under:

A C B

$$\begin{pmatrix} r_{1y} \\ r_{2y} \\ r_{3y} \\ . \\ r_{iy} \end{pmatrix} = \begin{pmatrix} 1 & r_{12} & r_{13} \ldots\ldots\ldots\ldots & r_{1i} \\ r_{21} & 1 & r_{23}\ldots\ldots\ldots\ldots & r_{2i} \\ r_{31} & r_{32} & 1 \ldots\ldots\ldots\ldots & r_{3i} \\ . & . & . & . \\ r_{i1} & r_{i2} & r_{i3}\ldots\ldots\ldots\ldots\ldots & 1 \end{pmatrix} \begin{pmatrix} p_{1y} \\ p_{2y} \\ p_{3y} \\ . \\ p_{iy} \end{pmatrix}$$

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

where,

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

Then, direct effects were calculated as follows:

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

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

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

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:

$$\text{Residual effect } (P_{RY}) = \sqrt{1-[P_{1y}r_{1y} + p_{2y}r_{2y} + \ldots\ldots\ldots + p_{iy}r_{iy}]^2}$$

where,

P_{RY} = Residual effect

p_{iy} = Direct effect of 'x_i' on 'y'

r_{iy} = Correlation coefficient of 'x_i' with 'y'.

The scales for path coefficients as proposed by Lenka and Mishra (1973) 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 & Discussion

Chapter – IV

RESULTS AND DISCUSSION

The present study on "**DUS characterization and diversity analysis of inbred lines in pearl millet (*Pennisetum glaucum* (L.) R. Br.)"** was conducted during *rabi*, 2021 for recording DUS traits using DUS guidelines and to study genetic divergence, genetic parameters, character association and path coefficient analysis in 70 inbred lines of pearl millet for 28 different DUS descriptors and 21 yield related parameters. The obtained results from the above investigation were presented here under.

4.1 DUS CHARACTERIZTION

The availability of diverse genetic resources is a prerequisite for genetic improvement of crop. Beside availability of genetic resources their characterization is essential for the effective utilization in crop improvement programmes (Reddy *et al*., 2009). Characterization based on visually assessed qualitative traits provides useful information on racial differentiation and varietal identification. DUS characterization of genotype plays a vital role in understanding phylogenetic relationship as well as in the maintenance, multiplication and seed certification of a variety. Hence, in the present investigation 70 inbred lines of pearl millet were characterized for 28 characters based on PPV&FRA, 2001 testing guidelines and data was furnished in table 4.1.

4.1.1 Plant anthocyanin coloration of first leaf sheath

Characterization of 70 germplasm accessions, on the basis of anthocyanin coloration of first leaf sheath revealed that it was absent in 34 accessions and present in 36 accessions. Similar results were reported by Kumar *et al.* (2005).

Table 4.1 DUS characterization in 70 inbred germplasm lines of pearl millet

S. No.	Name of the descriptor	Descriptor state	No. of accessions	Genotypes	Frequency (%)
1	Plant: Anthocyanin coloration of first leaf sheath	Absent	34	PPBi-2,3,5,7,9,11,12,14,15,16,18,19,20,22,28,30,37,43,44,45,47,48,49,50,52,53,55,56,61, 62,63,64,65,66,67,70	48.57
		Present	36	PPBi-1,4,6,8,10,13,17,21,23,24,25,26,27,29,31,32,33,34,35,36,38,39,40,41,42,46,51,54, 57,58,59,60,68,69	51.43
2	Plant: Growth habit	Erect	70	PPBi-1 to 70 (All 70 genotypes)	100
		Intermediate	0	--	-
		Spreading	0	--	-
3	Time of spike emergence (50%plants with atleast one spike emerged fully)	Very early (<43days)	0	--	-
		Early (43-46 days)	1	PPBi-44	14.29
		Medium (47-50)	0	--	-
		Late (51-54days)	11	PPBi-5,12,20,21,23,27,50,64,65,66,68	15.71
		Very late (>54days)	58	PPBi-1,2,3,4,6,7,8,9,10,11,13,14,15,16,17,18,19,22,24,25,26,28,29,30,31,32,33,34,35,36, 37,38,39,40,41,42,43,44,45,46,47,48,49,51,52,53,54,55,56,57,58,59,60,61,62,63,67,68, 69,70	82.86
4	Leaf: Sheath pubescence	Absent	69	PPBi-1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30, 31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,58, 59,60,61,62,63,64,65,66,67,69,70	98.57
		Present	1	PPBi-68	1.43
5	Leaf: Sheath length (cm)	Short (<11)	6	PPBi-21,23,39,54,67,68	8.57
		Medium (11-15)	57	PPBi-1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,20,22,25,26,27,28,30,31,32,33,34,35,36, 37,38,40,41,42,43,44,45,46,47,48,49,50,51,52,53,56,57,58,59,60,61,62,63,64,65,66	81.43
		Long (>15)	7	PPBi-18,19,24,29,55,69,70	10
6	Leaf : Blade length (cm)	Very short (<41)	13	PPBi-11,12,13,21,23,39,40,43,45,48,56,67,68	18.57
		Short (41-50)	43	PPBi-1,2,3,4,5,7,8,9,10,14,16,17,20,22,25,27,29,30,31,32,33,34,36,37,38,41,42,44,46, 47,49,51,54,57,58,59,61,62,63,64,65,66,70	61.43
		Medium (51-60)	13	PPBi-6,15,18,19,26,28,35,50,52,53,55,60,69	18.57
		Long (61-70)	1	PPBi-24	1.43
		Very long (>70)	0	--	-
7	Leaf : Blade width (at widest point) (cm)	Narrow (<3)	31	PPBi-1,7,11,12,13,15,16,18,20,23,29,30,34,36,39,40,42,45,47,48,50,51,54,56,62,63,65, 66,67,68,70	44.29

Cont.

Table 4.1 (cont.).

S. No.	Name of the descriptor	Descriptor state	No. of accessions	Genotypes	Frequency (%)
		Medium (3-4)	37	PPBi-2,3,4,5,8,9,10,14,17,19,21,22,24,25,26,27,31,32,33,35,37,38,41,43,44,46,49,52, 53,55,57,58,59,60,61,64,69	52.86
		Broad (>4)	2	PPBi-6,28	2.85
8	Spike: Stigma pigmentation	Absent	67	PPBi-3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31, 32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,52,53,54,55,56,57,58,59,60, 61,62,63,64,65,66,67,68,69,70	95.71
		Present	3	PPBi-1,2,51	4.29
9	Spike: Anther colour	Yellow	50	PPBi-3,4,5,7,9,12,14,16,20,21,22,23,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42, 43,44,45,46,47,49,50,54,55,56,57,58,59,60,62,63,64,67,68,69,70	71.43
		Brown	0	--	-
		Purple	20	PPBi-1,2,6,8,10,11,13,15,17,18,19,24,25,48,51,52,53,61,65,66	28.57
10	Plant: Node pubescence	Absent	57	PPBi-1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,18,19,20,21,22,23,24,25,26,27,28,29,30,32,34, 35,36,37,38,39,40,41,43,44,45,46,47,50,51,52,53,54,55,56,57,58,59,60,61,68,69,70	81.43
		Present	13	PPBi-16,17,31,33,42,48,49,62,63,64,65,66,67	18.57
11	Plant: Number of nodes	Low (<11)	70	PPBi-1 to 70 (All 70 genotypes)	100
		Medium (11-15)	0	--	-
		High (>15)	0	--	-
12	Plant: Node pigmentation	Whitish	0	--	-
		Green	47	PPBi-1,2,3,4,5,6,8,9,10,11,12,13,14,15,17,19,20,21,22,23,24,25,26,27,29,30,32,37,38, 40,41,42,43,45,46,47,51,53,54,55,57,58,59,60,67,68,69	67.14
		Brown	0	--	-
		Red	0	--	-
		Purple	23	PPBi-7,16,18,28,31,33,34,35,36,39,44,48,49,50,52,56,61,62,63,64,65,66,70	32.86
13	Plant: Internode pigmentation (between 3rd & 4th node from top)	Whitish	0		
		Green	67	PPBi-1,2,3,4,5,6,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,29,30,31,32, 33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60, 61,62,63,64,65,66,67,68,69	95.71
		Brown	0	--	-

Cont.

Table 4.1 (cont.).

S. No.	Name of the descriptor	Descriptor state	No. of accessions	Genotypes	Frequency (%)
		Red	0	--	-
		Purple	3	PPBi-7,28,70	4.29
14	Spike exertion	Incomplete	0	--	-
		Partial	1	PPBi-8	1.43
		Complete	69	PPBi-1,2,3,4,5,6,7,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31, 32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59, 60,61,62,63,64,65,66,67,68,69,70	98.57
15	Spike: Length (cm)	Very small (< 11)	0	--	-
		Small (11-20)	39	PPBi-3,7,10,12,13,17,20,21,23,27,29,30,31,33,34,37,38,39,40,42,43,45,46,48,49,54,56, 61,62,63,64,65,66,67,68,69,70	55.71
		Medium (21-30)	31	PPBi-1,2,4,5,6,8,9,11,14,15,16,18,19,22,24,25,26,28,32,35,36,41,44,47,50,51,52, 53,55,57,58,59,60	44.29
		Long (31-40)	0	--	-
		Very long (>40)	0	--	-
16	Spike : Anthocyanin pigmentation of glume	Absent	44	PPBi-1,2,6,7,10,12,14,15,16,18,20,21,22, 23,24,25,26,27,28,29,32,34,35,36,37,38, 40,42,43,44,47,53,55,58,59,60,61,63,65,66,67,68,69,70	62.86
		Present	26	PPBi-3,4,5,8,9,11,13,17,19,30,31,33,39,41,45,46,48,49,50,51,52,54,56,57,62,64	37.14
17	Spike: Bristle	Absent	62	PPBi-1,2,3,5,6,7,8,9,10,11,12,13,14,15,17,19,20,21,22,23,27,28,29,30,31,32,33,34,37, 38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65, 66,67,68,69,70	88.57
		Present	8	PPBi-4,16,18,24,25,26,35,36	11.43
18	Spike: Bristle colour	Yellow	2	PPBi-25,26	25
		Green	0	--	-
		Brown	4	PPBi-4,16,18,24	50
		Purple	2	PPBi-35,36	25
19	Spike: Bristle appearance	Non prominent (Bristle length <2mm from the ear head)	0	--	-
		Prominent (Bristle length > 2mm from the ear head)	8	PPBi-4,16,18,24,25,26,35,36	100

Cont.

Table 4.1 (cont.).

S. No.	Name of the descriptor	Descriptor state	No. of accessions	Genotypes	Frequency (%)
20	Spike: Girth at maximum point (excluding bristles) (cm)	Thin (<1.6)	0	--	-
		Medium (1.6-3.0)	67	PPBi-1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,19,20,21,22,23,26,27,28,29,30,31,32,33, 34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,61, 62,63,64,65,66,67,68,69,70	95.71
		Thick (>3.0)	3	PPBi-18,24,25	4.29
21	Plant: Number of productive tillers	Monoculm (<2)	36	PPBi-1,2,6,8,9,13,14,15,16,18,19,20,22,24,26,27,29,33,34,36,37,39,40,42,43,45,48,49,51, 52,53,55,61,62,66,68	51.43
		Low (2-3tillers)	33	PPBi-3,4,5,7,10,11,12,17,21,23,25,28,30,31,32,35,38,41,43,46,47,54,56,57,58,59,60,63, 64,65,67,69,70	47.14
		Medium (4-6tillers)	1	PPBi-50	1.42
		High (>6 tillers)	0	--	-
22	Plant: Height (including spike) (cm)	Very short (<101)	2	PPBi-67,68	2.86
		Short (101-150)	38	PPBi-2,5,10,11,12,13,17,20,21,23,26,27,29,30,31,34,37,38,39,40,42,43,44,46,48,54,56, 57,58,60,61,62,63,64,65,66,69,70	54.29
		Medium (151-200)	30	PPBi-1,3,4,6,7,8,9,14,15,16,18,19,22,24,25,28,32,33,35,36,41,45,47,49,50,51,52,53, 55,59	42.85
		Tall (201-250)	0	--	-
		Very tall (>250)	0	--	-
23	Spike shape	Cylindrical	12	PPBi-5,6,7,15,17,19,23,27,30,32,38,47	17.14
		Conical	18	PPBi-3,4,9,16,18,20,21,26,29,41,44,46,57,58,62,64,65,66	25.71
		Spindle	1	PPBi-25	1.43
		Candle	8	PPBi-10,11,12,24,28,35,37,48	11.43
		Lanceolate	30	PPBi-1,2,13,14,22,31,33,34,36,39,40,42,43,45,49,50,51,52,53,54,55,56,59,60,61,63,67, 68,69,70	42.86
		Dumb-bell	0	--	-
		Club	0	--	-
		Oblanceolate	1	PPBi-8	1.43
		Globose	0	--	-
24	Spike: Tip sterility	Absent	70	PPBi-1 to 70 (All 70 genotypes)	100
		Present	0	--	-

Cont.

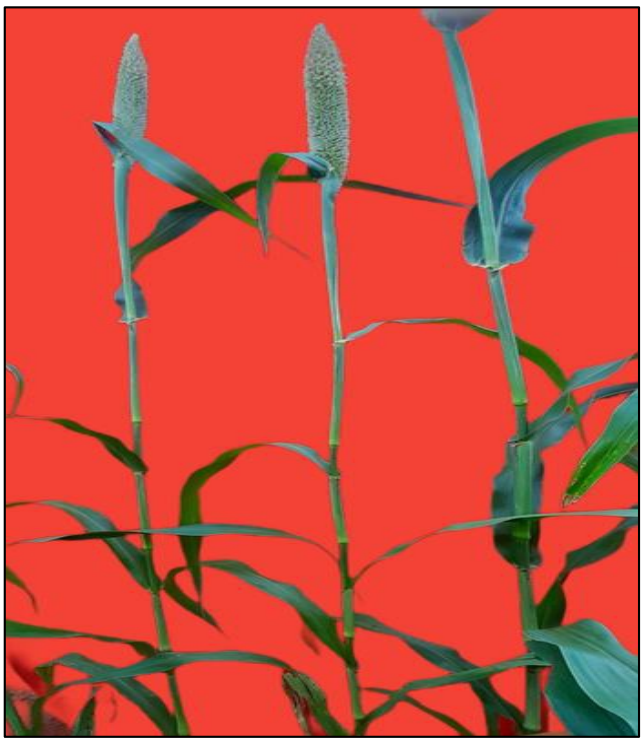
Table 4.1 (cont.).

S. No.	Name of the descriptor	Descriptor state	No. of accessions	Genotypes	Frequency (%)
25	Spike: Density	Loose	8	PPBi-23,30,31,38,62,64,67,68	11.43
		Semi-compact	36	PPBi-1,2,4,9,10,11,12,15,16,17,18,19,21,24,28,32,35,36,41,44,45,46,49,50,51,52,54,55, 56,58,59,60,63,65,66,70	51.43
		Compact	26	PPBi-3,5,6,7,8,13,14,20,22,25,26,27,29,33,34,37,39,40,42,43,47,48,53,57,61,69	37.14
26	Seed: Colour	Whitish	0	--	-
		Cream	1	PPBi-14	1.43
		Yellow	0	--	-
		Grey	18	PPBi-2,4,9,10,11,12,16,23,28,30,38,52,55,60,62,64,67,70	25.71
		Deep grey	23	PPBi-3,8,13,15,17,18,24,31,32,34,35,36,39,44,46,47,48,54,57,58,63,66,69	32.86
		Grey brown	25	PPBi-1,5,6,7,19,20,21,22,25,26,27,29,33,37,40,41,45,49,50,53,56,59,61,65,68	35.71
		Yellow brown	3	PPBi-42,43,51	4.29
27	Seed: Shape	Obovate	6	PPBi-11,12,37,39,61,69	8.57
		Elliptical	0	--	-
		Hexagonal	0	--	-
		Globular	64	PPBi-1,2,3,4,5,6,7,8,9,10,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32, 33,34,35,36,38,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,62,63, 64,65,66,67,68,70	91.43
28	Seed: Weight of 1000 grains (g)	Very low (<5)	0	--	-
		Small (5.0-7.5)	11	PPBi-11,34,40,42,43,44,48,54,55,57,60	15.71
		Medium (7.6-10.0)	17	PPBi-2,9,21,27,33,37,39,41,45,52,53,56,58,59,63,66,69	24.29
		Bold (10.1-12.5)	32	PPBi-1,3,6,8,10,12,13,14,16,19,22,24,25,26,28,29,30,31,32,35,36,38,49,50,51,61,62,64, 65,67,68,70	45.71
		Very bold (>12.5)	10	PPBi-4,5,7,15,17,18,20,23,46,47	14.29

Present (36 genotypes)

Absent (34 genotypes)

Plate 2. Plant anthocyanin coloration of first leaf sheath



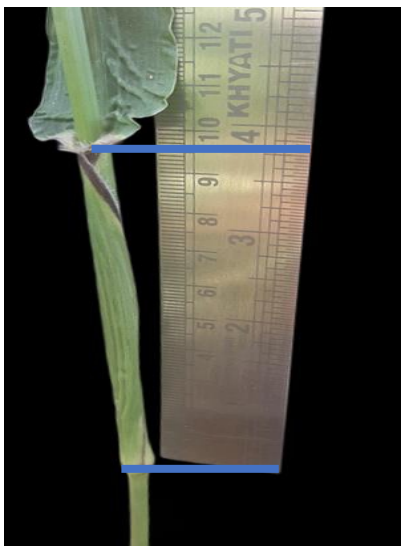
All genotypes are **ERECT**

Plate 3. Plant growth habit

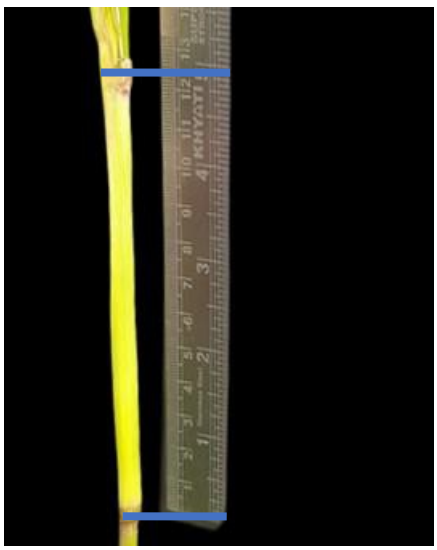
Present (1 genotype)

Absent (69 genotypes)

Plate 4. Leaf sheath pubescence



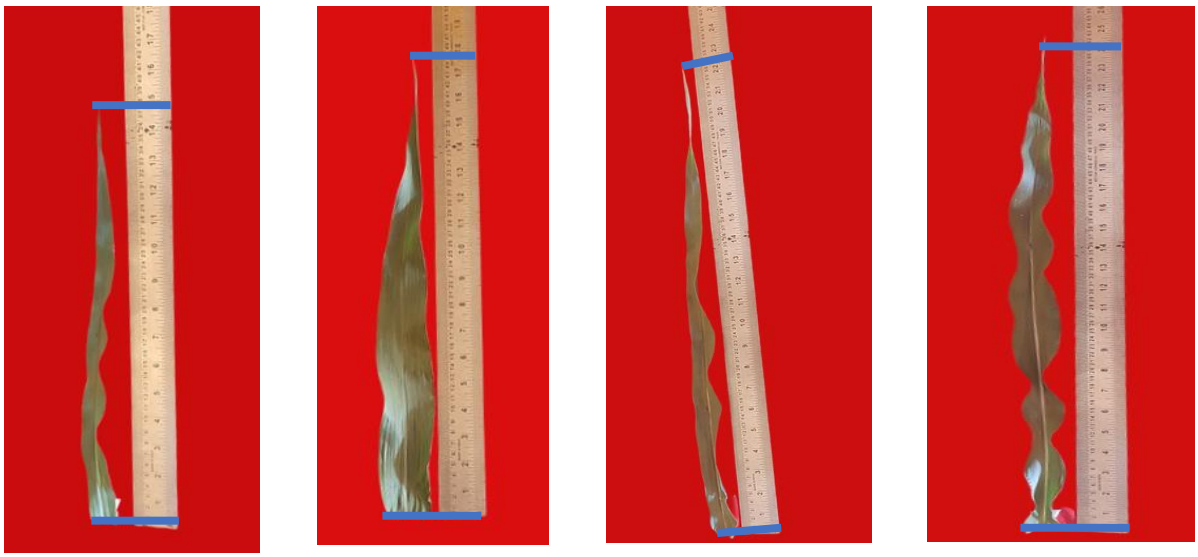
Short (6 genotypes)



Medium (57 genotypes)

Long (7 genotypes)

Plate 5. Leaf sheath length (cm)



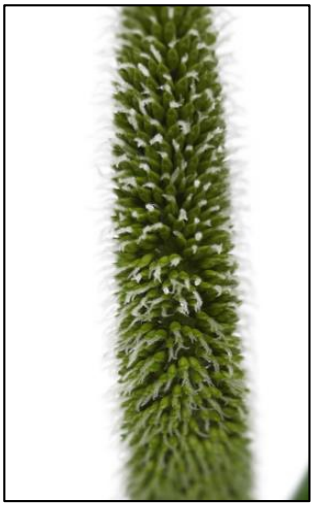
Very short (13 genotypes) | **Short (43 genotypes)** | **Medium (13 genotypes)** | **Long (1 genotype)**

Plate 6. Leaf blade length (cm)

Narrow (31 genotypes) | **Medium (37 genotypes)** | **Broad (2 genotypes)**

Plate 7. Leaf blade width (cm)

Present (3 genotypes)



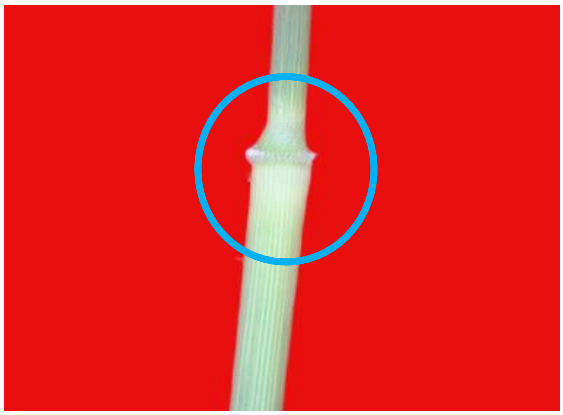
Absent (67 genotypes)

Plate 8. Spike stigma pigmentation

Yellow (50 genotypes)

Purple (20 genotypes)

Plate 9. Spike anther colour



Present (13 genotypes)

Absent (57 genotypes)

Plate 10. Plant: Node pubescence

Purple (23 genotypes)

Green (47 genotypes)

Plate 11. Plant node pigmentation

Purple (3 genotypes)

Green (67 genotypes)

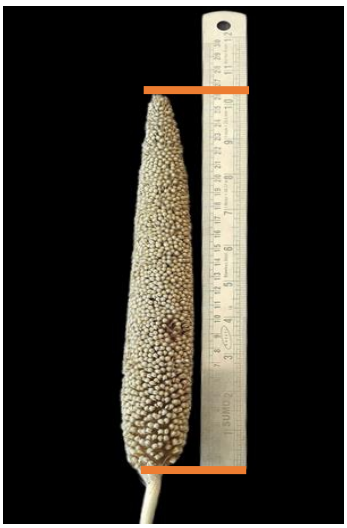
Plate 12. Plant internode pigmentation (between 3rd& 4th node from top)

Partial (1 genotype)

Complete (69 genotypes)

Plate 13. Spike exertion

Small (38 genotypes)



Medium(32 genotypes)

Plate 14. Spike length (cm)

Present (26 genotypes)

Absent (44 genotypes)

Plate 15. Spike anthocyanin pigmentation of glume

Absent (62 genotypes) **Present (8 genotypes)**

Plate 16. Spike bristle

Yellow (2 genotypes) **Brown (4 genotypes)** **Purple (2 genotypes)**

Plate 17. Spike bristle colour

Prominent (Bristle length> 2mm from the ear head)(8 genotypes)

Plate 18. Spike bristle appearance

Medium (67 genotypes)

Thick (3 genotypes)

Plate 19. Spike girth (cm)

Very short (2 genotypes)

Short (39 genotypes)

Medium(30 genotypes)

Plate 20. Plant height (cm)

Oblanceolate (1 genotype)

Candle (8 genotypes)

Spindle (1 genotype)

Plate 21. Spike shape

Cylindrical (12 genotypes)

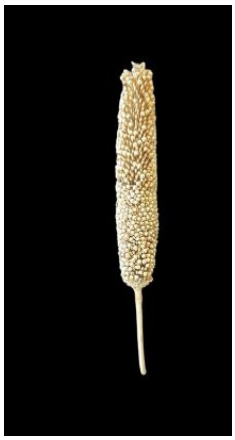
Lanceolate (30 genotypes)

Conical (18 genotypes)

Plate 21. Contd.

Compact (26 genotypes)

Semi-compact (36genotypes)



Loose (8 genotypes)

Plate 22. Spike density

Absent in all genotypes

Plate 23. Spike tip sterility

Cream (1 genotype)

Grey (18 genotypes)

Grey brown (25 genotypes)

Deep grey (23 genotypes)

Yellow brown (3 genotypes)

Plate 24. Seed colour

Obovate (6 genotypes)

Globular (64 genotypes)

Plate 25.Seed shape

4.1.2 Plant Growth Habit

Characterization of 70 germplasm accessions, on the basis of growth habit revealed that erect type is predominant (70) over other. Similar results were reported by Reddy *et al*. (2006) and Singh *et al*. (2016) for erect type of growth habit.

4.1.3 Time of Spike Emergence

On the basis of time of spike emergence, it was revealed that 58 accessions showed very late (>54 days) emergence, 11 accessions showed late (51-54 days) emergence and 1 accession shown early (43-46 days) emergence. This result was in agreement with the findings of Nehra *et al*. (2016) and Kalagarey *et al.* (2020).

Due to heavy rains and adverse environmental conditions during crop season vegetative period of crop was prolonged and caused delay in flowering, hence majority of the inbred lines were grouped into the category very late flowering.

4.1.4 Leaf Sheath Pubescence

69 germplasm accessions lacked pubescence whereas the rest showed pubescence on the leaf sheath. This result was in agreement with the findings of Nehra *et al*. (2016).

4.1.5 Leaf Sheath Length

Majority (57) of the germplasm accessions exhibited medium, 7 exhibited long while the remaining (6) were short for the trait, leaf sheath length. This result was in agreement with the findings of Singh *et al*. (2016) and Kalagarey *et al.* (2020).

4.1.6 Leaf Blade Length (cm)

Majority (43) of the germplasm accessions exhibited short, very short and medium were exhibited by 13 inbred lines each while the remaining one

was long for the trait, leaf blade length. This result is in accordance with the findings of Ahmed *et al*. (2017) and Kalagarey *et al.* (2020).

4.1.7 Leaf Blade Width (cm)

Medium blade width for leaf was observed in majority (37) of the germplasm accessions. Narrow was observed in 31 germplasm accessions, while remaining two inbred lines showed broad for the trait. Similar findings were also reported by Amarnath *et al*. (2019).

4.1.8 Spike Stigma Pigmentation

Characterization of 70 germplasm accessions, on the basis of spike stigma pigmentation revealed that, it is absent in 67 accessions and present in 3 accessions**.**

4.1.9 Spike Anther Color

Yellow anther colour for spike was observed in majority (50) of the germplasm accessions. While remaining (20) showed purple color for the trait. Similar classification was reported by Reddy *et al.* (2006) and Kalagarey *et al.* (2020) for this trait.

4.1.10 Plant Node Pubescence

Characterization of 70 germplasm accessions, on the basis of plant node pubescence revealed that it is absent in 57 accessions and present in 13 accessions**.** This result is in consonance with the findings of Nehra *et al*. (2016) and Singh *et al*. (2016).

4.1.11 Number of Nodes Plant^{-1}

Number of nodes plant^{-1} was low (<11) in all accessions.

4.1.12 Plant Node Pigmentation

Among the germplasm accessions studied, the trait was observed to be green (47) and purple (23). Similar result was reported by Kalagarey *et al.* (2020) for this character.

4.1.13 Plant Internode Pigmentation

Among the germplasm accessions studied, the trait was observed to be green (67) and purple (3). The results found were in conformity with the findings of Nehra *et al*. (2016) and Singh *et al*. (2016).

4.1.14 Spike Exertion

The trait spike exertion in the germplasm accessions was classified as complete (69) and partial (1). Similar results were reported by Ahmed *et al*. (2017) for this trait.

4.1.15 Spike Length (cm)

Majority (39) of the germplasm accessions exhibited short, while the remaining (31) were medium for the trait, spike length. The results found were in conformity with the findings of Bhattarai *et al.* (2014) and Nehra *et al*., (2016).

4.1.16 Spike Anthocyanin Pigmentation of Glume

Characterization of 70 germplasm accessions, on the basis of spike anthocyanin pigmentation of glume revealed that it is absent in 44 accessions and present in 26 accessions**.** Similar results were obtained by Ahmed *et al*. (2017) and Kalagarey *et al.* (2020) for this trait.

4.1.17 Spike Bristle

Characterization of 70 germplasm accessions, on the basis of spike bristle revealed that it is absent in 62 accessions and present in eight accessions**.** Similar result was obtained by Nehra *et al*. (2016) and Singh *et al*. (2016).

4.1.18 Spike Bristle Colour

Among the germplasm accessions studied, the trait was observed to be yellow (2), brown (4) and purple (2).

4.1.19 Spike Bristle Appearance

Among the germplasm accessions studied, the trait was observed to be prominent in 8 accessions only.

4.1.20 Spike Girth at Maximum Point

Characterization of 70 germplasm accessions, on the basis of spike girth at maximum point revealed that it is medium in 67 accessions and thick in three accessions.

4.1.21 Number of Productive Tillers Plant^{-1}

In the studied genotypes 36 accessions were found to be monoculm (single tiller), 33 accessions recorded 2-3 (low) and 4-6 (medium) in one accession.

4.1.22 Plant Height

Based on plant height, the germplasm accessions were categorized into very short (2), short (38) and medium (30).

4.1.23 Spike Shape

Based on spike shape, the germplasm accessions were categorized as cylindrical (12), conical (18), spindle (1), candle (8), lanceolate (30) and Oblanceolate (1). Similar result was obtained by Ahmed *et al*. (2017) for this trait.

4.1.24 Spike Tip Sterility

Among the germplasm accessions studied, the trait was observed to be absent in all accessions. This finding is complementary with the result obtained by Kalagarey *et al.* (2020) for this character.

4.1.25 Spike Density

Based on spike shape, the germplasm accessions were categorized as loose (8), semi-compact (36) and compact (26). Similar results were noted by Singh *et al*. (2016) for this trait.

4.1.26 Seed Colour

Based on seed colour, the germplasm accessions were categorized as cream (1), grey (18), deep grey (23), grey brown (25) and yellow brown (3). Similar results were observed by Bhattarai *et al.* (2014) and Nehra *et al.* (2016) for this trait.

4.1.27 Seed Shape

Among the germplasm accessions studied, the trait was observed to be obovate in 6 accessions and globular in 64 accessions. This finding is complementary with the results obtained by Reddy *et al*. (2006), Ahmed *et al.* (2017), Amarnath *et al*. (2019), Ankit *et al.* (2020) and Kalagarey *et al.* (2020) for this character.

4.1.28 Seed: Weight of 1000 Grains (g)

Among 70 germplasm accessions, 1000 grain weight was small in 11 accessions, medium in 17 accessions, bold in 32 accessions and very bold in 10 accessions. This result is in consonance with the findings of Amarnath *et al*. (2019), Ankit *et al.* (2020) and Kalagarey *et al.* (2020).

Morphological characterization of 70 pearl millet genotypes using 28 DUS traits highlighted the existence of sufficient variability for the characters studied. It was observed in the present study for character plant anthocyanin coloration of first leaf sheath, presence of pigmentation was predominant over absence of pigmentation; for character growth habit, erect was predominant; for character days to 50% flowering very late duration germplasm lines are predominant; for character leaf sheath pubescence, absence of leaf sheath pubescence was predominant over presence; for leaf sheath length medium types are predominant over short and long; for leaf blade length short types are predominant; for character leaf blade width medium types are predominant over narrow and broad; absence of spike stigma pigmentation is predominant over presence; for spike anther color yellow color was predominant; absence of plant node pubescence was predominant over

presence; number of nodes plant^{-1} was low in all; for character plant node pigmentation green was predominant; for plant internode pigmentation green was predominant; complete exertion of spike was predominant over partial exertion; short spike length was predominant over medium spike length; presence of spike anthocyanin pigmentation of glume was predominant over absence; absence of spike bristle was predominant over presence; brown coloured spike bristle colour was predominant over yellow and purple coloured spike bristles; medium spike girth was predominant over thick spike girth at maximum point; one productive tiller plant^{-1} was predominant; short plant height was predominant over very short and medium types; for character spike shape lanceolate type was predominant; absence of spike tip sertility in all genotypes; for character spike-density semi compact was predominant; for character seed color grey brown was predominant; globular seed shape was predominant over obovate seed shape; for character 1000 seed weight bold was predominant. Variability in DUS traits is depicted in Fig. 4.1.

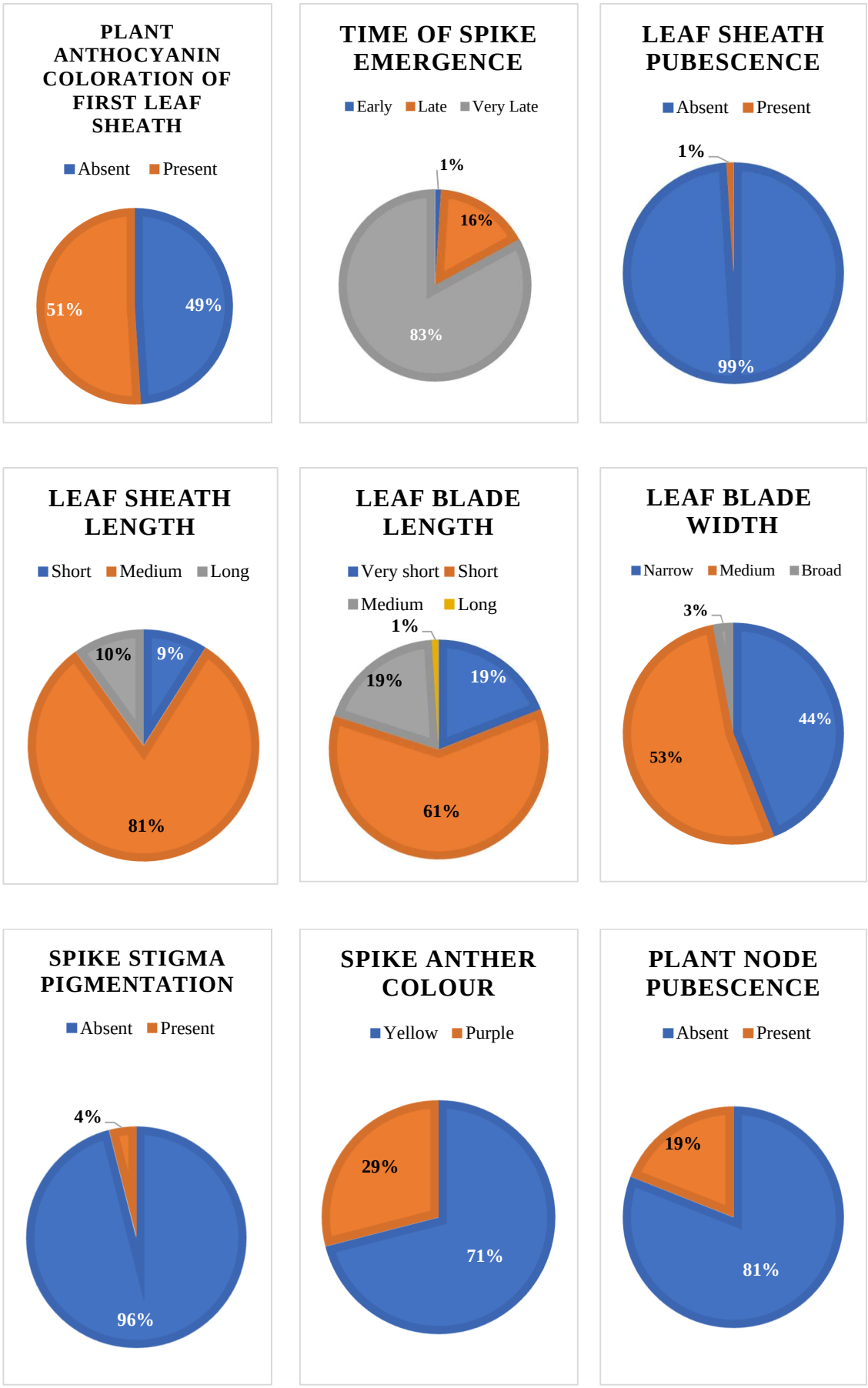


Fig. 4.1. Pie diagram depicting variability for DUS traits among 70 inbred lines of pearl millet

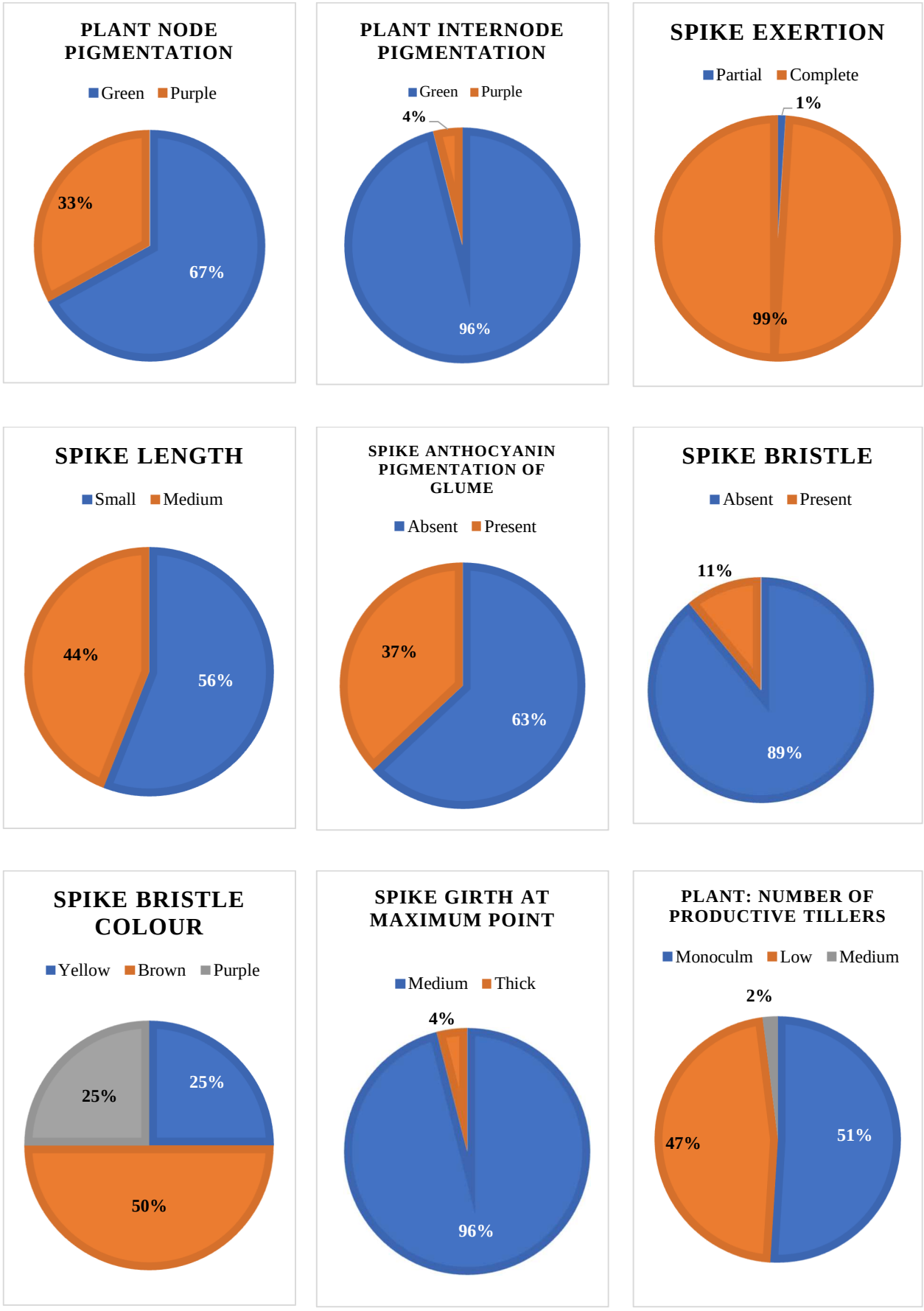

PLANT NODE PIGMENTATION
Green
Purple
33%
67%
PLANT INTERNODE PIGMENTATION
Green
Purple
4%
96%
SPIKE EXERTION
Partial
Complete
1%
99%
SPIKE LENGTH
Small
Medium
44%
56%
SPIKE ANTHOCYANIN PIGMENTATION OF GLUME
Absent
Present
37%
63%
SPIKE BRISTLE
Absent
Present
11%
89%
SPIKE BRISTLE COLOUR
Yellow
Brown
Purple
25%
25%
50%
SPIKE GIRTH AT MAXIMUM POINT
Medium
Thick
4%
96%
PLANT: NUMBER OF PRODUCTIVE TILLERS
Monoculm
Low
Medium
2%
47%
51%

Fig. 4.1 cont.

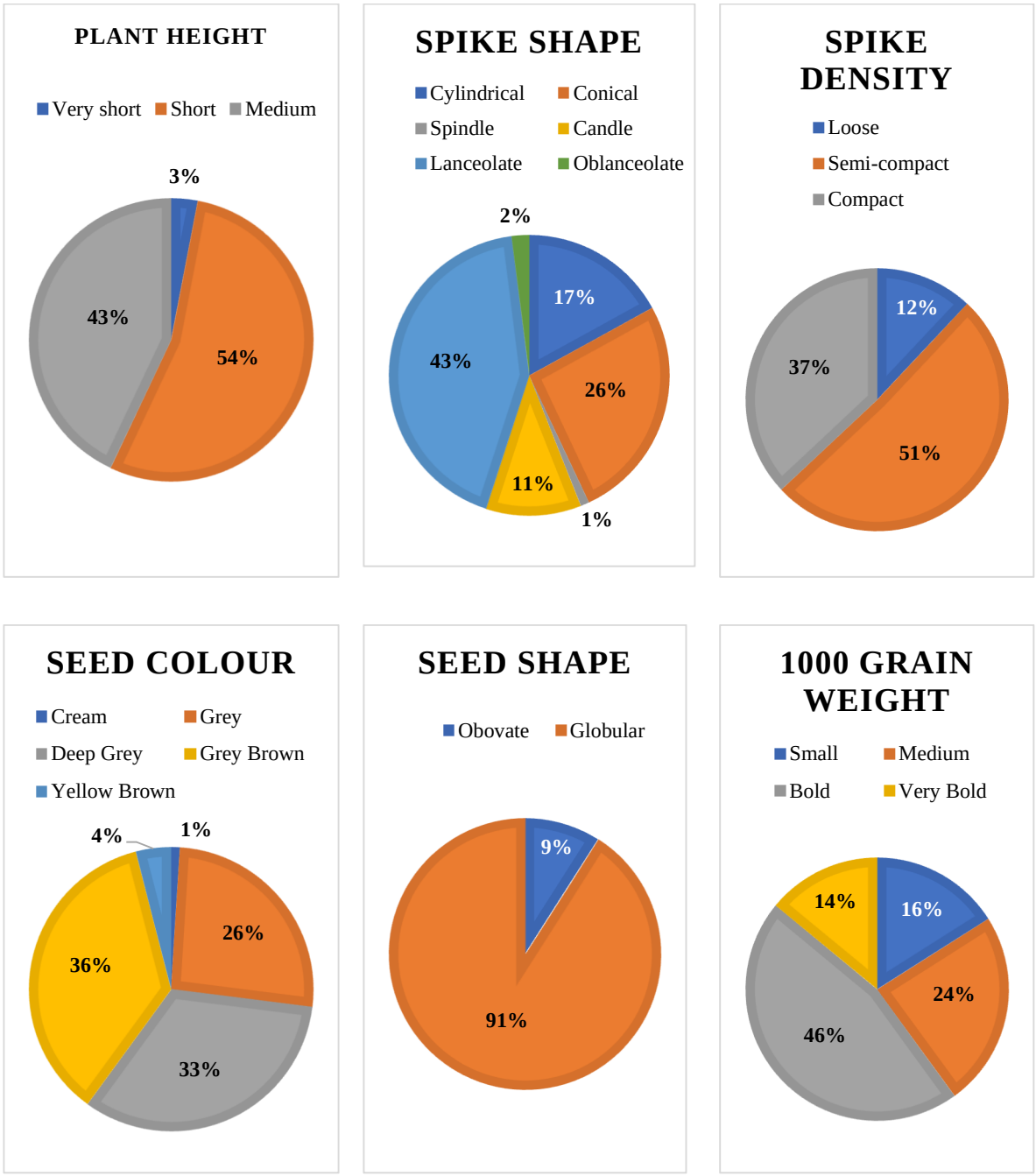

PLANT HEIGHT
Very short
Short
Medium
3%
43%
54%
SPIKE SHAPE
Cylindrical
Conical
Spindle
Candle
Lanceolate
Oblanceolate
2%
17%
43%
26%
11%
1%
SPIKE DENSITY
Loose
Semi-compact
Compact
12%
37%
51%
SEED COLOUR
Cream
Grey
Deep Grey
Grey Brown
Yellow Brown
4%
1%
26%
36%
33%
SEED SHAPE
Obovate
Globular
9%
91%
1000 GRAIN WEIGHT
Small
Medium
Bold
Very Bold
14%
16%
24%
46%

Fig. 4.1 cont.

4.2 ANALYSIS OF VARIANCE

Analysis of variance for 21 characters *viz.*, days to 50% flowering, days to maturity, SPAD chlorophyll meter reading at 45 DAS, SPAD chlorophyll meter reading at 65 DAS, specific leaf area at 45 DAS (cm^2 g^{-1}**)**, specific leaf area at 65 DAS (cm^2 g^{-1}**)**, leaf sheath length (cm), leaf blade length (cm), leaf blade width (cm), number of nodes $plant^{-1}$, spike length (cm), spike girth (cm), number of productive tillers $plant^{-1}$, plant height (cm), 1000 grain weight (g), panicle weight (g), green fodder yield $plant^{-1}$ (g), dry fodder yield $plant^{-1}$ (g), threshing (%), harvest index (%) and grain yield $plant^{-1}$ (g) were presented in the Table 4.2. The analysis of variance revealed that mean sum of squares were highly significant for all the characters studied, indicating the presence of ample amount of genetic variation among genotypes which can be exploited through selection.

4.3 MEAN PERFORMANCE

Mean is a relatively simple measure used in plant breeding to assess phenotypic variability and it serves as a basis for eliminating undesirable genotypes. It also measures the genetic potentiality of genotypes. The mean performance of 70 inbred lines of pearl millet for 21 yield and yield contributing characters is presented in Table 4.3.

4.3.1 Days to 50% Flowering

The mean performance for days to 50% flowering ranged from 44 days to 80.5 days with a general mean of 58.97 days. Among all inbred lines, PPBi-44 (44 days) was early to flowering and PPBi-6 (80.5 days) was late to flowering. The inbred lines PPBi-44, PPBi-12, PPBi-66, PPBi-64, PPBi-20, PPBi-23, PPBi-35 and PPBi-37 were the earliest one to flower. Therefore, these genotypes can be utilized in the hybridization programme as donor parents to evolve short duration hybrids. Out of 70 inbred lines evaluated, 41 inbred lines were earlier to flowering when compared with general mean (58.97 days).

Table 4.2 Analysis of variance for yield and yield attributes in 70 inbred lines of pearl millet

S. No.	Characters	Mean sum of squares		
		Replications	Treatments	Error
		(df=1)	(df=69)	(df=69)
1	Days to 50% flowering	16.457	93.477**	4.602
2	Days to maturity	13.207	87.208**	4.091
3	SPAD chlorophyll meter reading at 45 DAS	10.809	54.131**	19.152
4	SPAD chlorophyll meter reading at 65 DAS	15.114	104.664**	58.820
5	Specific leaf area at 45 DAS (cm^2 g^{-1})	807.408	1759.898**	511.374
6	Specific leaf area at 65 DAS (cm^2 g^{-1})	129.601	1891.645**	790.757
7	Leaf sheath length (cm)	1.629	7.452**	4.205
8	Leaf blade length (cm)	6.723	67.911**	17.149
9	Leaf blade width (cm)	0.394	0.384**	0.124
10	No of nodes $plant^{-1}$	0.833	0.977**	0.236
11	Spike length (cm)	0.003	27.541**	4.859
12	Spike girth (cm)	0.110	0.239**	0.037
13	Number of productive tillers $plant^{-1}$	0.001	0.759**	0.083
14	Plant height (cm)	219.250	917.970**	76.067
15	1000 grain weight (g)	2.345	10.607**	0.689
16	Panicle weight (g)	46.173	551.144**	45.659
17	Green fodder yield $plant^{-1}$ (g)	286.286	2270.019**	191.920
18	Dry fodder yield $plant^{-1}$ (g)	25.766	204.302**	21.248
19	Threshing (%)	0.140	198.391**	35.517
20	Harvest index (%)	1.783	98.552**	21.811
21	Grain yield $plant^{-1}$ (g)	20.034	152.866**	13.092

**Significant at 1% level.

Table 4.3 Mean performance of inbred lines of pearl millet for yield and its component characters

GENO-TYPES	DF	DM	SCMR 45	SCMR 65	SLA 45	SLA 65	LSL	LBL	LBW	NN	SL
PPBi-1	70.00	101.00	30.25	51.55	177.63	173.34	12.61	47.05	2.95	4.80	27.90
PPBi-2	65.00	98.00	33.75	51.90	136.33	145.37	13.47	49.95	3.18	5.70	22.10
PPBi-3	61.50	93.50	37.00	52.25	162.96	160.71	14.85	48.70	3.53	5.50	17.90
PPBi-4	55.00	86.00	42.25	59.05	146.43	171.32	14.90	48.85	3.62	5.90	21.00
PPBi-5	52.50	85.50	35.55	56.60	162.15	200.00	14.97	41.40	3.13	6.30	22.50
PPBi-6	80.50 **(Max)**	109.00	32.40	47.65	159.17	199.37	13.85	51.85	4.40 **(Max)**	5.70	26.40
PPBi-7	56.00	87.00	31.25	47.95	121.86	186.86	13.05	42.45	2.53	5.80	19.30
PPBi-8	58.50	91.50	36.20	54.95	162.46	113.10	12.81	41.75	3.18	5.20	22.40
PPBi-9	67.00	99.00	35.35	40.85	133.93	156.87	13.55	48.15	3.63	5.20	27.20
PPBi-10	66.00	97.00	36.35	74.50 **(Max)**	122.69	146.43	13.10	41.25	3.10	4.80	18.20
PPBi-11	54.50	87.50	39.45	57.30	134.14	164.77	11.45	37.90	2.64	4.80	26.60
PPBi-12	50.50	82.50	41.85	50.15	136.76	152.91	11.40	39.75	2.39	4.80	16.10
PPBi-13	55.00	86.00	42.85	44.95	122.30	130.93	11.45	39.40	2.64	4.90	19.00
PPBi-14	74.00	107.00	39.40	54.80	124.72	104.79 **(Min)**	14.30	46.95	3.87	5.20	24.90
PPBi-15	56.00	88.00	37.95	50.95	121.94	134.88	14.15	50.75	2.89	5.70	22.10
PPBi-16	71.00	102.00	31.60	49.95	190.08	211.30	14.05	48.40	2.87	6.10	21.10
PPBi-17	59.50	92.50	34.60	45.60	137.81	151.00	13.95	49.14	3.00	6.00	17.60
PPBi-18	72.50	104.50	34.40	54.80	181.61	155.94	18.40 **(Max)**	57.00	2.86	5.30	25.60
PPBi-19	61.50	92.50	31.90	46.90	156.66	142.11	18.15	54.40	3.47	5.40	21.90
PPBi-20	51.50	84.50	31.40	47.25	106.31	123.46	13.40	41.80	2.31 **(Min)**	5.50	17.10
PPBi-21	53.50	85.50	32.50	48.25	118.65	125.52	10.70	35.75	3.36	4.40	16.00
PPBi-22	62.50	93.50	36.95	53.85	133.03	146.26	14.52	44.05	3.24	6.80	21.80
PPBi-23	51.50	84.50	39.40	42.80	191.03	210.64	10.97	34.00	2.67	5.20	13.80
PPBi-24	67.00	99.00	25.55 **(Min)**	57.60	130.67	143.37	17.25	61.40 **(Max)**	3.28	4.70	28.20 **(Max)**
PPBi-25	58.00	89.00	35.85	53.35	181.43	182.79	14.95	48.50	3.20	5.70	22.00
PPBi-26	60.00	93.00	36.80	54.00	135.20	148.07	7.09 **(Min)**	50.10	3.17	5.70	21.90
PPBi-27	53.50	85.50	31.90	53.50	113.22	127.31	12.45	44.05	3.09	6.00	19.00
PPBi-28	54.50	85.50	44.20	54.60	142.09	143.54	14.50	52.30	4.39	5.70	22.10
PPBi-29	60.00	93.00	33.90	41.45	217.70	179.42	16.01	44.15	2.62	5.90	20.00
PPBi-30	63.50	95.50	36.85	48.60	155.86	164.46	13.30	45.25	2.99	6.00	17.10

Cont.

Table 4.3 (cont.).

GENO-TYPES	DF	DM	SCMR 45	SCMR 65	SLA 45	SLA 65	LSL	LBL	LBW	NN	SL
PPBi-31	67.50	98.50	28.30	46.80	118.20	131.76	11.14	48.05	3.18	5.40	19.70
PPBi-32	56.50	89.50	37.40	45.10	177.16	157.64	14.50	49.05	3.37	6.60	21.70
PPBi-33	57.00	88.50	31.05	33.90 **(Min)**	128.08	136.18	12.95	48.55	3.27	7.00	18.10
PPBi-34	60.00	91.50	30.00	34.50	244.31 **(Max)**	237.85 **(Max)**	13.20	45.60	2.32	4.90	20.20
PPBi-35	51.50	84.50	33.65	41.00	192.51	158.54	13.88	54.36	3.31	5.60	22.80
PPBi-36	59.00	91.00	45.55	53.80	156.22	224.36	14.60	49.40	2.59	6.10	21.70
PPBi-37	52.00	83.00	45.80	41.30	100.22	130.12	14.15	48.20	3.05	6.10	17.80
PPBi-38	54.00	87.00	27.85	45.90	173.54	194.80	14.17	44.40	3.24	5.00	17.90
PPBi-39	55.00	86.50	28.85	44.10	102.89	116.76	10.92	35.70	2.58	6.90	17.20
PPBi-40	54.00	85.00	28.60	45.10	165.26	172.05	12.90	36.70	2.42	4.40	18.50
PPBi-41	53.00	86.00	41.70	42.75	166.74	157.66	13.55	47.25	3.28	5.90	23.70
PPBi-42	53.50	85.50	40.05	60.60	113.76	154.42	13.70	48.65	2.74	5.70	17.50
PPBi-43	63.50	94.50	38.15	46.05	105.71	115.16	13.00	39.55	3.59	4.60	19.20
PPBi-44	44.00 **(Min)**	77.00 **(Min)**	34.50	65.45	163.19	173.68	11.60	40.50	3.29	4.60	20.40
PPBi-45	68.00	100.00	31.10	48.55	160.42	163.27	12.00	39.95	2.55	5.10	24.20
PPBi-46	54.50	85.50	38.85	51.15	153.91	153.78	12.58	49.24	3.19	6.20	18.20
PPBi-47	58.50	91.50	53.60 **(Max)**	55.60	129.10	128.13	14.45	42.55	2.71	7.30 **(Max)**	22.20
PPBi-48	59.50	91.50	41.70	41.90	152.74	129.65	13.95	38.10	2.80	5.30	13.40 **(Min)**
PPBi-49	63.50	95.00	43.80	46.05	141.85	236.40	14.70	44.29	3.43	6.70	17.20
PPBi-50	54.00	87.50	37.90	52.70	121.16	128.03	13.00	51.15	2.98	6.20	26.80
PPBi-51	55.00	87.00	42.45	51.80	144.45	187.23	12.70	45.85	2.95	5.40	23.80
PPBi-52	68.00	99.50	32.35	47.40	174.54	203.11	14.50	50.00	3.65	5.40	27.30
PPBi-53	76.00	109.00 **(Max)**	29.20	47.30	185.00	223.79	13.95	52.10	3.89	6.40	26.60
PPBi-54	58.00	90.00	33.00	45.30	189.11	155.32	10.55	40.90	2.60	4.90	17.20
PPBi-55	64.00	95.50	38.85	42.35	131.77	148.25	17.90	53.40	3.13	6.40	26.70
PPBi-56	57.50	90.50	33.55	50.60	116.28	127.15	13.50	34.35	2.68	4.30	18.10
PPBi-57	66.00	98.00	35.65	40.50	145.44	165.21	14.82	49.90	3.23	6.20	21.70
PPBi-58	60.50	92.00	34.10	47.05	163.80	160.55	13.85	45.65	3.60	6.20	23.50
PPBi-59	56.00	89.00	30.40	44.50	154.71	168.11	12.97	41.51	3.33	6.20	24.30
PPBi-60	56.50	88.50	29.20	36.60	143.47	160.69	14.79	50.75	3.03	5.70	23.30

Cont.

Table 4.3 (cont.).

GENO-TYPES	DF	DM	SCMR 45	SCMR 65	SLA 45	SLA 65	LSL	LBL	LBW	NN	SL
PPBi-61	54.50	86.00	46.35	47.70	122.95	169.41	12.30	47.30	3.10	5.40	17.80
PPBi-62	61.00	94.00	31.75	57.65	150.74	142.11	14.22	44.30	2.43	4.60	16.80
PPBi-63	55.00	87.00	40.80	41.90	195.14	172.98	13.99	40.70	2.83	4.80	17.90
PPBi-64	51.00	82.50	36.75	54.75	118.89	122.46	14.15	48.00	3.05	4.80	16.90
PPBi-65	54.00	87.00	35.80	54.90	111.21	134.65	14.10	44.20	2.97	5.50	18.90
PPBi-66	50.50	82.50	34.40	58.20	98.71 **(Min)**	199.51	13.50	41.70	2.89	4.90	15.40
PPBi-67	58.50	90.00	35.25	35.25	106.63	148.41	10.79	32.90 **(Min)**	2.55	4.70	15.00
PPBi-68	52.50	85.50	35.95	51.05	116.92	155.74	10.40	33.60	2.58	4.30 **(Min)**	14.80
PPBi-69	56.00	88.00	40.10	59.10	170.45	197.91	17.85	50.25	3.36	5.00	18.30
PPBi-70	57.00	88.50	37.80	58.70	132.62	208.53	16.75	45.50	2.90	5.60	17.40
General Mean	58.97	90.96	36.03	49.47	146.52	160.69	13.60	45.44	3.07	5.53	20.56
Minimum	44.00	77.00	25.55	33.90	98.71	104.79	7.09	32.90	2.31	4.30	13.40
Maximum	80.50	109.00	53.60	74.50	244.31	237.85	18.40	61.40	4.40	7.30	28.20
C.D. (at 5%)	4.28	4.04	8.73	15.30	45.11	56.10	4.09	8.26	0.70	0.97	4.40
S.E. (m)	1.51	1.42	3.07	3.57	4.35	5.13	5.92	6.70	7.48	8.26	1.55
S.E. (d)	2.15	2.02	4.38	7.67	22.61	28.12	2.05	4.14	0.35	0.49	2.20
C.V. (%)	3.64	2.22	12.15	15.50	15.43	17.50	15.08	9.11	11.46	8.79	10.72

Cont.

Table 4.3 (cont.).

GENO-TYPES	SG	NPT	PH	1000 GW	PW	GFY	DFY	TH	HI	GYP
PPBi-1	2.88	1.20	152.90	10.87	51.60	116.60	34.98	33.43	19.92	17.25
PPBi-2	2.19	1.30	139.00	7.64	32.00	66.60	19.98	35.47	21.92	11.35
PPBi-3	2.33	3.40	151.10	10.02	73.70	168.70 **(Max)**	50.61 **(Max)**	47.36	28.06	34.84
PPBi-4	2.97	1.70	160.60	14.58 **(Max)**	38.60	96.70	29.01	50.20	28.82	19.49
PPBi-5	2.41	1.70	144.10	14.46	40.10	72.70	21.81	46.07	29.78	18.22
PPBi-6	2.69	1.20	164.40	11.74	54.60	109.50	32.85	43.88	27.27	23.85
PPBi-7	2.25	2.30	151.80	12.72	44.90	110.80	33.24	50.90	28.08	21.70
PPBi-8	2.96	1.30	158.70	11.37	60.50	111.20	33.36	42.42	27.30	25.81
PPBi-9	2.69	1.40	152.60	8.59	56.20	134.50	40.35	26.60	15.48	14.95
PPBi-10	2.47	2.00	127.20	10.79	37.00	65.70	19.71	52.11	34.14	19.40
PPBi-11	2.25	1.70	120.10	5.92	24.20	32.90	9.87	44.05	31.57	10.61
PPBi-12	2.41	2.90	116.00	10.91	40.80	54.60	16.38	53.25	38.87	21.80
PPBi-13	2.69	1.40	138.30	12.36	39.00	81.50	24.45	66.59	40.81	25.70
PPBi-14	2.95	1.40	177.40	11.37	45.80	92.90	27.87	40.16	25.06	18.61
PPBi-15	2.38	1.40	153.80	14.23	44.00	66.40	19.92	61.77	43.53	27.10
PPBi-16	2.49	1.30	189.60	12.20	32.90	100.50	30.15	48.76	25.45	16.11
PPBi-17	2.89	1.60	137.20	13.77	49.70	95.80	28.74	48.23	31.15	23.95
PPBi-18	3.05	1.20	192.90 **(Max)**	13.66	39.20	81.30	24.39	40.38	25.06	15.90
PPBi-19	2.59	1.10	174.80	11.84	38.30	63.00	18.90	43.12	28.37	15.70
PPBi-20	1.98	1.40	139.60	14.31	22.30	42.50	12.75	67.26	42.58	14.93
PPBi-21	2.38	2.10	101.70	8.85	19.90	40.60	12.18	60.88	37.13	11.84
PPBi-22	2.71	1.20	161.40	11.14	40.60	84.10	25.23	54.22	33.25	21.85
PPBi-23	1.99	2.00	115.30	12.62	16.50	29.60	8.88	67.28	42.23	10.52
PPBi-24	3.32 **(Max)**	1.20	155.60	12.44	48.60	120.70	36.21	41.57	23.81	20.32
PPBi-25	3.05	2.60	170.20	10.93	75.80	129.60	38.88	51.53	34.01	39.00
PPBi-26	2.98	1.20	140.80	10.89	31.00	51.10	15.33	52.52	35.15	16.28
PPBi-27	2.79	1.00	136.00	8.95	46.90	77.60	23.28	49.18	32.68	23.40
PPBi-28	2.92	1.50	157.70	12.39	48.90	102.40	30.72	56.05	34.40	27.55
PPBi-29	1.90	1.20	135.40	10.82	24.20	51.10	15.33	29.01	17.63	7.05
PPBi-30	2.62	2.30	141.20	10.48	34.10	78.60	23.58	42.76	25.29	14.60

Cont.

Table 4.3 (cont.).

GENO-TYPES	SG	NPT	PH	1000 GW	PW	GFY	DFY	TH	HI	GYP
PPBi-31	2.30	2.30	129.40	10.73	32.40	67.50	20.25	53.16	31.97	17.70
PPBi-32	2.66	1.70	156.30	10.42	43.20	138.90	41.67	51.60	26.29	22.51
PPBi-33	2.60	1.20	150.90	7.86	28.00	67.30	20.19	60.27	35.03	16.88
PPBi-34	1.87	1.40	129.80	6.87	25.80	72.50	21.75	47.36	25.70	12.22
PPBi-35	2.24	1.90	155.70	12.47	50.40	122.20	36.66	52.54	30.46	26.50
PPBi-36	2.72	1.40	166.80	11.14	45.70	99.60	29.88	63.96	38.74	29.45
PPBi-37	2.03	1.20	138.40	9.98	25.20	53.60	16.08	75.98 **(Max)**	46.39 **(Max)**	19.15
PPBi-38	1.69 **(Min)**	1.60	128.00	10.96	11.00 **(Min)**	34.10	10.23	47.96	24.96	5.28 **(Min)**
PPBi-39	1.80	1.00 **(Min)**	130.60	8.04	13.20	31.40	9.42	56.32	32.92	7.44
PPBi-40	1.89	2.40	136.50	5.54 **(Min)**	23.10	66.10	19.83	49.42	26.62	11.42
PPBi-41	2.30	2.10	156.80	8.92	47.30	92.30	27.69	43.25	27.22	20.40
PPBi-42	2.07	1.30	129.80	6.60	16.70	37.60	11.28	47.79	28.15	7.87
PPBi-43	2.32	1.90	148.10	5.58	43.90	106.60	31.98	24.82 **(Min)**	14.29 **(Min)**	10.80
PPBi-44	2.39	1.30	102.70	7.32	26.80	57.80	17.34	35.25	21.40	9.45
PPBi-45	2.50	1.40	161.30	9.49	47.80	103.00	30.90	39.30	23.77	18.70
PPBi-46	2.78	2.90	139.60	13.54	64.60	116.60	34.98	53.69	34.83	34.41
PPBi-47	2.87	1.50	192.50	12.98	54.10	129.00	38.70	58.16	33.89	31.45
PPBi-48	2.40	1.20	120.30	7.47	14.50	42.40	12.72	46.11	25.06	6.70
PPBi-49	2.40	1.20	163.20	10.10	30.10	86.40	25.92	56.36	30.86	17.12
PPBi-50	2.51	4.20 **(Max)**	156.90	10.24	101.80 **(Max)**	165.30	49.59	57.40	38.61	58.42 **(Max)**
PPBi-51	2.96	1.10	150.70	10.41	36.10	77.00	23.10	65.89	40.02	23.75
PPBi-52	2.87	1.40	160.50	8.84	42.60	122.20	36.66	49.78	26.74	21.20
PPBi-53	3.01	1.10	171.50	7.72	54.60	118.20	35.46	44.95	27.26	24.55
PPBi-54	2.45	1.60	133.70	7.43	28.00	92.70	27.81	56.09	28.16	15.75
PPBi-55	2.07	1.20	151.60	6.93	25.50	75.40	22.62	45.93	24.14	11.70
PPBi-56	2.57	1.50	114.40	8.77	32.10	63.60	19.08	45.47	27.42	13.50
PPBi-57	2.61	2.60	144.20	6.95	63.60	104.90	31.47	39.47	26.43	25.10
PPBi-58	2.03	1.70	149.30	7.97	33.50	96.20	28.86	44.94	24.14	15.05
PPBi-59	2.52	2.00	155.70	9.25	57.70	107.70	32.31	48.27	31.01	27.85
PPBi-60	2.25	1.50	149.80	7.08	44.30	79.80	23.94	49.89	31.95	21.85

Cont.

Table 4.3 (cont.).

GENO-TYPES	SG	NPT	PH	1000 GW	PW	GFY	DFY	TH	HI	GYP
PPBi-61	2.37	1.30	138.20	10.11	35.50	62.00	18.60	60.59	39.51	21.25
PPBi-62	2.06	1.20	112.80	10.03	16.80	33.50	10.05	48.97	32.55	8.25
PPBi-63	2.46	1.50	117.80	8.56	20.50	33.90	10.17	65.11	43.27	13.32
PPBi-64	2.40	1.60	113.50	11.62	22.90	41.70	12.51	57.87	37.65	13.40
PPBi-65	2.50	1.80	138.80	11.49	34.70	73.50	22.05	49.89	30.50	17.30
PPBi-66	2.39	1.40	113.90	9.04	18.60	30.40	9.12	51.64	34.62	9.81
PPBi-67	2.39	2.15	99.70	11.06	35.00	56.40	16.92	46.50	31.46	16.10
PPBi-68	2.37	1.30	95.10 **(Min)**	11.41	16.60	24.60 **(Min)**	7.38 **(Min)**	66.38	45.82	11.28
PPBi-69	2.61	1.70	131.80	9.44	42.10	75.00	22.50	64.43	42.12	27.33
PPBi-70	2.61	3.30	137.80	13.60	63.60	121.40	36.42	47.13	30.01	29.95
General Mean	2.49	1.68	143.31	10.24	38.88	81.57	24.47	50.23	30.87	19.17
Minimum	1.69	1.00	95.10	5.54	11.00	24.60	7.38	24.82	14.29	5.28
Maximum	3.32	4.20	192.90	14.58	101.80	168.70	50.61	75.98	46.39	58.42
C.D. (at 5%)	0.38	0.38	0.38	1.66	13.48	27.64	9.20	11.89	9.32	7.22
S.E. (m)	0.13	0.20	6.12	0.58	4.74	9.73	3.24	4.18	3.28	2.54
S.E. (d)	0.19	0.29	8.72	0.83	6.76	13.85	4.61	5.96	4.67	3.62
C.V. (%)	7.70	17.23	6.09	8.11	17.38	16.98	18.84	11.86	15.13	18.88

DF : Days to 50% flowering
DM : Days to maturity
SCMR 45 : SPAD chlorophyll meter reading at 45 DAS
SCMR 65 : SPAD chlorophyll meter reading at 65 DAS
SLA 45 : Specific leaf area at 45 DAS ($cm^2 g^{-1}$)
SLA 65 : Specific leaf area at 65 DAS ($cm^2 g^{-1}$)
LSL : Leaf sheath length (cm)
LBL : Leaf blade length (cm)
LBW : Leaf blade width (cm)
NN : No of nodes $plant^{-1}$
SL : Spike length (cm)
SG : Spike girth (cm)
NPT : Number of productive tillers $plant^{-1}$
PH : Plant height (cm)
1000 GW : 1000 grain weight (g)
PW : Panicle weight (g)
GFY : Green fodder yield $plant^{-1}$ (g)
DFY : Dry fodder yield $plant^{-1}$ (g)
TH : Threshing (%)
HI : Harvest index (%)
GYP : Grain yield $plant^{-1}$ (g)

4.3.2 Days to Maturity

Days to maturity ranged from 77 days to 109 days with a general mean of 90.96 days. Maturity was early in PPBi-44 (77 days) and late in PPBi-53 (109 days). The inbred lines *viz.*, PPBi-44, PPBi-12, PPBi-64, PPBi-66, PPBi-37, PPBi-20, PPBi-23, PPBi-35 and PPBi-40 were found to be early maturing. Therefore, these genotypes can be utilized in the hybridization programme as donor parents to evolve short duration hybrids. Out of 70 inbred lines evaluated, 39 inbred lines were earlier to maturity than general mean (90.96 days).

4.3.3 SPAD Chlorophyll Meter Reading at 45 DAS

The SPAD chlorophyll meter reading at 45 DAS ranged from 25.55 to 53.6. High reading was observed in PPBi-47 (53.6), whereas PPBi-24 (25.55) was found to be low. 32 out of 70 inbred lines recorded higher values when compared to general mean (36.03).

Significant positive correlation between SCMR and WUE and a negative correlation between SCMR and SLA were considered as good indicators of high WUE. Hence, genotypes *viz.*, PPBi-50, PPBi-28, PPBi-14, PPBi-42 and PPBi-43 with high SCMR can be utilized for development of hybrids tolerant to drought.

4.3.4 SPAD Chlorophyll Meter Reading at 65 DAS

SPAD chlorophyll meter reading at 65 DAS ranged from 33.9 to 74.5. High reading was observed in PPBi-33 (33.9), whereas PPBi-10 (74.5) was found to be low. 34 out of 70 inbred lines had higher values of SPAD readings when compared to general mean (49.47).

4.3.5 Specific Leaf Area at 45 DAS ($cm^2\ g^{-1}$)

The mean values for SLA at 45 DAS ranged from 98.71 $cm^2\ g^{-1}$ (PPBi-66) to 244.31 $cm^2\ g^{-1}$ (PPBi-34) with a general mean of 146.52 $cm^2\ g^{-1}$. 39 inbred lines recorded low SLA at 45 DAS than the general mean.

4.3.6 Specific Leaf Area at 65 DAS ($cm^2 g^{-1}$)

Among 70 inbred lines, PPBI-14 recorded the lowest specific leaf area at 65 DAS of 104.79 $cm^2 g^{-1}$, while PPBi-34 recorded the highest specific leaf area at 65 DAS of 237.85 $cm^2 g^{-1}$. 40 inbred lines recorded less specific leaf area at 65 DAS compared to the general mean (160.69 $cm^2 g^{-1}$).

4.3.7 Leaf Sheath Length (cm)

The mean values for leaf sheath length ranged from 7.09 cm to 18.4 cm. PPBi-26 showed the shortest leaf sheath length (7.09 cm) and PPBi-18 showed the longest leaf sheath length (18.40 cm). Out of 70 inbred lines evaluated, 36 inbred lines showed longest leaf blade length than general mean (13.6 cm).

4.3.8 Leaf Blade Length (cm)

Among 70 inbred lines studied, PPBi-67 showed shortest leaf blade length (32.9 cm), while PPBi-24 showed longest leaf blade length (61.4 cm). 38 inbred lines recorded longest leaf blade length when compared to the general mean (45.44 cm).

4.3.9 Leaf Blade Width (cm)

The leaf blade width ranged from 2.31 cm (PPBi-20) to 4.4 cm (PPBi-06) with a general mean of 3.07 cm. Out of 70 inbred lines evaluated, 35 inbred lines showed largest leaf blade width than general mean.

4.3.10 Number of Nodes $Plant^{-1}$

The lowest number of nodes $plant^{-1}$ was recorded by PPBi-56 (4.3), while the highest was recorded by PPBi-47 (7.3). 34 inbred lines recorded low number of nodes $plant^{-1}$ than the general mean of 5.53.

4.3.11 Spike Length (cm)

Among 70 inbred lines evaluated, PPBi-48 (13.4 cm) showed minimum spike length, while the maximum was registered by PPBi-24 (28.2 cm). 33 inbred lines were recorded high compared to the general mean of 20.56.

4.3.12 Spike Girth (cm)

The inbred line PPBi-38 (1.69 cm) recorded minimum spike girth, while the inbred line PPBi-24 (3.32 cm) exhibited maximum. 34 inbred lines recorded maximum value compared to the general mean (2.49 cm).

4.3.13 Number of Productive Tillers Plant^{-1}

Number of productive tillers plant^{-1} ranged from 1 to 4.2 with a general mean of 1.68. PPBi-27 recorded the lowest (1) and PPBi-50 recorded the highest (4.2). 44 out of 70 inbred lines exhibited lower than general mean (1.68).

4.3.14 Plant Height (cm)

Among 70 inbred lines, PPBi-68 (95.1) recorded the lowest plant height, while the highest was recorded by PPBi-18 (192.9). 35 inbred lines recorded highest plant height when compared to the general mean (143.31).

4.3.15 1000 Grain Weight (g)

PPBi-40 had the lowest 1000 grain weight (5.54), while PPBi-4 had the highest (14.58). 38 out of 70 inbred lines had significantly high 1000 grain weight than the general mean (10.24).

4.3.16 Panicle Weight (g)

The mean values for panicle weight ranged from 11 g (PPBi-38) to 101.8 g (PPBi-50) with a general mean of 38.88 g. 34 out of 70 inbred lines recorded high panicle weight than the general mean (38.88 g).

4.3.17 Green Fodder Yield Plant^{-1} (g)

The mean values for green fodder yield plant^{-1} ranged from 24.6 g (PPBi-68) to 168.7 g (PPBi-3) with a general mean of 81.57 g. 31 out of 70 inbred lines recorded high green fodder yield plant^{-1} than the general mean (81.57 g).

4.3.18 Dry Fodder Yield Plant^{-1} (g)

The mean values for dry fodder yield plant^{-1} ranged from 7.38 g (PPBi-68) to 50.61 g (PPBi-3) with a general mean of 24.47 g. 31 out of 70 inbred lines recorded high dry fodder yield plant^{-1} than the general mean (24.47 g).

4.3.19 Threshing (%)

The mean values for threshing percentage ranged from 24.82% (PPBi-43) to 75.98% (PPBi-37) with a general mean of 50.23 %. 39 out of 70 inbred lines recorded high threshing percentage than the general mean (50.23 %).

4.3.20 Harvest Index (%)

The mean values for harvest index ranged from 14.29 % (PPBi-38) to 46.39 % (PPBi-50) with a general mean of 30.87 %. 33 out of 70 inbred lines recorded high harvest index than the general mean (30.87 %).

High harvest index of genotypes represents an increased physiological capacity to mobilize and translocate photosynthates efficiently towards higher grain yield.

4.3.21 Grain Yield Plant^{-1} (g)

The mean values for grain yield plant^{-1} ranged from 5.28 g (PPBi-38) to 58.42 g (PPBi-50) with a general mean of 19.17 g. 31 out of 70 inbred lines recorded high grain yield plant^{-1} than the general mean (19.17 g). The lines *viz.*, PPBi-50, PPBi-25, PPBi-3, PPBi-46, PPBi-47, PPBi-70, PPBi-36, PPBi-59, PPBi-28 and PPBi-69 exhibited superior mean performance for grain yield plant^{-1}.

List of potential genotypes identified based on *per se* performance for grain yield and its components was furnished in Table 4.4. Mean performance of top ten high yielding genotypes for different attributes were presented in Table 4.5.

Considering early maturity traits, the inbred lines PPBi-44, PPBi-12, PPBi-66, PPBi-64 and PPBi-20 registered low mean values for days to 50% flowering and days to maturity. Therefore, these genotypes could be suitable for hybridization programme as donor parents to develop short duration hybrids.

Considering the water use efficiency traits, the genotypes *viz.,* PPBi-50, PPBi-28, PPBi-14, PPBi-42 and PPBi-43 registered low SLA with high SCMR mean values which confers the drought tolerant ability of these lines. For plant height the genotypes, PPBi-68, PPBi-67 followed by PPBi-21, PPBi- 44 and PPBi-62 registered lower *per se* performance hence, these lines could be utilized for developing dwarf hybrids with lodging resistance.

For the remaining traits, maximum *per se* performance was registered by the lines PPBi-18 and PPBi-19 for leaf sheath length, PPBi-24 and PPBi-18 for leaf blade length, PPBi-6 and PPBi-28 for leaf blade width, PPBi-47 and PPBi-33 for number of nodes plant^{-1}, PPBi-24 and PPBi-1 for spike length, PPBi-24 and PPBi-18 for panicle girth, PPBi-50 and PPBi-3 for number of productive tillers plant^{-1}, green fodder yield plant^{-1} and dry fodder yield plant^{-1}, PPBi-4 and PPBi-5 for 1000 grain weight, PPBi-50 and PPBi-25 for panicle weight, PPBi-3 and PPBi-25 for panicle weight, PPBi-37 and PPBi-23 for threshing percentage, PPBi-37 and PPBi-68 for harvest index.

By and large from the foregoing discussion, it can be concluded that the inbred lines *viz.,* PPBi-50, PPBi-25, PPBi-3, PPBi-46 and PPBi-47 could be utilized as potential inbred lines in future breeding programme for improving yield and yield attributes coupled with early maturing traits.

Table 4.4 Summary of top genotypes based on *per se* performance for 21 quantitative characters in 70 inbred lines of pearl millet

S. No.	Characters	Genotypes
1	Days to 50% flowering	PPBi-44, PPBi-12, PPBi-66, PPBi-64, PPBi-20, PPBi-23, PPBi-35, PPBi-37, PPBi-5, PPBi-68
2	Days to maturity	PPBi-44, PPBi-12, PPBi-64, PPBi-66, PPBi-37, PPBi-20, PPBi-23, PPBi-35, PPBi-40, PPBi-5, PPBi-21, PPBi-27, PPBi-28, PPBi-42, PPBi-46, PPBi-68
3	SPAD chlorophyll meter reading at 45 DAS	PPBi-47, PPBi-61, PPBi-37, PPBi-36, PPBi-28, PPBi-49, PPBi-13, PPBi-51, PPBi-4, PPBi-12
4	SPAD chlorophyll meter reading at 65 DAS	PPBi-10, PPBi-44, PPBi-42, PPBi-69, PPBi-4, PPBi-70, PPBi-66, PPBi-62, PPBi-24, PPBi-11
5	Specific leaf area at 45 DAS (cm^2 g^{-1})	PPBi-66, PPBi-37, PPBi-39, PPBi-43, PPBi-20, PPBi-67, PPBi-65, PPBi-27, PPBi-42, PPBi-56
6	Specific leaf area at 65 DAS (cm^2 g^{-1})	PPBi-14, PPBi-8, PPBi-43, PPBi-39, PPBi-64, PPBi-20, PPBi-21, PPBi-56, PPBi-27, PPBi-50
7	Leaf sheath length (cm)	PPBi-18, PPBi-19, PPBi-55, PPBi-69, PPBi-24, PPBi-70, PPBi-29, PPBi-5, PPBi-25, PPBi-4
8	Leaf blade length (cm)	PPBi-24, PPBi-18, PPBi-19, PPBi-35, PPBi-55, PPBi-28, PPBi-53, PPBi-6, PPBi-50, PPBi-15, PPBi-60
9	Leaf blade width (cm)	PPBi-6, PPBi-28, PPBi-53, PPBi-14, PPBi-52, PPBi-9, PPBi-4, PPBi-58, PPBi-43, PPBi-3
10	No of nodes $plant^{-1}$	PPBi-47, PPBi-33, PPBi-39, PPBi-22, PPBi-49, PPBi-32, PPBi-53, PPBi-55, PPBi-5, PPBi-46, PPBi-50, PPBi-57, PPBi-58, PPBi-59
11	Spike length (cm)	PPBi-24, PPBi-1, PPBi-52, PPBi-9, PPBi-50, PPBi-55, PPBi-11, PPBi-53, PPBi-6, PPBi-18
12	Spike girth (cm)	PPBi-24, PPBi-18, PPBi-25, PPBi-53, PPBi-26, PPBi-4, PPBi-8, PPBi-51, PPBi-14, PPBi-28
13	Number of productive tillers $plant^{-1}$	PPBi-50, PPBi-3, PPBi-70, PPBi-12, PPBi-46, PPBi-25, PPBi-57, PPBi-40, PPBi-7, PPBi-30, PPBi-31
14	Plant height (cm)	PPBi-18, PPBi-47, PPBi-16, PPBi-14, PPBi-19, PPBi-53, PPBi-25, PPBi-36, PPBi-6, PPBi-49
15	1000 grain weight (g)	PPBi-4, PPBi-5, PPBi-20, PPBi-15, PPBi-17, PPBi-18, PPBi-70, PPBi-46, PPBi-47, PPBi-7
16	Panicle weight (g)	PPBi-50, PPBi-25, PPBi-3, PPBi-46, PPBi-57, PPBi-70, PPBi-8, PPBi-59, PPBi-9, PPBi-6, PPBi-53, PPBi-47
17	Green fodder yield $plant^{-1}$ (g)	PPBi-3, PPBi-50, PPBi-32, PPBi-9, PPBi-25, PPBi-47, PPBi-35, PPBi-52, PPBi-70, PPBi-24
18	Dry fodder yield $plant^{-1}$ (g)	PPBi-3, PPBi-50, PPBi-32, PPBi-9, PPBi-25, PPBi-47, PPBi-35, PPBi-52, PPBi-70, PPBi-24
19	Threshing (%)	PPBi-37, PPBi-23, PPBi-20, PPBi-13, PPBi-68, PPBi-51, PPBi-63, PPBi-69, PPBi-36, PPBi-15
20	Harvest index (%)	PPBi-37, PPBi-68, PPBi-15, PPBi-63, PPBi-20, PPBi-23, PPBi-69, PPBi-13, PPBi-51, PPBi-61
21	Grain yield $plant^{-1}$ (g)	PPBi-50, PPBi-25, PPBi-3, PPBi-46, PPBi-47, PPBi-70, PPBi-36, PPBi-59, PPBi-28, PPBi-69

Table 4.5 Identification of top ten high yielding inbred lines of pearl millet for promising characters

S. No.	Genotype	Grain yield/plant (g)	Characters
1	PPBi-50	58.42	DF, DM, SCMR 45, SCMR 65, SLA 45, SLA 65, LBL, NN, SL, SG, NPT, PH, 1000 GW, PW, GFY, DFY, TH, HI
2	PPBi-25	39.00	DF, DM, SCMR 65, LSL, LBL, LBW, NN, SL, SG, NPT, PH, 1000 GW, PW, GFY, DFY, TH, HI
3	PPBi-3	34.84	SCMR 45, SCMR 65, LSL, LBL, LBW, NPT, PH, PW, GFY, DFY
4	PPBi-46	34.41	DF, DM, SCMR 45, SCMR 65, SLA 65, LBL, LBW, NN, SG, NPT, 1000 GW, PW, GFY, DFY, TH, HI
5	PPBi-47	31.45	DF, SCMR 45, SCMR 65, SLA 45, SLA 65, LSL, NN, SL, SG, PH, 1000 GW, PW, GFY, DFY, TH, HI
6	PPBi-70	29.95	DF, DM, SCMR 45, SCMR 65, SLA 45, LSL, LBL, NN, SG, NPT, 1000 GW, PW, GFY, DFY
7	PPBi-36	29.45	SCMR 45, SCMR 65, LSL, LBL, NN, SL, SG, PH, 1000 GW, PW, GFY, DFY, TH, HI
8	PPBi-59	27.85	DF, DM, LBW, NN, SL, SG, NPT, PH, PW, GFY, DFY, HI
9	PPBi-28	27.55	DF, DM, SCMR 45, SCMR 65, SLA 45, SLA 65, LSL, LBL, LBW, NN, SL, SG, PH, 1000 GW, PW, GFY, DFY, TH, HI
10	PPBi-69	27.33	DF, DM, SCMR 45, SCMR 65, LSL, LBL, LBW, SG, NPT, PW, TH, HI

DF : Days to 50% flowering
DM : Days to maturity
SCMR 45 : SPAD chlorophyll meter reading at 45 DAS
SCMR 65 : SPAD chlorophyll meter reading at 65 DAS
SLA 45 : Specific leaf area at 45 DAS (cm^2g^{-1})
SLA 65 : Specific leaf area at 65 DAS (cm^2g^{-1})
LSL : Leaf sheath length (cm)
LBL : Leaf blade length (cm)
LBW : Leaf blade width (cm)
NN : No of nodes $plant^{-1}$
SL : Spike length (cm)
SG : Spike girth (cm)
NPT : Number of productive tillers $plant^{-1}$
PH : Plant height (cm)
1000 GW : 1000 grain weight (g)
PW : Panicle weight (g)
GFY : Green fodder yield $plant^{-1}$ (g)
DFY : Dry fodder yield $plant^{-1}$ (g)
TH : Threshing (%)
HI : Harvest index (%)
GYP : Grain yield $plant^{-1}$ (g)

PPBi-50 **PPBi-25**

PPBi-3

Plate 26. Top ten high yielding inbred lines of pearl millet for promising characters

PPBi-46

PPBi-47

PPBi-70

Plate 26. Cont.

PPBi-36

PPBi-59

PPBi-28

PPBi-69

Plate 26. Cont.

4.4 GENETIC PARAMETERS

The estimates of phenotypic and genotypic coefficient of variation (PCV and GCV), heritability in broad sense, genetic advance and genetic advance as per cent of mean for 21 characters involving 70 inbred lines of pearl millet were furnished in Table 4.6.

4.4.1 Variability

In the present study, phenotypic coefficient of variation was of higher magnitude than genotypic coefficient of variation for all characters indicating the influence of environment on the expression of these characters (Table 4.6).

The characters such as number of productive tillers plant^{-1} (GCV: 34.70%; PCV: 38.74%), 1000 grain weight (GCV: 21.75%; PCV: 23.22%), panicle weight (GCV: 40.89%; PCV: 44.43%), green fodder yield plant^{-1} (GCV: 39.52%; PCV: 43.01%), dry fodder yield plant^{-1} (GCV: 39.09%; PCV: 43.40%) and harvest index (GCV: 20.07%; PCV: 25.13%) and grain yield plant^{-1} (GCV: 43.61%; PCV: 47.52%) showed higher estimates of coefficient of variation indicating the ample amount of variation among the inbred lines. Therefore, simple selection would be effective for further improvement of these characters. This was in conformity with the findings of Yaqoob *et al*. (2015), Nehra *et al*. (2017), Ravindrakumar *et al.* (2020), Narasimhulu *et al.* (2021) and Shashibushan *et al.* (2021) for number of productive tillers plant^{-1}; Saikumar *et al.* (2020) and Madhavilatha *et al.* (2021) for green fodder yield plant^{-1}; Bhasker *et al*. (2017a), Nehra *et al*. (2017) and Madhavilatha *et al.* (2021) for dry fodder yield plant^{-1}; and Dehinwal *et al*. (2016) and Saikumar *et al.* (2020) for panicle weight; Talawar *et al*. (2017) and Annamalai *et al.* (2020) for 1000 grain weight; Bind *et al*. (2015), Anuradha *et al.* (2018) and Shailja *et al.* (2020) for grain yield plant^{-1} which corroborates with the findings of the present study.

Table 4.6 Estimates of mean, range and genetic parameters for yield and yield attributes in 70 inbred lines of pearl millet

S. No.	Characters	Mean	Range		Variance		Coefficient of Variation		Heritability (Broad sense) (%)	Genetic advance (GA)	Genetic advance as percent of mean (%)
			Min.	Max.	Genotypic	Phenotypic	Genotypic (%)	Phenotypic (%)			
1	Days to 50% flowering	58.97	44.00	80.50	44.44	49.04	11.30	11.88	90.62	13.07	22.17
2	Days to maturity	90.96	77.00	109.00	41.56	45.65	7.09	7.43	91.04	12.67	13.93
3	SPAD chlorophyll meter reading at 45 DAS	36.03	25.55	53.60	17.49	36.64	11.61	16.80	47.73	5.95	16.52
4	SPAD chlorophyll meter reading at 65 DAS	49.47	33.90	74.50	22.92	81.74	9.68	18.28	28.04	5.22	10.56
5	Specific leaf area at 45 DAS ($cm^2\ g^{-1}$)	146.52	98.71	244.31	624.26	1135.64	17.05	23.00	54.97	38.16	26.05
6	Specific leaf area at 65 DAS ($cm^2\ g^{-1}$)	160.69	104.79	237.85	550.44	1341.20	14.60	22.79	41.04	30.96	19.27
7	Leaf sheath length (cm)	13.60	7.09	18.40	1.62	5.83	9.37	17.75	27.85	1.39	10.19
8	Leaf blade length (cm)	45.44	32.90	61.40	25.38	42.53	11.09	14.35	59.68	8.02	17.65
9	Leaf blade width (cm)	3.07	2.31	4.40	0.13	0.25	11.75	16.42	51.24	0.53	17.33
10	No of nodes $plant^{-1}$	5.53	4.30	7.30	0.37	0.61	11.01	14.09	61.10	0.98	17.73
11	Spike length (cm)	20.56	13.40	28.20	11.34	16.20	16.38	19.58	70.00	5.80	28.24
12	Spike girth (cm)	2.49	1.69	3.32	0.10	0.14	12.81	14.95	73.47	0.56	22.62
13	Number of productive tillers $plant^{-1}$	1.68	1.00	4.20	0.34	0.42	34.70	38.74	80.23	1.07	64.02
14	Plant height (cm)	143.31	95.10	192.90	420.95	497.02	14.32	15.56	84.70	38.90	27.14
15	1000 grain weight (g)	10.24	5.54	14.58	4.96	5.65	21.75	23.22	87.80	4.30	41.99
16	Panicle weight (g)	38.88	11.00	101.80	252.74	298.40	40.89	44.43	84.70	30.14	77.52
17	Green fodder yield $plant^{-1}$ (g)	81.57	24.60	168.70	1039.05	1230.97	39.52	43.01	84.41	61.01	74.79
18	Dry fodder yield $plant^{-1}$ (g)	24.47	7.38	50.61	91.53	112.78	39.09	43.40	81.16	17.76	72.55
19	Threshing (%)	50.23	24.82	75.98	81.44	116.95	17.97	21.53	69.63	15.51	30.88
20	Harvest index (%)	30.87	14.29	46.39	38.37	60.18	20.07	25.13	63.76	10.19	33.01
21	Grain yield $plant^{-1}$ (g)	19.17	5.28	58.42	69.89	82.98	43.61	47.52	84.22	15.80	82.45

Moderate estimates of coefficient of variation were observed for days to 50% flowering (GCV: 11.30%; PCV:11.88%), SPAD chlorophyll meter reading at 45 DAS (GCV: 11.61%; PCV:16.80%), specific leaf area at 45 DAS (GCV: 17.05%; PCV: 23.00%), specific leaf area at 65 DAS (GCV: 14.60%; PCV: 22.79%), leaf blade length (GCV: 11.09; PCV: 4.35%), leaf blade width (GCV: 11.75%; PCV: 16.42%), number of nodes plant^{-1} (GCV: 11.01%; PCV: 14.09%), spike length (GCV: 16.38%; PCV: 19.58%), spike girth (GCV: 12.81%; PCV: 14.95%), plant height (GCV: 14.32%; PCV: 15.56%) and threshing percentage (GCV: 17.97%; PCV: 21.53%). This indicated the existence of sufficient variability for attempting selection to improve these traits in the genotypes studied. These findings were in consonance with Choudhary *et al*. (2013), Sathya *et al*. (2013) and Sowmiya *et al*. (2016) for both plant height and panicle girth and Priyanka *et al.* (2019) for specific leaf area at 45 DAS.

Low estimates of GCV and moderate estimates of PCV were observed for SPAD chlorophyll meter reading at 65 DAS (GCV: 9.68%; PCV:18.28%) and leaf sheath length (GCV: 9.37%; PCV: 17.75%).

The character days to maturity (GCV: 7.09%; PCV: 7.43%) exhibited low estimates of coefficient of variation. Similar kind of results were also reported by Sharma *et al*. (2018), Patel *et al*. (2019) and Saikumar *et al.* (2020) for days to maturity. Since low range of variation was observed for these characters in the inbred lines, there is a little scope for further improvement of these characters through selection.

4.4.2 Heritability

The knowledge of heritability enables the plant breeder to decide the course of selection procedure to be followed under a given situation. Broad sense heritability (h^2_b) is an estimate of the total contribution of the genetic variance to the total phenotypic variance of trait. Coefficient of variation together with heritability estimates would give the best picture of the amount

of advance to be expected from selection. In the present study, heritability in broad sense was estimated and presented in Table 4.6.

Out of 21 traits studied, high heritability was observed for 14 characters *viz.,* days to maturity (91.04%), days to 50% flowering (90.62%), 1000 grain weight (87.80%), plant height (84.70%), panicle weight (87.70%), green fodder yield plant^{-1} (84.41%), grain yield plant^{-1} (84.22%), dry fodder yield plant^{-1} (81.16%), number of productive tillers plant^{-1} (80.23%), spike girth (73.47%), spike length (70.00%), harvest index (63.76%), threshing percentage (69.63%) and number of nodes plant^{-1} (61.10%) in decreasing order of magnitude indicating that these characters were less influenced by environment. Higher values of heritability indicated that it may be due to higher contribution of genetic component and these traits were expected to remain stable under varied environmental conditions. Therefore, for improving these traits the selection will be more effective in early generation on the basis of *per se* performance of these traits.

Moderate estimates of heritability were observed for leaf blade length (59.68%), specific leaf area at 45 DAS (54.97%), leaf blade width (52.24%), SPAD chlorophyll meter reading at 45 DAS (47.73%) and specific leaf area at 65 DAS (41.04%).

Lower estimates of heritability were observed for SPAD chlorophyll meter reading at 65 DAS (28.04%) and leaf sheath length (27.85%).

4.4.3 Genetic Advance (GA)

Knowledge of heritability coupled with genetic advance is most useful in predicting the scope for genetic improvement through selection. Selection made on the basis of heritability alone is likely to be misleading and it becomes necessary to determine the parameters under targeted production environment. Thus, selection of traits based on heritability and genetic advance as per cent of mean is of great importance to the breeder for making criteria for improvement in a complex character. Genetic advance is the

improvement in the mean of selected families over the base population (Lush, 1940). It is the measure of genetic gain under selection. Since, magnitude of genetic advance is influenced by units of measurement, genetic advance as per cent of mean was computed.

In the present study, high genetic advance was observed for green fodder yield plant^{-1} (61.01), plant height (38.30), specific leaf area at 45 DAS (38.16), specific leaf area at 65 DAS (30.96) and panicle weight (30.14) whereas dry fodder yield plant^{-1} (17.76), grain yield plant^{-1} (15.80), threshing (15.51), days to 50% flowering (13.07), days to maturity (12.67) and harvest index (10.19) registered moderate genetic advance. The remaining characters *viz.,* leaf blade length (8.02), SPAD chlorophyll meter reading at 45 DAS (5.95), spike length (5.80), SPAD chlorophyll meter reading at 65 DAS (5.22), 1000 grain weight (4.30), leaf sheath length (1.39), number of productive tillers plant^{-1} (1.07), number of nodes plant^{-1} (0.98), spike girth (0.56) and leaf blade width (0.53) exhibited low genetic advance.

4.4.4 Genetic Advance as Percent of Mean (GAM)

The characters *viz.*, grain yield plant^{-1} (82.45%), panicle weight (77.52%), green fodder yield plant^{-1} (74.79%), dry fodder yield plant^{-1} (72.55%), number of productive tillers plant^{-1} (64.02%), 1000 grain weight (41.99%), harvest index (33.01%), threshing percentage (30.88%), spike length (28.24%), plant height (27.14%), specific leaf area at 45 DAS (26.05%), spike girth (22.62%) and days to 50% flowering (22.17%) exhibited high genetic advance as per cent of mean. Moderate estimates of genetic advance as percent of mean were exhibited by specific leaf area at 65 DAS (19.27%), number of nodes plant^{-1} (17.73%), leaf blade length (17.65%), leaf blade width (17.33%), SPAD chlorophyll meter reading at 45 DAS (16.52%), days to maturity (13.93%), SPAD chlorophyll meter reading at 65 DAS (10.56%) and leaf sheath length (10.19%).

In the present investigation, high heritability coupled with high genetic advance as percent of mean was observed days for 50% flowering

(h^2_b = 90.62%, GAM = 22.17%), spike length (h^2_b = 70.00%, GAM = 28.24%), spike girth (h^2_b = 73.47%, GAM = 22.62%), number of productive tillers plant^{-1} (h^2_b = 80.23%, GAM = 64.02%), plant height (h^2_b = 84.70%, GAM = 27.14%), 1000 grain weight (h^2_b = 87.80%, GAM = 41.99%), panicle weight (h^2_b = 84.70%, GAM = 77.52%), green fodder yield plant^{-1} (h^2_b = 84.41%, GAM = 74.79%), dry fodder yield plant^{-1} (h^2_b = 81.16%, GAM = 72.55%), threshing percentage (h^2_b = 69.63%, GAM = 30.88%), harvest index (h^2_b = 63.76%, GAM = 33.01%) and grain yield plant^{-1} (h^2_b = 84.22%, GAM = 82.45%) indicating the predominance of additive gene action. Early and simple selection could be exercised due to fixable additive gene effects. These results corroborates the findings of Bhasker *et al.* (2017a), Patel *et al.* (2019), Shashibushan *et al.* (2021) and Yadav *et al.* (2022) for plant height; Sumathi *et al.* (2010), Talawar *et al.* (2017) and Singh *et al.* (2018) for spike length; Patel *et al.* (2019) and Yadav *et al.* (2020) for spike girth; Singh *et al*. (2014) and Thomas *et al.* (2018) for green fodder yield plant^{-1}; Bind *et al.* (2015), Bhasker *et al.* (2017a) and Thomas *et al.* (2018) for dry fodder yield plant^{-1}; Dehinwal *et al.* (2016) for panicle weight; Talawar *et al.* (2017) and Kaushik *et al.* (2019) for 1000 grain weight; Patel *et al.* (2019) and Sai kumar *et al.* (2020) for harvest index; Dehinwal *et al.* (2016), Talawar *et al.* (2017), Ravindrakumar *et al.* (2020) and Shailja *et al.* (2020) for grain yield plant^{-1}.

High heritability coupled with moderate genetic advance as per cent of mean was recorded for days to maturity (h^2_b = 91.04%, GAM = 13.93%) and number of nodes plant^{-1} (h^2_b = 61.10%, GAM = 17.73%) indicating that these characters were governed by additive gene effects and may express consistently in succeeding generations leading to greater efficiency of breeding programme. The results are akin with the findings of Shashibushan *et al.* (2021) for days to maturity.

Moderate heritability coupled with high genetic advance as per cent of mean was observed for specific leaf area at 45 DAS (h^2_b = 54.97%, GAM =

26.05%), while SPAD chlorophyll meter reading at 45 DAS (h^2_b = 47.73%, GAM = 16.52%), specific leaf area at 65 DAS (h^2_b = 41.04%, GAM = 19.27%), leaf blade length (h^2_b = 59.68%, GAM = 17.65%) and leaf blade width (h^2_b = 51.24%, GAM = 17.33%) registered moderate estimates of both heritability and genetic advance as per cent of mean which indicated the preponderance of non-additive gene action. Hence, it could be suggested that improvement of these characters might be difficult through simple selection. These findings corroborates with Ravi (2013) for specific leaf area at 45 DAS.

Low heritability coupled with moderate genetic advance as per cent of mean was observed for SPAD chlorophyll meter reading at 65 DAS (h^2_b = 28.04%, GAM = 10.56%) and leaf sheath length (h^2_b = 27.85%, GAM = 10.89%). It indicates that the character is highly influenced by environmental effects and selection would be ineffective.

4.5 GENETIC DIVERGENCE

For a successful breeding programme, genetic divergence in the population, especially with respect to the character in which improvement is desired for, is of utmost importance because the crosses made between the parents with maximum genetic divergence are more likely to yield better recombinants in the progenies.

Analysis of genetic divergence has been used

(a) To quantify the genetic distance between the genotypes.

(b) To identify specific parents to initiate crossing programme.

Greater the genetic diversity in crop species better is the chance of evolving promising and desired types. Various techniques have been advocated by several workers, such as metroglyph analysis and hierarchial methods to estimate genetic divergence in crop plants. However, multivariate analysis using Mahalanobis's D^2 statistics provides a useful statistical tool for measuring the genetic diversity in germplasm collections and to classify the genotypes on the basis of genetic diversity. It also provides a quantitative

measure of association between geographic and genetic diversity based on generalized distance (Mahalanobis, 1936).

In the present study, D^2 analysis has been applied to assess the diversity available among inbred lines of pearl millet. It helps in identifying the divergent inbred lines to perform large number of hybrid combinations within a short time and evade the advancement and evaluation of redundant hybrids.

The data collected on 70 genotypes for the 21 characters were used for quantitative assessment of genetic divergence by adopting Mahalanobis D^2 statistics. The results obtained from D^2 analysis were discussed here under.

4.5.1 Test of Significance

Wilks ' Λ ' (statistic) criterion was used to test the significant differences among the genotypes based on the pooled effects of all the characters. The significance of ' Λ ' (statistic) value was tested by χ^2 at 1449 degrees of freedom. The calculated value of ' Λ ' (statistic) was highly significant (more than the tabulated χ^2 value) indicating that genotypes differed significantly when all the characters studied were considered simultaneously together (Table 4.7). Hence, further analysis was made to estimate the D^2 values.

Table 4.7 Analysis of variance for dispersion in 70 inbred lines of pearl millet

Source of variation	Degrees of freedom	Mean sum of Squares
Genotypes	69	-3.2270E+17
Error	68	3.2744E+17
Total	137	0.00E+00

4.5.2 Estimation of D^2 Values

The mean values of 70 genotypes (X_1-X_2) were transformed into standardized uncorrelated mean values using pivotal condensation method

(Y_1-Y_2). The D^2 values were computed for all the possible 2415 pairs [70 (70-1)/2] of genotypes.

4.5.3 Grouping of Genotypes into Clusters

All the 70 genotypes of pearl millet were grouped into 12 distinct and non-overlapping clusters using Tocher's method (Rao, 1952) such that the genotypes belonging to same cluster had an average smaller D^2 values than those belonging to different clusters. The distribution of genotypes into various clusters was presented in Table 4.8

Out of 12 clusters, cluster I was the largest one comprising of 33 genotypes followed by cluster IX with 12 genotypes, cluster V with ten genotypes and cluster VI contains seven genotypes. Whereas, clusters II, III, IV, VII, VIII, X, XI and XII had only one genotype indicating high degree of heterogeneity among the genotypes. The genotypes of the solitary clusters may be unique and very useful for breeding purpose. In the present study the genotypes identified in solitary clusters are cluster II, cluster III, cluster IV, cluster VII, cluster VIII, cluster X, cluster XI and cluster XII. Study of clustering pattern with respect to pedigree of genotypes revealed that genotypes with common parentage fell in either same cluster or in different clusters with low inter cluster distances which indicated presence of parallelism between genetic divergence and pedigree.

4.5.4 Intra and Inter-Cluster Average Distance

The average intra and inter-cluster D^2 and D values among 12 clusters were given in Table 4.9.

The average intra cluster distance ranged from 0.00 to 88.81. Maximum intra cluster distance was observed in cluster IX (88.81), followed by cluster VI (65.36) and cluster V (54.96) indicating that some divergence still existed among the genotypes of same cluster, which could be made use in the yield improvement through recombination breeding. Such intra cluster

Table 4.8 Distribution of 70 pearl millet inbred lines into 12 clusters based on Tocher's method

S. No.	Cluster number	Number of genotypes	Genotypes
1	I	33	PPBi-4,7,8,13,17,19,22,26,27,28,30,32,33,35,36,37,41,42,45,48,49,51,54,56,58,59,60,61,63,64,65,66,69
2	II	1	PPBi-67
3	III	1	PPBi-1
4	IV	1	PPBi-52
5	V	10	PPBi-2,10,11,29,31,34,38,39,55,62
6	VI	7	PPBi-6,9,14,16,18,24,53
7	VII	1	PPBi-5
8	VIII	1	PPBi-68
9	IX	12	PPBi-3,12,15,20,21,23,25,40,44,46,57,70
10	X	1	PPBi-43
11	XI	1	PPBi-47
12	XII	1	PPBi-50

Table 4.9 Average Inter (above diagonal) and Intra cluster (diagonal) D^2 and D values (in parenthesis) for 12 clusters in 70 inbred lines of pearl millet

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	**47.73 (6.91)**	61.42 (7.84)	73.34 (8.56)	72.72 (8.53)	66.57 (8.16)	106.58 (10.32)	62.69 (7.92)	79.60 (8.92)	79.27 (8.90)	97.61 (9.88)	100.94 (10.05)	190.99 (13.82)
II		**0.00 (0.00)**	101.39 (10.07)	118.20 (10.87)	75.37 (8.68)	154.20 (12.42)	67.04 (8.19)	37.90 (6.16)	60.48 (7.78)	105.99 (10.30)	161.43 (12.71)	161.27 (12.70)
III			**0.00 (0.00)**	17.55 (4.19)	72.53 (8.52)	41.27 (6.42)	105.21 (10.26)	119.29 (10.92)	125.09 (11.18)	65.05 (8.07)	143.57 (11.98)	296.42 (17.22)
IV				**0.00 (0.00)**	72.28 (8.50)	43.88 (6.62)	123.13 (11.10)	139.98 (11.83)	131.49 (11.47)	64.43 (8.03)	147.66 (12.15)	289.85 (17.02)
V					**54.96 (7.41)**	104.45 (10.22)	76.70 (8.76)	84.61 (9.20)	100.91 (10.05)	103.78 (10.19)	154.78 (12.44)	247.42 (15.73)
VI						**65.36 (8.08)**	138.75 (11.78)	172.28 (13.13)	170.20 (13.05)	112.04 (10.58)	146.29 (12.10)	337.24 (18.36)
VII							**0.00 (0.00)**	60.14 (7.75)	74.54 (8.63)	173.02 (13.15)	99.46 (9.97)	200.1 (14.15)
VIII								**0.00 (0.00)**	80.74 (8.99)	157.95 (12.57)	194.89 (13.96)	272.26 (16.50)
IX									**88.81 (9.42)**	142.53 (11.94)	163.01 (12.77)	178.44 (13.36)
X										**0.00 (0.00)**	197.90 (14.07)	304.13 (17.44)
XI											**0.00 (0.00)**	196.70 (14.02)
XII												**0.00 (0.00)**

genetic diversity among the inbred lines within the same cluster could be due to heterogeneity, degree of general combining ability (GCA) and their pedigree. Therefore, selection within these clusters could be based on highest mean performance for desirable traits. While the clusters II, III, IV, VII, VIII, X, XI and XII recorded zero values as they included only single genotype in each of them.

While, the inter-cluster D^2 values ranged from 17.55 to 337.24, the maximum inter cluster distance (337.24) was observed between cluster VI and XII followed by cluster X and XII (304.13), cluster III and XII (296.42), cluster IV and XII (289.85) and cluster VIII and XII (272.26). Whereas, minimum inter cluster distance of 17.55 was recorded between cluster III and IV, followed by cluster II and VIII (37.9) and between cluster III and VI (41.27) indicating that genotypes of these clusters were genetically close and had maximum number of gene complexes.

Inter-cluster distances were higher than intra-cluster distance indicating the presence of wider genetic diversity between the clusters rather than within the clusters. Based on inter cluster distances the cluster combinations *viz.*, VI ×XII, X× XII, III × XII, IV × XII and VIII × XII were found to be more divergent with high mean performance.

4.5.5 Cluster Means for Yield and Yield Attributes

The cluster means for 21 characters are presented in Table 4.10. Considerable variation among the cluster means for all the characters indicated the divergent nature of clusters formed.

Early flowering was observed in the genotypes of cluster VII (52.5 days) and cluster VIII (52.5 days) while delayed flowering in the genotypes of cluster VI (72.57 days). Days to maturity ranged from (85.5 days) in cluster VII and cluster VIII to (104.21 days) in cluster VI.

The genotypes of cluster XI recorded high SPAD chlorophyll meter reading at 45 DAS (53.6), while genotypes of cluster III had low SPAD

chlorophyll meter reading at 45 DAS (30.25). The genotypes of cluster VII recorded high SPAD chlorophyll meter reading at 65 DAS (56.6), while genotypes of cluster II had low SPAD chlorophyll meter reading at 65 DAS (35.25). Specific leaf area at 45 DAS ranged from 105.71 $cm^2 g^{-1}$ in cluster X to 177.63 $cm^2 g^{-1}$ in cluster III. Specific leaf area at 65 DAS ranged from 115.16 $cm^2 g^{-1}$ in cluster X to 203.11 $cm^2 g^{-1}$ in cluster IV.

The genotypes of cluster VI showed high leaf sheath length (15.05 cm), while genotypes of cluster VIII showed low leaf sheath length (10.4 cm). The genotypes of cluster VI recorded high leaf blade length (52.26 cm), whereas genotypes of cluster II had leaf blade length value (32.9 cm). The genotypes of cluster IV showed high leaf blade width (3.65 cm), whereas genotypes of cluster II showed low leaf blade width (2.55 cm). The genotypes of cluster XI recorded high number of nodes $plant^{-1}$ (7.3), while genotypes of cluster VIII had low number of nodes $plant^{-1}$ (4.3 cm).

The genotypes of cluster III recorded high spike length (27.9 cm), while genotypes of cluster VIII had low spike length (14.8 cm). The genotypes of cluster VI showed high spike girth (2.89 cm), while genotypes of cluster V showed low spike girth (2.06 cm).

Similarly, number of productive tillers $plant^{-1}$ ranged from 1.2 in cluster III to 4.2 in cluster XII, whereas plant height was highest in cluster XI (192.5 cm) and shortest in cluster VIII (95.1 cm). 1000 grain weight ranged from 5.58 gm in cluster X to 14.46 gm in cluster VII. Panicle weight ranged from 16.6 gm in cluster VIII to 101.8 gm in cluster XII. The genotypes of cluster XII showed high grain yield $plant^{-1}$ (58.42 g), while genotypes in cluster X showed low grain yield $plant^{-1}$ (10.8 g).

The genotypes of cluster XII showed high green fodder yield $plant^{-1}$ (165.3 g), while genotypes in cluster VIII showed low green fodder yield $plant^{-1}$ (24.6 g). Cluster means for dry fodder yield $plant^{-1}$ varied from 7.38 g (cluster VIII) to 49.59 g (cluster XII).

Table 4.10 Cluster means with respect to yield, yield attributes and overall character wise score in 70 inbred lines of pearl millet

Clusters	Characters											
	DF	DM	SCMR 45	SCMR 65	SLA 45	SLA 65	LSL	LBL	LBW	NN	SL	SG
I	56.89 (5)	88.88 (5)	37.41 (4)	48.83 (9)	143.81 (6)	158.46 (6)	13.59 (5)	45.78 (5)	3.09 (5)	5.65 (4)	19.90 (8)	2.54 (5)
II	58.50 (7)	90.00 (6)	35.25 (8)	35.25 (12)	106.63 (2)	148.41 (4)	10.79 (11)	32.90 (12)	2.55 (12)	4.70 (10)	15.00 (11)	2.39 (9)
III	70.00 (11)	101.00 (11)	30.25 (12)	51.55 (4)	177.63 (12)	173.34 (10)	12.61 (10)	47.05 (4)	2.95 (7)	4.80 (9)	**27.90 (1)**	2.88 (2)
IV	68.00 (10)	99.50 (10)	32.35 (11)	47.40 (10)	174.54 (11)	203.11 (12)	14.50 (3)	50.00 (3)	**3.65 (1)**	5.40 (7)	27.30 (2)	2.87 (3)
V	60.70 (8)	92.85 (8)	32.91 (9)	49.65 (8)	153.23 (8)	160.75 (7)	13.56 (6)	44.47 (6)	2.84 (9)	5.44 (6)	20.54 (7)	2.06 (12)
VI	72.57 (12)	104.21 (12)	32.56 (10)	50.40 (7)	157.88 (9)	170.77 (9)	**15.05 (1)**	**52.26 (1)**	3.54 (3)	5.51 (5)	25.71 (4)	**2.89 (1)**
VII	**52.50 (1)**	**85.50 (1)**	35.55 (7)	**56.60 (1)**	162.15 (10)	200.00 (11)	14.97 (2)	41.40 (9)	3.13 (4)	6.30 (2)	22.50 (5)	2.41 (7)
VIII	**52.50 (1)**	**85.50 (1)**	35.95 (5)	51.05 (5)	116.92 (3)	155.74 (5)	10.40 (12)	33.60 (11)	2.58 (11)	4.30 (12)	14.80 (12)	2.37 (10)
IX	54.83 (4)	86.79 (3)	35.95 (5)	50.49 (6)	148.29 (7)	163.68 (8)	13.26 (7)	43.42 (7)	2.95 (7)	5.32 (8)	18.43 (10)	2.40 (8)
X	63.50 (9)	94.50 (9)	38.15 (2)	46.05 (11)	**105.71 (1)**	**115.16 (1)**	13.00 (8)	39.55 (10)	3.59 (2)	4.60 (11)	19.20 (9)	2.32 (11)
XI	58.50 (6)	91.50 (7)	**53.60 (1)**	55.60 (2)	129.10 (5)	128.13 (3)	14.45 (4)	42.55 (8)	2.71 (10)	**7.30 (1)**	22.20 (6)	2.87 (3)
XII	54.00 (3)	87.50 (4)	37.90 (3)	52.70 (3)	121.16 (4)	128.03 (2)	13.00 (8)	51.15 (2)	2.98 (6)	6.20 (3)	26.80 (3)	2.51 (6)

Cont.

Table 4.10 (Cont..)

Clusters	Characters									Productivity Traits	
	NPT	PH	1000GW	PW	GFY	DFY	TH	HI	GYP	Total score	Final Rank
I	1.51 (6)	144.41 (7)	10.18 (9)	37.19 (9)	79.68 (8)	23.91 (8)	53.12 (4)	32.35 (5)	19.44 (5)	128	4
II	2.15 (3)	99.70 (11)	11.06 (5)	35.00 (10)	56.40 (10)	16.92 (10)	46.50 (7)	31.46 (6)	16.10 (9)	175	11
III	1.20 (12)	152.90 (5)	10.87 (6)	51.60 (3)	116.60 (4)	34.98 (4)	33.43 (11)	19.92 (11)	17.25 (8)	157	8
IV	1.40 (9)	160.50 (3)	8.84 (11)	42.60 (7)	122.20 (3)	36.66 (3)	49.78 (6)	26.74 (9)	21.20 (4)	138	7
V	1.49 (8)	130.39 (10)	8.87 (10)	24.21 (11)	53.07 (11)	15.92 (11)	46.03 (9)	27.75 (8)	11.10 (11)	183	12
VI	1.26 (11)	172.00 (2)	11.10 (4)	47.41 (4)	108.23 (5)	32.47 (5)	40.90 (10)	24.20 (10)	19.18 (6)	131	6
VII	1.70 (5)	144.10 (8)	**14.46 (1)**	40.10 (8)	72.70 (9)	21.81 (9)	46.07 (8)	29.78 (7)	18.22 (7)	122	3
VIII	1.30 (10)	95.10 (12)	11.41 (3)	16.60 (12)	24.60 (12)	7.38 (12)	**66.38 (1)**	**45.82 (1)**	11.28 (10)	161	10
IX	2.36 (2)	134.04 (9)	10.73 (7)	44.56 (5)	83.23 (7)	24.97 (7)	52.86 (5)	33.81 (4)	22.53 (3)	129	5
X	1.90 (4)	148.10 (6)	5.58 (12)	43.90 (6)	106.60 (6)	31.98 (6)	24.82 (12)	14.29 (12)	10.80 (12)	160	9
XI	1.50 (7)	**192.50 (1)**	12.98 (2)	54.10 (2)	129.00 (2)	38.70 (2)	58.16 (2)	33.89 (3)	31.45 (2)	79	2
XII	**4.20 (1)**	156.90 (4)	10.24 (8)	**101.80 (1)**	**165.30 (1)**	**49.59 (1)**	57.40 (3)	38.61 (2)	**58.42 (1)**	**68**	1

Note: Numbers in the parenthesis indicates the ranks based on cluster mean. Total score is the summation of rank numbers for all characters, based on which final rank indicated. Bold numbers indicated highest mean values for each character.

DF : Days to 50% flowering
DM : Days to maturity
SCMR 45 : SPAD chlorophyll meter reading at 45 DAS
SCMR 65 : SPAD chlorophyll meter reading at 65 DAS
SLA 45 : Specific leaf area at 45 DAS ($cm^2 g^{-1}$)
SLA 65 : Specific leaf area at 65 DAS ($cm^2 g^{-1}$)
LSL : Leaf sheath length (cm)
LBL : Leaf blade length (cm)
LBW : Leaf blade width (cm)
NN : No of nodes $plant^{-1}$
SL : Spike length (cm)
SG : Spike girth (cm)
NPT : Number of productive tillers $plant^{-1}$
PH : Plant height (cm)
1000 GW : 1000 grain weight (g)
PW : Panicle weight (g)
GFY : Green fodder yield $plant^{-1}$ (g)
DFY : Dry fodder yield $plant^{-1}$ (g)
TH : Threshing (%)
HI : Harvest index (%)
GYP : Grain yield $plant^{-1}$ (g)

Threshing percentage cluster means varied from 24.82 % (cluster X) to 66.38 % (cluster VIII). Harvest index ranged from 14.29 % in cluster X to 45.82 % in cluster VIII.

4.5.6 Cluster mean analysis

Cluster means of different characters help the breeder to know the performance of genotypes with better mean performance against cluster means. All the means were scored across the cluster for all the 21 characters. The highest cluster mean was given the first rank and the clusters possessing next best means were given second, third and so on upto twelfth rank for all the traits except days to 50 percent flowering, days to maturity, specific leaf area at 45 DAS and specific leaf area at 65 DAS for which the lowest mean was given the first rank. If mean values of two clusters are similar, then same rank was given for both the clusters. Accordingly, cluster XII (PPBi-50) secured first rank with overall score of 68 among the 12 clusters followed by cluster XI (PPBi-47) and cluster VII (PPBi-5) indicating the presence of most promising genotypes in them and can be extensively used for further crop improvement programme. The least ranking was recorded by cluster V followed by II, VIII and X.

Cluster VII and cluster VIII registered minimum values for days to 50% flowering and days to maturity which is desirable and also had lowest cluster means for plant height, panicle weight and green fodder yield plant^{-1}. Of the inbreds evaluated, PPBi-5, PPBi-68 both alone remained as single apart in their respective clusters stating that they are highly diverse and can be used for development of short duration hybrids.

Furthermore, genotype PPBi-50 of cluster VIII is highly diversified among 70 genotypes and recorded highest mean value for most of the traits *viz*., number of productive tillers plant^{-1}, panicle weight, green fodder yield plant^{-1}, dry fodder yield plant^{-1} and grain yield plant^{-1} which can be used as a potential line to develop dual purpose hybrids with high grain and fodder

yield potential. Contrastingly, genotypes of cluster V were inferior for most of the characters. Therefore, genotypes superior for specific characters from different clusters may be selected for further utilization in breeding programme.

4.5.7 Relative Contribution of Each Character towards Diversity

Apart from divergence, the performance of genotypes and the character with maximum contribution towards genetic divergence should also be given due consideration for effective selection of pearl millet genotypes. The number of times each of the 21 characters appeared in first rank and its respective per cent contribution towards diversity was presented in Table 4.11.

Among all the characters studied, maximum contribution towards genetic divergence is recorded by 1000 grain weight (21.66%) by taking first rank in 523 times out of 2415 combinations, followed by days to 50% flowering (17.81%), number of productive tillers plant^{-1} (12.75%), panicle weight (9.86%), plant height (8.57%), green fodder yield plant^{-1} (5.09%), grain yield plant^{-1} (4.93%), spike girth (4.89%), threshing percentage (4.18%) and harvest index (2.65%). The characters leaf blade width (1.66%), number of nodes plant^{-1} (1.45%), specific leaf area at 45 DAS (1.20%), spike length (1.12%), leaf blade length (0.66%), leaf sheath length (0.41%), specific leaf area at 65 DAS (0.37%), SPAD chlorophyll meter reading at 45 DAS (0.33%), days to maturity (0.25%) and SPAD chlorophyll meter reading at 65 DAS (0.17%) contributed least towards genetic divergence. Contribution of dry fodder yield plant^{-1} (0.00%) was nil to genetic divergence in the study.

In the present study, 1000 grain weight, days to 50% flowering, number of productive tillers plant^{-1}, panicle weight and plant height were found the best discriminatory characters for better selection of diverse genotypes and contributing maximum towards divergence in inbred lines of pearl millet, so these traits could be exploited maximum in order to get superior hybrids with higher yield.

Table 4.11 Relative contribution of various characters towards genetic divergence in 70 inbred lines of pearl millet

S. No.	Characters	Number of times ranked first	Contribution (%)
1	Days to 50% flowering	430	17.81%
2	Days to maturity	6	0.25%
3	SPAD chlorophyll meter reading at 45 DAS	8	0.33%
4	SPAD chlorophyll meter reading at 65 DAS	4	0.17%
5	Specific leaf area at 45 DAS ($cm^2 g^{-1}$)	29	1.20%
6	Specific leaf area at 65 DAS ($cm^2 g^{-1}$)	9	0.37%
7	Leaf sheath length (cm)	10	0.41%
8	Leaf blade length (cm)	16	0.66%
9	Leaf blade width (cm)	40	1.66%
10	No of nodes $plant^{-1}$	35	1.45%
11	Spike length (cm)	27	1.12%
12	Spike girth (cm)	118	4.89%
13	Number of productive tillers $plant^{-1}$	308	12.75%
14	Plant height (cm)	207	8.57%
15	1000 grain weight (g)	523	21.66%
16	Panicle weight (g)	238	9.86%
17	Green fodder yield $plant^{-1}$ (g)	123	5.09%
18	Dry fodder yield $plant^{-1}$ (g)	0	0.00%
19	Threshing (%)	101	4.18%
20	Harvest index (%)	64	2.65%
21	Grain yield $plant^{-1}$ (g)	119	4.93%

Similar results were recorded by the earlier researchers for 1000 grain weight (Ramya *et al.* 2017., Singh *et al.* 2018 and Saikumar *et al.* 2021); for days to 50% flowering (Singh *et al.* 2018 and Saikumar *et al.* 2021); for number of productive tillers plant^{-1} (Jyothi *et al.* 2016, Ramya *et al*. 2017 and Shasibhusan *et al.* 2022); for panicle weight (Basavaraj *et al.* 2017 and Kumar *et al.* 2022); for plant height (Jyothi *et al.* 2016 and Ramya *et al.* 2017); and for spike girth (Athoni *et al.* 2016., Basavaraj *et al.* 2017., Singh *et al.* 2018 and Kumar *et al.* 2022)

Therefore, hybridization between genotypes from widely divergent clusters which showed higher inter cluster distances and high mean values for the respective traits to be improved would be beneficial in developing promising hybrids.

4.6 CORRELATION COEFFICIENT ANALYSIS

Yield amelioration is the ultimate aim of plant breeder in any crop improvement programme which can be achieved through gaining insight knowledge on association of component characters with grain yield. Correlation coefficient is a statistical measure, which is used to find out the degree of relationship between two or more variables. Hence, correlation studies were undertaken to identify the magnitude and direction of association of yield attributes and other traits of interest with grain yield.

Phenotypic and genotypic correlation coefficients were worked out in order to assess the nature of association existing between grain yield and yield components and also among themselves. The results of phenotypic and genotypic correlation analysis were presented in Table 4.12. Genotypic correlation coefficients were greater than phenotypic correlation coefficients, indicating the preponderance of genetic variance in expression of characters as well as masking effect of environmental phenotypic level. In the present study, correlation coefficients estimated between productivity traits were discussed here under.

Table 4.12 Phenotypic (r_p) and Genotypic (r_g) correlation coefficients among grain yield and its components in 70 inbred lines of pearl millet

Trait		DF	DM	SCMR 45	SCMR 65	SLA 45	SLA 65	LSL	LBL	LBW	NN	SL
DF	r_p	**1.000**	0.989**	-0.220**	-0.042	0.178*	0.133	0.215*	0.340**	0.305**	0.088	0.464**
	r_g	**1.000**	0.996**	-0.327**	-0.056	0.239**	0.135	0.372**	0.457**	0.494**	0.142	0.572**
DM	r_p		**1.000**	-0.218**	-0.035	0.200*	0.128	0.215*	0.341**	0.294**	0.082	0.481**
	r_g		**1.000**	-0.345**	-0.044	0.247**	0.109	0.354**	0.440**	0.459**	0.155	0.589**
SCMR 45	r_p			**1.000**	0.185*	-0.107	0.008	0.102	-0.011	0.079	0.139	-0.101
	r_g			**1.000**	0.163	-0.313**	-0.184*	-0.119	-0.125	-0.074	0.355**	-0.238**
SCMR 65	r_p				**1.000**	-0.162	-0.039	0.151	0.089	0.107	-0.127	0.056
	r_g				**1.000**	-0.389**	-0.078	-0.088	0.009	0.046	-0.301**	0.074
SLA 45	r_p					**1.000**	0.511 **	0.161	0.142	-0.058	0.021	0.177 *
	r_g					**1.000**	0.727**	0.345**	0.255**	0.198*	-0.046	0.291**
SLA 65	r_p						**1.000**	0.120	0.083	0.017	0.018	0.091
	r_g						**1.000**	0.337**	0.126	0.015	0.208*	0.060
LSL	r_p							**1.000**	0.519**	0.277**	0.147	0.237**
	r_g							**1.000**	0.761**	0.205*	0.417**	0.441**
LBL	r_p								**1.000**	0.476**	0.288**	0.495**
	r_g								**1.000**	0.524**	0.448**	0.699**
LBW	r_p									**1.000**	0.175*	0.381**
	r_g									**1.000**	0.325**	0.501**
NN	r_p										**1.000**	0.159
	r_g										**1.000**	0.293**
SL	r_p											**1.000**
	r_g											**1.000**

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

Cont.

Table 4.12 (Cont.).

Trait		SG	NPT	PH	1000 GW	PW	GFY	DFY	TH	HI	GYP
DF	r_p	0.330**	-0.170*	0.507**	-0.022	0.247**	0.358**	0.354**	-0.429**	-0.439**	0.027
	r_g	0.411**	-0.221**	0.571**	-0.025	0.251**	0.401**	0.407**	-0.505**	-0.558**	0.019
DM	r_p	0.334**	-0.171*	0.508**	-0.024	0.253**	0.359**	0.354**	-0.453**	-0.453**	0.025
	r_g	0.410**	-0.227**	0.563**	-0.029	0.252**	0.398**	0.403**	-0.526**	-0.573**	0.013
SCMR 45	r_p	0.118	0.094	0.088	0.143	0.059	0.033	0.040	0.317**	0.302**	0.217*
	r_g	0.247**	0.019	0.119	0.217**	0.135	0.034**	0.022	0.448**	0.526**	0.331**
SCMR 65	r_p	0.265**	0.074	0.023	0.181*	0.124	0.064	0.067	-0.061	-0.013	0.134
	r_g	0.495**	0.014	-0.046	0.465**	0.094	-0.094	-0.100	0.035	0.280**	0.152
SLA 45	r_p	-0.020	-0.007	0.206*	-0.040	0.075	0.184*	0.176*	-0.190*	-0.237**	0.008
	r_g	-0.013	-0.064	0.276**	-0.053	0.041	0.249**	0.260**	-0.236**	-0.400**	-0.038
SLA 65	r_p	-0.053	0.022	0.090	0.019	0.010	0.093	0.098	-0.031	-0.088	0.009
	r_g	-0.043	-0.023	0.157	-0.036	-0.026	0.117	0.109	0.081	-0.027	0.005
LSL	r_p	0.115	-0.063	0.362**	0.125	0.170*	0.190*	0.182*	-0.140	-0.146	0.121
	r_g	0.237**	-0.040	0.746**	0.308**	0.317**	0.494**	0.513**	-0.321**	-0.424**	0.213*
LBL	r_p	0.331**	-0.027	0.547**	0.180*	0.390**	0.413**	0.413**	-0.129	-0.131	0.345**
	r_g	0.509**	-0.103	0.700**	0.241**	0.464**	0.555**	0.555**	-0.146	-0.196*	0.428**
LBW	r_p	0.353**	-0.034	0.344**	0.043	0.326**	0.359**	0.362**	-0.174*	-0.180*	0.228**
	r_g	0.516**	-0.070	0.473**	-0.011	0.426**	0.547**	0.544**	-0.360**	-0.394**	0.250**
NN	r_p	0.107	0.013	0.502**	0.115	0.264**	0.307**	0.299**	0.106	0.040	0.334**
	r_g	0.099	-0.073	0.659**	0.202*	0.313**	0.407**	0.419**	0.124	-0.032	0.381**
SL	r_p	0.424**	-0.102	0.610**	-0.015	0.470**	0.511**	0.511**	-0.347**	-0.322**	0.313**
	r_g	0.430**	-0.150	0.696**	-0.047	0.543**	0.620**	0.620**	-0.497**	-0.498**	0.341**

Cont.

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

Table 4.12 (Cont.).

Trait		SG	NPT	PH	1000 GW	PW	GFY	DFY	TH	HI	GYP
SG	r_p	**1.000**	-0.055	0.467**	0.330**	0.496**	0.461**	0.461**	-0.069	-0.017	0.446**
	r_g	**1.000**	-0.052	0.483**	0.374**	0.611**	0.573**	0.575**	-0.113	-0.034	0.536**
NPT	r_p		**1.000**	-0.056	0.070	0.549**	0.406**	0.405**	0.001	0.073	0.559**
	r_g		**1.000**	-0.128	0.116	0.565**	0.408**	0.410**	0.044	0.110	0.581**
PH	r_p			**1.000**	0.247**	0.513**	0.636**	0.637**	-0.164	-0.246**	0.436**
	r_g			**1.000**	0.289**	0.560**	0.701**	0.701**	-0.199*	-0.301**	0.477**
1000 GW	r_p				**1.000**	0.227**	0.152	0.150	0.228 **	0.266**	0.316**
	r_g				**1.000**	0.251**	0.176*	0.178*	0.325**	0.382**	0.372**
PW	r_p					**1.000**	0.851**	0.843**	-0.198 *	-0.082	0.890**
	r_g					**1.000**	0.909**	0.919**	-0.199*	-0.137	0.906**
GFY	r_p						**1.000**	0.996**	-0.255**	-0.335**	0.718**
	r_g						**1.000**	1.006**	-0.301**	-0.342**	0.770**
DFY	r_p							**1.000**	-0.249**	-0.342**	0.712**
	r_g							**1.000**	-0.310**	-0.331**	0.777**
TH	r_p								**1.000**	0.903**	0.238**
	r_g								**1.000**	0.973**	0.209*
HI	r_p									**1.000**	0.307**
	r_g									**1.000**	0.253**
GYP	r_p										**1.000**
	r_g										**1.000**

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

DF : Days to 50% flowering
DM : Days to maturity
SCMR 45 : SPAD chlorophyll meter reading at 45 DAS
SCMR 65 : SPAD chlorophyll meter reading at 65 DAS
SLA 45 : Specific leaf area at 45 DAS ($cm^2\ g^{-1}$)
SLA 65 : Specific leaf area at 65 DAS ($cm^2\ g^{-1}$)
LSL : Leaf sheath length (cm)
LBL : Leaf blade length (cm)
LBW : Leaf blade width (cm)
NN : No of nodes $plant^{-1}$
SL : Spike length (cm)
SG : Spike girth (cm)
NPT : Number of productive tillers $plant^{-1}$
PH : Plant height (cm)
1000 GW : 1000 grain weight (g)
PW : Panicle weight (g)
GFY : Green fodder yield $plant^{-1}$ (g)
DFY : Dry fodder yield $plant^{-1}$ (g)
TH : Threshing (%)
HI : Harvest index (%)
GYP : Grain yield $plant^{-1}$ (g)

4.6.1 Correlation between Grain Yield Plant^{-1} (g) and its Yield Components

Grain yield plant^{-1} had highly significant positive correlation with panicle weight (r_p=0.890**; r_g=0.906**), followed by green fodder yield plant^{-1} (r_p=0.718**; r_g=0.770**), dry fodder yield plant^{-1} (r_p=0.712**; r_g=0.777**), number of productive tillers plant^{-1} (r_p=0.559**; r_g=0.581**), spike girth (r_p=0.446**; r_g=0.536**), plant height (r_p=0.436**; r_g=0.477**), leaf blade length (r_p=0.345**; r_g=0.428**), number of nodes plant^{-1} (r_p=0.334**; r_g=0.381**), 1000 grain weight (r_p=0.316**; r_g=0.372**), spike length (r_p=0.313**; r_g=0.341**), harvest index (r_p=0.307**; r_g=0.253**), threshing percentage (r_p=0.238**; r_g=0.209**), leaf blade width (r_p=0.228**; r_g=0.250**) and specific leaf area at 45DAS (r_p= 0.217*; r_g= 0.331*) at both phenotypic and genotypic levels.

Non-significant positive correlation of grain yield plant^{-1} was observed with specific leaf area at 65 DAS (r_p= 0.134; r_g= 0.152), days to 50% flowering (r_p= 0.027; r_g= 0.019), days to maturity (r_p= 0.025; r_g= 0.013), SPAD chlorophyll meter reading at 65 DAS (r_p= 0.009; r_g= 0.005) and SPAD chlorophyll meter reading at 45 DAS (r_p= 0.008; r_g= -0.038).

Similar kind of highly significant positive association of grain yield plant^{-1} with panicle weight was reported by Dehinwal *et al* (2017); with dry fodder yield plant^{-1} by Vinodhana *et al.* (2013), Dehinwal *et al* (2017), Patil *et al.* (2021) and Yadav *et al.* (2022); with 1000 grain weight by Naveen *et al.* (2016), Talawar *et al.* (2017), Singh *et al.* (2018) and Patil *et al.* (2021);with harvest index by Dapke *et al.* (2014), Kumar *et al.* (2016) and Singh *et al.* (2018) and Patil *et al.* (2021). Similarly, positive association of grain yield plant^{-1} with plant height, number of productive tillers plant^{-1}, panicle length and panicle girth was reported earlier by Bhasker *et al.* (2017b), Anuradha *et al.* (2018), Patil *et al.* (2021), Shasibhusan *et al.* (2021) and Yadav *et al.* (2022).

4.6.2 *Inter-se* Correlation Among Yield and Yield Components

The studies on *inter-se* association among yield components will reveal the favourable or unfavourable association among themselves as well as with grain yield. The improvement in favourable components will in turn cause the improvement in yield. The *inter-se* correlations among the characters were assessed in the present study and were briefly discussed here under.

4.6.2.1 Days to 50% flowering

Days to 50% flowering showed highly significant positive association with days to maturity (r_p= 0.989**; r_g= 0.996**), plant height (r_p= 0.507**; r_g= 0.571**), spike length (r_p= 0.464**; r_g= 0.572**), green fodder yield plant^{-1} (r_p= 0.358**; r_g= 0.401**), spike girth (r_p= 0.330**; r_g= 0.411**), dry fodder yield plant^{-1} (r_p= 0.354**; r_g= 0.407**) leaf blade length (r_p= 0.340**; r_g= 0.457**), leaf blade width (r_p= 0.305**; r_g= 0.494**), panicle weight (r_p= 0.247**; r_g= 0.251**), leaf sheath length (r_p= 0.215*; r_g= 0.372**) and specific leaf area at 45 DAS (r_p= 0.178*; r_g= 0.239**) which was also confirmed by Dadarwal *et al.* (2020), Pallavi *et al.* (2020), Anuradha *et al.* (2021) and Patil *et al.* (2021) for days to maturity; Pallavi *et al.* (2020), Patil *et al.* (2021) and kumar *et al.* (2022) for plant height; Pallavi *et al.* (2020) and Patil *et al.* (2021) for spike length; Anuradha *et al.* (2021) and Patil *et al.* (2021) for green fodder yield plant^{-1} and dry fodder yield plant^{-1} . It showed non-significant positive association with specific leaf area at 65 DAS (r_p= 0.133; r_g= 0.135) and number of nodes plant^{-1} (r_p= 0.088; r_g= 0.142).

Days to 50% flowering exhibited significant and positive association with days to maturity indicating selection of early flowering and high yielding genotypes would result in reduction of maturity duration.

Contrarily, it expressed negative significant association with SPAD chlorophyll meter reading at 45 DAS (r_p= -0.220**; r_g= -0.327**), number of productive tillers plant^{-1} (r_p= -0.170*; r_g= -0.221**), threshing percentage (r_p=-0.429**; r_g=-0.505**), harvest index (r_p= -0.439**; r_g= -0.558**). It

expressed negative non-significant association with SPAD chlorophyll meter reading at 65 DAS (r_p= -0.042; r_g=-0.056) and 1000 grain weight (r_p= -0.022; r_g= -0.025). Similar results were reported by Bhaskar *et al.* (2017) and Rasitha *et al*. (2019) for number of productive tillers plant^{-1}; Anuradha *et al*. (2018), Pallavi *et al.* (2020) and Patil *et al.* (2021) for 1000 grain weight; Izge *et al*. (2006) for threshing percentage; Patil *et al.* (2021) for harvest index.

4.6.2.2 Days to maturity

Days to maturity showed significant positive association with leaf sheath length (r_p= 0.215*; r_g= 0.354**), leaf blade length (r_p= 0.341**; r_g= 0.440**), leaf blade width (r_p= 0.294**; r_g= 0.459**), spike length (r_p= 0.481**; r_g= 0.589**), spike girth (r_p= 0.334**; r_g= 0.410**), plant height (r_p= 0.508**; r_g= 0.563**), panicle weight (r_p= 0.253**; r_g= 0.252**), green fodder yield plant^{-1} (r_p= 0.359**; r_g= 0.398**) and dry fodder yield plant^{-1} (r_p= 0.354**; r_g= 0.403**). It showed non-significant positive association with specific leaf area at 45 DAS (r_p= 0.200*; r_g= 0.247**), specific leaf area at 65 DAS (r_p= 0.128; r_g= 0.109) and number of nodes plant^{-1} (r_p= 0.082; r_g= 0.155). Similar results were also confirmed by Dapke *et al.* (2014), Pallavi *et al.* (2020) and Patil *et al.* (2021) for spike length; Patil *et al.* (2021) and Yadav *et al.* (2022) for plant height.

On contrary, it displayed significant negative association with threshing percentage (r_p= -0.453**; r_g=-0.526**), harvest index (r_p= -0.453**; r_g=-0.573**), SPAD chlorophyll meter reading at 45 DAS (r_p= -0.218**; r_g= -0.345**) and number of productive tillers plant^{-1} (r_p= -0.171*; r_g= -0.227**). It displayed non-significant negative association with SPAD chlorophyll meter reading at 65 DAS (r_p= -0.035; r_g= -0.044) and1000 grain weight (r_p= -0.024; r_g= -0.029).Similar results were obtained for number of productive tillers plant^{-1} and harvest index by Kumar *et al*. (2016); productive tillers plant^{-1}by Pallavi *et al.* (2020) and Shasibhusan *et al.* (2021); 1000 grain weight by Anuradha *et al*. (2018), Pallavi *et al.* (2020), Patil *et al.* (2021) and

Shasibhusan *et al.* (2021); harvest index by Patil *et al.* (2021) and Yadav *et al.* (2022).

4.6.2.3 SPAD chlorophyll meter reading at 45 DAS

SPAD chlorophyll meter reading at 45 DAS recorded highly significant positive association with threshing percentage (r_p= 0.317**; r_g= 0.448**), harvest index (r_p= 0.302**; r_g= 0.526**), SPAD chlorophyll meter reading at 65 DAS (r_p= 0.185*; r_g= 0.163). It showed positive and non-significant association with specific leaf area at 65 DAS (r_p= 0.008; r_g= -0.184*), 1000 grain weight (r_p= 0.143; r_g= 0.217**), number of nodes plant^{-1} (r_p= 0.139; r_g= 0.355**), spike girth (r_p= 0.118; r_g= 0.247**), leaf sheath length (r_p= 0.102; r_g= -0.119), number of productive tillers plant^{-1} (r_p= 0.094; r_g= 0.019), plant height (r_p= 0.088; r_g= 0.119), leaf blade width (r_p= 0.079; r_g= -0.074), panicle weight (r_p= 0.059; r_g= 0.135), dry fodder yield plant^{-1} (r_p= 0.040; r_g= 0.022) and green fodder yield plant^{-1} (r_p= 0.033; r_g= 0.034**). While, it has negative and non-significant correlation with leaf blade length (r_p= -0.011; r_g= -0.125) and spike length (r_p= -0.101; r_g= -0.238**).

4.6.2.4 SPAD chlorophyll meter reading at 65 DAS

SPAD chlorophyll meter reading at 65 DAS recorded highly significant positive association with spike girth (r_p= 0.265**; r_g= 0.495**) and 1000 grain weight (r_p= 0.181*; r_g= 0.465**).

It showed positive and non-significant association with leaf sheath length (r_p= 0.151; r_g= -0.088), panicle weight (r_p= 0.124; r_g= 0.094), leaf blade width (r_p= 0.107; r_g= 0.046), leaf blade length (r_p= 0.089; r_g= 0.009), number of productive tillers plant^{-1} (r_p= 0.074; r_g= 0.014), green fodder yield plant^{-1} (r_p= 0.064; r_g= -0.094), dry fodder yield plant^{-1} (r_p= 0.067; r_g= -0.100), spike length (r_p= 0.056; r_g= 0.074) and plant height (r_p= 0.023; r_g= -0.046).

It showed negative and non-significant association with specific leaf area at 45 DAS (r_p= -0.162; r_g= -0.389**), number of nodes plant^{-1} (r_p= -0.127; r_g= -0.301**), threshing percentage (r_p= -0.061; r_g= 0.035),

specific leaf area at 65 DAS (r_p= -0.039; r_g= -0.078) and harvest index (r_p= -0.013; r_g= 0.280**).

4.6.2.5 Specific leaf area at 45 DAS (cm^2 g^{-1})

Specific leaf area at 45 DAS registered significant positive association with specific leaf area at 65 DAS (r_p= 0.511**; r_g= 0.727**), plant height (r_p= 0.206*; r_g= 0.276**), green fodder yield $plant^{-1}$ (r_p= 0.184*; r_g= 0.249**), spike length (r_p= 0.177*; r_g= 0.291**) and dry fodder yield $plant^{-1}$ (r_p= 0.176*; r_g= 0.260**).

It showed positive non-significant association with leaf sheath length (r_p= 0.161; r_g= 0.345**), leaf blade length (r_p= 0.142; r_g= 0.255**), panicle weight (r_p= 0.075; r_g= 0.041) and number of nodes $plant^{-1}$ (r_p= 0.021; r_g= -0.046).

It showed negative significant association with threshing percentage (r_p= -0.190*; r_g= 0.236**) and harvest index (r_p= -0.237**; r_g= -0.400**).

It showed negative non-significant association with leaf blade width (r_p= 0.058; r_g= 0.198*), spike girth (r_p= -0.020; r_g= -0.013), number of productive tillers $plant^{-1}$ (r_p= -0.007; r_g= -0.064) and 1000 grain weight (r_p= -0.040; r_g= -0.053).

4.6.2.6 Specific leaf area at 65 DAS (cm^2 g^{-1})

SLA at 65 DAS registered significant positive association with plant height (r_p= 0.362**; r_g= 0.746**), panicle weight (r_p= 0.170*; r_g= 0.317**), green fodder yield $plant^{-1}$ (r_p= 0.190*; r_g= 0.494**) and dry fodder yield $plant^{-1}$ (r_p= 0.182*; r_g= 0.513**).

It showed positive non-significant association with leaf sheath length (r_p= 0.120; r_g= 0.337**), 1000 grain weight (r_p= 0.125; r_g= 0.308**), spike length (r_p= 0.091; r_g= 0.060), leaf blade length (r_p= 0.083; r_g= 0.126), number of nodes $plant^{-1}$ (r_p= 0.018; r_g= 0.208*), leaf blade width (r_p= 0.017; r_g= 0.015) and spike girth (r_p= 0.115; r_g= 0.237**).

It showed negative non-significant association with number of productive tillers plant^{-1} (r_p= -0.063; r_g= -0.040), threshing percentage (r_p= -0.140; r_g= -0.321**) and harvest index (r_p= -0.146; r_g= -0.424**).

4.6.2.7 Leaf sheath length (cm)

Leaf sheath length registered significant positive association with leaf blade length (r_p= 0.519**; r_g= 0.761**), plant height (r_p= 0.362**; r_g= 0.746**), leaf blade width (r_p= 0.277**; r_g= 0.205**), spike length (r_p= 0.237**; r_g= 0.441**), green fodder yield plant^{-1} (r_p= 0.190**; r_g= 0.494**), dry fodder yield plant^{-1} (r_p= 0.182*; r_g= 0.513**) and panicle weight (r_p= 0.170*; r_g= 0.317**). These findings are in accordance with Rasitha *et al.* (2019) for leaf blade length, spike length and plant height.

It showed positive non-significant association with number of nodes plant^{-1} (r_p= 0.147; r_g= 0.417**), 1000 grain weight (r_p= 0.125; r_g= 0.308**) and spike girth (r_p= 0.115; r_g= 0.237**).

It showed negative non-significant association with harvest index (r_p= -0.146; r_g= -0.424**), threshing percentage (r_p= -0.140; r_g= -0.321**) and number of productive tillers plant^{-1} (r_p= -0.063; r_g= -0.040).

4.6.2.8 Leaf blade length (cm)

Leaf blade length showed highly significant positive association with plant height (r_p= 0.547**; r_g= 0.700**), spike length (r_p= 0.495**; r_g= 0.699**), leaf blade width (r_p= 0.476**; r_g= 0.524**), green fodder yield plant^{-1} (r_p= 0.413**; r_g= 0.555**), dry fodder yield plant^{-1} (r_p= 0.413**; r_g= 0.555**), panicle weight (r_p= 0.390**; r_g= 0.464**), spike girth (r_p= 0.331**; r_g= 0.509**), number of nodes plant^{-1} (r_p= 0.288**; r_g= 0.448**) and 1000 grain weight (r_p= 0.180*; r_g= 0.241**).

It showed negative non-significant association with harvest index (r_p= -0.131; r_g= -0.196*), threshing percentage (r_p= -0.129; r_g= -0.146) and number of productive tillers plant^{-1} (r_p= -0.027; r_g= -0.103). These results are

in agreement with Rasitha *et al.* (2019) for leaf blade length, number of productive tillers plant^{-1}, spike length, spike girth and plant height.

4.6.2.9 Leaf blade width (cm)

Leaf blade width showed highly significant positive association with spike length (r_p= 0.381**; r_g= 0.501**), dry fodder yield plant^{-1} (r_p= 0.362**; r_g= 0.544**), spike girth (r_p= 0.353**; r_g= 0.516**), green fodder yield plant^{-1} (r_p= 0.359**; r_g= 0.547**), plant height (r_p= 0.344**; r_g= 0.473**), panicle weight (r_p= 0.326**; r_g= 0.426**) and number of nodes plant^{-1} (r_p= 0.175*; r_g= 0.325**).

It showed positive non-significant association with 1000 grain weight (r_p= 0.043; r_g= -0.011).

It displayed negative significant association with threshing percentage (r_p= -0.174*; r_g= -0.360**) and harvest index (r_p= -0.180*; r_g= -0.394**).

It showed negative non-significant association with number of productive tillers plant^{-1} (r_p= -0.034; r_g= -0.070).

Similar results are obtained for Rasitha *et al.* (2019) for number of productive tillers plant^{-1}, spike girth, plant height and 1000 grain weight.

4.6.2.10 Number of nodes plant^{-1}

Number of nodes plant^{-1} showed highly significant positive association with plant height (r_p= 0.502**; r_g= 0.659**), panicle weight (r_p= 0.264**; r_g= 0.313**), green fodder yield plant^{-1} (r_p= 0.307**; r_g= 0.407**) and dry fodder yield plant^{-1} (r_p= 0.299**; r_g= 0.419**).

It showed positive non-significant association with spike length (r_p= 0.159; r_g= 0.293**), number of nodes plant^{-1} (r_p= 0.175*; r_g= 0.325**), spike girth (r_p= 0.107; r_g= 0.099), threshing percentage (r_p= 0.106; r_g= 0.124), 1000 grain weight (r_p= 0.115; r_g= 0.202*), number of productive tillers plant^{-1} (r_p= 0.013; r_g= -0.073, and harvest index (r_p= 0.040; r_g= -0.032).

4.6.2.11 Spike length (cm)

Spike length showed highly significant positive association with plant height (r_p= 0.610**; r_g= 0.696**), green fodder yield plant^{-1} (r_p= 0.511**; r_g= 0.620**), dry fodder yield plant^{-1} (r_p= 0.511**; r_g= 0.620**), panicle weight (r_p= 0.470**; r_g= 0.543**) and spike girth (r_p= 0.424**; r_g= 0.430**). These results are in agreement with Bhasker *et al*. (2017b), Rasitha *et al.* (2019), Dadarwal *et al.* (2020) and Patil *et al.* (2021) for spike girth; Kumar *et al*. (2020a) for panicle weight; Kaushik *et al*. (2018), Patil *et al.* (2021) and Shasibhusan *et al.* (2021) for green fodder yield plant^{-1}; Kumar *et al*. (2020a), Patil *et al.* (2021), Shasibhusan *et al.* (2021) and Yadav *et al.* (2022) for dry fodder yield plant^{-1}.

It displayed negative significant association with threshing percentage (r_p= -0.347**; r_g= -0.497**) and harvest index (r_p= -0.322**; r_g= -0.498**).

It showed negative non-significant association with number of productive tillers plant^{-1} (r_p= -0.102; r_g= -0.150) and 1000 grain weight (r_p= -0.015; r_g= -0.047) which were supported by Pallavi *et al.* (2020), Anuradha *et al.* (2021) and Yadav *et al.* (2022).

4.6.2.12 Spike girth (cm)

Spike girth showed highly significant positive association with panicle weight (r_p= 0.496**; r_g= 0.611**), plant height (r_p= 0.467**; r_g= 0.483**), green fodder yield plant^{-1} (r_p= 0.461**; r_g= 0.573**), dry fodder yield plant^{-1} (r_p= 0.461**; r_g= 0.575**) and 1000 grain weight (r_p= 0.330**; r_g= 0.374**). These findings are in accordance with Naveen *et al.* (2016) for panicle weight; Sowmiya *et al.* (2016), Anuradha *et al.* (2018), Rasitha *et al.* (2019), Dadarwal *et al.* (2020), Pallavi *et al.* (2020) and Patil *et al.* (2021) for 1000 grain weight; Dadarwal *et al.* (2020) and Shasibhusan *et al.* (2021) for green fodder yield plant^{-1}; Dehinwal *et al*. (2017), Dadarwal *et al.* (2020) and Shasibhusan *et al.* (2021) for dry fodder yield plant^{-1}.

It showed negative non-significant association with threshing percentage (r_p= -0.069; r_g= -0.113), number of productive tillers plant^{-1} (r_p= -0.055; r_g= -0.052) and harvest index (r_p= -0.017; r_g= -0.034).

4.6.2.13 Number of productive tillers plant^{-1}

Number of productive tillers plant^{-1} showed highly significant positive association with panicle weight (r_p= 0.549**; r_g= 0.565**), green fodder yield plant^{-1} (r_p= 0.406**; r_g= 0.408**) and dry fodder yield plant^{-1} (r_p= 0.405**; r_g= 0.410**). Similar kind of association was revealed earlier by Ram *et al.* (2007) and Kaushik *et al*. (2018), Shasibhusan *et al.* (2021) and Yadav *et al.* (2022) for green fodder yield plant^{-1} and dry fodder yield plant^{-1}; Naveen *et al.* (2016) and Dehinwal *et al*. (2017) for panicle weight.

It showed positive non-significant association with 1000 grain weight (r_p= 0.070; r_g= 0.116), harvest index (r_p= 0.073; r_g= 0.110) and threshing percentage (r_p= 0.001; r_g= 0.044) which were akin with the findings of Dadarwal *et al.* (2020) for 1000 grain weight; Patil *et al.* (2021) for harvest index.

It showed negative non-significant association with plant height (r_p= -0.056; r_g= -0.128).

4.6.2.14 Plant height (cm)

Plant height showed highly significant positive association with green fodder yield plant^{-1} (r_p= 0.636**; r_g= 0.701**), dry fodder yield plant^{-1} (r_p= 0.637**; r_g= 0.701**), panicle weight (r_p= 0.513**; r_g= 0.560**) and 1000 Grain weight (r_p= 0.247**; r_g= 0.289**).

It displayed negative significant association with harvest index (r_p= -0.246**; r_g= -0.301**).

It showed negative non-significant association with threshing percentage (r_p= -0.164; r_g= -0.199*).

These results are in consonance with Sowmiya *et al.* (2016), Dehinwal *et al.* (2017) and Anuradha *et al.* (2018) for panicle weight; Kaushik *et al.* (2018) for green fodder yield plant^{-1}, dry fodder yield plant^{-1} and 1000 grain weight; Rasitha *et al.* (2019) and Dadarwal *et al.* (2020) for 1000 grain weight; Patil *et al.* (2021) and Yadav *et al.* (2022) for harvest index.

4.6.2.15 1000 grain weight (g)

It recorded highly significant positive association with harvest index (r_p= 0.266**; r_g= 0.382**), threshing percentage (r_p= 0.228**; r_g= 0.325**) and panicle weight (r_p= 0.227**; r_g= 0.251**).

It showed positive non-significant association with green fodder yield plant^{-1} (r_p= 0.152; r_g= 0.176*) and dry fodder yield plant^{-1} (r_p= 0.150; r_g= 0.178*).

These results corroborates with the findings of Naveen *et al.* (2016), Sowmiya *et al.* (2016) and Sumathi *et al.* (2016) for panicle weight and Rasitha *et al.* (2019) for dry fodder yield plant^{-1}; Patil *et al.* (2021) and Yadav *et al.* (2022) for harvest index; Izge *et al*. (2006) for threshing percentage.

4.6.2.16 Panicle weight (g)

Panicle weight exhibited highly significant positive association with green fodder yield plant^{-1} (r_p= 0.851**; r_g= 0.909**) and dry fodder yield plant^{-1} (r_p= 0.843**; r_g= 0.919**).

It displayed negative significant association with threshing percentage (r_p= -0.198*; r_g= -0.199*).

It showed negative non-significant association with harvest index (r_p= -0.082; r_g= -0.137).

These results corroborates with the findings of Naveen *et al.* (2016), Sowmiya *et al.* (2016) and Sumathi *et al.* (2016) for dry fodder yield plant^{-1} and grain yield plant^{-1}.

4.6.2.17 Green fodder yield plant^{-1} (g)

This character had registered high significant positive association with dry fodder yield plant^{-1} (r_p= 0.996**; r_g= 1.006**).

It displayed negative significant association with harvest index (r_p= -0.335**; r_g= -0.342**) and threshing percentage (r_p= -0.255**; r_g= -0.301**).

The observed correlations are in consonance with the findings of Ravi (2013) and Kaushik *et al*. (2018) for dry fodder yield plant^{-1}.

4.6.2.18 Dry fodder yield plant^{-1} (g)

It displayed negative significant association with threshing percentage (r_p= -0.249**; r_g= -0.310**) and harvest index (r_p= -0.342**; r_g= -0.331**)

Similar results were reported by Patil *et al.* (2021) and Yadav *et al.* (2022) for harvest index.

4.6.2.19 Threshing (%)

It had recorded highly significant positive association with harvest index (r_p= 0.903**; r_g= 0.973**).

Foregoing discussion on character association studies revealed significant and positive correlation of grain yield plant^{-1} with panicle weight followed by green fodder yield plant^{-1}, dry fodder yield plant^{-1}, number of productive tillers plant^{-1}, spike girth, plant height, leaf blade length, number of nodes plant^{-1}, spike length, harvest index, threshing percentage, leaf blade width and specific leaf area at 45 DAS at both phenotypic and genotypic levels. This indicated possibility of simultaneous selection of all these characters for yield improvement.

4.7 PATH COEFFICIENT ANALYSIS

Path coefficient analysis defines partitioning of correlation coefficient into direct and indirect effects to know relative importance of the component characters. It provides a clear cut picture about cause and effect relationship

between yield and yield attributes which is useful to formulate effective selection criterion.

In the present study, path coefficient analysis was conducted using grain yield plant^{-1} as dependent variable and all other characters which showed significant correlations with grain yield plant^{-1} as independent variables. Various direct and indirect effects of component traits on grain yield were discussed here under and the results were presented in Table 4.13 and 4.14.

4.7.1 Direct Effects of Yield Components on Grain Yield Plant^{-1} (g)

Among the yield components, panicle weight (P=1.011; G=-0.297) had very high positive direct effect on grain yield plant^{-1}. Threshing percentage (P=0.530; G=-0.571) exhibited a high positive direct effect on single plant grain yield. Hence direct selection based on these characters would be rewarded in increasing the grain yield plant^{-1}. Green fodder yield plant^{-1} (P=0.139; G=-3.382) exhibited a low positive direct effect on single plant grain yield. The characters *viz.,* number of productive tillers plant^{-1} (P=0.056, G=0.540), leaf blade length (P=0.041, G=0.132), number of nodes plant^{-1} (P=0.039, G=0.503), spike length (P=0.032, G=0.794), SPAD chlorophyll meter reading at 45 DAS (P=0.031, G=-0.288), spike girth (P=0.018, G=0.626) exerted negligible positive direct effect on grain yield plant^{-1} indicating direct selection for improving these characters might be ineffective.

Similar positive direct effects of component traits observed with grain yield plant^{-1} were reported by Dapke *et al*. (2014) and Nehra *et al.* (2017) for leaf blade length; Dapke *et al*. (2014), Kumar *et al*. (2014b) and Naveen *et al.* (2016) for spike length; Dapke *et al*. (2014) and Naveen *et al*. (2016) for panicle weight and Nehra *et al*. (2017) for green fodder yield plant^{-1}.

On contrary, the traits *viz.,* 1000 grain weight (P=-0.002, G=-0.352), plant height (P=-0.017, G=-0.335), leaf blade width (P=-0.034, G=0.253), harvest index (P=-0.136, G=1.729), dry fodder yield plant^{-1} (P=-0.139, G=3.820)

Table 4.13 Estimates of genotypic path coefficients among grain yield and its components in 70 inbred lines of pearl millet

Trait	SCMR 45	LSL	LBL	LBW	NN	SL	SG	NPT	PH	TSW	PW	GFY	DFY	TH	HI	Correlation with GYP
SCMR 45	**-0.288**	-0.111	0.127	-0.019	0.178	-0.189	0.154	0.010	-0.040	-0.076	-0.040	-0.114	0.084	-0.256	0.909	**0.331****
LSL	0.034	**0.926**	-0.775	0.052	0.210	0.350	0.149	-0.021	-0.250	-0.108	-0.094	-1.670	1.961	0.184	-0.733	**0.213***
LBL	0.036	0.704	**-1.019**	0.132	0.225	0.555	0.318	-0.056	-0.235	-0.085	-0.138	-1.876	2.121	0.083	-0.338	**0.428****
LBW	0.021	0.190	0.534	**0.253**	0.163	0.402	0.323	-0.038	-0.159	0.004	-0.126	-1.850	2.076	0.205	-0.682	**0.250****
NN	-0.102	0.386	0.456	0.082	**0.503**	0.233	0.062	-0.039	-0.221	-0.071	-0.093	-1.377	1.601	-0.071	-0.056	**0.381****
SL	0.069	0.408	-0.712	0.128	0.148	**0.794**	0.269	-0.081	-0.233	0.017	-0.161	-2.096	2.369	0.284	-0.861	**0.341****
SG	-0.071	0.220	-0.519	0.130	0.050	0.342	**0.626**	-0.028	-0.162	-0.132	-0.181	-1.939	2.195	0.064	-0.059	**0.536****
NPT	-0.006	-0.037	-0.105	-0.018	-0.037	-0.119	-0.033	**0.540**	0.043	-0.041	-0.168	-1.381	1.566	-0.025	0.190	**0.581****
PH	-0.034	0.690	-0.714	0.119	0.331	0.552	0.302	-0.069	**-0.335**	-0.102	-0.166	-2.370	2.678	0.114	-0.520	**0.477****
TSW	-0.063	0.285	-0.245	-0.003	0.102	-0.037	0.234	0.063	-0.097	**-0.352**	-0.074	-0.595	0.681	-0.186	0.660	**0.372****
PW	-0.039	0.294	-0.473	0.108	0.157	0.431	0.383	0.305	-0.188	-0.088	**-0.297**	-3.075	3.512	0.114	-0.237	**0.906****
GFY	-0.010	0.457	-0.566	0.138	0.205	0.492	0.359	0.220	-0.235	-0.062	-0.270	**-3.382**	3.841	0.172	-0.591	**0.770****
DFY	-0.006	0.475	-0.566	0.137	0.211	0.492	0.360	0.221	-0.235	-0.063	-0.273	-3.400	**3.820**	0.177	-0.573	**0.777****
TH	-0.129	-0.298	0.149	-0.091	0.062	-0.395	-0.071	0.024	0.067	-0.114	0.059	1.019	-1.184	**-0.571**	1.682	**0.209****
HI	-0.151	-0.393	0.199	-0.100	-0.016	-0.395	-0.021	0.059	0.101	-0.134	0.041	1.156	-1.266	-0.556	**1.729**	**0.253****

* Significant at 5% level; ** Significant at 1 % level; Genotypic residual effect: 0.191.

SCMR 45 : SPAD chlorophyll meter reading at 45 DAS
LSL : Leaf sheath length (cm)
LBL : Leaf blade length (cm)
LBW : Leaf blade width (cm)
NN : No of nodes plant^{-1}
SL : Spike length (cm)
SG : Spike girth (cm)
NPT : Number of productive tillers plant^{-1}
PH : Plant height (cm)
1000 GW : 1000 grain weight (g)
PW : Panicle weight (g)
GFY : Green fodder yield plant^{-1} (g)
DFY : Dry fodder yield plant^{-1} (g)
TH : Threshing (%)
HI : Harvest index (%)
GYP : Grain yield plant^{-1} (g)

Table 4.14 Estimates of phenotypic path coefficients among grain yield and its components in 70 inbred lines of pearl millet

Trait	SCMR 45	LBL	LBW	NN	SL	SG	NPT	PH	TSW	PW	GFY	DFY	TH	HI	Correlation with GYP
SCMR 45	**0.031**	0.000	-0.003	0.005	-0.003	0.002	0.005	-0.002	0.000	0.060	0.005	-0.010	0.168	-0.041	**0.217***
LBL	0.000	**0.041**	-0.016	0.011	0.016	0.006	-0.002	-0.009	0.000	0.394	0.057	-0.102	-0.068	0.018	**0.345****
LBW	0.002	0.019	**-0.034**	0.007	0.012	0.006	-0.002	-0.006	0.000	0.330	0.050	-0.089	-0.092	0.025	**0.228****
NN	0.004	0.012	-0.006	**0.039**	0.005	0.002	0.001	-0.009	0.000	0.267	0.043	-0.074	0.056	-0.005	**0.334****
SL	-0.003	0.020	-0.013	0.006	**0.032**	0.008	-0.006	-0.011	0.000	0.475	0.071	-0.126	-0.184	0.044	**0.313****
SG	0.004	0.014	-0.012	0.004	0.013	**0.018**	-0.003	-0.008	-0.001	0.501	0.064	-0.114	-0.036	0.002	**0.446****
NPT	0.003	-0.001	0.001	0.001	-0.003	-0.001	**0.056**	0.001	0.000	0.555	0.057	-0.100	0.001	-0.010	**0.559****
PH	0.003	0.022	-0.012	0.020	0.019	0.008	-0.003	**-0.017**	-0.001	0.519	0.089	-0.157	-0.087	0.033	**0.436****
TSW	0.004	0.007	-0.002	0.005	-0.001	0.006	0.004	-0.004	**-0.002**	0.230	0.021	-0.037	0.121	-0.036	**0.316****
PW	0.002	0.016	-0.011	0.010	0.015	0.009	0.031	-0.009	-0.001	**1.011**	0.118	-0.208	-0.105	0.011	**0.890****
GFY	0.001	0.017	-0.012	0.012	0.016	0.008	0.023	-0.011	0.000	0.861	**0.139**	-0.246	-0.135	0.046	**0.718****
DFY	0.001	0.017	-0.012	0.012	0.016	0.008	0.023	-0.011	0.000	0.853	0.139	**-0.247**	-0.132	0.047	**0.712****
TH	0.010	-0.005	0.006	0.004	-0.011	-0.001	0.000	0.003	-0.001	-0.200	-0.036	0.062	**0.530**	-0.123	**0.238****
HI	0.009	-0.005	0.006	0.002	-0.010	0.000	0.004	0.004	-0.001	-0.083	-0.047	0.085	0.478	**-0.136**	**0.307****

* Significant at 5% level; ** Significant at 1 % level; Phenotypic residual effect: 0.158.

SCMR 45 : SPAD chlorophyll meter reading at 45 DAS
LBL : Leaf blade length (cm)
LBW : Leaf blade width (cm)
NN : No of nodes plant^{-1}
SL : Spike length (cm)
SG : Spike girth (cm)
NPT : Number of productive tillers plant^{-1}
PH : Plant height (cm)
1000 GW : 1000 grain weight (g)
PW : Panicle weight (g)
GFY : Green fodder yield plant^{-1} (g)
DFY : Dry fodder yield plant^{-1} (g)
TH : Threshing (%)
HI : Harvest index (%)
GYP : Grain yield plant^{-1} (g)

depicted negligible and negative direct effect on grain yield plant^{-1}. Similar results were revealed by Dehinwal *et al*. (2017) and Nehra *et al*. (2017) for leaf blade width; Dapke *et al*. (2014) for plant height and Yadav *et al*. (2022) for 1000 grain weight.

4.7.2 Indirect Effects of Yield Components on Grain Yield Plant^{-1}

4.7.2.1 SPAD chlorophyll meter reading at 45 DAS

SPAD chlorophyll meter reading at 45 DAS registered significant positive association with grain yield plant^{-1} (r_p= 0.217*; r_g= 0.331**). The direct effect of this trait on grain yield plant^{-1} was positive but negligible (P=0.031; G=-0.288). It showed positive and low indirect effects on grain yield plant^{-1} *via* threshing percentage (P=0.168, G=-0.256). It showed positive and negligible indirect effects on grain yield plant^{-1} via panicle weight (P=0.060, G=-0.040), number of productive tillers plant^{-1} (P=0.005, G=0.010), green fodder yield plant^{-1} (P=0.005, G=-0.114), number of nodes plant^{-1} (P=0.005, G=0.178), spike girth (P=0.002, G=0.154), leaf blade length (P=0, G=-0.019) and 1000 grain weight (P=0.000, G=-0.076).

On contrary, it had negative and negligible indirect effect on grain yield through plant height (P=-0.002, G=-0.04), spike length (P=-0.003, G=-0.189), dry fodder yield plant^{-1} (P=-0.01, G=0.084), leaf blade width (P=-0.03, G=-0.019), harvest index (P=-0.041, G=0.909). The present results were in consonance with Naveen *et al*. (2016) for spike length and panicle weight.

4.7.2.2 Leaf sheath length (cm)

Leaf sheath length exhibited significant positive association with grain yield plant^{-1} at both phenotypic and genotypic levels (r_p= 0.215*; r_g=0.372**). Direct effect was high and positive on grain yield plant^{-1} (G=0.926).

This trait exhibited low positive indirect effect on grain yield plant^{-1} via leaf blade width (G=0.190); moderate indirect effect via spike girth (G=0.220), 1000 grain weight (G=0.285) and panicle weight (G=0.293); whereas high positive direct effects via number of nodes plant^{-1} (G=0.386),

spike length (G=0.408), green fodder yield plant^{-1} (G=0.457), dry fodder yield plant^{-1} (G=0.475) and leaf blade length (G=0.704).

However, it showed negative negligible indirect effects on grain yield plant^{-1} via number of productive tillers plant^{-1} (G=-0.037), negative low indirect effects via SPAD chlorophyll meter reading at 45 DAS (G=-0.111); moderate negative indirect effects via threshing percentage (G=-0.298), whereas high negative indirect effects via harvest index (G=-0.393). Similar results were revealed by Nehra *et al*. (2017) for leaf blade width and Yadav *et al*. (2022) for 1000 grain weight.

4.7.2.3 Leaf blade length (cm)

The direct effect of days to maturity on grain yield plant^{-1} was positive but negligible (P=0.041; G=0.132). Its significant positive association (r_p= 0.345**; r_g= 0.428**) with grain yield plant^{-1} was due to moderate and positive indirect effect by panicle weight (P=0.394, G=-0.138) coupled with positive and negligible indirect effect through green fodder yield plant^{-1} (P=0.057, G=-1.876), spike length (P=0.016, G=0.555), number of nodes plant^{-1} (P=0.011, G=0.225), harvest index (P=0.018, G=-0.338), spike girth (P=0.006, G=0.318), SPAD chlorophyll meter reading at 45 DAS (P=0.000, G=0.036) and 1000 grain weight (P=0.000, G=-0.085)

It exerted negative and negligible indirect effects through number of productive tillers plant^{-1} (P=-0.002, G=-0.056), plant height (P=-0.009, G=-0.235), leaf blade width (P=-0.016, G=0.132), threshing percentage (P=-0.068, G=0.083). It exerted negative and low indirect effects through dry fodder yield plant^{-1} (P=-0.102, G=2.121). These findings were supported by reports of Dehinwal *et al*. (2017) for number of productive tillers plant^{-1}, plant height, leaf blade width, spike length, spike girth and 1000 grain weight.

4.7.2.4 Leaf blade width (cm)

Leaf blade width exhibited significant positive association with grain yield plant^{-1} (r_p=0.228**; r_g= 0.250**). The direct effect of this trait on grain

yield plant^{-1} was negative and negligible (P=-0.034; G=0.253). It showed positive and moderate indirect effect on grain yield plant^{-1} through panicle weight (P=0.330, G=-0.126), along with positive negligible indirect effect *via* green fodder yield plant^{-1} (P=0.050, G=-1.85), harvest index (P=0.025, G=-0.682), leaf blade length (P=0.019, G=0.253), spike length (P=0.012, G=0.402), number of nodes plant^{-1} (P=0.007, G=0.163), spike girth (P=0.006, G=0.323), SPAD chlorophyll meter reading at 45 DAS (P=0.002, G=0.021) and 1000 grain weight (P=0.000, G=0.004).

On contrary, it had negative and negligible indirect effect through number of productive tillers plant^{-1} (P=-0.002, G=-0.038), plant height (P=-0.006, G=-0.159), dry fodder yield plant-1 (P=-0.089, G=2.076), threshing percentage (P=-0.092, G=0.205). These findings were supported by reports of Dehinwal *et al*. (2017) for number of productive tillers plant^{-1}, plant height, leaf blade length.

4.7.2.5 Number of nodes plant^{-1}

Number of nodes plant^{-1} exhibited significant and positive correlation with grain yield plant^{-1} (r_p=0.334**; r_g= 0.381**). The direct effect of this trait on grain yield plant^{-1} was positive and negligible (P=0.039; G=0.503). It expressed moderate positive indirect effect on grain yield plant^{-1} *via* panicle weight (P=0.267, G=-0.093). Similarly, it showed negligible positive indirect effects through threshing (P=0.056, G=-0.071), green fodder yield plant^{-1} (P=0.043, G=-1.377), leaf blade length (P=0.012, G=0.082), spike length (P=0.005, G=0.233), SPAD chlorophyll meter reading at 45 DAS (P=0.004, G=-0.102), spike girth (P=0.002, G=0.062), number of productive tillers plant^{-1} (P=0.001, G=-0.039) and 1000 grain weight (P=0.000, G=-0.071).

It exerted negative and negligible indirect effect through the traits *viz.*, harvest index (P=-0.005, G=-0.056), leaf blade width (P=-0.006, G=0.082), plant height (P=-0.009, G=-0.221), dry fodder yield plant^{-1} (P=-0.074, G=1.601). Similar results were obtained by Kumar *et al*. (2014b) for plant

height and Nehra *et al*. (2017) for plant height, leaf blade width and dry fodder yield plant^{-1}.

4.7.2.6 Spike length (cm)

Spike length registered significant positive correlation with grain yield plant^{-1} (r_p=0.313**; r_g= 0.341**). The direct effect of this trait on grain yield plant^{-1} was positive and negligible (P=0.032; G=0.794). It showed high positive indirect effect on grain yield plant^{-1} *via* panicle weight (P=0.475, G=-0.161) and negligible positive indirect effects through green fodder yield plant^{-1} (P=0.071, G=-2.096), harvest index (P=0.044, G=-0.861), leaf blade length (P=0.020, G=0.128), number of nodes plant^{-1} (P=0.006, G=0.148), spike girth (P=0.008, G=0.269) and 1000 grain weight (P=0.000, G=0.017).

The characters SPAD chlorophyll meter reading at 45 DAS (P=-0.003, G=0.069), number of productive tillers plant^{-1} (P=-0.006, G=-0.081), plant height (P=-0.011, G=-0.233) and leaf blade width (P=-0.013, G=0.128) registered negative and negligible indirect effect on grain yield plant^{-1}. The characters dry fodder yield plant^{-1} (P=-0.126, G=2.369), threshing (P=-0.184, G=0.284) registered low and negative indirect effect on grain yield plant^{-1}. These findings were in agreement with Kumar *et al*. (2014b) for spike girth and number of nodes plant^{-1}; Kumar *et al*. (2022) for plant height; Shasibhusan *et al.* (2021) for spike girth; Talawar *et al*. (2017) for number of productive tillers plant^{-1}; Dehinwal *et al*. (2017) for spike girth, plant height and leaf blade width; Yadav *et al*. (2022) for 1000 grain weight; Dapke *et al*. (2014) for threshing percentage.

4.7.2.7 Spike girth (cm)

Spike girth had positive and significant association with grain yield plant^{-1} (r_p=0.446**; r_g= 0.536**). The direct effect of this trait on grain yield plant^{-1} was positive and negligible (P=0.018; G=0.626). It showed high positive indirect effect on grain yield plant^{-1} *via* panicle weight (P=0.501, G=-0.181). It exhibited negligible positive indirect effect on grain yield plant^{-1} *via*

green fodder yield plant^{-1} (P=0.064, G=-0.181) followed by SPAD chlorophyll meter reading at 45 DAS (P=0.040, G=-0.071), leaf blade length (P=0.014, G=0.130), spike length (P=0.013, G=0.342), number of nodes plant^{-1} (P=0.004, G=0.050), harvest index (P=0.002, G=-0.059),

On contrary, it registered negative and negligible indirect effects through 1000 grain weight (P=-0.001, G=-0.132), number of productive tillers plant^{-1} (P=-0.003, G=-0.028), plant height (P=-0.008, G=-0.162), leaf blade width (P=-0.012, G=0.130), threshing percentage (P=-0.036, G=0.064). It registered negative and low indirect effects through dry fodder yield plant^{-1} (P=-0.114, G=2.195)

Such conformity results were also given Kumar *et al*. (2014b) for number of productive tillers plant^{-1}; Shasibhusan *et al.* (2021) for number of productive tillers plant^{-1} and spike length; Dehinwal *et al*. (2017) for spike length, plant height, 1000 grain weight and leaf blade width; Yadav *et al*. (2022) for 1000 grain weight; Naveen *et al*. (2016) for SPAD chlorophyll meter reading at 45 DAS; Kumar *et al.* (2014) for plant height.

4.7.2.8 Number of productive tillers plant^{-1}

Number of productive tillers plant^{-1} recorded significant and positive correlation with grain yield plant^{-1} (r_p=0.559**; r_g= 0.581**). The direct effect of this trait on grain yield plant^{-1} was positive and negligible (P=0.056; G=0.54). Positive correlation was mainly due to high positive indirect effect through panicle weight (P=0.555, G=-0.168) on grain yield plant^{-1} and negligible positive indirect effect through green fodder yield plant^{-1} (P=0.057, G=-1.381), SPAD chlorophyll meter reading at 45 DAS (P=0.003, G=-0.006), leaf blade width (P=0.001, G=-0.018), number of nodes plant^{-1} (P=0.001, G=-0.037), plant height (P=0.001, G=0.043), threshing percentage (P=0.001, G=-0.025) and 1000 grain weight (P=0.000, G=-0.041).

Whereas, it exerted negative and negligible indirect effect on grain yield plant^{-1} through leaf blade length (P=-0.001, G=-0.018), spike girth (P=-

0.001, G=-0.033), spike length (P=-0.003, G=-0.119), harvest index (P=-0.01, G=0.19). It exerted negative and low indirect effect on dry fodder yield plant^{-1} (P=-0.100, G=1.566). These results corroborates with the findings of Dapke *et al*. (2014) for panicle weight and dry fodder yield plant^{-1}; Kumar *et al*. (2014b) for spike length; Naveen *et al*. (2016) for SPAD chlorophyll meter reading at 45 DAS, plant height and 1000 grain weight; Dehinwal *et al*. (2017) for leaf blade length, spike girth, 1000 grain weight and leaf blade width; Shasibhusan *et al.* (2021) for spike girth and Yadav *et al.* (2022) for 1000 grain weight.

4.7.2.9 Plant height (cm)

Plant height recorded significant positive correlation with grain yield plant^{-1} (r_p=0.436**; r_g= 0.477**). It displayed negligible and negative direct effect on grain yield plant^{-1} (P=-0.017; G =-0.335) and showed high positive indirect effect on grain yield plant^{-1} through panicle weight (P=0.519, G=-0.166). It expressed negligible positive indirect effects on grain yield plant^{-1} *via* green fodder yield plant^{-1} (P=0.089, G=-2.370), harvest index (P=0.033, G=-0.52), leaf blade length (P=0.022, G=0.119), number of nodes plant^{-1} (P=0.02, G=0.331), spike length (P=0.019, G=0.552), spike girth (P=0.008, G=0.302) and SPAD chlorophyll meter reading at 45 DAS (P=0.003, G=-0.034)

While, negative and negligible indirect effect was recorded through 1000 grain weight (P=-0.001, G=-0.102), number of productive tillers plant^{-1} (P=-0.003, G=-0.069), leaf blade width (P=-0.012, G=0.119), threshing percentage (P=-0.087, G=0.114). Negative and low indirect effect was recorded through dry fodder yield plant^{-1} (P=-0.157, G=2.678).

Such conformity results were also given by Dapke *et al*. (2014) for spike length and harvest index; Kumar *et al*. (2014b) for spike length and spike girth; Dehinwal *et al*. (2017) for leaf blade length, plant height, 1000 grain weight and leaf blade width; Kumar *et al*. (2022) for spike girth.

4.7.2.10 1000 Grain weight (g)

1000 grain weight registered significant positive correlation with grain yield plant^{-1} (r_p=0.316**; r_g= 0.372**). The direct effect of this trait on grain yield plant^{-1} was negative and negligible (P=-0.002; G=-0.352). It exhibited moderate positive indirect effect on grain yield plant^{-1} through panicle weight (P=0.230, G=-0.074). It expressed negligible positive indirect effects on grain yield plant^{-1} *via* green fodder yield plant^{-1} (P=0.021, G=-0.595), leaf blade length (P=0.007, G=-0.003), spike girth (P=0.006, G=0.234), number of nodes plant^{-1} (P=0.005, G=0.102), number of productive tillers plant^{-1} (P=0.004, G=0.063) and SPAD chlorophyll meter reading at 45 DAS (P=0.004, G=-0.063).

It also showed negative and negligible indirect effect through spike length (P=-0.001, G=-0.037), leaf blade width (P=-0.002, G=-0.003), plant height (P=-0.004, G=-0.097), harvest index (P=-0.036, G=0.66) and dry fodder yield plant^{-1} (P=-0.037, G=0.681). It showed negative and low indirect effect through threshing (P=0.121, G=-0.186). Similar results were revealed by Naveen *et al.* (2016) for SPAD chlorophyll meter reading at 45 DAS and spike girth ; Nehra *et al.* (2017) for days to 50% flowering.

4.7.2.11 Panicle weight (g)

Panicle weight displayed highly significant and positive correlation with grain yield plant^{-1} (r_p=0.890**; r_g= 0.906**) due to high positive direct effect on grain yield plant^{-1} (P=1.011; G=-0.297). It expressed low positive indirect effect on green fodder yield plant^{-1} (P=0.118, G=-3.075). It expressed negligible positive indirect effect on grain yield plant^{-1} *via* number of productive tillers plant^{-1} (P=0.031, G=0.305), leaf blade length (P=0.016, G=0.108), spike length (P=0.015, G=0.431), harvest index (P=0.011, G=-0.237), number of nodes plant^{-1} (P=0.010, G=0.157), spike girth (P=0.009, G=0.383) and SPAD chlorophyll meter reading at 45 DAS (P=0.002, G=-0.039).

On contrary, it exerted negative and negligible indirect effect through 1000 grain weight (P=-0.001, G=-0.088), plant height (P=-0.009, G=-0.188), leaf blade width (P=-0.011, G=0.108). It exerted negative and low indirect effect through threshing (P=-0.105, G=0.114). It exerted negative and moderate effect through dry fodder yield plant^{-1} (P=-0.208, G=3.512).

4.7.2.12 Green fodder yield plant^{-1} (g)

Green fodder yield plant^{-1} recorded significant and positive correlation with grain yield plant^{-1} (r_p=0.718**; r_g= 0.770**). The direct effect of this trait on grain yield plant^{-1} was positive and low (P=0.139; G=-3.382). The positive correlation was mainly due to high positive indirect effect of panicle weight (P=0.861, G=-0.270) on grain yield plant^{-1} and negligible positive indirect effect *via* harvest index (P=0.046, G=-0.591), number of productive tillers plant^{-1} (P=0.023, G=0.220), leaf blade length (P=0.017, G=0.138), spike length (P=0.016, G=0.492), number of nodes plant^{-1} (P=0.012, G=0.205), spike girth (P=0.008, G=0.359), SPAD chlorophyll meter reading at 45 DAS (P=0.001, G=-0.010) and 1000 grain weight (P=0.000, G=-0.062).

On contrary, it showed negative and negligible indirect effect *via* plant height (P=-0.011, G=-0.235), leaf blade width (P=-0.012, G=0.138). It showed negative and low indirect effect through threshing percentage (P=-0.135, G=0.172). It showed negative and moderate effect through dry fodder yield plant^{-1} (P=-0.246, G=3.841). The present findings were in conformity with Nehra *et al.* (2017) for leaf blade length, number of nodes plant^{-1}, spike length, spike girth and 1000 grain weight.

4.7.2.13 Dry fodder yield plant^{-1} (g)

Dry fodder yield plant^{-1} showed negative and moderate direct effect (P=-0.247; G=3.82) on grain yield plant^{-1} and displayed significant and positive correlation with grain yield plant^{-1} (r_p=0.712**; r_g= 0.777**). The positive association was due to high positive indirect contribution through panicle weight (P=0.853, G=-0.273). It showed positive and low association

with green fodder yield plant^{-1} (P=0.139, G=-3.400). It showed positive and negligible association with harvest index (P=0.047, G=-0.573), number of productive tillers plant^{-1} (P=0.023, G=0.221), leaf blade length (P=0.017, G=0.137), spike length (P=0.016, G=0.492), number of nodes plant^{-1} (P=0.012, G=0.211), spike girth (P=0.008, G=0.36), SPAD chlorophyll meter reading at 45 DAS (P=0.001, G=-0.006) and 1000 grain weight (P=0.000, G=-0.063).

On contrary, it registered negative and negligible indirect effects *via* plant height (P=-0.011, G=-0.235) and leaf blade width (P=-0.012, G=0.137). It registered negative and low association with threshing (P=-0.132, G=0.177). The present findings were in conformity with Nehra *et al.* (2017) for leaf blade width, number of nodes plant^{-1}, number of productive tillers plant^{-1}and 1000 grain weight.

4.7.2.14 Threshing (%)

Threshing percentage exerted significant positive association with grain yield plant^{-1} (r_p=0.238**; r_g= 0.209**). The direct effect was positive and high (P =0.530; G =-0.571) on grain yield plant^{-1}. It expressed negligible positive indirect effects on grain yield plant^{-1} *via* SPAD chlorophyll meter reading at 45 DAS (P=0.01, G=-0.129), leaf blade width (P=0.006, G=-0.091), number of nodes plant^{-1} (P=0.004, G=0.062), plant height (P=0.003, G=0.067) and number of productive tillers plant^{-1} (P=0.000, G=0.024).

It also showed negative and negligible indirect effect *via* spike girth (P=-0.001, G=-0.071), 1000 grain weight (P=-0.001, G=-0.114), leaf blade length (P=-0.005, G=-0.091), spike length (P=-0.011, G=-0.395), green fodder yield plant^{-1} (P=-0.036, G=1.019) and dry fodder yield plant^{-1} (P=0.062, G=-1.184). It showed negative and low indirect effect through harvest index (P=-0.123, G=1.682). It showed negative and moderate effect through panicle weight (P=-0.200, G=0.059).

4.7.2.15 Harvest index (%)

Harvest Index exerted significant positive association with grain yield plant^{-1} (r_p=0.307**; r_g=0.253**). The direct effect was negative and low (P =-0.136; G=1.729) on grain yield plant^{-1}. It showed positive and negligible effect through SPAD chlorophyll meter reading at 45 DAS (P=0.009, G=-0.151), leaf blade width (P=0.006, G=-0.100), number of productive tillers plant^{-1} (P=0.004, G=0.059), plant height (P=0.004, G=0.101), number of nodes plant^{-1} (P=0.002, G=-0.016) and spike girth (P=0.000, G=-0.021).

It showed negative and negligible association with 1000 grain weight (P=-0.001, G=-0.134), leaf blade length (P=-0.005, G=-0.100), spike length (P=-0.010, G=-0.395), green fodder yield plant^{-1} (P=-0.047, G=1.156), panicle weight (P=-0.083, G=0.041), dry fodder yield plant^{-1} (P=0.085, G=-1.266). It showed negative and high association with threshing percentage (P=0.478, G=-0.556).

Similar results were observed by; Dapke *et al*. (2014) for number of productive tillers plant^{-1} and Yadav *et al*. (2022) for 1000 grain weight.

Path coefficient analysis reflected that panicle weight had very high positive direct effect on grain yield plant^{-1} and most of the characters exerted high positive indirect effect through panicle weight. While, threshing percentage exhibited a high direct and positive effect on grain yield plant^{-1}. Results further revealed that grain yield was mainly a product of direct and indirect effects of panicle weight, threshing percentage and green fodder yield plant^{-1}. Hence, major emphasis should be given on these characters in selection programme to isolate superior parental lines with higher genetic potential for grain yield.

In the present study, phenotypic (0.158) and genotypic (0.191) residual effects were of low magnitude, indicating the appropriateness of characters chosen and insignificant effect of other characters not included in the present study.

To sum up with genetic parameters, high GCV, heritability and genetic advance as per cent of mean were observed for number of productive tillers plant^{-1}, 1000 grain weight, panicle weight, green fodder yield plant^{-1}, dry fodder yield plant^{-1}, threshing percentage, harvest index and grain yield plant^{-1} indicating scope for genetic improvement through simple selection for all these traits with an implication of genetic variation mainly due to the presence of additive gene action.

The characters *viz.,* 1000 grain weight, days to 50% flowering, number of productive tillers plant^{-1}, panicle weight and plant height were contributing maximum towards divergence in inbred lines of pearl millet, so these traits could be exploited maximum in order to get superior hybrids with higher yield.

Correlation and path analysis in inbred lines of pearl millet suggested that characters like panicle weight, threshing percentage and green fodder yield plant^{-1} should be considered as major components for selection of parental lines in breeding programmes for developing high yielding hybrids in pearl millet.

From the above results, it is to conclude that inbred lines *viz.*, PPBi-50, PPBi-47 and PPBi-5 belongs to different divergent clusters with considerable phenotypic diversity and possess desirable combination of characters studied. Hence, these promising lines can be exploited in future hybridization programme to obtain superior heterotic expression in F_1's for yield and yield attributes in pearl millet.

The genetically diverse genotypes for specific characters can be used in hybridization programme to bring the new gene pool in population and to expand the range of adaptation.

Chapter - V

Summary & Conclusions

Chapter V

SUMMARY AND CONCLUSIONS

The present work titled **"DUS characterization and diversity analysis of inbred lines in pearl millet (*Pennisetum glaucum* (L.) R. Br.)"** was conducted at Agricultural Research Station, Perumallapalle, Tirupati during *rabi*, 2021 in a RBD with two replications. In this study 70 inbred lines of pearl millet were comprehensively characterized for 28 DUS traits and genetic parameters were estimated for 21 quantitative traits *viz*., days to 50% flowering, days to maturity, SPAD chlorophyll meter reading at 45 DAS, SPAD chlorophyll meter reading at 65 DAS, specific leaf area at 45 DAS (cm^2 g^{-1}**)**, specific leaf area at 65 DAS (cm^2 g^{-1}**)**, leaf sheath length (cm), leaf blade length (cm), leaf blade width (cm), number of nodes $plant^{-1}$, spike length (cm), spike girth (cm), number of productive tillers $plant^{-1}$, plant height (cm), 1000 grain weight (g), panicle weight (g), green fodder yield $plant^{-1}$ (g), dry fodder yield $plant^{-1}$ (g), threshing (%), harvest index (%) and grain yield $plant^{-1}$ (g).

DUS characterization of 70 pearl millet genotypes using 28 DUS traits revealed existence of abundant diversity for these characters. In the present studied pearl millet inbred lines appreciable differences were observed for the traits viz., anthocyanin pigmentation, leaf sheath length, leaf blade length, leaf blade width, spike stigma pigmentation, anther colour, plant node pubescence, number of nodes $plant^{-1}$, node pigmentation, internode pigmentation, spike length, anthocyanin pigmentation of glume, spike bristle, spike bristle colour, bristle appearance, spike girth, number of productive tillers $plant^{-1}$, plant height, spike shape, spike-density, seed color, seed shape and 1000 seed weight. Based on the DUS descriptors inbred lines were characterized effectively which would be useful for their documentation and registration. These descriptors would aid in explicit identity of inbred lines and help in maintenance of their purity in field for use in future breeding programmes.

Table 5.1 Distinguishable characters of top ten high yielding inbred lines of pearl millet

S. No.	Genotype	Characters
1	PPBi-50	Yellow anthers, purple node and green internode, semi-compact lanceolate spike, medium number of productive tillers, globular grey brown bold seed
2	PPBi-25	Purple anthers, green node and internode, medium spike length and girth, yellow prominent bristle, compact spindle spike, globular grey brown bold seed
3	PPBi-3	Yellow anthers, green node and internode, compact conical spike, globular deep grey bold seed
4	PPBi-46	Yellow anthers, green node and internode, semi-compact conical spike, globular deep grey very bold seed
5	PPBi-47	Yellow anthers, green node and internode, cylindrical compact spike, globular deep grey very bold seed
6	PPBi-70	Yellow anthers, purple node and internode, semi-compact lanceolate spike, globular grey bold seed
7	PPBi-36	Yellow anthers, purple node and green internode, purple prominent bristle, semi-compact lanceolate spike, globular deep grey bold seed
8	PPBi-59	Yellow anthers, green node and internode, semi-compact lanceolate spike, globular grey brown medium seed
9	PPBi-28	Yellow anthers, purple node and internode, semi-compact candle spike, globular grey bold seed
10	PPBi-69	Yellow anthers, green node and internode, compact lanceolate spike, obovate deep grey medium seed

The analysis of variance revealed the existence of highly significant differences among the genotypes for all the characters studied. On critical observation of mean performance, the inbred lines PPBi-50, PPBi-25, PPBi-3, PPBi-46, PPBi-47, PPBi-70, PPBi-36, PPBi-59, PPBi-28 and PPBi-69 have registered desirable *per se* performance for most of the yield contributing and physiological traits.

The high estimates of GCV and PCV recorded for grain yield plant^{-1} followed by 1000 grain weight, panicle weight, green fodder yield plant^{-1}, dry fodder yield plant^{-1} and harvest index indicated the presence of high genetic variability for these characters. Thus, direct selection for these traits could result in further improvement of grain yield.

Moderate GCV and PCV values were observed for days to 50 % flowering, SPAD chlorophyll meter reading at 45 DAS, specific leaf area at 45 DAS, specific leaf area at 65 DAS, leaf blade length, leaf blade width, no of nodes plant^{-1}, spike length, spike girth, plant height and threshing percentage. Contrarily, low estimates of coefficients of variation were recorded for SPAD chlorophyll meter reading at 65 DAS and leaf sheath length which indicated that these characters were highly influenced by the environment and selection would be ineffective.

High heritability coupled with high genetic advance as per cent of mean was recorded for days to 50 % flowering, spike length, spike girth, number of productive tillers plant^{-1}, plant height, 1000 grain, panicle weight, green fodder yield plant^{-1}, dry fodder yield plant^{-1}, threshing percentage, harvest index and grain yield plant^{-1} indicating the preponderance of additive gene action. These characters can be further improved by following simple selection procedure. Whereas, days to maturity and number of nodes plant^{-1} showed high heritability combined with moderate genetic advance as percent of mean.

Moderate heritability coupled with high genetic advance as per cent of mean was observed for specific leaf area at 45 DAS, while SPAD chlorophyll

meter reading at 45 DAS, specific leaf area at 65 DAS, leaf blade length and leaf blade width registered moderate estimates of both heritability and genetic advance as per cent of mean which indicated the preponderance of non-additive gene action. Low heritability coupled with moderate genetic advance as per cent of mean was observed for SPAD chlorophyll meter reading at 65 DAS and leaf sheath length indicating the environmental effects and selection would be ineffective in those characters.

Based on divergence studies through D^2 statistics, the experimental material was assigned into 12 clusters with wide range of inter cluster distances, revealing the existence of substantial diversity among the inbred lines for the traits studied. Cluster I was the largest one comprising of 33 genotypes followed by cluster IX with 12 genotypes, cluster V with ten genotypes and cluster VI contains seven genotypes. While, remaining clusters II, III, IV, VII, VIII, X, XI and XII were solitary demonstrating the impact of selection pressure towards genetic diversity.

Higher inter cluster distance was recorded between cluster VI and XII followed by cluster X and XII , cluster III and XII and cluster IV and XII. The clusters XII and VIII recorded high mean values for yield components like SPAD chlorophyll meter reading at 45 DAS, number of productive tillers plant^{-1}, plant height, panicle weight, green fodder yield plant^{-1}, dry fodder yield plant^{-1}, threshing percentage, harvest index and grain yield plant^{-1} and also they were divergent from each other. Genotypes from divergent clusters with high mean performance for the respective traits to be improved may be selected depending on the objective of the breeding programme.

The maximum contribution towards genetic divergence was recorded by 1000 grain weight followed by days to 50% flowering, number of productive tillers plant^{-1}, panicle weight, plant height, green fodder yield plant^{-1}, grain yield plant^{-1}, spike girth, threshing percentage and harvest index. Hence, major emphasis could be given to these characters to formulate selection procedures.

Correlation studies revealed that characters *viz.*, panicle weight followed by green fodder yield plant^{-1}, dry fodder yield plant^{-1}, number of productive tillers plant^{-1}, spike girth, plant height, leaf blade length, number of nodes plant^{-1}, 1000 grain weight, spike length, harvest index, threshing percentage, leaf blade width and specific leaf area at 45 DAS had significant positive association with grain yield plant^{-1} at both phenotypic and genotypic levels. This indicated possibility of simultaneous selection of all these characters for yield improvement.

Critical analysis of path analysis results implied that panicle weight followed by threshing percentage, green fodder yield plant^{-1}, number of productive tillers plant^{-1}, leaf blade length, number of nodes plant^{-1}, spike length, SPAD chlorophyll meter reading at 45 DAS, spike girth showed positive direct effect on grain yield plant^{-1}. The maximum positive indirect effects on grain yield plant^{-1} were exerted by spike length, number of productive tillers plant^{-1}, plant height, green fodder yield plant^{-1}, dry fodder yield plant^{-1} *via* panicle weight. Hence, direct selection for yield improvement through these characters would be rewarded. Low residual effects at both phenotypic and genotypic level demonstrated that choice of traits in the present study were able to explain most of the effects on grain yield.

In conclusion, it is evident that grain yield could be improved by selecting the inbred lines for higher number of productive tillers plant^{-1}, panicle weight, green fodder yield plant^{-1}, dry fodder yield plant^{-1} and threshing percentage.

Differentiation of selected inbred lines into B and R lines upon test crossing with a male sterile line and observation of F_1 for sterility/fertility. Then the selected inbred lines based on test cross may be tested for GCA to know its performance in series of crosses and the identified ones will be converted into A lines by backcrossing.

FUTURE LINE OF WORK

1. Superior inbred lines PPBi-3, PPBi-46, PPBi-47, PPBi-50 and PPBi-59 identified in the present study could be utilized for the development of composites.

2. Developing heterotic pools of B and R lines, utilization of diverse inbreds for production of promising hybrids and synthetics.

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Appendices

APPENDIX 1

MEAN MONTHLY METEOROLOGICAL DATA RECORDED AT AGRICULTURAL RESEARCH STATION, PERUMALLAPALLE

Standard Week	Date & Month	Temperature				Relative Humidity (%)		Rainfall (mm)		Number of rainy days		Evaporation (mm day^{-1})		Bright sunshine (hours day^{-1})	
		Maximum		Minimum											
		A	DN	A	DN	A	DN	A	DN	A	DN	A	DN	A	DN
40	01 Oct. – 07 Oct.	32.3	-0.7	23.2	-0.2	79.1	11.2	71	11.6	5.0	2.7	2.7	1.8	5.9	0.6
41	08 Oct – 14 Oct	32.4	-0.9	24.5	0.2	74.6	9.7	10.0	13.4	2.0	2.1	4.3	1.6	5.3	0.5
42	15 Oct – 21 Oct	33.2	-0.3	24.2	0.5	74.0	7.4	85.8	54.6	5.0	0.6	3.2	-4.8	4.5	-0.5
43	22 Oct – 28 Oct	31.7	-0.5	22.6	0.8	73.3	10.3	94.4	68.2	2.0	0.5	3.8	-5.3	4.9	-0.4
44	29 Oct – 04 Nov	29.04	-2.08	23.1	0.8	87.4	20.3	83	39.6	5	2.6	1.6	-2.2		-2.8
45	05 Nov – 11 Nov	27.04	-4.52	22.1	1.5	82	16.6	116.8	81.3	5	3.9	1.4	-3.6	1.0	-5.0
46	12 Nov – 18 Nov	29.28	-0.66	22.6	2.7	83.6	17.8	215.2	172.6	5	3.5	1.8	-2.2	2.3	-3.1
47	19 Nov – 25 Nov	30.1	0.1	22.7	2.3	78.6	11.4	166	125.9	5	3.2	2.5	-1.5	4.4	-1.3
48	26 Nov - 2 Dec	28.4	-0.9	23.1	3.3	80.7	3.2	74	37.6	6	4.7	1.6	-1.8	2.3	-2.1
49	3 Dec- 9 Dec	31.5	2.4	21.1	1.1	71.0	-5.7	2	-31.2	0	-1.6	3.5	0.0	5.4	0.8
50	10 Dec- 16 Dec	29.3	-0.2	20.9	1.9	75.1	0.4	12.2	-8.5	1	0	3.6	-0.4	4.7	-1.0
51	17 Dec- 23 Dec	28.9	0.1	16.8	-1.2	62.9	-9.2	0	-0.9	0	-0.1	4.7	1.0	7.5	1.1
52	24 Dec-31 Dec	29.6	-0.2	17.1	-1.7	68.1	-3.7	19	8.2	1	0.6	4.4	0.4	6.4	-0.2
1	1 Jan - 7 Jan	29.0	-0.4	18.7	0.3	71.1	-0.4	5	-1.1	1	0.7	3.4	-0.1	7.1	0.5
2	8 Jan - 14 Jan	30.4	1.3	20.0	2.6	70.0	-0.7	8	7.4	1	0.9	4.5	0.7	7.5	0.4
3	15 Jan - 21 Jan	30.4	0.6	18.9	2.4	66.9	-1.2	0	-0.1	0	0	4.5	0.2	7.0	0.2
4	22 Jan – 28 Jan	30.3	0.3	20.4	3.1	67.5	-1.3	5.4	5.4	2	1.9	4.3	-0.2	6.5	-1.2
5	29 Jan – 04 Feb	31.1	0.8	19.3	2.6	64.4	-1.4	0	-3.0	0	-0.1	4.2	-0.8	6.8	-0.7

A: Actual **DN: Deviation from normal (Decennial mean)**

DUS CHARACTERIZATION AND DIVERSITY ANALYSIS OF INBRED LINES IN PEARL MILLET (*Pennisetum glaucum* (L.) R. Br.)

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ABSTRACT

The present investigation was conducted at Agricultural Research Station (ARS), Perumallapalle, Tirupati during *rabi*, 2021 to characterize pearl millet inbred lines for DUS traits and to identify potential germplasm lines by estimating genetic parameters (variability, heritability and genetic advance), genetic divergence, character association and path coefficient. DUS characterization of 70 pearl millet genotypes using 28 DUS traits revealed existence of abundant diversity for these characters. In the present studied pearl millet inbred lines appreciable differences were observed for the traits *viz.*, anthocyanin pigmentation, leaf sheath length, leaf blade length, leaf blade width, spike stigma pigmentation, anther colour, plant node pubescence, number of nodes plant^{-1}, node pigmentation, internode pigmentation, spike length, anthocyanin pigmentation of glume, spike bristle, spike bristle colour, bristle appearance, spike girth, number of productive tillers plant^{-1}, plant height, spike shape, spike-density, seed color, seed shape and 1000 seed weight. Based on the DUS descriptors inbred lines were characterized effectively which would be useful for their documentation and registration. These descriptors would aid in explicit identity of inbred lines and help in maintenance of their purity in field for use in future breeding programmes.

The analysis of variance carried out among 70 germplasm lines for 21 yield and yield attributes revealed significant differences for all the characters indicating the presence of considerable amount of genetic variability for the characters in the studied material. The characters such as grain yield plant^{-1}, 1000 grain weight panicle weight, green fodder yield plant^{-1}, dry fodder yield plant^{-1} and harvest index showed higher estimates of PCV and GCV indicating ample amount of variation among germplasm lines for these traits. Thus, direct selection for these traits would result in further improvement of grain yield. High heritability coupled with high genetic advance as per cent of mean was observed for days to 50 % flowering, spike length, spike girth, number of productive tillers plant^{-1}, plant height, 1000 grain, panicle weight, green fodder yield plant^{-1}, dry fodder yield plant^{-1}, threshing percentage, harvest index and grain yield plant^{-1} indicating the predominance of additive gene action and direct selection would be effective for improvement of these traits. D^2 analysis grouped 70 inbred lines into 12 clusters. Among all the characters studied, 1000 grain weight, days to 50% flowering and number of productive tillers plant^{-1} contributed relatively maximum towards the total genetic divergence. Inter cluster distance was observed maximum between cluster VI and XII followed by cluster X and XII, cluster III and XII and cluster IV and XII representing that germplasm lines belonging to these clusters are more divergent. Correlation studies revealed that characters *viz.*, panicle weight followed by green fodder yield plant^{-1}, dry fodder yield plant^{-1}, number of productive tillers plant^{-1}, spike girth, plant height, leaf blade length, number of nodes plant^{-1}, 1000 grain weight, spike length, harvest index, threshing percentage, leaf blade width and specific leaf area at 45 DAS had significant positive association with grain yield plant^{-1} indicating simultaneous selection of these traits would result in improvement of grain yield. Further, path analysis estimates in the present investigation revealed that panicle weight followed by threshing percentage, green fodder yield plant^{-1} had true relationship with grain yield plant^{-1} by establishing significant positive association and high positive direct effect on grain yield plant^{-1}. Low residual effects at both phenotypic and genotypic level demonstrated that choice of traits in the present study were able to explain most of the effects on grain yield. Superior inbred lines PPBi-3, PPBi-46, PPBi-47, PPBi-50 and PPBi-59 identified in the present study could be utilized for the development of composites.